

Mus musculus (607)
Unknown (13)

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_BP_FAT	GO:0006091--generation of precursor metabolites and energy	94	17.18464351	2.E-68	18746, 226646, 66377, 100041835, 1770	491	261	13588	1.E+01	3.E-65	3.E-65
GOTERM_BP_FAT	GO:0006412--translation	99	18.09872029	3.E-65	666899, 100048462, 13667, 13669, 1000	491	319	13588	9.E+00	7.E-62	3.E-62
GOTERM_BP_FAT	GO:0022900--electron transport chain	51	9.323583181	2.E-42	70316, 672195, 226646, 100041273, 66	491	112	13588	1.E+01	3.E-39	1.E-39
GOTERM_BP_FAT	GO:0055114--oxidation reduction	91	16.63619744	2.E-28	66885, 226646, 66377, 56348, 17705, 1	491	672	13588	4.E+00	4.E-25	1.E-25
GOTERM_BP_FAT	GO:0006119--oxidative phosphorylation	27	4.936014625	4.E-23	228033, 66416, 100041835, 66043, 1770	491	56	13588	1.E+01	8.E-20	2.E-20
GOTERM_BP_FAT	GO:0006096--glycolysis	24	4.387568556	4.E-22	18746, 68263, 100042746, 15275, 1527	491	44	13588	2.E+01	8.E-19	1.E-19
GOTERM_BP_FAT	GO:0006007--glucose catabolic process	24	4.387568556	5.E-20	18746, 68263, 100042746, 15275, 1527	491	52	13588	1.E+01	1.E-16	1.E-17
GOTERM_BP_FAT	GO:0019320--hexose catabolic process	24	4.387568556	5.E-20	18746, 68263, 100042746, 15275, 1527	491	52	13588	1.E+01	1.E-16	1.E-17
GOTERM_BP_FAT	GO:0044275--cellular carbohydrate catabolic process	25	4.570383912	1.E-19	18746, 68263, 100042746, 15275, 1527	491	60	13588	1.E+01	3.E-16	4.E-17
GOTERM_BP_FAT	GO:0046365--monosaccharide catabolic process	24	4.387568556	1.E-19	18746, 68263, 100042746, 15275, 1527	491	54	13588	1.E+01	3.E-16	3.E-17
GOTERM_BP_FAT	GO:0035023--regulation of Rho protein signal transduction	28	5.118829982	1.E-18	22324, 13605, 16800, 442801, 53972, 2	491	86	13588	9.E+00	2.E-15	2.E-16
GOTERM_BP_FAT	GO:0006413--translational initiation	20	3.65630713	5.E-18	13684, 13667, 66235, 13669, 56347, 53	491	38	13588	1.E+01	1.E-14	9.E-16
GOTERM_BP_FAT	GO:0007242--intracellular signaling cascade	88	16.08775137	2.E-17	228543, 14685, 12190, 22324, 19247, 1	491	915	13588	3.E+00	4.E-14	3.E-15
GOTERM_BP_FAT	GO:0046164--alcohol catabolic process	24	4.387568556	2.E-17	18746, 68263, 100042746, 15275, 1527	491	65	13588	1.E+01	4.E-14	3.E-15
GOTERM_BP_FAT	GO:0016052--carbohydrate catabolic process	25	4.570383912	4.E-16	18746, 68263, 100042746, 15275, 1527	491	81	13588	9.E+00	9.E-13	7.E-14
GOTERM_BP_FAT	GO:0007264--small GTPase mediated signal transduction	40	7.31261426	2.E-14	228543, 117600, 11852, 11854, 246710, 1	491	258	13588	4.E+00	5.E-11	3.E-12
GOTERM_BP_FAT	GO:0042773--ATP synthesis coupled electron transport	13	2.376599634	6.E-14	66416, 17719, 675851, 17705, 17706, 1	491	18	13588	2.E+01	1.E-10	8.E-12
GOTERM_BP_FAT	GO:0006006--glucose metabolic process	29	5.301645338	1.E-13	18746, 68263, 100042746, 15275, 1527	491	140	13588	6.E+00	2.E-10	1.E-11
GOTERM_BP_FAT	GO:0022904--respiratory electron transport chain	15	2.742230347	1.E-13	66416, 17719, 675851, 17705, 17706, 1	491	28	13588	1.E+01	3.E-10	2.E-11
GOTERM_BP_FAT	GO:0045333--cellular respiration	19	3.473491773	1.E-12	66416, 17448, 17719, 675851, 17705, 1	491	59	13588	9.E+00	3.E-09	1.E-10
GOTERM_BP_FAT	GO:0019318--hexose metabolic process	29	5.301645338	1.E-11	18746, 68263, 100042746, 15275, 1527	491	169	13588	5.E+00	3.E-08	1.E-09
GOTERM_BP_FAT	GO:0046578--regulation of Ras protein signal transduction	30	5.484460695	1.E-11	22324, 13605, 442801, 16800, 53972, 2	491	181	13588	5.E+00	3.E-08	1.E-09
GOTERM_BP_FAT	GO:0015985--energy coupled proton transport, down electrochemi	15	2.742230347	1.E-11	228033, 100041835, 67126, 66043, 1770	491	37	13588	1.E+01	3.E-08	1.E-09
GOTERM_BP_FAT	GO:0015986--ATP synthesis coupled proton transport	15	2.742230347	1.E-11	228033, 100041835, 67126, 66043, 1770	491	37	13588	1.E+01	3.E-08	1.E-09
GOTERM_BP_FAT	GO:0005996--monosaccharide metabolic process	30	5.484460695	5.E-11	18746, 68263, 100042746, 15275, 1527	491	191	13588	4.E+00	1.E-07	4.E-09
GOTERM_BP_FAT	GO:0034220--ion transmembrane transport	15	2.742230347	1.E-10	228033, 100041835, 67126, 66043, 1770	491	42	13588	1.E+01	2.E-07	9.E-09
GOTERM_BP_FAT	GO:0016310--phosphorylation	63	11.51736746	1.E-10	19247, 100041835, 13665, 17705, 1770	491	718	13588	2.E+00	2.E-07	9.E-09
GOTERM_BP_FAT	GO:0042775--mitochondrial ATP synthesis coupled electron transpc	10	1.828153565	2.E-10	67530, 17719, 675851, 67264, 17705, 1	491	14	13588	2.E+01	3.E-07	1.E-08
GOTERM_BP_FAT	GO:0015980--energy derivation by oxidation of organic compounds	21	3.839122486	2.E-10	17448, 66416, 17719, 675851, 17705, 1	491	98	13588	6.E+00	5.E-07	2.E-08
GOTERM_BP_FAT	GO:0015992--proton transport	16	2.925045704	2.E-10	228033, 100041835, 67126, 66043, 1770	491	52	13588	9.E+00	5.E-07	2.E-08
GOTERM_BP_FAT	GO:0006818--hydrogen transport	16	2.925045704	3.E-10	228033, 100041835, 67126, 66043, 1770	491	53	13588	8.E+00	7.E-07	2.E-08
GOTERM_BP_FAT	GO:0051056--regulation of small GTPase mediated signal transducti	30	5.484460695	3.E-09	22324, 13605, 442801, 16800, 53972, 2	491	228	13588	4.E+00	7.E-06	2.E-07
GOTERM_BP_FAT	GO:0006796--phosphate metabolic process	64	11.70018282	7.E-08	19247, 100041835, 13665, 17705, 1770	491	866	13588	2.E+00	1.E-04	4.E-06
GOTERM_BP_FAT	GO:0006793--phosphorus metabolic process	64	11.70018282	7.E-08	19247, 100041835, 13665, 17705, 1770	491	866	13588	2.E+00	1.E-04	4.E-06
GOTERM_BP_FAT	GO:0009260--ribonucleotide biosynthetic process	19	3.473491773	8.E-08	228033, 100041835, 67126, 66043, 1770	491	111	13588	5.E+00	2.E-04	5.E-06
GOTERM_BP_FAT	GO:0009259--ribonucleotide metabolic process	20	3.65630713	1.E-07	228033, 100041835, 67126, 66043, 1770	491	125	13588	4.E+00	2.E-04	7.E-06
GOTERM_BP_FAT	GO:0046034--ATP metabolic process	17	3.10786106	1.E-07	228033, 100041835, 67126, 66043, 1770	491	90	13588	5.E+00	2.E-04	7.E-06
GOTERM_BP_FAT	GO:0007265--Ras protein signal transduction	14	2.559414991	1.E-07	117600, 14674, 192662, 69581, 11848, 1	491	59	13588	7.E+00	3.E-04	8.E-06
GOTERM_BP_FAT	GO:0006754--ATP biosynthetic process	16	2.925045704	2.E-07	228033, 100041835, 67126, 66043, 1770	491	82	13588	5.E+00	4.E-04	1.E-05
GOTERM_BP_FAT	GO:0009205--purine ribonucleoside triphosphate metabolic process	17	3.10786106	6.E-07	228033, 100041835, 67126, 66043, 1770	491	101	13588	5.E+00	1.E-03	3.E-05
GOTERM_BP_FAT	GO:0009199--ribonucleoside triphosphate metabolic process	17	3.10786106	7.E-07	228033, 100041835, 67126, 66043, 1770	491	102	13588	5.E+00	1.E-03	4.E-05
GOTERM_BP_FAT	GO:0009201--ribonucleoside triphosphate biosynthetic process	16	2.925045704	1.E-06	228033, 100041835, 67126, 66043, 1770	491	93	13588	5.E+00	2.E-03	6.E-05
GOTERM_BP_FAT	GO:0009206--purine ribonucleoside triphosphate biosynthetic proce	16	2.925045704	1.E-06	228033, 100041835, 67126, 66043, 1770	491	93	13588	5.E+00	2.E-03	6.E-05
GOTERM_BP_FAT	GO:0009144--purine nucleoside triphosphate metabolic process	17	3.10786106	1.E-06	228033, 100041835, 67126, 66043, 1770	491	106	13588	4.E+00	2.E-03	6.E-05
GOTERM_BP_FAT	GO:0009150--purine ribonucleotide metabolic process	18	3.290676417	1.E-06	228033, 100041835, 67126, 66043, 1770	491	119	13588	4.E+00	3.E-03	6.E-05
GOTERM_BP_FAT	GO:0009165--nucleotide biosynthetic process	22	4.021937843	1.E-06	228033, 21915, 100041835, 66043, 1770	491	174	13588	3.E+00	3.E-03	6.E-05
GOTERM_BP_FAT	GO:0009145--purine nucleoside triphosphate biosynthetic process	16	2.925045704	1.E-06	228033, 100041835, 67126, 66043, 1770	491	94	13588	5.E+00	3.E-03	6.E-05
GOTERM_BP_FAT	GO:0009152--purine ribonucleotide biosynthetic process	17	3.10786106	1.E-06	228033, 100041835, 67126, 66043, 1770	491	107	13588	4.E+00	3.E-03	6.E-05
GOTERM_BP_FAT	GO:0009142--nucleoside triphosphate biosynthetic process	16	2.925045704	1.E-06	228033, 100041835, 67126, 66043, 1770	491	95	13588	5.E+00	3.E-03	7.E-05
GOTERM_BP_FAT	GO:0034404--nucleobase, nucleoside and nucleotide biosynthetic p	22	4.021937843	2.E-06	228033, 21915, 100041835, 66043, 1770	491	179	13588	3.E+00	4.E-03	9.E-05
GOTERM_BP_FAT	GO:0034654--nucleobase, nucleoside, nucleotide and nucleic acid b	22	4.021937843	2.E-06	228033, 21915, 100041835, 66043, 1770	491	179	13588	3.E+00	4.E-03	9.E-05
GOTERM_BP_FAT	GO:0009141--nucleoside triphosphate metabolic process	17	3.10786106	4.E-06	228033, 100041835, 67126, 66043, 1770	491	115	13588	4.E+00	7.E-03	2.E-04
GOTERM_BP_FAT	GO:0007169--transmembrane receptor protein tyrosine kinase sign	22	4.021937843	6.E-06	13649, 19247, 56338, 18479, 18791, 13	491	192	13588	3.E+00	1.E-02	3.E-04
GOTERM_BP_FAT	GO:0006120--mitochondrial electron transport, NADH to ubiquinon	5	0.914076782	8.E-06	17719, 675851, 67264, 17717, 13382, 6	491	5	13588	3.E+01	2.E-02	3.E-04



GOTERM_BP_FAT	GO:0006957~complement activation, alternative pathway	6	1.096892139	1.E-05 12266, 12279, 230558, 69379, 15139, 1770	491	10	13588	2.E+01	3.E-02	5.E-04
GOTERM_BP_FAT	GO:0006164~purine nucleotide biosynthetic process	17	3.10786106	3.E-05 228033, 100041835, 67126, 66043, 1770	491	137	13588	3.E+00	7.E-02	1.E-03
GOTERM_BP_FAT	GO:0007266~Rho protein signal transduction	8	1.462522852	4.E-05 80837, 117600, 57874, 14674, 192662, 1	491	27	13588	8.E+00	7.E-02	1.E-03
GOTERM_BP_FAT	GO:0007167~enzyme linked receptor protein signaling pathway	25	4.570383912	5.E-05 13649, 19247, 18791, 21844, 13645, 18	491	273	13588	3.E+00	1.E-01	2.E-03
GOTERM_BP_FAT	GO:0006163~purine nucleotide metabolic process	18	3.290676417	7.E-05 228033, 100041835, 67126, 66043, 1770	491	160	13588	3.E+00	1.E-01	3.E-03
GOTERM_BP_FAT	GO:0030029~actin filament-based process	19	3.473491773	7.E-05 11350, 26934, 94190, 73167, 11856, 16	491	176	13588	3.E+00	1.E-01	3.E-03
GOTERM_BP_FAT	GO:0030036~actin cytoskeleton organization	18	3.290676417	1.E-04 11350, 26934, 94190, 73167, 11856, 16	491	165	13588	3.E+00	2.E-01	4.E-03
GOTERM_BP_FAT	GO:0008202~steroid metabolic process	17	3.10786106	2.E-04 13121, 11816, 56348, 22359, 65969, 16	491	161	13588	3.E+00	4.E-01	8.E-03
GOTERM_BP_FAT	GO:0008360~regulation of cell shape	9	1.645338208	2.E-04 80837, 14163, 14674, 104215, 76117, 1	491	47	13588	5.E+00	4.E-01	9.E-03
GOTERM_BP_FAT	GO:0042325~regulation of phosphorylation	24	4.387568556	3.E-04 13649, 19247, 20416, 13645, 18709, 21	491	290	13588	2.E+00	5.E-01	1.E-02
GOTERM_BP_FAT	GO:0043087~regulation of GTPase activity	12	2.193784278	5.E-04 22324, 71709, 228359, 57257, 228998, 1	491	93	13588	4.E+00	6.E-01	2.E-02
GOTERM_BP_FAT	GO:0051174~regulation of phosphorus metabolic process	24	4.387568556	6.E-04 13649, 19247, 20416, 13645, 18709, 21	491	301	13588	2.E+00	7.E-01	2.E-02
GOTERM_BP_FAT	GO:0019220~regulation of phosphate metabolic process	24	4.387568556	6.E-04 13649, 19247, 20416, 13645, 18709, 21	491	301	13588	2.E+00	7.E-01	2.E-02
GOTERM_BP_FAT	GO:0006958~complement activation, classical pathway	7	1.279707495	6.E-04 12266, 12258, 12279, 230558, 69379, 1	491	30	13588	6.E+00	7.E-01	2.E-02
GOTERM_BP_FAT	GO:0044271~nitrogen compound biosynthetic process	24	4.387568556	6.E-04 228033, 21915, 100041835, 66043, 1770	491	302	13588	2.E+00	7.E-01	2.E-02
GOTERM_BP_FAT	GO:0006122~mitochondrial electron transport, ubiquinol to cytochr	4	0.731261426	9.E-04 67530, 66594, 66576, 22273	491	6	13588	2.E+01	8.E-01	3.E-02
GOTERM_BP_FAT	GO:0007243~protein kinase cascade	20	3.65630713	9.E-04 13131, 14674, 19247, 14678, 20416, 13	491	236	13588	2.E+00	9.E-01	3.E-02
GOTERM_BP_FAT	GO:0006694~steroid biosynthetic process	10	1.828153565	1.E-03 13121, 100043456, 14137, 56348, 1307	491	71	13588	4.E+00	9.E-01	3.E-02
GOTERM_BP_FAT	GO:0032268~regulation of cellular protein metabolic process	22	4.021937843	1.E-03 13684, 15170, 13649, 12258, 13665, 11	491	280	13588	2.E+00	9.E-01	4.E-02
GOTERM_BP_FAT	GO:0002443~leukocyte mediated immunity	11	2.010968921	1.E-03 15170, 12266, 18753, 12258, 12279, 23	491	89	13588	3.E+00	9.E-01	4.E-02
GOTERM_BP_FAT	GO:0001932~regulation of protein amino acid phosphorylation	13	2.376599634	1.E-03 13649, 15170, 13645, 224014, 15129, 1	491	121	13588	3.E+00	9.E-01	4.E-02
GOTERM_BP_FAT	GO:0002455~humoral immune response mediated by circulating ir	7	1.279707495	1.E-03 12266, 12258, 12279, 230558, 69379, 1	491	35	13588	6.E+00	9.E-01	4.E-02
GOTERM_BP_FAT	GO:0002541~activation of plasma proteins involved in acute inflam	7	1.279707495	2.E-03 12266, 12258, 12279, 230558, 69379, 1	491	36	13588	5.E+00	1.E+00	5.E-02
GOTERM_BP_FAT	GO:0006956~complement activation	7	1.279707495	2.E-03 12266, 12258, 12279, 230558, 69379, 1	491	36	13588	5.E+00	1.E+00	5.E-02
GOTERM_BP_FAT	GO:0044093~positive regulation of molecular function	23	4.204753199	2.E-03 13131, 672195, 19247, 12279, 14678, 1	491	306	13588	2.E+00	1.E+00	5.E-02
GOTERM_BP_FAT	GO:0007623~circadian rhythm	7	1.279707495	2.E-03 11865, 12753, 12952, 18626, 12953, 18	491	37	13588	5.E+00	1.E+00	5.E-02
GOTERM_BP_FAT	GO:0002252~immune effector process	13	2.376599634	2.E-03 15170, 12266, 12258, 12279, 16423, 69	491	126	13588	3.E+00	1.E+00	5.E-02
GOTERM_BP_FAT	GO:0051336~regulation of hydrolase activity	17	3.10786106	2.E-03 672195, 22324, 12279, 228359, 57257, 1	491	196	13588	2.E+00	1.E+00	5.E-02
GOTERM_BP_FAT	GO:0022604~regulation of cell morphogenesis	11	2.010968921	3.E-03 80837, 14163, 14674, 18049, 104215, 7	491	97	13588	3.E+00	1.E+00	7.E-02
GOTERM_BP_FAT	GO:0031399~regulation of protein modification process	15	2.742230347	3.E-03 15170, 13649, 13645, 224014, 15129, 1	491	165	13588	3.E+00	1.E+00	7.E-02
GOTERM_BP_FAT	GO:0009725~response to hormone stimulus	15	2.742230347	3.E-03 19247, 18709, 20848, 18708, 21813, 20	491	165	13588	3.E+00	1.E+00	7.E-02
GOTERM_BP_FAT	GO:0009719~response to endogenous stimulus	16	2.925045704	3.E-03 19247, 18227, 18709, 20848, 18708, 21	491	184	13588	2.E+00	1.E+00	7.E-02
GOTERM_BP_FAT	GO:0048511~rhythmic process	11	2.010968921	3.E-03 11865, 13667, 12753, 12952, 18626, 12	491	98	13588	3.E+00	1.E+00	7.E-02
GOTERM_BP_FAT	GO:0043085~positive regulation of catalytic activity	20	3.65630713	3.E-03 13131, 672195, 19247, 12279, 14678, 1	491	261	13588	2.E+00	1.E+00	7.E-02
GOTERM_BP_FAT	GO:0006928~cell motion	25	4.570383912	4.E-03 117600, 13649, 16392, 238055, 18791, 1	491	367	13588	2.E+00	1.E+00	9.E-02
GOTERM_BP_FAT	GO:0002253~activation of immune response	10	1.828153565	4.E-03 15170, 12266, 12258, 12279, 230558, 6	491	86	13588	3.E+00	1.E+00	9.E-02
GOTERM_BP_FAT	GO:0006606~protein import into nucleus	8	1.462522852	4.E-03 11865, 664868, 56338, 19384, 231103, 1	491	56	13588	4.E+00	1.E+00	9.E-02
GOTERM_BP_FAT	GO:0051170~nuclear import	8	1.462522852	5.E-03 11865, 664868, 56338, 19384, 231103, 1	491	58	13588	4.E+00	1.E+00	1.E-01
GOTERM_BP_FAT	GO:0006084~acetyl-CoA metabolic process	6	1.096892139	5.E-03 17448, 235339, 78920, 67834, 15929, 6	491	31	13588	5.E+00	1.E+00	1.E-01
GOTERM_BP_FAT	GO:0002449~lymphocyte mediated immunity	9	1.645338208	6.E-03 15170, 12266, 18753, 12258, 12279, 23	491	76	13588	3.E+00	1.E+00	1.E-01
GOTERM_BP_FAT	GO:0034504~protein localization in nucleus	8	1.462522852	6.E-03 11865, 664868, 56338, 19384, 231103, 1	491	61	13588	4.E+00	1.E+00	1.E-01
GOTERM_BP_FAT	GO:0006800~oxygen and reactive oxygen species metabolic proces	7	1.279707495	7.E-03 18126, 672195, 68349, 227197, 17717, 1	491	47	13588	4.E+00	1.E+00	1.E-01
GOTERM_BP_FAT	GO:0010001~glial cell differentiation	7	1.279707495	7.E-03 13667, 13867, 224045, 217715, 16000, 1	491	48	13588	4.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0016064~immunoglobulin mediated immune response	8	1.462522852	7.E-03 12266, 18753, 12258, 12279, 230558, 6	491	63	13588	4.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0019441~tryptophan catabolic process to kynurenine	3	0.548446069	7.E-03 71562, 15930, 56720	491	4	13588	2.E+01	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0009611~response to wounding	23	4.204753199	8.E-03 15170, 12266, 14674, 15930, 12258, 16	491	347	13588	2.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0000165~MAPKKK cascade	11	2.010968921	8.E-03 57874, 19247, 19713, 14784, 14678, 13	491	114	13588	3.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0019835~cytolysis	5	0.914076782	9.E-03 12279, 230558, 69379, 15139, 110382	491	23	13588	6.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0002526~acute inflammatory response	9	1.645338208	9.E-03 20848, 12266, 12258, 15930, 12279, 23	491	81	13588	3.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0051605~protein maturation by peptide bond cleavage	8	1.462522852	9.E-03 12266, 12258, 11487, 12279, 230558, 6	491	65	13588	3.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0019724~B cell mediated immunity	8	1.462522852	9.E-03 12266, 18753, 12258, 12279, 230558, 6	491	65	13588	3.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0009820~alkaloid metabolic process	5	0.914076782	1.E-02 98256, 21991, 17969, 103988, 14381	491	24	13588	6.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0006769~nicotinamide metabolic process	5	0.914076782	1.E-02 98256, 21991, 17969, 103988, 14381	491	24	13588	6.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0046496~nicotinamide nucleotide metabolic process	5	0.914076782	1.E-02 98256, 21991, 17969, 103988, 14381	491	24	13588	6.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0018108~peptidyl-tyrosine phosphorylation	6	1.096892139	1.E-02 11350, 20779, 14158, 16451, 13645, 16	491	37	13588	4.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0042552~myelination	6	1.096892139	1.E-02 13667, 13866, 224045, 12527, 217715, 1	491	37	13588	4.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0018212~peptidyl-tyrosine modification	6	1.096892139	1.E-02 11350, 20779, 14158, 16451, 13645, 16	491	37	13588	4.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0042551~neuron maturation	4	0.731261426	1.E-02 19713, 12577, 11820, 18227	491	13	13588	9.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0043547~positive regulation of GTPase activity	4	0.731261426	1.E-02 71709, 11856, 19765, 19417	491	13	13588	9.E+00	1.E+00	2.E-01



GOTERM_BP_FAT	GO:0042063~gliogenesis	7	1.279707495	1.E-02 13667, 13867, 224045, 217715, 16000, 1	491	52	13588	4.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0002250~adaptive immune response	9	1.645338208	1.E-02 12266, 18753, 12258, 12279, 230558, 69	491	84	13588	3.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0002460~adaptive immune response based on somatic recomb	9	1.645338208	1.E-02 12266, 18753, 12258, 12279, 230558, 69	491	84	13588	3.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0050730~regulation of peptidyl-tyrosine phosphorylation	7	1.279707495	1.E-02 15170, 13649, 18753, 18754, 14600, 136	491	53	13588	4.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0060416~response to growth hormone stimulus	3	0.548446069	1.E-02 20848, 14600, 16452	491	5	13588	2.E+01	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0042436~indole derivative catabolic process	3	0.548446069	1.E-02 71562, 15930, 56720	491	5	13588	2.E+01	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0006569~tryptophan catabolic process	3	0.548446069	1.E-02 71562, 15930, 56720	491	5	13588	2.E+01	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0046218~indolalkylamine catabolic process	3	0.548446069	1.E-02 71562, 15930, 56720	491	5	13588	2.E+01	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0060396~growth hormone receptor signaling pathway	3	0.548446069	1.E-02 20848, 14600, 16452	491	5	13588	2.E+01	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0030879~mammary gland development	9	1.645338208	1.E-02 12190, 21813, 20779, 11855, 15277, 129	491	86	13588	3.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0007272~ensheathment of neurons	6	1.096892139	1.E-02 13667, 13866, 224045, 12527, 217715, 1	491	39	13588	4.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0008366~axon ensheathment	6	1.096892139	1.E-02 13667, 13866, 224045, 12527, 217715, 1	491	39	13588	4.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0043603~cellular amide metabolic process	6	1.096892139	1.E-02 98256, 21991, 17969, 14600, 103988, 14	491	39	13588	4.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0014003~oligodendrocyte development	4	0.731261426	1.E-02 13667, 224045, 217715, 108067	491	14	13588	8.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0006739~NADP metabolic process	4	0.731261426	1.E-02 21991, 17969, 103988, 14381	491	14	13588	8.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0006959~humoral immune response	7	1.279707495	1.E-02 12266, 12258, 12279, 230558, 69379, 11	491	54	13588	4.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0050817~coagulation	8	1.462522852	1.E-02 14060, 14674, 12258, 16644, 12279, 74	491	70	13588	3.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0007596~blood coagulation	8	1.462522852	1.E-02 14060, 14674, 12258, 16644, 12279, 74	491	70	13588	3.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0009743~response to carbohydrate stimulus	5	0.914076782	1.E-02 21813, 230163, 224045, 217715, 103988	491	26	13588	5.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0007599~hemostasis	8	1.462522852	1.E-02 14060, 14674, 12258, 16644, 12279, 74	491	71	13588	3.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0006732~coenzyme metabolic process	12	2.193784278	1.E-02 98256, 17448, 235339, 74147, 78920, 2	491	143	13588	2.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0019362~pyridine nucleotide metabolic process	5	0.914076782	2.E-02 98256, 21991, 17969, 103988, 14381	491	28	13588	5.E+00	1.E+00	3.E-01
GOTERM_BP_FAT	GO:0048584~positive regulation of response to stimulus	14	2.559414991	2.E-02 15170, 12266, 15930, 12258, 12279, 16	491	186	13588	2.E+00	1.E+00	3.E-01
GOTERM_BP_FAT	GO:0042159~lipoprotein catabolic process	3	0.548446069	2.E-02 11816, 238055, 16835	491	6	13588	1.E+01	1.E+00	3.E-01
GOTERM_BP_FAT	GO:0032870~cellular response to hormone stimulus	7	1.279707495	2.E-02 18709, 20848, 18708, 19247, 104215, 14	491	58	13588	3.E+00	1.E+00	3.E-01
GOTERM_BP_FAT	GO:0048469~cell maturation	8	1.462522852	2.E-02 12190, 19713, 12577, 11820, 18551, 18	491	75	13588	3.E+00	1.E+00	3.E-01
GOTERM_BP_FAT	GO:0033674~positive regulation of kinase activity	11	2.010968921	2.E-02 13131, 21813, 19247, 14678, 22359, 57	491	130	13588	2.E+00	1.E+00	3.E-01
GOTERM_BP_FAT	GO:0009109~coenzyme catabolic process	5	0.914076782	2.E-02 17448, 78920, 67834, 15929, 17969	491	29	13588	5.E+00	1.E+00	3.E-01
GOTERM_BP_FAT	GO:0042060~wound healing	10	1.828153565	2.E-02 14060, 14674, 21813, 12258, 16644, 12	491	112	13588	2.E+00	1.E+00	3.E-01
GOTERM_BP_FAT	GO:0043434~response to peptide hormone stimulus	9	1.645338208	2.E-02 18709, 20848, 18708, 104215, 230163, 1	491	95	13588	3.E+00	1.E+00	3.E-01
GOTERM_BP_FAT	GO:0019228~regulation of action potential in neuron	6	1.096892139	2.E-02 13667, 13866, 224045, 12527, 217715, 1	491	45	13588	4.E+00	1.E+00	3.E-01
GOTERM_BP_FAT	GO:0006913~nucleocytoplasmic transport	9	1.645338208	2.E-02 11865, 664868, 56338, 19384, 11487, 2	491	96	13588	3.E+00	1.E+00	3.E-01
GOTERM_BP_FAT	GO:0040008~regulation of growth	17	3.10786106	2.E-02 19247, 67184, 11816, 68349, 11820, 15	491	256	13588	2.E+00	1.E+00	3.E-01
GOTERM_BP_FAT	GO:0006568~tryptophan metabolic process	3	0.548446069	2.E-02 71562, 15930, 56720	491	7	13588	1.E+01	1.E+00	3.E-01
GOTERM_BP_FAT	GO:0051347~positive regulation of transferase activity	11	2.010968921	2.E-02 13131, 21813, 19247, 14678, 22359, 57	491	135	13588	2.E+00	1.E+00	3.E-01
GOTERM_BP_FAT	GO:0006468~protein amino acid phosphorylation	34	6.215722121	3.E-02 13649, 19247, 13665, 20416, 12912, 13	491	640	13588	1.E+00	1.E+00	3.E-01
GOTERM_BP_FAT	GO:0051169~nuclear transport	9	1.645338208	3.E-02 11865, 664868, 56338, 19384, 11487, 2	491	98	13588	3.E+00	1.E+00	3.E-01
GOTERM_BP_FAT	GO:0050778~positive regulation of immune response	11	2.010968921	3.E-02 15170, 12266, 12258, 15930, 12279, 23	491	136	13588	2.E+00	1.E+00	3.E-01
GOTERM_BP_FAT	GO:0051345~positive regulation of hydrolase activity	8	1.462522852	3.E-02 672195, 71709, 12279, 11856, 67469, 14	491	81	13588	3.E+00	1.E+00	4.E-01
GOTERM_BP_FAT	GO:0051187~cofactor catabolic process	5	0.914076782	3.E-02 17448, 78920, 67834, 15929, 17969	491	32	13588	4.E+00	1.E+00	4.E-01
GOTERM_BP_FAT	GO:0048514~blood vessel morphogenesis	14	2.559414991	3.E-02 14674, 11852, 11816, 238055, 20416, 1	491	198	13588	2.E+00	1.E+00	4.E-01
GOTERM_BP_FAT	GO:0007010~cytoskeleton organization	20	3.65630713	3.E-02 14163, 11350, 26934, 94190, 73167, 11	491	326	13588	2.E+00	1.E+00	4.E-01
GOTERM_BP_FAT	GO:0017038~protein import	8	1.462522852	3.E-02 11865, 664868, 56338, 19384, 231103, 1	491	82	13588	3.E+00	1.E+00	4.E-01
GOTERM_BP_FAT	GO:0048870~cell motility	18	3.290676417	3.E-02 117600, 13649, 13131, 16392, 14389, 2	491	284	13588	2.E+00	1.E+00	4.E-01
GOTERM_BP_FAT	GO:0051674~localization of cell	18	3.290676417	3.E-02 117600, 13649, 13131, 16392, 14389, 2	491	284	13588	2.E+00	1.E+00	4.E-01
GOTERM_BP_FAT	GO:0032321~positive regulation of Rho GTPase activity	3	0.548446069	3.E-02 71709, 19765, 19417	491	8	13588	1.E+01	1.E+00	4.E-01
GOTERM_BP_FAT	GO:0001568~blood vessel development	16	2.925045704	3.E-02 14674, 11852, 11816, 12929, 238055, 2	491	244	13588	2.E+00	1.E+00	4.E-01
GOTERM_BP_FAT	GO:0009894~regulation of catabolic process	6	1.096892139	3.E-02 11865, 14447, 282663, 67469, 19697, 2	491	50	13588	3.E+00	1.E+00	4.E-01
GOTERM_BP_FAT	GO:0048709~oligodendrocyte differentiation	4	0.731261426	3.E-02 13667, 224045, 217715, 108067	491	20	13588	6.E+00	1.E+00	4.E-01
GOTERM_BP_FAT	GO:0006954~inflammatory response	15	2.742230347	3.E-02 12266, 15930, 12258, 12279, 16644, 69	491	225	13588	2.E+00	1.E+00	4.E-01
GOTERM_BP_FAT	GO:0001944~vasculature development	16	2.925045704	4.E-02 14674, 11852, 11816, 12929, 238055, 2	491	250	13588	2.E+00	1.E+00	4.E-01
GOTERM_BP_FAT	GO:0051270~regulation of cell motion	9	1.645338208	4.E-02 18708, 14674, 73167, 74144, 11491, 11	491	107	13588	2.E+00	1.E+00	4.E-01
GOTERM_BP_FAT	GO:0048011~nerve growth factor receptor signaling pathway	3	0.548446069	4.E-02 20779, 19247, 20662	491	9	13588	9.E+00	1.E+00	4.E-01
GOTERM_BP_FAT	GO:0030031~cell projection assembly	7	1.279707495	4.E-02 19354, 104394, 30938, 57257, 12540, 1	491	70	13588	3.E+00	1.E+00	4.E-01
GOTERM_BP_FAT	GO:0008203~cholesterol metabolic process	7	1.279707495	4.E-02 13121, 11816, 14137, 22359, 65969, 16	491	70	13588	3.E+00	1.E+00	4.E-01
GOTERM_BP_FAT	GO:0030030~cell projection organization	19	3.473491773	4.E-02 104394, 19247, 16392, 11820, 57257, 1	491	319	13588	2.E+00	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0050878~regulation of body fluid levels	8	1.462522852	4.E-02 14060, 14674, 12258, 16644, 12279, 74	491	89	13588	2.E+00	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0009746~response to hexose stimulus	4	0.731261426	4.E-02 21813, 224045, 217715, 103988	491	22	13588	5.E+00	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0009749~response to glucose stimulus	4	0.731261426	4.E-02 21813, 224045, 217715, 103988	491	22	13588	5.E+00	1.E+00	5.E-01



GOTERM_BP_FAT	GO:0034284~response to monosaccharide stimulus	4	0.731261426	4.E-02 21813, 224045, 217715, 103988	491	22	13588	5.E+00	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0016485~protein processing	8	1.462522852	4.E-02 12266, 12258, 11487, 12279, 230558, 69	491	90	13588	2.E+00	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0001508~regulation of action potential	6	1.096892139	4.E-02 13667, 13866, 224045, 12527, 217715, :	491	54	13588	3.E+00	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0043549~regulation of kinase activity	13	2.376599634	5.E-02 13131, 15170, 19247, 14678, 11820, 57:	491	192	13588	2.E+00	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0006733~oxidoreduction coenzyme metabolic process	5	0.914076782	5.E-02 98256, 21991, 17969, 103988, 14381	491	38	13588	4.E+00	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0046626~regulation of insulin receptor signaling pathway	3	0.548446069	5.E-02 18753, 20779, 12702	491	10	13588	8.E+00	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0033143~regulation of steroid hormone receptor signaling path	3	0.548446069	5.E-02 20779, 16000, 11848	491	10	13588	8.E+00	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0032320~positive regulation of Ras GTPase activity	3	0.548446069	5.E-02 71709, 19765, 19417	491	10	13588	8.E+00	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0030334~regulation of cell migration	8	1.462522852	5.E-02 18708, 14674, 73167, 74144, 11855, 20:	491	92	13588	2.E+00	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0021782~glial cell development	4	0.731261426	5.E-02 13667, 224045, 217715, 108067	491	23	13588	5.E+00	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0006099~tricarboxylic acid cycle	4	0.731261426	5.E-02 17448, 78920, 67834, 15929	491	23	13588	5.E+00	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0031960~response to corticosteroid stimulus	4	0.731261426	5.E-02 20779, 11409, 230163, 94284, 394436	491	23	13588	5.E+00	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0019221~cytokine-mediated signaling pathway	6	1.096892139	5.E-02 20848, 15170, 16195, 20846, 16451, 16:	491	56	13588	3.E+00	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0001525~angiogenesis	10	1.828153565	5.E-02 14674, 21813, 14751, 11852, 74144, 20:	491	133	13588	2.E+00	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0030155~regulation of cell adhesion	8	1.462522852	5.E-02 18708, 22324, 13131, 20779, 11487, 56:	491	94	13588	2.E+00	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0040014~regulation of multicellular organism growth	7	1.279707495	5.E-02 20848, 19247, 11816, 11820, 12912, 14:	491	75	13588	3.E+00	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0016477~cell migration	15	2.742230347	5.E-02 117600, 13649, 13131, 16392, 14389, 5:	491	240	13588	2.E+00	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0048732~gland development	13	2.376599634	5.E-02 12190, 13649, 16392, 12929, 11855, 15:	491	197	13588	2.E+00	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0045834~positive regulation of lipid metabolic process	4	0.731261426	5.E-02 11816, 57257, 67469, 12540	491	24	13588	5.E+00	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0046356~acetyl-CoA catabolic process	4	0.731261426	5.E-02 17448, 78920, 67834, 15929	491	24	13588	5.E+00	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0021675~nerve development	4	0.731261426	5.E-02 12064, 13867, 68193, 18205	491	24	13588	5.E+00	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0051338~regulation of transferase activity	13	2.376599634	6.E-02 13131, 15170, 19247, 14678, 11820, 57:	491	199	13588	2.E+00	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0030035~microspike assembly	3	0.548446069	6.E-02 30938, 12540, 224014	491	11	13588	8.E+00	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0007173~epidermal growth factor receptor signaling pathway	3	0.548446069	6.E-02 13649, 20779, 13645	491	11	13588	8.E+00	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0009074~aromatic amino acid family catabolic process	3	0.548446069	6.E-02 71562, 15930, 56720	491	11	13588	8.E+00	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0051604~protein maturation	8	1.462522852	6.E-02 12266, 12258, 11487, 12279, 230558, 69	491	96	13588	2.E+00	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0016125~sterol metabolic process	7	1.279707495	6.E-02 13121, 11816, 14137, 22359, 65969, 16:	491	77	13588	3.E+00	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0051272~positive regulation of cell motion	5	0.914076782	6.E-02 18708, 73167, 11491, 11855, 20339	491	41	13588	3.E+00	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0007162~negative regulation of cell adhesion	4	0.731261426	6.E-02 18708, 13131, 11487, 11947	491	25	13588	4.E+00	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0006090~pyruvate metabolic process	4	0.731261426	6.E-02 14751, 235339, 21991, 230163	491	25	13588	4.E+00	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0033365~protein localization in organelle	8	1.462522852	6.E-02 11865, 664868, 56338, 19384, 231103, :	491	97	13588	2.E+00	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0048545~response to steroid hormone stimulus	6	1.096892139	6.E-02 21813, 20779, 11409, 230163, 16847, 9:	491	60	13588	3.E+00	1.E+00	6.E-01
GOTERM_BP_FAT	GO:0051186~cofactor metabolic process	12	2.193784278	7.E-02 98256, 17448, 235339, 74147, 78920, 2:	491	182	13588	2.E+00	1.E+00	6.E-01
GOTERM_BP_FAT	GO:0001909~leukocyte mediated cytotoxicity	3	0.548446069	7.E-02 15170, 13035, 17969	491	12	13588	7.E+00	1.E+00	6.E-01
GOTERM_BP_FAT	GO:0006414~translational elongation	5	0.914076782	7.E-02 56040, 13627, 13628, 66656, 55949	491	43	13588	3.E+00	1.E+00	6.E-01
GOTERM_BP_FAT	GO:0006631~fatty acid metabolic process	12	2.193784278	7.E-02 70316, 66885, 15107, 11409, 74147, 22:	491	184	13588	2.E+00	1.E+00	6.E-01
GOTERM_BP_FAT	GO:0002684~positive regulation of immune system process	13	2.376599634	7.E-02 15170, 12266, 15930, 12258, 12279, 69:	491	206	13588	2.E+00	1.E+00	6.E-01
GOTERM_BP_FAT	GO:0032615~interleukin-12 production	2	0.365630713	7.E-02 18753, 14381	491	2	13588	3.E+01	1.E+00	6.E-01
GOTERM_BP_FAT	GO:0001732~formation of translation initiation complex	2	0.365630713	7.E-02 13669, 55944	491	2	13588	3.E+01	1.E+00	6.E-01
GOTERM_BP_FAT	GO:0032613~interleukin-10 production	2	0.365630713	7.E-02 18753, 14381	491	2	13588	3.E+01	1.E+00	6.E-01
GOTERM_BP_FAT	GO:0009060~aerobic respiration	4	0.731261426	7.E-02 17448, 78920, 67834, 15929	491	27	13588	4.E+00	1.E+00	6.E-01
GOTERM_BP_FAT	GO:0042326~negative regulation of phosphorylation	4	0.731261426	7.E-02 15170, 18753, 12577, 16476	491	27	13588	4.E+00	1.E+00	6.E-01
GOTERM_BP_FAT	GO:0021700~developmental maturation	8	1.462522852	7.E-02 12190, 19713, 12577, 11820, 18551, 18:	491	101	13588	2.E+00	1.E+00	6.E-01
GOTERM_BP_FAT	GO:0006586~indolalkylamine metabolic process	3	0.548446069	8.E-02 71562, 15930, 56720	491	13	13588	6.E+00	1.E+00	6.E-01
GOTERM_BP_FAT	GO:0042430~indole and derivative metabolic process	3	0.548446069	8.E-02 71562, 15930, 56720	491	13	13588	6.E+00	1.E+00	6.E-01
GOTERM_BP_FAT	GO:0043467~regulation of generation of precursor metabolites anc	3	0.548446069	8.E-02 14447, 103988, 208727	491	13	13588	6.E+00	1.E+00	6.E-01
GOTERM_BP_FAT	GO:0048639~positive regulation of developmental growth	3	0.548446069	8.E-02 21813, 18049, 74318	491	13	13588	6.E+00	1.E+00	6.E-01
GOTERM_BP_FAT	GO:0042434~indole derivative metabolic process	3	0.548446069	8.E-02 71562, 15930, 56720	491	13	13588	6.E+00	1.E+00	6.E-01
GOTERM_BP_FAT	GO:0042130~negative regulation of T cell proliferation	4	0.731261426	8.E-02 15170, 208154, 13866, 15930	491	28	13588	4.E+00	1.E+00	6.E-01
GOTERM_BP_FAT	GO:0045860~positive regulation of protein kinase activity	9	1.645338208	8.E-02 13131, 21813, 19247, 14678, 22359, 20:	491	124	13588	2.E+00	1.E+00	6.E-01
GOTERM_BP_FAT	GO:0046660~female sex differentiation	6	1.096892139	8.E-02 12190, 13667, 16847, 224045, 217715, :	491	64	13588	3.E+00	1.E+00	6.E-01
GOTERM_BP_FAT	GO:0046700~heterocycle catabolic process	5	0.914076782	8.E-02 71562, 72269, 15930, 56720, 99586	491	46	13588	3.E+00	1.E+00	6.E-01
GOTERM_BP_FAT	GO:0010563~negative regulation of phosphorus metabolic process	4	0.731261426	9.E-02 15170, 18753, 12577, 16476	491	29	13588	4.E+00	1.E+00	6.E-01
GOTERM_BP_FAT	GO:0045936~negative regulation of phosphate metabolic process	4	0.731261426	9.E-02 15170, 18753, 12577, 16476	491	29	13588	4.E+00	1.E+00	6.E-01
GOTERM_BP_FAT	GO:0046887~positive regulation of hormone secretion	3	0.548446069	9.E-02 19247, 12912, 103988	491	14	13588	6.E+00	1.E+00	7.E-01
GOTERM_BP_FAT	GO:0010906~regulation of glucose metabolic process	3	0.548446069	9.E-02 14447, 103988, 208727	491	14	13588	6.E+00	1.E+00	7.E-01
GOTERM_BP_FAT	GO:0032319~regulation of Rho GTPase activity	3	0.548446069	9.E-02 71709, 19765, 19417	491	14	13588	6.E+00	1.E+00	7.E-01
GOTERM_BP_FAT	GO:0045087~innate immune response	8	1.462522852	9.E-02 15170, 12266, 12258, 12279, 230558, 69	491	107	13588	2.E+00	1.E+00	7.E-01
GOTERM_BP_FAT	GO:0007422~peripheral nervous system development	4	0.731261426	9.E-02 18049, 13867, 13866, 18205	491	30	13588	4.E+00	1.E+00	7.E-01



GOTERM_BP_FAT	GO:0006979~response to oxidative stress	7	1.279707495	9.E-02 226646, 19053, 56338, 11816, 22229, 21	491	87	13588	2.E+00	1.E+00	7.E-01
GOTERM_BP_FAT	GO:0008361~regulation of cell size	8	1.462522852	1.E-01 104394, 18049, 67184, 72269, 68349, 1	491	108	13588	2.E+00	1.E+00	7.E-01
GOTERM_BP_FAT	GO:0031175~neuron projection development	13	2.376599634	1.E-01 19247, 16392, 11820, 18479, 18227, 17	491	218	13588	2.E+00	1.E+00	7.E-01
GOTERM_BP_FAT	GO:0048608~reproductive structure development	9	1.645338208	1.E-01 12190, 13667, 20779, 16847, 224045, 2	491	130	13588	2.E+00	1.E+00	7.E-01
GOTERM_BP_FAT	GO:0046364~monosaccharide biosynthetic process	4	0.731261426	1.E-01 14751, 21991, 230163, 14381	491	31	13588	4.E+00	1.E+00	7.E-01
GOTERM_CC_FAT	GO:0070469~respiratory chain	52	9.506398537	1.E-63 70316, 672195, 226646, 100041273, 66	419	65	12504	2.E+01	3.E-61	3.E-61
GOTERM_CC_FAT	GO:0005840~ribosome	66	12.06581353	3.E-48 666899, 100048462, 20103, 100044516,	419	192	12504	1.E+01	8.E-46	4.E-46
GOTERM_CC_FAT	GO:0005743~mitochondrial inner membrane	76	13.89396709	1.E-45 226646, 100041273, 66377, 100041835,	419	296	12504	8.E+00	4.E-43	1.E-43
GOTERM_CC_FAT	GO:0019866~organelle inner membrane	77	14.07678245	7.E-45 226646, 100041273, 66377, 100041835,	419	312	12504	7.E+00	2.E-42	5.E-43
GOTERM_CC_FAT	GO:0031966~mitochondrial membrane	79	14.44241316	2.E-41 226646, 100041273, 66377, 100041835,	419	368	12504	6.E+00	7.E-39	1.E-39
GOTERM_CC_FAT	GO:0044429~mitochondrial part	91	16.63619744	5.E-40 66885, 226646, 66377, 100041835, 142	419	524	12504	5.E+00	2.E-37	3.E-38
GOTERM_CC_FAT	GO:0005740~mitochondrial envelope	79	14.44241316	2.E-39 226646, 100041273, 66377, 100041835,	419	391	12504	6.E+00	7.E-37	1.E-37
GOTERM_CC_FAT	GO:0031967~organelle envelope	88	16.08775137	2.E-36 226646, 66377, 100041835, 14270, 177	419	540	12504	5.E+00	6.E-34	8.E-35
GOTERM_CC_FAT	GO:0031975~envelope	88	16.08775137	3.E-36 226646, 66377, 100041835, 14270, 177	419	542	12504	5.E+00	9.E-34	1.E-34
GOTERM_CC_FAT	GO:0005739~mitochondrion	127	23.21755027	2.E-29 18746, 226646, 66885, 66377, 1000445	419	1322	12504	3.E+00	6.E-27	6.E-28
GOTERM_CC_FAT	GO:0030529~ribonucleoprotein complex	69	12.6142596	6.E-26 666899, 100048462, 20103, 100044516,	419	462	12504	4.E+00	2.E-23	2.E-24
GOTERM_CC_FAT	GO:0031090~organelle membrane	86	15.72212066	4.E-22 226646, 100041273, 66377, 100041835,	419	809	12504	3.E+00	1.E-19	1.E-20
GOTERM_CC_FAT	GO:0045259~proton-transporting ATP synthase complex	16	2.925045704	2.E-19 228033, 100041835, 67126, 66043, 177	419	19	12504	3.E+01	6.E-17	4.E-18
GOTERM_CC_FAT	GO:0044455~mitochondrial membrane part	20	3.65630713	4.E-16 226646, 67184, 67126, 68349, 17705, 1	419	49	12504	1.E+01	1.E-13	9.E-15
GOTERM_CC_FAT	GO:0005852~eukaryotic translation initiation factor 3 complex	11	2.010968921	1.E-13 27979, 66085, 13669, 16341, 53356, 56	419	12	12504	3.E+01	3.E-11	2.E-12
GOTERM_CC_FAT	GO:0033279~ribosomal subunit	20	3.65630713	2.E-13 100048462, 20103, 100039355, 100043	419	66	12504	9.E+00	7.E-11	5.E-12
GOTERM_CC_FAT	GO:0022626~cytosolic ribosome	12	2.193784278	1.E-12 100048462, 19944, 100042832, 20103, 1	419	18	12504	2.E+01	4.E-10	2.E-11
GOTERM_CC_FAT	GO:0016469~proton-transporting two-sector ATPase complex	16	2.925045704	2.E-12 228033, 100041835, 67126, 66043, 177	419	42	12504	1.E+01	7.E-10	4.E-11
GOTERM_CC_FAT	GO:0045263~proton-transporting ATP synthase complex, coupling	10	1.828153565	3.E-11 228033, 100041835, 17705, 17706, 274	419	13	12504	2.E+01	9.E-09	5.E-10
GOTERM_CC_FAT	GO:0005746~mitochondrial respiratory chain	10	1.828153565	2.E-10 226646, 67184, 67264, 68349, 12862, 2	419	15	12504	2.E+01	6.E-08	3.E-09
GOTERM_CC_FAT	GO:0044445~cytosolic part	16	2.925045704	2.E-09 100048462, 20103, 100043391, 18709, 1	419	63	12504	8.E+00	5.E-07	2.E-08
GOTERM_CC_FAT	GO:0043228~non-membrane-bounded organelle	111	20.29250457	3.E-09 666899, 100048462, 13669, 100044516,	419	1919	12504	2.E+00	8.E-07	4.E-08
GOTERM_CC_FAT	GO:0043232~intracellular non-membrane-bounded organelle	111	20.29250457	3.E-09 666899, 100048462, 13669, 100044516,	419	1919	12504	2.E+00	8.E-07	4.E-08
GOTERM_CC_FAT	GO:0005753~mitochondrial proton-transporting ATP synthase complex	7	1.279707495	9.E-09 11950, 100042348, 67126, 17705, 2742	419	7	12504	3.E+01	3.E-06	1.E-07
GOTERM_CC_FAT	GO:0033177~proton-transporting two-sector ATPase complex, prot	10	1.828153565	2.E-08 228033, 100041835, 17705, 17706, 274	419	22	12504	1.E+01	5.E-06	2.E-07
GOTERM_CC_FAT	GO:0015935~small ribosomal subunit	11	2.010968921	2.E-08 20103, 100039355, 677113, 20102, 200	419	29	12504	1.E+01	5.E-06	2.E-07
GOTERM_CC_FAT	GO:0000276~mitochondrial proton-transporting ATP synthase complex	6	1.096892139	2.E-07 11950, 100042348, 17705, 27425, 1770	419	6	12504	3.E+01	7.E-05	3.E-06
GOTERM_CC_FAT	GO:0030964~NADH dehydrogenase complex	6	1.096892139	2.E-07 226646, 67264, 68349, 227197, 17993, 1	419	6	12504	3.E+01	7.E-05	3.E-06
GOTERM_CC_FAT	GO:0045271~respiratory chain complex I	6	1.096892139	2.E-07 226646, 67264, 68349, 227197, 17993, 1	419	6	12504	3.E+01	7.E-05	3.E-06
GOTERM_CC_FAT	GO:0005747~mitochondrial respiratory chain complex I	6	1.096892139	2.E-07 226646, 67264, 68349, 227197, 17993, 1	419	6	12504	3.E+01	7.E-05	3.E-06
GOTERM_CC_FAT	GO:0045261~proton-transporting ATP synthase complex, catalytic c	6	1.096892139	2.E-07 66043, 67126, 11947, 11949, 28080, 10	419	6	12504	3.E+01	7.E-05	3.E-06
GOTERM_CC_FAT	GO:0022625~cytosolic large ribosomal subunit	6	1.096892139	8.E-07 100048462, 20005, 110954, 100042832,	419	7	12504	3.E+01	2.E-04	9.E-06
GOTERM_CC_FAT	GO:0005579~membrane attack complex	5	0.914076782	6.E-06 12279, 230558, 69379, 15139, 110382	419	5	12504	3.E+01	2.E-03	6.E-05
GOTERM_CC_FAT	GO:0005851~eukaryotic translation initiation factor 2B complex	5	0.914076782	2.E-05 13667, 13665, 224045, 217715, 108067	419	6	12504	2.E+01	5.E-03	2.E-04
GOTERM_CC_FAT	GO:0015934~large ribosomal subunit	9	1.645338208	4.E-05 100048462, 100042832, 19921, 100043	419	39	12504	7.E+00	1.E-02	4.E-04
GOTERM_CC_FAT	GO:0005759~mitochondrial matrix	17	3.10786106	1.E-04 672195, 66885, 68263, 15107, 17448, 1	419	163	12504	3.E+00	3.E-02	1.E-03
GOTERM_CC_FAT	GO:0031980~mitochondrial lumen	17	3.10786106	1.E-04 672195, 66885, 68263, 15107, 17448, 1	419	163	12504	3.E+00	3.E-02	1.E-03
GOTERM_CC_FAT	GO:0033178~proton-transporting two-sector ATPase complex, cata	6	1.096892139	2.E-04 66043, 67126, 11947, 11949, 28080, 10	419	17	12504	1.E+01	5.E-02	2.E-03
GOTERM_CC_FAT	GO:0005829~cytosol	36	6.581352834	2.E-04 100048462, 672195, 27041, 20103, 100	419	549	12504	2.E+00	5.E-02	2.E-03
GOTERM_CC_FAT	GO:0022627~cytosolic small ribosomal subunit	4	0.731261426	7.E-04 20103, 20085, 677113, 20088, 20068	419	6	12504	2.E+01	2.E-01	6.E-03
GOTERM_CC_FAT	GO:0005853~eukaryotic translation elongation factor 1 complex	3	0.548446069	6.E-03 13628, 66656, 55949	419	4	12504	2.E+01	9.E-01	5.E-02
GOTERM_CC_FAT	GO:0000015~phosphopyruvate hydratase complex	3	0.548446069	6.E-03 433182, 13807, 13806, 13808, 1000442	419	4	12504	2.E+01	9.E-01	5.E-02
GOTERM_CC_FAT	GO:0005626~insoluble fraction	29	5.301645338	1.E-02 13121, 14685, 19247, 12955, 11852, 66	419	528	12504	2.E+00	1.E+00	9.E-02
GOTERM_CC_FAT	GO:0000267~cell fraction	31	5.667276051	2.E-02 13121, 14685, 672195, 19247, 12955, 1	419	596	12504	2.E+00	1.E+00	1.E-01
GOTERM_CC_FAT	GO:0005624~membrane fraction	27	4.936014625	2.E-02 13121, 14685, 19247, 11852, 665032, 2	419	510	12504	2.E+00	1.E+00	2.E-01
GOTERM_CC_FAT	GO:0031974~membrane-enclosed lumen	52	9.506398537	3.E-02 672195, 66885, 68263, 101206, 12912, 1	419	1174	12504	1.E+00	1.E+00	2.E-01
GOTERM_CC_FAT	GO:0046930~pore complex	7	1.279707495	3.E-02 664868, 12279, 230558, 69379, 15139, 1	419	73	12504	3.E+00	1.E+00	2.E-01
GOTERM_CC_FAT	GO:0005667~transcription factor complex	14	2.559414991	5.E-02 11865, 12753, 104394, 16911, 12912, 1	419	234	12504	2.E+00	1.E+00	3.E-01
GOTERM_CC_FAT	GO:0043233~organelle lumen	49	8.957952468	5.E-02 672195, 66885, 68263, 101206, 12912, 1	419	1136	12504	1.E+00	1.E+00	3.E-01
GOTERM_CC_FAT	GO:0030027~lamellipodium	6	1.096892139	6.E-02 12549, 14163, 170758, 224014, 106952,	419	63	12504	3.E+00	1.E+00	3.E-01
GOTERM_CC_FAT	GO:0070013~intracellular organelle lumen	48	8.775137112	7.E-02 66885, 672195, 68263, 101206, 12912, 1	419	1133	12504	1.E+00	1.E+00	4.E-01
GOTERM_CC_FAT	GO:0005905~coated pit	4	0.731261426	9.E-02 22359, 11820, 65969, 16835	419	32	12504	4.E+00	1.E+00	5.E-01
GOTERM_CC_FAT	GO:0030426~growth cone	5	0.914076782	9.E-02 18479, 170758, 53972, 19417, 24001	419	51	12504	3.E+00	1.E+00	5.E-01
GOTERM_CC_FAT	GO:0030427~site of polarized growth	5	0.914076782	9.E-02 18479, 170758, 53972, 19417, 24001	419	51	12504	3.E+00	1.E+00	5.E-01



GOTERM_CC_FAT	GO:0005751~mitochondrial respiratory chain complex IV	2	0.365630713	1.E-01 12862, 12861	419	3	12504	2.E+01	1.E+00	5.E-01
GOTERM_CC_FAT	GO:0045277~respiratory chain complex IV	2	0.365630713	1.E-01 12862, 12861	419	3	12504	2.E+01	1.E+00	5.E-01
GOTERM_CC_FAT	GO:0030141~secretory granule	8	1.462522852	1.E-01 26934, 18551, 13035, 18791, 71326, 13						



GOTERM_MF_FAT	GO:0019206~nucleoside kinase activity	4	0.731261426	3.E-03 80914, 68556, 22245, 21877	476	9	13288	1.E+01	8.E-01	4.E-02
GOTERM_MF_FAT	GO:0016229~steroid dehydrogenase activity	6	1.096892139	3.E-03 100043456, 56348, 15493, 15492, 1549	476	29	13288	6.E+00	8.E-01	4.E-02
GOTERM_MF_FAT	GO:0004739~pyruvate dehydrogenase (acetyl-transferring) activity	3	0.548446069	4.E-03 68263, 18597, 18598	476	3	13288	3.E+01	8.E-01	4.E-02
GOTERM_MF_FAT	GO:0005094~Rho GDP-dissociation inhibitor activity	3	0.548446069	4.E-03 14570, 192662, 11857	476	3	13288	3.E+01	8.E-01	4.E-02
GOTERM_MF_FAT	GO:0004738~pyruvate dehydrogenase activity	3	0.548446069	4.E-03 68263, 18597, 18598	476	3	13288	3.E+01	8.E-01	4.E-02
GOTERM_MF_FAT	GO:0019904~protein domain specific binding	16	2.925045704	4.E-03 11350, 13131, 20401, 15170, 228359, 1	476	192	13288	2.E+00	9.E-01	4.E-02
GOTERM_MF_FAT	GO:0004634~phosphopyruvate hydratase activity	3	0.548446069	7.E-03 433182, 13807, 13806, 13808, 1000442	476	4	13288	2.E+01	1.E+00	7.E-02
GOTERM_MF_FAT	GO:0004459~L-lactate dehydrogenase activity	3	0.548446069	7.E-03 16828, 16833, 16832	476	4	13288	2.E+01	1.E+00	7.E-02
GOTERM_MF_FAT	GO:0004849~uridine kinase activity	3	0.548446069	7.E-03 80914, 68556, 22245	476	4	13288	2.E+01	1.E+00	7.E-02
GOTERM_MF_FAT	GO:0004769~steroid delta-isomerase activity	3	0.548446069	7.E-03 15493, 15492, 15497	476	4	13288	2.E+01	1.E+00	7.E-02
GOTERM_MF_FAT	GO:0046906~tetrapyrrole binding	13	2.376599634	8.E-03 13121, 672195, 15930, 76279, 65969, 6	476	151	13288	2.E+00	1.E+00	8.E-02
GOTERM_MF_FAT	GO:0017076~purine nucleotide binding	86	15.72212066	1.E-02 18746, 228543, 14685, 66885, 26905, 1	476	1871	13288	1.E+00	1.E+00	1.E-01
GOTERM_MF_FAT	GO:0016860~intramolecular oxidoreductase activity	6	1.096892139	1.E-02 14751, 74147, 21991, 15493, 15492, 15	476	38	13288	4.E+00	1.E+00	1.E-01
GOTERM_MF_FAT	GO:0030676~Rac guanyl-nucleotide exchange factor activity	3	0.548446069	1.E-02 22324, 57257, 16800	476	5	13288	2.E+01	1.E+00	1.E-01
GOTERM_MF_FAT	GO:0004332~fructose-bisphosphate aldolase activity	3	0.548446069	1.E-02 230163, 11676, 11674	476	5	13288	2.E+01	1.E+00	1.E-01
GOTERM_MF_FAT	GO:0031405~lipoic acid binding	3	0.548446069	1.E-02 235339, 27402, 78920	476	5	13288	2.E+01	1.E+00	1.E-01
GOTERM_MF_FAT	GO:0004457~lactate dehydrogenase activity	3	0.548446069	1.E-02 16828, 16833, 16832	476	5	13288	2.E+01	1.E+00	1.E-01
GOTERM_MF_FAT	GO:0016863~intramolecular oxidoreductase activity, transposing C=	4	0.731261426	1.E-02 74147, 15493, 15492, 15497	476	14	13288	8.E+00	1.E+00	1.E-01
GOTERM_MF_FAT	GO:0020037~heme binding	12	2.193784278	1.E-02 13121, 672195, 15930, 76279, 66445, 1	476	144	13288	2.E+00	1.E+00	1.E-01
GOTERM_MF_FAT	GO:0032553~ribonucleotide binding	81	14.80804388	2.E-02 18746, 228543, 14685, 26905, 13627, 1	476	1796	13288	1.E+00	1.E+00	2.E-01
GOTERM_MF_FAT	GO:0032555~purine ribonucleotide binding	81	14.80804388	2.E-02 18746, 228543, 14685, 26905, 13627, 1	476	1796	13288	1.E+00	1.E+00	2.E-01
GOTERM_MF_FAT	GO:0005158~insulin receptor binding	4	0.731261426	2.E-02 18708, 27261, 13449, 13448	476	17	13288	7.E+00	1.E+00	2.E-01
GOTERM_MF_FAT	GO:0003746~translation elongation factor activity	5	0.914076782	2.E-02 13627, 13628, 13629, 66656, 55949	476	31	13288	5.E+00	1.E+00	2.E-01
GOTERM_MF_FAT	GO:0016832~aldehyde-lyase activity	3	0.548446069	2.E-02 230163, 11676, 11674	476	7	13288	1.E+01	1.E+00	2.E-01
GOTERM_MF_FAT	GO:0019200~carbohydrate kinase activity	4	0.731261426	3.E-02 15275, 15277, 103988, 212032	476	20	13288	6.E+00	1.E+00	2.E-01
GOTERM_MF_FAT	GO:0004713~protein tyrosine kinase activity	12	2.193784278	3.E-02 13836, 11350, 13649, 14191, 20779, 13	476	164	13288	2.E+00	1.E+00	2.E-01
GOTERM_MF_FAT	GO:0042625~ATPase activity, coupled to transmembrane movemen	7	1.279707495	4.E-02 100042348, 66043, 67126, 11947, 2742	476	69	13288	3.E+00	1.E+00	3.E-01
GOTERM_MF_FAT	GO:0019205~nucleobase, nucleoside, nucleotide kinase activity	5	0.914076782	4.E-02 80914, 21915, 68556, 22245, 21877	476	36	13288	4.E+00	1.E+00	3.E-01
GOTERM_MF_FAT	GO:0010181~FMN binding	3	0.548446069	6.E-02 18126, 17995, 18984	476	11	13288	8.E+00	1.E+00	4.E-01
GOTERM_MF_FAT	GO:0016836~hydro-lyase activity	5	0.914076782	6.E-02 12350, 74147, 433182, 13807, 13806, 1	476	42	13288	3.E+00	1.E+00	4.E-01
GOTERM_MF_FAT	GO:0003913~DNA photolyase activity	2	0.365630713	7.E-02 12952, 12953	476	2	13288	3.E+01	1.E+00	4.E-01
GOTERM_MF_FAT	GO:0004833~tryptophan 2,3-dioxygenase activity	2	0.365630713	7.E-02 15930, 56720	476	2	13288	3.E+01	1.E+00	4.E-01
GOTERM_MF_FAT	GO:0005093~Rab GDP-dissociation inhibitor activity	2	0.365630713	7.E-02 14567, 14569	476	2	13288	3.E+01	1.E+00	4.E-01
GOTERM_MF_FAT	GO:0017077~oxidative phosphorylation uncoupler activity	2	0.365630713	7.E-02 22227, 22229	476	2	13288	3.E+01	1.E+00	4.E-01
GOTERM_MF_FAT	GO:0031406~carboxylic acid binding	7	1.279707495	8.E-02 70316, 18126, 11409, 235339, 13350, 2	476	85	13288	2.E+00	1.E+00	5.E-01
GOTERM_MF_FAT	GO:0016620~oxidoreductase activity, acting on the aldehyde or oxi	4	0.731261426	8.E-02 100040053, 100042746, 14433, 14447, 1	476	29	13288	4.E+00	1.E+00	5.E-01
GOTERM_MF_FAT	GO:0042169~SH2 domain binding	3	0.548446069	9.E-02 15170, 13131, 11487	476	14	13288	6.E+00	1.E+00	5.E-01
GOTERM_MF_FAT	GO:0008553~hydrogen-exporting ATPase activity, phosphorylative r	3	0.548446069	9.E-02 100042348, 67126, 11947, 27425	476	14	13288	6.E+00	1.E+00	5.E-01
GOTERM_MF_FAT	GO:0004697~protein kinase C activity	3	0.548446069	1.E-01 18753, 18762, 18754	476	15	13288	6.E+00	1.E+00	5.E-01
BIOCARTA	m_egfPathway:EGF Signaling Pathway	11	2.010968921	9.E-05 20848, 18708, 13649, 20846, 14784, 20	109	28	1171	4.E+00	2.E-02	2.E-02
BIOCARTA	m_her2Pathway:Role of ERBB2 in Signal Transduction and Oncology	9	1.645338208	4.E-04 20848, 18708, 13649, 16195, 13867, 13	109	22	1171	4.E+00	8.E-02	4.E-02
BIOCARTA	m_tffPathway:Trefoil Factors Initiate Mucosal Healing	9	1.645338208	6.E-04 18708, 13649, 672195, 13866, 14784, 2	109	23	1171	4.E+00	1.E-01	4.E-02
BIOCARTA	m_metPathway:Signaling of Hepatocyte Growth Factor Receptor	10	1.828153565	2.E-03 20848, 18708, 20779, 19247, 14784, 20	109	32	1171	3.E+00	3.E-01	7.E-02
BIOCARTA	m_il6Pathway:IL 6 signaling pathway	8	1.462522852	2.E-03 20848, 16195, 19247, 14784, 20662, 16	109	21	1171	4.E+00	3.E-01	6.E-02
BIOCARTA	m_eifPathway:Eukaryotic protein translation	5	0.914076782	2.E-03 13669, 217869, 13664, 13629, 67204, 1	109	7	1171	8.E+00	3.E-01	6.E-02
BIOCARTA	m_gleevecPathway:Inhibition of Cellular Proliferation by Gleevec	8	1.462522852	2.E-03 18708, 20846, 14784, 20662, 16476, 12	109	22	1171	4.E+00	4.E-01	6.E-02
BIOCARTA	m_pdgfrPathway:PDGF Signaling Pathway	9	1.645338208	3.E-03 20848, 18708, 20846, 14784, 20662, 16	109	28	1171	3.E+00	4.E-01	6.E-02
BIOCARTA	m_TPOPathway:TPO Signaling Pathway	8	1.462522852	3.E-03 20848, 18708, 20846, 14784, 20662, 16	109	23	1171	4.E+00	5.E-01	6.E-02
BIOCARTA	m_il22bPathway:IL22 Soluble Receptor Signaling Pathway	5	0.914076782	4.E-03 20848, 20846, 12702, 16451, 16154	109	8	1171	7.E+00	5.E-01	6.E-02
BIOCARTA	m_rhoPathway:Rho cell motility signaling pathway	7	1.279707495	5.E-03 20779, 94190, 11856, 11855, 171207, 1	109	19	1171	4.E+00	6.E-01	9.E-02
BIOCARTA	m_HBxPathway:Calcium Signaling by HBx of Hepatitis B virus	5	0.914076782	6.E-03 20779, 14784, 20662, 20416, 12912	109	9	1171	6.E+00	7.E-01	9.E-02
BIOCARTA	m_alternativePathway:Alternative Complement Pathway	5	0.914076782	6.E-03 12266, 12279, 15139, 12417, 12274	109	9	1171	6.E+00	7.E-01	9.E-02
BIOCARTA	m_pyk2Pathway:Links between Pyk2 and Map Kinases	8	1.462522852	9.E-03 20779, 14784, 20662, 16476, 12929, 18	109	27	1171	3.E+00	8.E-01	1.E-01
BIOCARTA	m_igf1Pathway:IGF-1 Signaling Pathway	7	1.279707495	9.E-03 18708, 19247, 14784, 20662, 16476, 20	109	21	1171	4.E+00	8.E-01	1.E-01
BIOCARTA	m_AtrPathway:Angiotensin II mediated activation of JNK Pathway	8	1.462522852	1.E-02 13649, 20779, 14784, 20662, 16476, 18	109	28	1171	3.E+00	9.E-01	1.E-01
BIOCARTA	m_spryPathway:Sprouty regulation of tyrosine kinase signals	6	1.096892139	1.E-02 13649, 20779, 14784, 20662, 20416, 13	109	16	1171	4.E+00	9.E-01	1.E-01
BIOCARTA	m_circadianPathway:Circadian Rhythms	4	0.731261426	1.E-02 11865, 12753, 12952, 18626	109	6	1171	7.E+00	9.E-01	1.E-01
BIOCARTA	m_integrinPathway:Integrin Signaling Pathway	8	1.462522852	1.E-02 20779, 14784, 20662, 16476, 12929, 10	109	29	1171	3.E+00	9.E-01	1.E-01
BIOCARTA	m_il2rbPathway:IL-2 Receptor Beta Chain in T cell Activation	9	1.645338208	1.E-02 18708, 15170, 13555, 12702, 14784, 20	109	36	1171	3.E+00	9.E-01	1.E-01



BIOCARTA	m_ghPathway:Growth Hormone Signaling Pathway	7	1.279707495	2.E-02 18708, 15170, 14784, 20662, 20416, 164	109	25	1171	3.E+00	1.E+00	2.E-01
BIOCARTA	m_fcer1Pathway:Fc Epsilon Receptor I Signaling in Mast Cells	8	1.462522852	2.E-02 18708, 18783, 22324, 14784, 20662, 164	109	32	1171	3.E+00	1.E+00	2.E-01
BIOCARTA	m_classicPathway:Classical Complement Pathway	5	0.914076782	3.E-02 12266, 12279, 15139, 12417, 12274	109	13	1171	4.E+00	1.E+00	2.E-01
BIOCARTA	m_lectinPathway:Lectin Induced Complement Pathway	5	0.914076782	3.E-02 12266, 12279, 15139, 12417, 12274	109	13	1171	4.E+00	1.E+00	2.E-01
BIOCARTA	m_igf1mrtorPathway:Skeletal muscle hypertrophy is regulated via AK	6	1.096892139	3.E-02 13684, 18708, 26905, 13665, 67204, 164	109	20	1171	3.E+00	1.E+00	2.E-01
BIOCARTA	m_epoPathway:EPO Signaling Pathway	6	1.096892139	4.E-02 15170, 14784, 20662, 16476, 20416, 164	109	21	1171	3.E+00	1.E+00	3.E-01
BIOCARTA	m_cdc42racPathway:Role of PI3K subunit p85 in regulation of Actin	4	0.731261426	4.E-02 18708, 12540, 18479, 11848	109	9	1171	5.E+00	1.E+00	3.E-01
BIOCARTA	m_insulinPathway:Insulin Signaling Pathway	6	1.096892139	4.E-02 18708, 19247, 14784, 20662, 16476, 204	109	22	1171	3.E+00	1.E+00	3.E-01
BIOCARTA	m_il3Pathway:IL 3 signaling pathway	5	0.914076782	5.E-02 15170, 14784, 20662, 20416, 16452	109	16	1171	3.E+00	1.E+00	3.E-01
BIOCARTA	m_cardiacegfPathway:Role of EGF Receptor Transactivation by GPCR	5	0.914076782	6.E-02 13649, 11489, 16476, 13645, 11848	109	17	1171	3.E+00	1.E+00	3.E-01
BIOCARTA	m_longevityPathway:The IGF-1 Receptor and Longevity	4	0.731261426	7.E-02 18708, 20416, 14600, 16000	109	11	1171	4.E+00	1.E+00	4.E-01
BIOCARTA	m_d4gdiPathway:D4-GDI Signaling Pathway	4	0.731261426	7.E-02 672195, 16476, 11855, 11857, 13063	109	11	1171	4.E+00	1.E+00	4.E-01
BIOCARTA	m_eif2Pathway:Regulation of eIF2	4	0.731261426	7.E-02 217869, 26905, 13665, 67204, 10004761	109	11	1171	4.E+00	1.E+00	4.E-01
BIOCARTA	m_compPathway:Complement Pathway	5	0.914076782	8.E-02 12266, 12279, 15139, 12417, 12274	109	18	1171	3.E+00	1.E+00	4.E-01
BIOCARTA	m_agrPathway:Agrin in Postsynaptic Differentiation	6	1.096892139	8.E-02 73341, 13649, 20779, 16476, 12540, 184	109	26	1171	2.E+00	1.E+00	4.E-01
BIOCARTA	m_arenr2Pathway:Oxidative Stress Induced Gene Expression Via Nr	5	0.914076782	9.E-02 16476, 12912, 18984, 94284, 394436, 1	109	19	1171	3.E+00	1.E+00	4.E-01
BIOCARTA	m_ngfPathway:Nerve growth factor pathway (NGF)	5	0.914076782	9.E-02 18708, 14784, 20662, 16476, 20416	109	19	1171	3.E+00	1.E+00	4.E-01
BIOCARTA	m_ecmPathway:Erk and PI-3 Kinase Are Necessary for Collagen Binc	5	0.914076782	9.E-02 18708, 20779, 11855, 20416, 11848	109	19	1171	3.E+00	1.E+00	4.E-01
BIOCARTA	m_cblPathway:CBL mediated ligand-induced downregulation of EGF	4	0.731261426	9.E-02 13649, 20779, 14784, 13645	109	12	1171	4.E+00	1.E+00	4.E-01
BIOCARTA	mIRESPathway:Internal Ribosome entry pathway	3	0.548446069	1.E-01 13684, 13669, 13681	109	6	1171	5.E+00	1.E+00	4.E-01
BIOCARTA	m_ifngPathway:IFN gamma signaling pathway	3	0.548446069	1.E-01 20846, 16451, 16452	109	6	1171	5.E+00	1.E+00	4.E-01
BIOCARTA	m_ErbB3Pathway:Neuregulin receptor degradation protein-1 Con	3	0.548446069	1.E-01 13649, 13867, 13645	109	6	1171	5.E+00	1.E+00	4.E-01
KEGG_PATHWAY	mmu03010:Ribosome	64	11.70018282	3.E-56 666899, 100048462, 20103, 100044516,	372	89	5738	1.E+01	4.E-54	4.E-54
KEGG_PATHWAY	mmu00190:Oxidative phosphorylation	69	12.6142596	8.E-48 70316, 226646, 100041273, 66377, 1000	372	130	5738	8.E+00	1.E-45	6.E-46
KEGG_PATHWAY	mmu05012:Parkinson's disease	68	12.43144424	1.E-45 70316, 672195, 226646, 100041273, 663	372	133	5738	8.E+00	2.E-43	5.E-44
KEGG_PATHWAY	mmu05010:Alzheimer's disease	68	12.43144424	5.E-35 70316, 226646, 672195, 100041273, 663	372	182	5738	6.E+00	8.E-33	2.E-33
KEGG_PATHWAY	mmu05016:Huntington's disease	68	12.43144424	8.E-35 70316, 672195, 226646, 100041273, 663	372	183	5738	6.E+00	1.E-32	2.E-33
KEGG_PATHWAY	mmu00010:Glycolysis / Gluconeogenesis	35	4.570383912	1.E-12 18746, 68263, 100042746, 15275, 1527	372	68	5738	6.E+00	2.E-10	4.E-11
KEGG_PATHWAY	mmu04062:Chemokine signaling pathway	32	5.850091408	4.E-07 12765, 22324, 20416, 20418, 21844, 18	372	182	5738	3.E+00	7.E-05	1.E-05
KEGG_PATHWAY	mmu05212:Pancreatic cancer	18	3.290676417	2.E-06 12190, 13649, 170758, 13645, 18709, 7	372	72	5738	4.E+00	3.E-04	4.E-05
KEGG_PATHWAY	mmu04722:Neurotrophin signaling pathway	25	4.570383912	2.E-06 19247, 192662, 20416, 11857, 20418, 11	372	130	5738	3.E+00	3.E-04	4.E-05
KEGG_PATHWAY	mmu04260:Cardiac muscle contraction	17	3.10786106	3.E-05 66694, 17705, 17706, 66445, 66142, 17	372	78	5738	3.E+00	4.E-03	4.E-04
KEGG_PATHWAY	mmu05220:Chronic myeloid leukemia	16	2.925045704	8.E-05 11350, 19247, 14389, 12929, 20416, 204	372	76	5738	3.E+00	1.E-02	1.E-03
KEGG_PATHWAY	mmu04710:Circadian rhythm	7	1.279707495	8.E-05 11865, 12753, 12952, 18626, 12953, 186	372	13	5738	8.E+00	1.E-02	1.E-03
KEGG_PATHWAY	mmu00020:Citrate cycle (TCA cycle)	10	1.828153565	1.E-04 68263, 17448, 235339, 18597, 78920, 21	372	31	5738	5.E+00	2.E-02	1.E-03
KEGG_PATHWAY	mmu04012:ErbB signaling pathway	17	3.10786106	1.E-04 11350, 13649, 12929, 18479, 20416, 204	372	87	5738	3.E+00	2.E-02	1.E-03
KEGG_PATHWAY	mmu00030:Pentose phosphate pathway	9	1.645338208	2.E-04 14751, 110639, 230163, 72157, 11676, 1	372	26	5738	5.E+00	2.E-02	2.E-03
KEGG_PATHWAY	mmu00620:Pyruvate metabolism	11	2.010968921	2.E-04 18746, 16828, 68263, 17448, 235339, 11	372	41	5738	4.E+00	3.E-02	2.E-03
KEGG_PATHWAY	mmu05214:Glioma	13	2.376599634	7.E-04 13649, 20416, 20418, 13645, 18709, 18	372	64	5738	3.E+00	1.E-01	6.E-03
KEGG_PATHWAY	mmu00150:Androgen and estrogen metabolism	9	1.645338208	9.E-04 100043456, 56348, 54200, 15493, 1549	372	33	5738	4.E+00	1.E-01	8.E-03
KEGG_PATHWAY	mmu04930:Type II diabetes mellitus	11	2.010968921	1.E-03 18746, 18709, 18708, 18753, 18762, 18	372	49	5738	3.E+00	1.E-01	8.E-03
KEGG_PATHWAY	mmu04510:Focal adhesion	25	4.570383912	2.E-03 13649, 22324, 11855, 20416, 170758, 20	372	198	5738	2.E+00	3.E-01	1.E-02
KEGG_PATHWAY	mmu00140:Steroid hormone biosynthesis	10	1.828153565	2.E-03 100043456, 56348, 13074, 54200, 1549	372	45	5738	3.E+00	3.E-01	1.E-02
KEGG_PATHWAY	mmu04610:Complement and coagulation cascades	13	2.376599634	3.E-03 12266, 12258, 12279, 16644, 69379, 15	372	75	5738	3.E+00	3.E-01	2.E-02
KEGG_PATHWAY	mmu00983:Drug metabolism	10	1.828153565	3.E-03 76654, 80914, 68556, 72269, 22245, 72	372	48	5738	3.E+00	4.E-01	2.E-02
KEGG_PATHWAY	mmu05215:Prostate cancer	14	2.559414991	5.E-03 13649, 12912, 13645, 12914, 18709, 18	372	90	5738	2.E+00	5.E-01	3.E-02
KEGG_PATHWAY	mmu05211:Renal cell carcinoma	12	2.193784278	5.E-03 18709, 18708, 19247, 14784, 20662, 20	372	70	5738	3.E+00	5.E-01	3.E-02
KEGG_PATHWAY	mmu04662:B cell receptor signaling pathway	13	2.376599634	5.E-03 22324, 15170, 57257, 170758, 18709, 1	372	80	5738	3.E+00	5.E-01	3.E-02
KEGG_PATHWAY	mmu05200:Pathways in cancer	34	6.215722121	5.E-03 12190, 22029, 13649, 672195, 170758, 1	372	323	5738	2.E+00	6.E-01	3.E-02
KEGG_PATHWAY	mmu04664:Fc epsilon RI signaling pathway	13	2.376599634	6.E-03 22324, 14389, 57257, 170758, 18709, 11	372	82	5738	2.E+00	6.E-01	3.E-02
KEGG_PATHWAY	mmu05020:Prion diseases	8	1.462522852	6.E-03 12279, 230558, 69379, 19108, 15139, 1	372	35	5738	4.E+00	6.E-01	3.E-02
KEGG_PATHWAY	mmu05223:Non-small cell lung cancer	10	1.828153565	7.E-03 18709, 18708, 13649, 13555, 242705, 1	372	54	5738	3.E+00	7.E-01	4.E-02
KEGG_PATHWAY	mmu00500:Starch and sucrose metabolism	8	1.462522852	7.E-03 14751, 14387, 15275, 72157, 15277, 10	372	36	5738	3.E+00	7.E-01	3.E-02
KEGG_PATHWAY	mmu04910:Insulin signaling pathway	18	3.290676417	7.E-03 13684, 12929, 15275, 15277, 20416, 204	372	138	5738	2.E+00	7.E-01	3.E-02
KEGG_PATHWAY	mmu04520:Adherens junction	12	2.193784278	9.E-03 15170, 19354, 13649, 21813, 20779, 131	372	76	5738	2.E+00	7.E-01	4.E-02
KEGG_PATHWAY	mmu04650:Natural killer cell mediated cytotoxicity	16	2.925045704	1.E-02 22324, 15170, 19247, 57257, 18479, 204	372	122	5738	2.E+00	8.E-01	5.E-02
KEGG_PATHWAY	mmu05322:Systemic lupus erythematosus	14	2.559414991	1.E-02 621893, 12266, 12279, 15078, 69379, 11	372	103	5738	2.E+00	9.E-01	6.E-02
KEGG_PATHWAY	mmu04630:Jak-STAT signaling pathway	18	3.290676417	2.E-02 15170, 19247, 12914, 18709, 20848, 16	372	152	5738	2.E+00	9.E-01	7.E-02
KEGG_PATHWAY	mmu04670:Leukocyte transendothelial migration	15	2.742230347	2.E-02 22324, 69524, 19247, 14678, 17972, 57	372	119	5738	2.E+00	1.E+00	8.E-02



KEGG_PATHWAY	mmu05210:Colorectal cancer	12	2.193784278	2.E-02 672195, 13649, 170758, 18709, 19354, 1	372	86	5738	2.E+00	1.E+00	8.E-02
KEGG_PATHWAY	mmu04666:Fc gamma R-mediated phagocytosis	13	2.376599634	2.E-02 22324, 14389, 12929, 57257, 18479, 18	372	98	5738	2.E+00	1.E+00	9.E-02
KEGG_PATHWAY	mmu00052:Galactose metabolism	6	1.096892139	3.E-02 14387, 15275, 72157, 15277, 103988, 2	372	27	5738	3.E+00	1.E+00	1.E-01
KEGG_PATHWAY	mmu00051:Fructose and mannose metabolism	7	1.279707495	3.E-02 15275, 21991, 230163, 15277, 11676, 1	372	37	5738	3.E+00	1.E+00	1.E-01
KEGG_PATHWAY	mmu04810:Regulation of actin cytoskeleton	22	4.021937843	4.E-02 14163, 13649, 22324, 14674, 12929, 57	372	217	5738	2.E+00	1.E+00	1.E-01
KEGG_PATHWAY	mmu00640:Propanoate metabolism	6	1.096892139	4.E-02 16828, 74147, 73724, 68738, 16833, 16	372	30	5738	3.E+00	1.E+00	1.E-01
KEGG_PATHWAY	mmu00380:Tryptophan metabolism	7	1.279707495	4.E-02 98256, 71562, 15107, 74147, 15930, 56	372	40	5738	3.E+00	1.E+00	1.E-01
KEGG_PATHWAY	mmu00240:Pyrimidine metabolism	12	2.193784278	4.E-02 76654, 80914, 20020, 21915, 68556, 72	372	96	5738	2.E+00	1.E+00	1.E-01
KEGG_PATHWAY	mmu05213:Endometrial cancer	8	1.462522852	5.E-02 18709, 18708, 13649, 13866, 14784, 20	372	52	5738	2.E+00	1.E+00	1.E-01
KEGG_PATHWAY	mmu04010:MAPK signaling pathway	25	4.570383912	6.E-02 13649, 170758, 13645, 18205, 18783, 2	372	265	5738	1.E+00	1.E+00	2.E-01
KEGG_PATHWAY	mmu00280:Valine, leucine and isoleucine degradation	7	1.279707495	7.E-02 66885, 15107, 11409, 74147, 73724, 13	372	46	5738	2.E+00	1.E+00	2.E-01
KEGG_PATHWAY	mmu04660:T cell receptor signaling pathway	13	2.376599634	8.E-02 22324, 15170, 57257, 18479, 11848, 18	372	118	5738	2.E+00	1.E+00	2.E-01
KEGG_PATHWAY	mmu00650:Butanoate metabolism	6	1.096892139	9.E-02 68263, 15107, 11409, 74147, 18597, 18	372	37	5738	3.E+00	1.E+00	2.E-01
KEGG_PATHWAY	mmu00100:Steroid biosynthesis	4	0.731261426	9.E-02 13121, 14137, 16987, 20775	372	17	5738	4.E+00	1.E+00	2.E-01
KEGG_PATHWAY	mmu04912:GnRH signaling pathway	11	2.010968921	9.E-02 18783, 13649, 18753, 20779, 14784, 20	372	97	5738	2.E+00	1.E+00	3.E-01
KEGG_PATHWAY	mmu05222:Small cell lung cancer	10	1.828153565	1.E-01 18709, 22029, 18708, 18126, 672195, 1	372	85	5738	2.E+00	1.E+00	2.E-01

Annotation Cluster 1	Enrichment Score: 38.77025233959643										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_BP_FAT	GO:0006091~generation of precursor metabolites and energy	94	17.18464351	2.E-68	18746, 226646, 66377, 100041835, 1770	491	261	13588	1.E+01	3.E-65	3.E-65
SP_PIR_KEYWORDS	respiratory chain	52	9.506398537	1.E-67	70316, 672195, 226646, 100041273, 66377, 100041835, 1770	541	62	17854	3.E+01	4.E-65	4.E-65
GOTERM_CC_FAT	GO:0070469~respiratory chain	52	9.506398537	1.E-63	70316, 672195, 226646, 100041273, 66377, 100041835, 1770	419	65	12504	2.E+01	3.E-61	3.E-61
KEGG_PATHWAY	mmu00190:Oxidative phosphorylation	69	12.6142596	8.E-48	70316, 226646, 100041273, 66377, 100041835, 1770	372	130	5738	8.E+00	1.E-45	6.E-46
SP_PIR_KEYWORDS	mitochondrion inner membrane	62	11.3345521	6.E-47	226646, 100041273, 66377, 22227, 5950	541	183	17854	1.E+01	2.E-44	5.E-45
SP_PIR_KEYWORDS	electron transport	49	8.957952468	3.E-46	70316, 672195, 226646, 100041273, 66377, 100041835, 1770	541	100	17854	2.E+01	1.E-43	2.E-44
KEGG_PATHWAY	mmu05012:Parkinson's disease	68	12.43144424	1.E-45	70316, 672195, 226646, 100041273, 66377, 100041835, 1770	372	133	5738	8.E+00	2.E-43	5.E-44
GOTERM_CC_FAT	GO:0005743~mitochondrial inner membrane	76	13.89396709	1.E-45	226646, 100041273, 66377, 100041835, 1770	419	296	12504	8.E+00	4.E-43	1.E-43
GOTERM_CC_FAT	GO:0019866~organelle inner membrane	77	14.07678245	7.E-45	226646, 100041273, 66377, 100041835, 1770	419	312	12504	7.E+00	2.E-42	5.E-43
GOTERM_BP_FAT	GO:0022900~electron transport chain	51	9.323583181	2.E-42	70316, 672195, 226646, 100041273, 66377, 100041835, 1770	491	112	13588	1.E+01	3.E-39	1.E-39
GOTERM_CC_FAT	GO:0031966~mitochondrial membrane	79	14.44241316	2.E-41	226646, 100041273, 66377, 100041835, 1770	419	368	12504	6.E+00	7.E-39	1.E-39
SP_PIR_KEYWORDS	mitochondrion	108	19.7440585	8.E-41	226646, 66885, 66377, 100041835, 2430	541	790	17854	5.E+00	3.E-38	4.E-39
GOTERM_CC_FAT	GO:0044429~mitochondrial part	91	16.63619744	5.E-40	66885, 226646, 66377, 100041835, 1420	419	524	12504	5.E+00	2.E-37	3.E-38
GOTERM_CC_FAT	GO:0005740~mitochondrial envelope	79	14.44241316	2.E-39	226646, 100041273, 66377, 100041835, 1770	419	391	12504	6.E+00	7.E-37	1.E-37
GOTERM_CC_FAT	GO:0031967~organelle envelope	88	16.08775137	2.E-36	226646, 66377, 100041835, 14270, 1770	419	540	12504	5.E+00	6.E-34	8.E-35
GOTERM_CC_FAT	GO:0031975~envelope	88	16.08775137	3.E-36	226646, 66377, 100041835, 14270, 1770	419	542	12504	5.E+00	9.E-34	1.E-34
KEGG_PATHWAY	mmu05010:Alzheimer's disease	68	12.43144424	5.E-35	70316, 226646, 672195, 100041273, 66377, 100041835, 1770	372	182	5738	6.E+00	8.E-33	2.E-33
KEGG_PATHWAY	mmu05016:Huntington's disease	68	12.43144424	8.E-35	70316, 672195, 226646, 100041273, 66377, 100041835, 1770	372	183	5738	6.E+00	1.E-32	2.E-33
GOTERM_CC_FAT	GO:0005739~mitochondrion	127	23.21755027	2.E-29	18746, 226646, 66885, 66377, 10004450	419	1322	12504	3.E+00	6.E-27	6.E-28
GOTERM_BP_FAT	GO:0055114~oxidation reduction	91	16.63619744	2.E-28	66885, 226646, 66377, 56348, 17705, 100041835, 1770	491	672	13588	4.E+00	4.E-25	1.E-25
GOTERM_CC_FAT	GO:0031090~organelle membrane	86	15.72212066	4.E-22	226646, 100041273, 66377, 100041835, 1770	419	809	12504	3.E+00	1.E-19	1.E-20
SP_PIR_KEYWORDS	transit peptide	57	10.42047532	2.E-19	70316, 66885, 226646, 68263, 66377, 100041835, 1770	541	457	17854	4.E+00	9.E-17	6.E-18
UP_SEQ_FEATURE	transit peptide:Mitochondrion	57	10.42047532	9.E-18	70316, 66885, 226646, 68263, 66377, 100041835, 1770	537	449	16021	4.E+00	1.E-14	4.E-15
SP_PIR_KEYWORDS	transport	84	15.35648995	3.E-07	70316, 226646, 672195, 100041273, 66377, 100041835, 1770	541	1571	17854	2.E+00	1.E-04	5.E-06

Annotation Cluster 2	Enrichment Score: 37.33499997534053										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
SMART	SM00324:RhoGAP	45	8.226691042	6.E-54	117600, 94190, 228482, 243362, 11856,	248	67	9131	2.E+01	8.E-52	8.E-52
INTERPRO	IPR000198:RhoGAP	45	8.226691042	5.E-51	117600, 94190, 228482, 243362, 11856,	535	67	17763	2.E+01	5.E-48	5.E-48
UP_SEQ_FEATURE	domain:Rho-GAP	41	7.495429616	2.E-46	117600, 228482, 94190, 243362, 11856,	537	57	16021	2.E+01	3.E-43	3.E-43
GOTERM_MF_FAT	GO:0030695~GTPase regulator activity	74	13.52833638	5.E-35	13667, 22324, 228482, 94190, 192662, 1	476	361	13288	6.E+00	2.E-32	1.E-32



SP_PIR_KEYWORDS	GTPase activation	46	8.409506399	1.E-34	117600, 94190, 228482, 192662, 24336:	541	136	17854	1.E+01	4.E-32	5.E-33
GOTERM_MF_FAT	GO:0060589~nucleoside-triphosphatase regulator activity	74	13.52833638	2.E-34	13667, 22324, 228482, 94190, 192662, :	476	367	13288	6.E+00	8.E-32	3.E-32
GOTERM_MF_FAT	GO:0005096~GTPase activator activity	48	8.775137112	1.E-26	117600, 94190, 228482, 192662, 24336:	476	192	13288	7.E+00	7.E-24	1.E-24
GOTERM_MF_FAT	GO:0008047~enzyme activator activity	49	8.957952468	3.E-22	94190, 228482, 243362, 192662, 14270,	476	249	13288	5.E+00	1.E-19	1.E-20

Annotation Cluster 4	Enrichment Score: 36.729385477891206										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
SP_PIR_KEYWORDS	respiratory chain	52	9.506398537	1.E-67	70316, 672195, 226646, 100041273, 66:	541	62	17854	3.E+01	4.E-65	4.E-65
GOTERM_CC_FAT	GO:0070469~respiratory chain	52	9.506398537	1.E-63	70316, 672195, 226646, 100041273, 66:	419	65	12504	2.E+01	3.E-61	3.E-61
SP_PIR_KEYWORDS	electron transport	49	8.957952468	3.E-46	70316, 672195, 226646, 100041273, 66:	541	100	17854	2.E+01	1.E-43	2.E-44
GOTERM_BP_FAT	GO:0022900~electron transport chain	51	9.323583181	2.E-42	70316, 672195, 226646, 100041273, 66:	491	112	13588	1.E+01	3.E-39	1.E-39
GOTERM_MF_FAT	GO:0050136~NADH dehydrogenase (quinone) activity	22	4.021937843	5.E-28	226646, 100041273, 66416, 67184, 177:	476	24	13288	3.E+01	2.E-25	6.E-26
GOTERM_MF_FAT	GO:0008137~NADH dehydrogenase (ubiquinone) activity	22	4.021937843	5.E-28	226646, 100041273, 66416, 67184, 177:	476	24	13288	3.E+01	2.E-25	6.E-26
GOTERM_MF_FAT	GO:0003954~NADH dehydrogenase activity	22	4.021937843	5.E-28	226646, 100041273, 66416, 67184, 177:	476	24	13288	3.E+01	2.E-25	6.E-26
GOTERM_MF_FAT	GO:0016655~oxidoreductase activity, acting on NADH or NADPH, c	22	4.021937843	6.E-26	226646, 100041273, 66416, 67184, 177:	476	27	13288	2.E+01	3.E-23	5.E-24
GOTERM_MF_FAT	GO:0016651~oxidoreductase activity, acting on NADH or NADPH	26	4.753199269	4.E-23	226646, 100041273, 66416, 67184, 177:	476	51	13288	1.E+01	2.E-20	2.E-21
SP_PIR_KEYWORDS	ubiquinone	18	3.290676417	3.E-21	70316, 226646, 17718, 17719, 68349, 6:	541	24	17854	2.E+01	1.E-18	9.E-20

Annotation Cluster 6		Enrichment Score: 17.001426294210617									
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_MF_FAT	GO:0030695~GTPase regulator activity	74	13.52833638		5.E-35 13667, 22324, 228482, 94190, 192662, :	476	361	13288	6.E+00	2.E-32	1.E-32
GOTERM_MF_FAT	GO:0060589~nucleoside-triphosphatase regulator activity	74	13.52833638		2.E-34 13667, 22324, 228482, 94190, 192662, :	476	367	13288	6.E+00	8.E-32	3.E-32
SMART	SM00325:RhoGEF	25	4.570383912		1.E-21 22324, 13605, 16800, 442801, 53972, 2,	248	65	9131	1.E+01	2.E-19	8.E-20
INTERPRO	IPR000219:DbI homology (DH) domain	25	4.570383912		2.E-20 22324, 13605, 16800, 442801, 53972, 2,	535	65	17763	1.E+01	2.E-17	1.E-17
GOTERM_BP_FAT	GO:0035023~regulation of Rho protein signal transduction	28	5.118829982		1.E-18 22324, 13605, 16800, 442801, 53972, 2,	491	86	13588	9.E+00	2.E-15	2.E-16
UP_SEQ_FEATURE	domain:DH	23	4.204753199		2.E-18 14163, 277360, 22324, 13605, 101497, :	537	56	16021	1.E+01	2.E-15	1.E-15
GOTERM_MF_FAT	GO:0005083~small GTPase regulator activity	42	7.678244973		2.E-18 117600, 22324, 192662, 13605, 11856, :	476	223	13288	5.E+00	1.E-15	9.E-17
GOTERM_MF_FAT	GO:0005089~Rho guanyl-nucleotide exchange factor activity	25	4.570383912		1.E-17 22324, 13605, 16800, 442801, 53972, 2,	476	71	13288	1.E+01	6.E-15	4.E-16
INTERPRO	IPR001331:Guanine-nucleotide dissociation stimulator, CDC24, cons	21	3.839122486		2.E-17 14163, 277360, 22324, 13605, 101497, :	535	53	17763	1.E+01	2.E-14	6.E-15
GOTERM_MF_FAT	GO:0005088~Ras guanyl-nucleotide exchange factor activity	25	4.570383912		7.E-16 22324, 13605, 16800, 442801, 53972, 2,	476	83	13288	8.E+00	4.E-13	2.E-14
SMART	SM00233:PH	36	6.581352834		2.E-15 22324, 94190, 16800, 75415, 53972, 21,	248	261	9131	5.E+00	3.E-13	7.E-14
SP_PIR_KEYWORDS	guanine-nucleotide releasing factor	25	4.570383912		3.E-15 22324, 13605, 16800, 442801, 53972, 2,	541	102	17854	8.E+00	1.E-12	7.E-14
GOTERM_MF_FAT	GO:0005085~guanyl-nucleotide exchange factor activity	30	5.484460695		4.E-14 22324, 13667, 13605, 442801, 16800, 5:	476	147	13288	6.E+00	2.E-11	1.E-12
INTERPRO	IPR011993:Pleckstrin homology-type	38	6.946983547		9.E-14 94190, 16800, 75415, 20416, 53972, 21,	535	289	17763	4.E+00	9.E-11	2.E-11
INTERPRO	IPR001849:Pleckstrin homology	36	6.581352834		1.E-13 22324, 94190, 16800, 75415, 53972, 21,	535	261	17763	5.E+00	1.E-10	2.E-11
GOTERM_BP_FAT	GO:0046578~regulation of Ras protein signal transduction	30	5.484460695		1.E-11 22324, 13605, 442801, 16800, 53972, 2,	491	181	13588	5.E+00	3.E-08	1.E-09
GOTERM_BP_FAT	GO:0051056~regulation of small GTPase mediated signal transducti	30	5.484460695		3.E-09 22324, 13605, 442801, 16800, 53972, 2,	491	228	13588	4.E+00	7.E-06	2.E-07



UP_SEQ_FEATURE	domain:PH	25	4.570383912	7.E-08	22324, 94190, 13605, 16800, 75415, 530	537	202	16021	4.E+00	1.E-04	2.E-05
Annotation Cluster 7											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
SP_PIR_KEYWORDS	glycolysis	23	4.204753199	7.E-23	18746, 68263, 100042746, 15275, 1527	541	42	17854	2.E+01	3.E-20	2.E-21
GOTERM_BP_FAT	GO:0006096~glycolysis	24	4.387568556	4.E-22	18746, 68263, 100042746, 15275, 1527	491	44	13588	2.E+01	8.E-19	1.E-19
GOTERM_BP_FAT	GO:0006007~glucose catabolic process	24	4.387568556	5.E-20	18746, 68263, 100042746, 15275, 1527	491	52	13588	1.E+01	1.E-16	1.E-17
GOTERM_BP_FAT	GO:0019320~hexose catabolic process	24	4.387568556	5.E-20	18746, 68263, 100042746, 15275, 1527	491	52	13588	1.E+01	1.E-16	1.E-17
GOTERM_BP_FAT	GO:0044275~cellular carbohydrate catabolic process	25	4.570383912	1.E-19	18746, 68263, 100042746, 15275, 1527	491	60	13588	1.E+01	3.E-16	4.E-17
GOTERM_BP_FAT	GO:0046365~monosaccharide catabolic process	24	4.387568556	1.E-19	18746, 68263, 100042746, 15275, 1527	491	54	13588	1.E+01	3.E-16	3.E-17
GOTERM_BP_FAT	GO:0046164~alcohol catabolic process	24	4.387568556	2.E-17	18746, 68263, 100042746, 15275, 1527	491	65	13588	1.E+01	4.E-14	3.E-15
GOTERM_BP_FAT	GO:0016052~carbohydrate catabolic process	25	4.570383912	4.E-16	18746, 68263, 100042746, 15275, 1527	491	81	13588	9.E+00	9.E-13	7.E-14
GOTERM_BP_FAT	GO:0006006~glucose metabolic process	29	5.301645338	1.E-13	18746, 68263, 100042746, 15275, 1527	491	140	13588	6.E+00	2.E-10	1.E-11
KEGG_PATHWAY	mmu00010:Glycolysis / Gluconeogenesis	25	4.570383912	1.E-12	18746, 68263, 100042746, 15275, 1527	372	68	5738	6.E+00	2.E-10	4.E-11
GOTERM_BP_FAT	GO:0019318~hexose metabolic process	29	5.301645338	1.E-11	18746, 68263, 100042746, 15275, 1527	491	169	13588	5.E+00	3.E-08	1.E-09
GOTERM_BP_FAT	GO:0005996~monosaccharide metabolic process	30	5.484460695	5.E-11	18746, 68263, 100042746, 15275, 1527	491	191	13588	4.E+00	1.E-07	4.E-09
UP_SEQ_FEATURE	binding_site:Substrate	23	4.204753199	1.E-04	18746, 66885, 22245, 56348, 15929, 11	537	275	16021	2.E+00	2.E-01	2.E-02
KEGG_PATHWAY	mmu00620:Pyruvate metabolism	11	2.010968921	2.E-04	18746, 16828, 68263, 17448, 235339, 1	372	41	5738	4.E+00	3.E-02	2.E-03
Annotation Cluster 8											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_BP_FAT	GO:0006119~oxidative phosphorylation	27	4.936014625	4.E-23	228033, 66416, 100041835, 66043, 1770	491	56	13588	1.E+01	8.E-20	2.E-20
GOTERM_BP_FAT	GO:0042773~ATP synthesis coupled electron transport	13	2.376599634	6.E-14	66416, 17719, 675851, 17705, 17706, 1	491	18	13588	2.E+01	1.E-10	8.E-12
GOTERM_BP_FAT	GO:0022904~respiratory electron transport chain	15	2.742230347	1.E-13	66416, 17719, 675851, 17705, 17706, 1	491	28	13588	1.E+01	3.E-10	2.E-11
GOTERM_BP_FAT	GO:0045333~cellular respiration	19	3.473491773	1.E-12	66416, 17448, 17719, 675851, 17705, 1	491	59	13588	9.E+00	3.E-09	1.E-10
GOTERM_BP_FAT	GO:0042775~mitochondrial ATP synthesis coupled electron transpc	10	1.828153565	2.E-10	67530, 17719, 675851, 67264, 17705, 1	491	14	13588	2.E+01	3.E-07	1.E-08
GOTERM_BP_FAT	GO:0015980~energy derivation by oxidation of organic compounds	21	3.839122486	2.E-10	17448, 66416, 17719, 675851, 17705, 1	491	98	13588	6.E+00	5.E-07	2.E-08
GOTERM_BP_FAT	GO:0006120~mitochondrial electron transport, NADH to ubiquinon	5	0.914076782	8.E-06	17719, 675851, 67264, 17717, 13382, 6	491	5	13588	3.E+01	2.E-02	3.E-04
Annotation Cluster 9											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_CC_FAT	GO:0033279~ribosomal subunit	20	3.65630713	2.E-13	100048462, 20103, 100039355, 100043	419	66	12504	9.E+00	7.E-11	5.E-12
GOTERM_CC_FAT	GO:0022626~cytosolic ribosome	12	2.193784278	1.E-12	100048462, 19944, 100042832, 20103, :	419	18	12504	2.E+01	4.E-10	2.E-11
GOTERM_CC_FAT	GO:0044445~cytosolic part	16	2.925045704	2.E-09	100048462, 20103, 100043391, 18709, :	419	63	12504	8.E+00	5.E-07	2.E-08
GOTERM_CC_FAT	GO:0022625~cytosolic large ribosomal subunit	6	1.096892139	8.E-07	100048462, 20005, 110954, 100042832,	419	7	12504	3.E+01	2.E-04	9.E-06
GOTERM_CC_FAT	GO:0015934~large ribosomal subunit	9	1.645338208	4.E-05	100048462, 100042832, 19921, 100043:	419	39	12504	7.E+00	1.E-02	4.E-04
Annotation Cluster 10											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
SMART	SM00252:SH2	22	4.021937843	1.E-12	11350, 15170, 22324, 19247, 12929, 57:	248	111	9131	7.E+00	2.E-10	4.E-11
SP_PIR_KEYWORDS	SH2 domain	22	4.021937843	3.E-12	11350, 15170, 22324, 19247, 12929, 57:	541	103	17854	7.E+00	1.E-09	6.E-11
INTERPRO	IPR000980:SH2 motif	22	4.021937843	1.E-11	11350, 15170, 22324, 19247, 12929, 57:	535	111	17763	7.E+00	1.E-08	2.E-09
UP_SEQ_FEATURE	domain:SH2	17	3.10786106	4.E-08	11350, 22324, 12929, 57257, 20416, 20:	537	90	16021	6.E+00	6.E-05	1.E-05
KEGG_PATHWAY	mmu04650:Natural killer cell mediated cytotoxicity	16	2.925045704	1.E-02	22324, 15170, 19247, 57257, 18479, 20:	372	122	5738	2.E+00	8.E-01	5.E-02
Annotation Cluster 11											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
SP_PIR_KEYWORDS	nad	29	5.301645338	2.E-13	226646, 100042746, 15929, 56847, 177:	541	169	17854	6.E+00	7.E-11	4.E-12
UP_SEQ_FEATURE	binding_site:NAD	12	2.193784278	2.E-07	15107, 100042746, 17448, 13382, 1000:	537	46	16021	8.E+00	3.E-04	5.E-05
UP_SEQ_FEATURE	nucleotide phosphate-binding region:NAD	10	1.828153565	7.E-04	15107, 100042746, 17448, 15929, 5684:	537	73	16021	4.E+00	6.E-01	6.E-02
Annotation Cluster 12											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_CC_FAT	GO:0005746~mitochondrial respiratory chain	10	1.828153565	2.E-10	226646, 67184, 67264, 68349, 12862, 2:	419	15	12504	2.E+01	6.E-08	3.E-09
GOTERM_CC_FAT	GO:0005747~mitochondrial respiratory chain complex I	6	1.096892139	2.E-07	226646, 67264, 68349, 227197, 17993, :	419	6	12504	3.E+01	7.E-05	3.E-06
GOTERM_CC_FAT	GO:0045271~respiratory chain complex I	6	1.096892139	2.E-07	226646, 67264, 68349, 227197, 17993, :	419	6	12504	3.E+01	7.E-05	3.E-06
GOTERM_CC_FAT	GO:0030964~NADH dehydrogenase complex	6	1.096892139	2.E-07	226646, 67264, 68349, 227197, 17993, :	419	6	12504	3.E+01	7.E-05	3.E-06
Annotation Cluster 13											
Enrichment Score: 6.725598209536165											







GOTERM_BP_FAT	GO:0009141~nucleoside triphosphate metabolic process	17	3.10786106	4.E-06	228033, 100041835, 67126, 66043, 1770	491	115	13588	4.E+00	7.E-03	2.E-04
SP_PIR_KEYWORDS	cf(1)	5	0.914076782	4.E-06	66043, 67126, 11947, 11949, 11946	541	5	17854	3.E+01	2.E-03	5.E-05
GOTERM_MF_FAT	GO:0046933~hydrogen ion transporting ATP synthase activity, rota	6	1.096892139	2.E-05	66043, 67126, 11947, 11949, 28080, 100	476	11	13288	2.E+01	1.E-02	4.E-04
GOTERM_BP_FAT	GO:0006164~purine nucleotide biosynthetic process	17	3.10786106	3.E-05	228033, 100041835, 67126, 66043, 1770	491	137	13588	3.E+00	7.E-02	1.E-03
GOTERM_BP_FAT	GO:0006163~purine nucleotide metabolic process	18	3.290676417	7.E-05	228033, 100041835, 67126, 66043, 1770	491	160	13588	3.E+00	1.E-01	3.E-03
GOTERM_MF_FAT	GO:0046961~proton-transporting ATPase activity, rotational mecha	6	1.096892139	1.E-04	66043, 67126, 11947, 11949, 28080, 100	476	15	13288	1.E+01	6.E-02	2.E-03
GOTERM_CC_FAT	GO:0033178~proton-transporting two-sector ATPase complex, cata	6	1.096892139	2.E-04	66043, 67126, 11947, 11949, 28080, 100	419	17	12504	1.E+01	5.E-02	2.E-03
GOTERM_BP_FAT	GO:0044271~nitrogen compound biosynthetic process	24	4.387568556	6.E-04	228033, 21915, 100041835, 66043, 1770	491	302	13588	2.E+00	7.E-01	2.E-02
GOTERM_MF_FAT	GO:0019829~cation-transporting ATPase activity	6	1.096892139	2.E-03	66043, 67126, 11947, 11949, 28080, 100	476	25	13288	7.E+00	6.E-01	2.E-02
GOTERM_MF_FAT	GO:0042625~ATPase activity, coupled to transmembrane movemen	7	1.279707495	4.E-02	100042348, 66043, 67126, 11947, 27425	476	69	13288	3.E+00	1.E+00	3.E-01
GOTERM_MF_FAT	GO:0008553~hydrogen-exporting ATPase activity, phosphorylative r	3	0.548446069	9.E-02	100042348, 67126, 11947, 27425	476	14	13288	6.E+00	1.E+00	5.E-01
GOTERM_MF_FAT	GO:0016820~hydrolase activity, acting on acid anhydrides, catalyzi	7	1.279707495	1.E-01	100042348, 66043, 67126, 11947, 27425	476	97	13288	2.E+00	1.E+00	6.E-01
GOTERM_MF_FAT	GO:0042626~ATPase activity, coupled to transmembrane movemen	7	1.279707495	1.E-01	100042348, 66043, 67126, 11947, 27425	476	97	13288	2.E+00	1.E+00	6.E-01
GOTERM_MF_FAT	GO:0043492~ATPase activity, coupled to movement of substances	7	1.279707495	1.E-01	100042348, 66043, 67126, 11947, 27425	476	97	13288	2.E+00	1.E+00	6.E-01
GOTERM_BP_FAT	GO:0015672~monovalent inorganic cation transport	16	2.925045704	1.E-01	228033, 100041835, 67126, 66043, 1770	491	303	13588	1.E+00	1.E+00	8.E-01
GOTERM_MF_FAT	GO:0042623~ATPase activity, coupled	12	2.193784278	2.E-01	67126, 66043, 27425, 100047429, 17925	476	223	13288	2.E+00	1.E+00	7.E-01
GOTERM_MF_FAT	GO:0015405~P-P-bond-hydrolysis-driven transmembrane transport	7	1.279707495	2.E-01	100042348, 66043, 67126, 11947, 27425	476	107	13288	2.E+00	1.E+00	7.E-01
GOTERM_MF_FAT	GO:0015399~primary active transmembrane transporter activity	7	1.279707495	2.E-01	100042348, 66043, 67126, 11947, 27425	476	108	13288	2.E+00	1.E+00	7.E-01
GOTERM_MF_FAT	GO:0016887~ATPase activity	12	2.193784278	4.E-01	67126, 66043, 27425, 100047429, 17925	476	281	13288	1.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0055085~transmembrane transport	18	3.290676417	5.E-01	228033, 100041835, 22227, 67126, 66043	491	460	13588	1.E+00	1.E+00	1.E+00
SP_PIR_KEYWORDS	ion transport	17	3.10786106	6.E-01	26934, 228033, 100041835, 67126, 66043	541	543	17854	1.E+00	1.E+00	9.E-01
GOTERM_MF_FAT	GO:0015662~ATPase activity, coupled to transmembrane movemen	3	0.548446069	6.E-01	100042348, 67126, 11947, 27425	476	57	13288	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0006812~cation transport	16	2.925045704	8.E-01	228033, 100041835, 67126, 66043, 1770	491	515	13588	9.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0006811~ion transport	18	3.290676417	1.E+00	26934, 228033, 100041835, 67126, 66043	491	712	13588	7.E-01	1.E+00	1.E+00
Annotation Cluster 15	Enrichment Score: 5.744088490606012										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
SP_PIR_KEYWORDS	rrna-binding	9	1.645338208	4.E-09	26961, 20084, 19983, 100043295, 6728	541	15	17854	2.E+01	1.E-06	5.E-08
GOTERM_MF_FAT	GO:0019843~rRNA binding	10	1.828153565	7.E-08	26961, 100042832, 20102, 268449, 1000	476	24	13288	1.E+01	4.E-05	2.E-06
SP_PIR_KEYWORDS	rna-binding	24	4.387568556	2.E-02	13684, 26961, 27041, 53356, 19934, 20	541	485	17854	2.E+00	1.E+00	1.E-01
Annotation Cluster 16	Enrichment Score: 5.422770109600319										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_MF_FAT	Term: Rho/Ras/Rac GTPase activator activity										
GOTERM_MF_FAT	GO:0005100~Rho GTPase activator activity	10	1.828153565	3.E-09	117600, 71709, 17925, 50768, 228359, 7	476	18	13288	2.E+01	2.E-06	9.E-08
GOTERM_MF_FAT	GO:0005099~Ras GTPase activator activity	11	2.010968921	9.E-05	117600, 71709, 17925, 50768, 228359, 7	476	65	13288	5.E+00	5.E-02	2.E-03
GOTERM_MF_FAT	GO:0030675~Rac GTPase activator activity	5	0.914076782	2.E-04	228359, 76117, 19765, 233071, 106952	476	9	13288	2.E+01	8.E-02	3.E-03
Annotation Cluster 17	Enrichment Score: 5.069580849538957										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
SMART	SM00326:SH3	22	4.021937843	2.E-07	117600, 11350, 22324, 17972, 12929, 14	248	211	9131	4.E+00	3.E-05	5.E-06
INTERPRO	IPR001452:Src homology-3 domain	22	4.021937843	2.E-06	117600, 11350, 22324, 17972, 12929, 14	535	211	17763	3.E+00	2.E-03	1.E-04
SP_PIR_KEYWORDS	sh3 domain	21	3.839122486	4.E-06	117600, 11350, 22324, 17972, 12929, 14	541	204	17854	3.E+00	2.E-03	5.E-05
UP_SEQ_FEATURE	domain:SH3	14	2.559414991	3.E-03	117600, 11350, 17972, 14270, 75415, 5	537	163	16021	3.E+00	1.E+00	2.E-01
Annotation Cluster 18	Enrichment Score: 4.949200698116412										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_MF_FAT	GO:0016675~oxidoreductase activity, acting on heme group of don	9	1.645338208	8.E-07	12868, 12858, 333182, 17705, 17706, 1	476	23	13288	1.E+01	4.E-04	2.E-05
GOTERM_MF_FAT	GO:0016676~oxidoreductase activity, acting on heme group of don	9	1.645338208	8.E-07	12868, 12858, 333182, 17705, 17706, 1	476	23	13288	1.E+01	4.E-04	2.E-05
GOTERM_MF_FAT	GO:0015002~heme-copper terminal oxidase activity	9	1.645338208	8.E-07	12868, 12858, 333182, 17705, 17706, 1	476	23	13288	1.E+01	4.E-04	2.E-05
GOTERM_MF_FAT	GO:0004129~cytochrome-c oxidase activity	9	1.645338208	8.E-07	12868, 12858, 333182, 17705, 17706, 1	476	23	13288	1.E+01	4.E-04	2.E-05
KEGG_PATHWAY	mmu04260:Cardiac muscle contraction	17	3.10786106	3.E-05	66694, 17705, 17706, 66445, 66142, 17	372	78	5738	3.E+00	4.E-03	4.E-04
UP_SEQ_FEATURE	topological domain:Mitochondrial matrix	3	0.548446069	2.E-01	12868, 66142, 12864	537	25	16021	4.E+00	1.E+00	1.E+00
Annotation Cluster 19	Enrichment Score: 4.397910316411424										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_MF_FAT	GO:0019992~diacylglycerol binding	13	2.376599634	9.E-07	22324, 26934, 70719, 57257, 16800, 18	476	59	13288	6.E+00	5.E-04	2.E-05
SMART	SM00109:C1	12	2.193784278	1.E-06	22324, 26934, 18753, 18762, 78816, 18	248	66	9131	7.E+00	2.E-04	3.E-05
INTERPRO	IPR002219:Protein kinase C-like, phorbol ester/diacylglycerol bindin	12	2.193784278	4.E-06	22324, 26934, 18753, 18762, 78816, 18	535	66	17763	6.E+00	4.E-03	3.E-04
UP_SEQ_FEATURE	zinc finger region:Phorbol-ester/DAG-type	9	1.645338208	3.E-05	22324, 26934, 18762, 78816, 17925, 70	537	38	16021	7.E+00	4.E-02	3.E-03



INTERPRO	IPR002219:Protein kinase C, phorbol ester/diacylglycerol binding	9	1.645338208	1.E-04	22324, 18753, 78816, 18754, 17925, 701	535	52	17763	6.E+00	1.E-01	8.E-03
GOTERM_MF_FAT	GO:0008289~lipid binding	26	4.753199269	7.E-04	22324, 228033, 100041835, 11816, 1680	476	345	13288	2.E+00	3.E-01	9.E-03
GOTERM_MF_FAT	GO:0030676~Rac guanyl-nucleotide exchange factor activity	3	0.548446069	1.E-02	22324, 57257, 16800	476	5	13288	2.E+01	1.E+00	1.E-01
Annotation Cluster 20	Enrichment Score: 4.372430901512718										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_MF_FAT	GO:0050662~coenzyme binding	20	3.65630713		4.E-06 66885, 226646, 100042746, 15929, 568	476	160	13288	3.E+00	2.E-03	8.E-05
GOTERM_MF_FAT	GO:0048037~cofactor binding	23	4.204753199		2.E-05 70316, 226646, 66885, 100042746, 159	476	226	13288	3.E+00	1.E-02	3.E-04
GOTERM_MF_FAT	GO:0051287~NAD or NADH binding	8	1.462522852		9.E-04 226646, 100042746, 15929, 67834, 568	476	44	13288	5.E+00	4.E-01	1.E-02
Annotation Cluster 21	Enrichment Score: 3.4307537983392056										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
SP_PIR_KEYWORDS	isopeptide bond	21	3.839122486		3.E-04 100048462, 13649, 19384, 665032, 100	541	277	17854	3.E+00	1.E-01	3.E-03
SP_PIR_KEYWORDS	ubiquitination	32	5.850091408		3.E-04 100048462, 13649, 19384, 665032, 660	541	524	17854	2.E+00	1.E-01	3.E-03
UP_SEQ_FEATURE	cross-link:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in	16	2.925045704		5.E-04 100048462, 19944, 621893, 78294, 136	537	168	16021	3.E+00	5.E-01	5.E-02
Annotation Cluster 22	Enrichment Score: 3.248784098355741										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_BP_FAT	GO:0030029~actin filament-based process	19	3.473491773		7.E-05 11350, 26934, 94190, 73167, 11856, 16	491	176	13588	3.E+00	1.E-01	3.E-03
GOTERM_BP_FAT	GO:0030036~actin cytoskeleton organization	18	3.290676417		1.E-04 11350, 26934, 94190, 73167, 11856, 16	491	165	13588	3.E+00	2.E-01	4.E-03
GOTERM_BP_FAT	GO:0007010~cytoskeleton organization	20	3.65630713		3.E-02 14163, 11350, 26934, 94190, 73167, 11	491	326	13588	2.E+00	1.E+00	4.E-01
Annotation Cluster 23	Enrichment Score: 3.1755602613864053										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
KEGG_PATHWAY	mmu04722:Neurotrophin signaling pathway	25	4.570383912		2.E-06 19247, 192662, 20416, 11857, 20418, 1	372	130	5738	3.E+00	3.E-04	4.E-05
KEGG_PATHWAY	mmu04012:ErbB signaling pathway	17	3.10786106		1.E-04 11350, 13649, 12929, 18479, 20416, 20	372	87	5738	3.E+00	2.E-02	1.E-03
KEGG_PATHWAY	mmu04510:Focal adhesion	25	4.570383912		2.E-03 13649, 22324, 11855, 20416, 170758, 2	372	198	5738	2.E+00	3.E-01	1.E-02
KEGG_PATHWAY	mmu05211:Renal cell carcinoma	12	2.193784278		5.E-03 18709, 18708, 19247, 14784, 20662, 20	372	70	5738	3.E+00	5.E-01	3.E-02
KEGG_PATHWAY	mmu04010:MAPK signaling pathway	25	4.570383912		6.E-02 13649, 170758, 13645, 18205, 18783, 2	372	265	5738	1.E+00	1.E+00	2.E-01
Annotation Cluster 24	Enrichment Score: 3.1656770876629574										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_BP_FAT	GO:0007169~transmembrane receptor protein tyrosine kinase signa	22	4.021937843		6.E-06 13649, 19247, 56338, 18479, 18791, 13	491	192	13588	3.E+00	1.E-02	3.E-04
GOTERM_BP_FAT	GO:0007167~enzyme linked receptor protein signaling pathway	25	4.570383912		5.E-05 13649, 19247, 18791, 21844, 13645, 18	491	273	13588	3.E+00	1.E-01	2.E-03
GOTERM_BP_FAT	GO:0007166~cell surface receptor linked signal transduction	45	8.226691042		1.E+00 14685, 12765, 22324, 13649, 19247, 18	491	2495	13588	5.E-01	1.E+00	1.E+00
Annotation Cluster 25	Enrichment Score: 3.0742474222776113										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_MF_FAT	GO:0008121~ubiquinol-cytochrome-c reductase activity	4	0.731261426		8.E-04 66694, 67530, 66594, 66576	476	6	13288	2.E+01	3.E-01	1.E-02
GOTERM_MF_FAT	GO:0016679~oxidoreductase activity, acting on diphenols and relat	4	0.731261426		8.E-04 66694, 67530, 66594, 66576	476	6	13288	2.E+01	3.E-01	1.E-02
GOTERM_MF_FAT	GO:0016681~oxidoreductase activity, acting on diphenols and relat	4	0.731261426		8.E-04 66694, 67530, 66594, 66576	476	6	13288	2.E+01	3.E-01	1.E-02
GOTERM_BP_FAT	GO:0006122~mitochondrial electron transport, ubiquinol to cytochr	4	0.731261426		9.E-04 67530, 66594, 66576, 22273	491	6	13588	2.E+01	8.E-01	3.E-02
Annotation Cluster 26	Enrichment Score: 3.0166448094191924										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_CC_FAT	GO:0005759~mitochondrial matrix	17	3.10786106		1.E-04 672195, 66885, 68263, 15107, 17448, 1	419	163	12504	3.E+00	3.E-02	1.E-03
GOTERM_CC_FAT	GO:0031980~mitochondrial lumen	17	3.10786106		1.E-04 672195, 66885, 68263, 15107, 17448, 1	419	163	12504	3.E+00	3.E-02	1.E-03
GOTERM_CC_FAT	GO:0070013~intracellular organelle lumen	48	8.775137112		7.E-02 66885, 672195, 68263, 101206, 12912, :	419	1133	12504	1.E+00	1.E+00	4.E-01
Annotation Cluster 27	Enrichment Score: 2.904269834034266										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_MF_FAT	GO:0005092~GDP-dissociation inhibitor activity	5	0.914076782		8.E-06 14570, 192662, 14567, 11857, 14569	476	5	13288	3.E+01	4.E-03	1.E-04
INTERPRO	IPR000406:RHO protein GDP dissociation inhibitor	3	0.548446069		3.E-03 14570, 192662, 11857	535	3	17763	3.E+01	9.E-01	8.E-02
GOTERM_MF_FAT	GO:0005094~Rho GDP-dissociation inhibitor activity	3	0.548446069		4.E-03 14570, 192662, 11857	476	3	13288	3.E+01	8.E-01	4.E-02
PIR_SUPERFAMILY	PIRSF015597:rho GDP dissociation inhibitor	3	0.548446069		6.E-03 14570, 192662, 11857	378	3	8136	2.E+01	9.E-01	4.E-01
PIR_SUPERFAMILY	PIRSF500829:animal rho GDP dissociation inhibitor	3	0.548446069		6.E-03 14570, 192662, 11857	378	3	8136	2.E+01	9.E-01	4.E-01
Annotation Cluster 28	Enrichment Score: 2.89587573395095										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini



GOTERM_MF_FAT	GO:0017124~SH3 domain binding	11	2.010968921	5.E-04	12549, 15170, 20401, 11489, 13858, 114	476	79	13288	4.E+00	2.E-01	7.E-03
UP_SEQ_FEATURE	short sequence motif:SH3-binding	8	1.462522852	9.E-04	14163, 20401, 11487, 14389, 228359, 11	537	47	16021	5.E+00	7.E-01	7.E-02
SP_PIR_KEYWORDS	sh3-binding	8	1.462522852	2.E-03	20401, 11489, 13858, 11487, 228359, 11	541	57	17854	5.E+00	4.E-01	1.E-02
GOTERM_MF_FAT	GO:0019904~protein domain specific binding	16	2.925045704	4.E-03	11350, 13131, 20401, 15170, 228359, 11	476	192	13288	2.E+00	9.E-01	4.E-02
Annotation Cluster 29	Enrichment Score: 2.8831827293662804										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_BP_FAT	GO:0042325~regulation of phosphorylation	24	4.387568556	3.E-04	13649, 19247, 20416, 13645, 18709, 21	491	290	13588	2.E+00	5.E-01	1.E-02
GOTERM_BP_FAT	GO:0051174~regulation of phosphorus metabolic process	24	4.387568556	6.E-04	13649, 19247, 20416, 13645, 18709, 21	491	301	13588	2.E+00	7.E-01	2.E-02
GOTERM_BP_FAT	GO:0019220~regulation of phosphate metabolic process	24	4.387568556	6.E-04	13649, 19247, 20416, 13645, 18709, 21	491	301	13588	2.E+00	7.E-01	2.E-02
GOTERM_BP_FAT	GO:0032268~regulation of cellular protein metabolic process	22	4.021937843	1.E-03	13684, 15170, 13649, 12258, 13665, 11	491	280	13588	2.E+00	9.E-01	4.E-02
GOTERM_BP_FAT	GO:0001932~regulation of protein amino acid phosphorylation	13	2.376599634	1.E-03	13649, 15170, 13645, 224014, 15129, 1	491	121	13588	3.E+00	9.E-01	4.E-02
GOTERM_BP_FAT	GO:0031399~regulation of protein modification process	15	2.742230347	3.E-03	15170, 13649, 13645, 224014, 15129, 1	491	165	13588	3.E+00	1.E+00	7.E-02
GOTERM_BP_FAT	GO:0050730~regulation of peptidyl-tyrosine phosphorylation	7	1.279707495	1.E-02	15170, 13649, 18753, 18754, 14600, 13	491	53	13588	4.E+00	1.E+00	2.E-01
Annotation Cluster 30	Enrichment Score: 2.8752650674824314										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
UP_SEQ_FEATURE	domain:PH 2	10	1.828153565	7.E-07	14163, 26382, 30938, 19417, 212285, 2	537	32	16021	9.E+00	1.E-03	1.E-04
UP_SEQ_FEATURE	domain:PH 1	10	1.828153565	9.E-07	14163, 26382, 30938, 19417, 212285, 2	537	33	16021	9.E+00	1.E-03	1.E-04
PIR_SUPERFAMILY	PIRSF037335:FYVE, RhoGEF and PH domain containing protein(1-4)	4	0.731261426	4.E-04	14163, 26382, 30938, 224014	378	4	8136	2.E+01	1.E-01	7.E-02
SMART	SM00064:FYVE	4	0.731261426	5.E-02	14163, 26382, 30938, 224014	248	30	9131	5.E+00	1.E+00	3.E-01
INTERPRO	IPR000306:Zinc finger, FYVE-type	4	0.731261426	6.E-02	14163, 26382, 30938, 224014	535	30	17763	4.E+00	1.E+00	7.E-01
INTERPRO	IPR017455:Zinc finger, FYVE-related	4	0.731261426	9.E-02	14163, 26382, 30938, 224014	535	35	17763	4.E+00	1.E+00	8.E-01
UP_SEQ_FEATURE	zinc finger region:FYVE-type	4	0.731261426	1.E-01	14163, 26382, 30938, 224014	537	37	16021	3.E+00	1.E+00	9.E-01
Annotation Cluster 31	Enrichment Score: 2.4400069010080054										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
INTERPRO	IPR011626:A-macroglobulin complement component	5	0.914076782	9.E-05	17836, 12266, 17837, 15139, 11287	535	9	17763	2.E+01	8.E-02	6.E-03
INTERPRO	IPR001599:Alpha-2-macroglobulin	5	0.914076782	9.E-05	17836, 12266, 17837, 15139, 11287	535	9	17763	2.E+01	8.E-02	6.E-03
INTERPRO	IPR011625:Alpha-2-macroglobulin, N-terminal 2	5	0.914076782	9.E-05	17836, 12266, 17837, 15139, 11287	535	9	17763	2.E+01	8.E-02	6.E-03
INTERPRO	IPR009048:Alpha-macroglobulin, receptor-binding	5	0.914076782	9.E-05	17836, 12266, 17837, 15139, 11287	535	9	17763	2.E+01	8.E-02	6.E-03
INTERPRO	IPR002890:Alpha-2-macroglobulin, N-terminal	5	0.914076782	1.E-04	17836, 12266, 17837, 15139, 11287	535	10	17763	2.E+01	1.E-01	9.E-03
INTERPRO	IPR019742:Alpha-2-macroglobulin, conserved site	5	0.914076782	2.E-04	17836, 12266, 17837, 15139, 11287	535	11	17763	2.E+01	2.E-01	1.E-02
PIR_SUPERFAMILY	PIRSF001635:alpha-2-macroglobulin	5	0.914076782	5.E-04	17836, 12266, 17837, 15139, 11287	378	9	8136	1.E+01	2.E-01	6.E-02
SP_PIR_KEYWORDS	thioester bond	4	0.731261426	9.E-04	17836, 12266, 17837, 11287	541	7	17854	2.E+01	3.E-01	6.E-03
UP_SEQ_FEATURE	cross-link:isoglutamyl cysteine thioester (Cys-Gln)	4	0.731261426	1.E-03	17836, 12266, 17837, 11287	537	7	16021	2.E+01	8.E-01	9.E-02
INTERPRO	IPR019565:Alpha-2-macroglobulin, thiol-ester bond-forming	4	0.731261426	1.E-03	17836, 12266, 17837, 11287	535	8	17763	2.E+01	7.E-01	5.E-02
UP_SEQ_FEATURE	region of interest:Bait region	3	0.548446069	6.E-03	17836, 17837, 11287	537	4	16021	2.E+01	1.E+00	3.E-01
SP_PIR_KEYWORDS	bait region	3	0.548446069	1.E-02	17836, 17837, 11287	541	6	17854	2.E+01	1.E+00	6.E-02
SP_PIR_KEYWORDS	Serine protease inhibitor	7	1.279707495	4.E-02	17836, 17837, 12258, 282663, 21789, 1	541	82	17854	3.E+00	1.E+00	1.E-01
SP_PIR_KEYWORDS	protease inhibitor	8	1.462522852	5.E-02	17836, 17837, 12258, 16644, 282663, 2	541	109	17854	2.E+00	1.E+00	2.E-01
GOTERM_MF_FAT	GO:0004866~endopeptidase inhibitor activity	10	1.828153565	1.E-01	17836, 12266, 17837, 12258, 16644, 28	476	161	13288	2.E+00	1.E+00	6.E-01
GOTERM_MF_FAT	GO:0004857~enzyme inhibitor activity	13	2.376599634	2.E-01	12266, 56338, 12258, 16644, 282663, 1	476	243	13288	1.E+00	1.E+00	7.E-01
GOTERM_MF_FAT	GO:0030414~peptidase inhibitor activity	10	1.828153565	2.E-01	17836, 12266, 17837, 12258, 16644, 28	476	176	13288	2.E+00	1.E+00	7.E-01
GOTERM_MF_FAT	GO:0004867~serine-type endopeptidase inhibitor activity	7	1.279707495	2.E-01	17836, 17837, 12258, 282663, 21789, 1	476	115	13288	2.E+00	1.E+00	8.E-01
UP_SEQ_FEATURE	site:Reactive bond	4	0.731261426	3.E-01	12258, 282663, 21789, 11820	537	52	16021	2.E+00	1.E+00	1.E+00
Annotation Cluster 32	Enrichment Score: 2.3628521130317455										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_BP_FAT	GO:0008202~steroid metabolic process	17	3.10786106	2.E-04	13121, 11816, 56348, 22359, 65969, 16	491	161	13588	3.E+00	4.E-01	8.E-03
INTERPRO	IPR016040:NAD(P)-binding domain	14	2.559414991	6.E-04	100042746, 15107, 56348, 100041325, 9	535	151	17763	3.E+00	5.E-01	3.E-02
SP_PIR_KEYWORDS	steroidogenesis	5	0.914076782	7.E-04	100043456, 13074, 15493, 15492, 1549	541	14	17854	1.E+01	2.E-01	5.E-03
KEGG_PATHWAY	mmu00150:Androgen and estrogen metabolism	9	1.645338208	9.E-04	100043456, 56348, 54200, 15493, 1549	372	33	5738	4.E+00	1.E-01	8.E-03
GOTERM_BP_FAT	GO:0006694~steroid biosynthetic process	10	1.828153565	1.E-03	13121, 100043456, 14137, 56348, 1307	491	71	13588	4.E+00	9.E-01	3.E-02
GOTERM_MF_FAT	GO:0033764~steroid dehydrogenase activity, acting on the CH-OH	6	1.096892139	1.E-03	100043456, 56348, 15493, 15492, 1549	476	23	13288	7.E+00	4.E-01	1.E-02
SP_PIR_KEYWORDS	Steroid biosynthesis	7	1.279707495	1.E-03	13121, 100043456, 14137, 56348, 1549	541	40	17854	6.E+00	4.E-01	8.E-03
SP_PIR_KEYWORDS	intramolecular oxidoreductase	4	0.731261426	1.E-03	14751, 100043456, 21991, 15492, 1549	541	8	17854	2.E+01	4.E-01	9.E-03
KEGG_PATHWAY	mmu00140:Steroid hormone biosynthesis	10	1.828153565	2.E-03	100043456, 56348, 13074, 54200, 1549	372	45	5738	3.E+00	3.E-01	1.E-02
INTERPRO	IPR002225:3-beta hydroxysteroid dehydrogenase/isomerase	4	0.731261426	2.E-03	100043456, 15493, 15492, 15497, 1549	535	9	17763	1.E+01	8.E-01	6.E-02



GOTERM_MF_FAT	GO:0003854~3-beta-hydroxy-delta5-steroid dehydrogenase activity	4	0.731261426	3.E-03	100043456, 15493, 15492, 15497, 1549!	476	9	13288	1.E+01	8.E-01	4.E-02
GOTERM_MF_FAT	GO:0016229~steroid dehydrogenase activity	6	1.096892139	3.E-03	100043456, 56348, 15493, 15492, 1549!	476	29	13288	6.E+00	8.E-01	4.E-02
COG_ONTOLOGY	Cell envelope biogenesis, outer membrane / Carbohydrate transpor	4	0.731261426	4.E-03	100043456, 15493, 15492, 15497, 1549!	52	14	2040	1.E+01	6.E-02	3.E-02
PIR_SUPERFAMILY	PIRSF036679:bifunctional 3 beta-hydroxysteroid dehydrogenase/De	4	0.731261426	7.E-03	100043456, 15493, 15492, 15497, 1549!	378	9	8136	1.E+01	9.E-01	4.E-01
GOTERM_MF_FAT	GO:0004769~steroid delta-isomerase activity	3	0.548446069	7.E-03	15493, 15492, 15497	476	4	13288	2.E+01	1.E+00	7.E-02
SP_PIR_KEYWORDS	Isomerase	10	1.828153565	1.E-02	14751, 74147, 100043456, 73724, 2199!	541	118	17854	3.E+00	1.E+00	5.E-02
GOTERM_MF_FAT	GO:0016860~intramolecular oxidoreductase activity	6	1.096892139	1.E-02	14751, 74147, 21991, 15493, 15492, 15!	476	38	13288	4.E+00	1.E+00	1.E-01
GOTERM_MF_FAT	GO:0016863~intramolecular oxidoreductase activity, transposing C=	4	0.731261426	1.E-02	74147, 15493, 15492, 15497	476	14	13288	8.E+00	1.E+00	1.E-01
SP_PIR_KEYWORDS	multifunctional enzyme	6	1.096892139	3.E-02	74147, 14137, 15493, 14450, 15492, 15!	541	58	17854	3.E+00	1.E+00	1.E-01
SP_PIR_KEYWORDS	lipid synthesis	7	1.279707495	8.E-02	70316, 13121, 14137, 56348, 21991, 16!	541	99	17854	2.E+00	1.E+00	3.E-01
KEGG_PATHWAY	mmu00100:Steroid biosynthesis	4	0.731261426	9.E-02	13121, 14137, 16987, 20775	372	17	5738	4.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0008610~lipid biosynthetic process	14	2.559414991	2.E-01	13121, 70316, 56348, 16987, 10004345!	491	285	13588	1.E+00	1.E+00	9.E-01

Annotation Cluster 33	Enrichment Score: 2.3566737879175865										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
INTERPRO	IPR004161:Translation elongation factor EFTu/EF1A, domain 2	6	1.096892139		1.E-04 26905, 13627, 13628, 13629, 14852, 22!	535	17	17763	1.E+01	1.E-01	7.E-03
INTERPRO	IPR000795:Protein synthesis factor, GTP-binding	6	1.096892139		1.E-04 26905, 13627, 13628, 13629, 14852, 22!	535	18	17763	1.E+01	1.E-01	8.E-03
GOTERM_CC_FAT	GO:0005853~eukaryotic translation elongation factor 1 complex	3	0.548446069		6.E-03 13628, 66656, 55949	419	4	12504	2.E+01	9.E-01	5.E-02
SP_PIR_KEYWORDS	elongation factor	5	0.914076782		8.E-03 13627, 13628, 13629, 66656, 55949	541	27	17854	6.E+00	1.E+00	4.E-02
INTERPRO	IPR004160:Translation elongation factor EFTu/EF1A, C-terminal	3	0.548446069		2.E-02 13627, 13628, 14852	535	8	17763	1.E+01	1.E+00	4.E-01
GOTERM_MF_FAT	GO:0003746~translation elongation factor activity	5	0.914076782		2.E-02 13627, 13628, 13629, 66656, 55949	476	31	13288	5.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0006414~translational elongation	5	0.914076782		7.E-02 56040, 13627, 13628, 66656, 55949	491	43	13588	3.E+00	1.E+00	6.E-01

Annotation Cluster 34	Enrichment Score: 2.3262905438210764										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
SP_PIR_KEYWORDS	pentose phosphate pathway	4	0.731261426		1.E-04 21991, 11676, 11674, 14381	541	4	17854	3.E+01	4.E-02	1.E-03
KEGG_PATHWAY	mmu00030:Penrose phosphate pathway	9	1.645338208		2.E-04 14751, 110639, 230163, 72157, 11676, !	372	26	5738	5.E+00	2.E-02	2.E-03
SP_PIR_KEYWORDS	gluconeogenesis	5	0.914076782		1.E-03 100040053, 100042746, 14433, 14751, !	541	17	17854	1.E+01	4.E-01	9.E-03
UP_SEQ_FEATURE	active site:Schiff-base intermediate with dihydroxyacetone-P	3	0.548446069		3.E-03 230163, 11676, 11674	537	3	16021	3.E+01	1.E+00	2.E-01
UP_SEQ_FEATURE	site:Necessary for preference for fructose 1,6-bisphosphate over fru	3	0.548446069		3.E-03 230163, 11676, 11674	537	3	16021	3.E+01	1.E+00	2.E-01
INTERPRO	IPR000741:Fructose-bisphosphate aldolase, class-I	3	0.548446069		8.E-03 230163, 11676, 11674	535	5	17763	2.E+01	1.E+00	2.E-01
GOTERM_MF_FAT	GO:0004332~fructose-bisphosphate aldolase activity	3	0.548446069		1.E-02 230163, 11676, 11674	476	5	13288	2.E+01	1.E+00	1.E-01
GOTERM_MF_FAT	GO:0016832~aldehyde-lyase activity	3	0.548446069		2.E-02 230163, 11676, 11674	476	7	13288	1.E+01	1.E+00	2.E-01
KEGG_PATHWAY	mmu00051:Fructose and mannose metabolism	7	1.279707495		3.E-02 15275, 21991, 230163, 15277, 11676, 1!	372	37	5738	3.E+00	1.E+00	1.E-01
SP_PIR_KEYWORDS	Schiff base	3	0.548446069		3.E-02 230163, 11676, 11674	541	10	17854	1.E+01	1.E+00	1.E-01
INTERPRO	IPR013785:Aldolase-type TIM barrel	5	0.914076782		4.E-02 21991, 230163, 11676, 11674, 99586	535	43	17763	4.E+00	1.E+00	5.E-01

Annotation Cluster 35	Enrichment Score: 2.3073427423192534										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
COG_ONTOLOGY	Nucleotide transport and metabolism	5	0.914076782		1.E-04 80914, 68556, 22245, 67273, 99586	52	11	2040	2.E+01	1.E-03	1.E-03
KEGG_PATHWAY	mmu00983:Drug metabolism	10	1.828153565		3.E-03 76654, 80914, 68556, 72269, 22245, 72!	372	48	5738	3.E+00	4.E-01	2.E-02
GOTERM_MF_FAT	GO:0019206~nucleoside kinase activity	4	0.731261426		3.E-03 80914, 68556, 22245, 21877	476	9	13288	1.E+01	8.E-01	4.E-02
INTERPRO	IPR000764:Uridine kinase	3	0.548446069		5.E-03 80914, 68556, 22245	535	4	17763	2.E+01	1.E+00	1.E-01
INTERPRO	IPR006083:Phosphoribulokinase/uridine kinase	3	0.548446069		5.E-03 80914, 68556, 22245	535	4	17763	2.E+01	1.E+00	1.E-01
GOTERM_MF_FAT	GO:0004849~uridine kinase activity	3	0.548446069		7.E-03 80914, 68556, 22245	476	4	13288	2.E+01	1.E+00	7.E-02
GOTERM_MF_FAT	GO:0019205~nucleobase, nucleoside, nucleotide kinase activity	5	0.914076782		4.E-02 80914, 21915, 68556, 22245, 21877	476	36	13288	4.E+00	1.E+00	3.E-01
KEGG_PATHWAY	mmu00240:Pyrimidine metabolism	12	2.193784278		4.E-02 76654, 80914, 20020, 21915, 68556, 72!	372	96	5738	2.E+00	1.E+00	1.E-01

Annotation Cluster 36	Enrichment Score: 2.297462591660972										
Category	Term: SH2 domain	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
UP_SEQ_FEATURE	domain:SH2 2	4	0.731261426		3.E-03 18709, 18708, 15170, 19247	537	9	16021	1.E+01	1.E+00	2.E-01
UP_SEQ_FEATURE	domain:SH2 1	4	0.731261426		3.E-03 18709, 18708, 15170, 19247	537	9	16021	1.E+01	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0032870~cellular response to hormone stimulus	7	1.279707495		2.E-02 18709, 20848, 18708, 19247, 104215, 1!	491	58	13588	3.E+00	1.E+00	3.E-01

Annotation Cluster 37	Enrichment Score: 2.2847820981232796										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
UP_SEQ_FEATURE	nucleotide phosphate-binding region:NAD	10	1.828153565		7.E-04 15107, 100042746, 17448, 15929, 5684!	537	73	16021	4.E+00	6.E-01	6.E-02
INTERPRO	IPR001557:L-lactate/malate dehydrogenase	4	0.731261426		9.E-04 16828, 17448, 16833, 16832	535	7	17763	2.E+01	6.E-01	3.E-02
INTERPRO	IPR015955:Lactate dehydrogenase/glycoside hydrolase, family 4, C-	4	0.731261426		1.E-03 16828, 17448, 16833, 16832	535	8	17763	2.E+01	7.E-01	5.E-02



INTERPRO	IPR001236:Lactate/malate dehydrogenase	4	0.731261426	1-E-03 16828, 17448, 16833, 16832	535	8	17763	2.E+01	7.E-01	5.E-02
PIR_SUPERFAMILY	PIRSF000102:Lac_mal_DH	4	0.731261426	3-E-03 16828, 17448, 16833, 16832	378	7	8136	1.E+01	7.E-01	3.E-01
UP_SEQ_FEATURE	binding site:NAD or substrate	3	0.548446069	3-E-03 16828, 16833, 16832	537	3	16021	3.E+01	1.E+00	2.E-01
INTERPRO	IPR011304:L-lactate dehydrogenase	3	0.548446069	5-E-03 16828, 16833, 16832	535	4	17763	2.E+01	1.E+00	1.E-01
INTERPRO	IPR018177:L-lactate dehydrogenase, active site	3	0.548446069	5-E-03 16828, 16833, 16832	535	4	17763	2.E+01	1.E+00	1.E-01
GOTERM_MF_FAT	GO:0004459~L-lactate dehydrogenase activity	3	0.548446069	7-E-03 16828, 16833, 16832	476	4	13288	2.E+01	1.E+00	7.E-02
GOTERM_MF_FAT	GO:0004457~lactate dehydrogenase activity	3	0.548446069	1-E-02 16828, 16833, 16832	476	5	13288	2.E+01	1.E+00	1.E-01
KEGG_PATHWAY	mmu00640:Propanoate metabolism	6	1.096892139	4-E-02 16828, 74147, 73724, 68738, 16833, 16832	372	30	5738	3.E+00	1.E+00	1.E-01
KEGG_PATHWAY	mmu00270:Cysteine and methionine metabolism	4	0.731261426	4-E-01 16828, 13436, 16833, 16832	372	33	5738	2.E+00	1.E+00	6.E-01

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
KEGG_PATHWAY	mmu05220:Chronic myeloid leukemia	16	2.925045704	8.E-05	11350, 19247, 14389, 12929, 20416, 20416	372	76	5738	3.E+00	1.E-02	1.E-03
KEGG_PATHWAY	mmu04012:ErbB signaling pathway	17	3.10786106	1.E-04	11350, 13649, 12929, 18479, 20416, 20416	372	87	5738	3.E+00	2.E-02	1.E-03
KEGG_PATHWAY	mmu05214:Glioma	13	2.376599634	7.E-04	13649, 20416, 20418, 13645, 18709, 18709	372	64	5738	3.E+00	1.E-01	6.E-03
KEGG_PATHWAY	mmu05215:Prostate cancer	14	2.559414991	5.E-03	13649, 12912, 13645, 12914, 18709, 18709	372	90	5738	2.E+00	5.E-01	3.E-02
KEGG_PATHWAY	mmu05223:Non-small cell lung cancer	10	1.828153565	1.E-03	18709, 18708, 13649, 13555, 242705, 13555	372	54	5738	3.E+00	7.E-01	4.E-02
KEGG_PATHWAY	mmu04910:Insulin signaling pathway	18	3.290676417	7.E-03	13684, 12929, 15275, 15277, 20416, 20416	372	138	5738	2.E+00	7.E-01	3.E-02
KEGG_PATHWAY	mmu05213:Endometrial cancer	8	1.462522852	5.E-02	18709, 18708, 13649, 13866, 14784, 20416	372	52	5738	2.E+00	1.E+00	1.E-01
KEGG_PATHWAY	mmu05219:Bladder cancer	6	1.096892139	1.E-01	13649, 13555, 242705, 13866, 72962, 13555	372	42	5738	2.E+00	1.E+00	3.E-01
KEGG_PATHWAY	mmu05218:Melanoma	7	1.279707495	3.E-01	18709, 18708, 13649, 13555, 242705, 13555	372	71	5738	2.E+00	1.E+00	6.E-01

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_BP_FAT	GO:0043087~regulation of GTPase activity	12	2.193784278	5.E-04	22324, 71709, 228359, 57257, 228998, :	491	93	13588	4.E+00	6.E-01	2.E-02
GOTERM_BP_FAT	GO:0051336~regulation of hydrolase activity	17	3.10786106	2.E-03	672195, 22324, 12279, 228359, 57257, :	491	196	13588	2.E+00	1.E+00	5.E-02
GOTERM_BP_FAT	GO:0032318~regulation of Ras GTPase activity	6	1.096892139	2.E-01	71709, 228998, 19765, 19417, 212285, :	491	80	13588	2.E+00	1.E+00	8.E-01

[illegible]

Annotation	Cluster 41	Enrichment Score: 2.1866652810392004									
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
SP_PIR_KEYWORDS	thiamine pyrophosphate	5	0.914076782	2.E-04	68263, 18597, 18598, 18293, 21881	541	11	17854	2.E+01	8.E-02	2.E-03
SP_PIR_KEYWORDS	pyruvate	5	0.914076782	2.E-03	18746, 68263, 27402, 18597, 18598	541	18	17854	9.E+00	5.E-01	1.E-02
GOTERM_MF_FAT	GO:0016624~oxidoreductase activity, acting on the aldehyde or oxo-	4	0.731261426	3.E-03	68263, 18597, 18598, 18293	476	9	13288	1.E+01	8.E-01	4.E-02
GOTERM_MF_FAT	GO:0004738~pyruvate dehydrogenase activity	3	0.548446069	4.E-03	68263, 18597, 18598	476	3	13288	3.E+01	8.E-01	4.E-02
GOTERM_MF_FAT	GO:0004739~pyruvate dehydrogenase (acetyl-transferring) activity	3	0.548446069	4.E-03	68263, 18597, 18598	476	3	13288	3.E+01	8.E-01	4.E-02
INTERPRO	IPR001017:Dehydrogenase, E1 component	3	0.548446069	1.E-02	18597, 18598, 18293	535	6	17763	2.E+01	1.E+00	2.E-01
KEGG_PATHWAY	mmu00650:Butanoate metabolism	6	1.096892139	9.E-02	68263, 15107, 11409, 74147, 18597, 18598	372	37	5738	3.E+00	1.E+00	2.E-01
KEGG_PATHWAY	mmu00290:Valine, leucine and isoleucine biosynthesis	3	0.548446069	2.E-01	68263, 18597, 18598	372	11	5738	4.E+00	1.E+00	4.E-01

Annotation Cluster 42	Enrichment Score: 2.182208038139367										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
SP_PIR_KEYWORDS	iron-sulfur	8	1.46252852	5.E-04	66694, 226646, 17995, 227197, 225887,	541	47	17854	6.E+00	2.E-01	4.E-03
SP_PIR_KEYWORDS	4fe-4s	6	1.096892139	5.E-04	226646, 17995, 227197, 225887, 75406,	541	23	17854	9.E+00	2.E-01	4.E-03



GOTERM_MF_FAT	GO:0051539~4 iron, 4 sulfur cluster binding	6	1.096892139	1.E-03 226646, 17995, 227197, 225887, 75406,	476	23	13288	7.E+00	4.E-01	1.E-02	
GOTERM_MF_FAT	GO:0051536~iron-sulfur cluster binding	8	1.462522852	2.E-03 66694, 226646, 17995, 227197, 225887,	476	50	13288	4.E+00	6.E-01	2.E-02	
GOTERM_MF_FAT	GO:0051540~metal cluster binding	8	1.462522852	2.E-03 66694, 226646, 17995, 227197, 225887,	476	50	13288	4.E+00	6.E-01	2.E-02	
UP_SEQ_FEATURE	metal ion-binding site:Iron-sulfur 2 (4Fe-4S)	3	0.548446069	2.E-02 227197, 225887, 99586	537	6	16021	1.E+01	1.E+00	5.E-01	
UP_SEQ_FEATURE	metal ion-binding site:Iron-sulfur (4Fe-4S)	3	0.548446069	9.E-02 226646, 17995, 75406	537	15	16021	6.E+00	1.E+00	9.E-01	
SP_PIR_KEYWORDS	2Fe-2S	3	0.548446069	1.E-01 66694, 227197, 72900	541	19	17854	5.E+00	1.E+00	3.E-01	
GOTERM_MF_FAT	GO:0051537~2 iron, 2 sulfur cluster binding	3	0.548446069	1.E-01 66694, 227197, 72900	476	19	13288	4.E+00	1.E+00	6.E-01	
Annotation Cluster 43	Enrichment Score: 2.162097616773596										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
UP_SEQ_FEATURE	domain:Ras-associating	6	1.096892139	5.E-03 17925, 270163, 266781, 212285, 24486	537	34	16021	5.E+00	1.E+00	2.E-01	
SMART	SM00314:RA	6	1.096892139	6.E-03 17925, 270163, 266781, 212285, 24486	248	44	9131	5.E+00	6.E-01	6.E-02	
INTERPRO	IPR000159:Ras-association	6	1.096892139	1.E-02 17925, 270163, 266781, 212285, 24486	535	44	17763	5.E+00	1.E+00	2.E-01	
Annotation Cluster 44	Enrichment Score: 2.1365713181496915										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
KEGG_PATHWAY	mmu04710:Circadian_rhythm	7	1.279707495	8.E-05 11865, 12753, 12952, 18626, 12953, 18627, 18628	372	13	5738	8.E+00	1.E-02	1.E-03	
SP_PIR_KEYWORDS	biological rhythms	6	1.096892139	3.E-04 12753, 12952, 18626, 12953, 18627, 18628	541	21	17854	9.E+00	1.E-01	3.E-03	
SMART	SM00091:PAS	6	1.096892139	2.E-03 11865, 12753, 18626, 17979, 18627, 18628	248	32	9131	7.E+00	2.E-01	2.E-02	
INTERPRO	IPR013655:PAS fold-3	5	0.914076782	2.E-03 11865, 12753, 18626, 18627, 18628	535	18	17763	9.E+00	8.E-01	6.E-02	
GOTERM_BP_FAT	GO:0007623~circadian rhythm	7	1.279707495	2.E-03 11865, 12753, 12952, 18626, 12953, 18627, 18628	491	37	13588	5.E+00	1.E+00	5.E-02	
INTERPRO	IPR000014:PAS	6	1.096892139	2.E-03 11865, 12753, 18626, 17979, 18627, 18628	535	32	17763	6.E+00	9.E-01	7.E-02	
GOTERM_BP_FAT	GO:0048511~rhythmic process	11	2.010968921	3.E-03 11865, 13667, 12753, 12952, 18626, 12953, 18627, 18628	491	98	13588	3.E+00	1.E+00	7.E-02	
UP_SEQ_FEATURE	domain:RAS 1	5	0.914076782	3.E-03 11865, 12753, 18626, 18627, 18628	537	19	16021	8.E+00	1.E+00	2.E-01	
UP_SEQ_FEATURE	domain:RAS 2	5	0.914076782	3.E-03 11865, 12753, 18626, 18627, 18628	537	19	16021	8.E+00	1.E+00	2.E-01	
UP_SEQ_FEATURE	region of interest:CRY binding domain	3	0.548446069	3.E-03 18626, 18627, 18628	537	3	16021	3.E+01	1.E+00	2.E-01	
UP_SEQ_FEATURE	region of interest:CSNK1E binding domain	3	0.548446069	3.E-03 18626, 18627, 18628	537	3	16021	3.E+01	1.E+00	2.E-01	
SMART	SM00086:PAC	5	0.914076782	5.E-03 11865, 12753, 18626, 18627, 18628	248	26	9131	7.E+00	5.E-01	5.E-02	
INTERPRO	IPR001610:PAC motif	5	0.914076782	7.E-03 11865, 12753, 18626, 18627, 18628	535	26	17763	6.E+00	1.E+00	2.E-01	
UP_SEQ_FEATURE	domain:PAC	5	0.914076782	8.E-03 11865, 12753, 18626, 18627, 18628	537	24	16021	6.E+00	1.E+00	3.E-01	
BIOCARTA	m_circadianPathway:Circadian_Rhythms	4	0.731261426	1.E-02 11865, 12753, 12952, 18626	109	6	1171	7.E+00	9.E-01	1.E-01	
UP_SEQ_FEATURE	short sequence motif:Nuclear export signal	4	0.731261426	1.E-01 18626, 208727, 18627, 18628	537	36	16021	3.E+00	1.E+00	9.E-01	
GOTERM_BP_FAT	GO:0010553~negative regulation of specific transcription from RNA	3	0.548446069	2.E-01 18626, 18627, 18628	491	21	13588	4.E+00	1.E+00	8.E-01	
GOTERM_BP_FAT	GO:0032582~negative regulation of gene-specific transcription	3	0.548446069	2.E-01 18626, 18627, 18628	491	23	13588	4.E+00	1.E+00	9.E-01	
GOTERM_BP_FAT	GO:0010551~regulation of specific transcription from RNA polymer	4	0.731261426	3.E-01 18626, 208727, 18627, 18628	491	51	13588	2.E+00	1.E+00	9.E-01	
GOTERM_BP_FAT	GO:0032583~regulation of gene-specific transcription	4	0.731261426	4.E-01 18626, 208727, 18627, 18628	491	67	13588	2.E+00	1.E+00	1.E+00	
Annotation Cluster 45	Enrichment Score: 2.03155280082052										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_BP_FAT	GO:0016310~phosphorylation	63	11.51736746	1.E-10 19247, 100041835, 13665, 17705, 17706, 17707, 17708, 17709, 17710, 17711, 17712, 17713, 17714, 17715, 17716, 17717, 17718, 17719, 17720, 17721, 17722, 17723, 17724, 17725, 17726, 17727, 17728, 17729, 17730, 17731, 17732, 17733, 17734, 17735, 17736, 17737, 17738, 17739, 17740, 17741, 17742, 17743, 17744, 17745, 17746, 17747, 17748, 17749, 17750, 17751, 17752, 17753, 17754, 17755, 17756, 17757, 17758, 17759, 17760, 17761, 17762, 17763, 17764, 17765, 17766, 17767, 17768, 17769, 17770, 17771, 17772, 17773, 17774, 17775, 17776, 17777, 17778, 17779, 17780, 17781, 17782, 17783, 17784, 17785, 17786, 17787, 17788, 17789, 17790, 17791, 17792, 17793, 17794, 17795, 17796, 17797, 17798, 17799, 17800, 17801, 17802, 17803, 17804, 17805, 17806, 17807, 17808, 17809, 17810, 17811, 17812, 17813, 17814, 17815, 17816, 17817, 17818, 17819, 17820, 17821, 17822, 17823, 17824, 17825, 17826, 17827, 17828, 17829, 17830, 17831, 17832, 17833, 17834, 17835, 17836, 17837, 17838, 17839, 17840, 17841, 17842, 17843, 17844, 17845, 17846, 17847, 17848, 17849, 17850, 17851, 17852, 17853, 17854, 17855, 17856, 17857, 17858, 17859, 17860, 17861, 17862, 17863, 17864, 17865, 17866, 17867, 17868, 17869, 17870, 17871, 17872, 17873, 17874, 17875, 17876, 17877, 17878, 17879, 17880, 17881, 17882, 17883, 17884, 17885, 17886, 17887, 17888, 17889, 17890, 17891, 17892, 17893, 17894, 17895, 17896, 17897, 17898, 17899, 17900, 17901, 17902, 17903, 17904, 17905, 17906, 17907, 17908, 17909, 17910, 17911, 17912, 17913, 17914, 17915, 17916, 17917, 17918, 17919, 17920, 17921, 17922, 17923, 17924, 17925, 17926, 17927, 17928, 17929, 17930, 17931, 17932, 17933, 17934, 17935, 17936, 17937, 17938, 17939, 17940, 17941, 17942, 17943, 17944, 17945, 17946, 17947, 17948, 17949, 17950, 17951, 17952, 17953, 17954, 17955, 17956, 17957, 17958, 17959, 17960, 17961, 17962, 17963, 17964, 17965, 17966, 17967, 17968, 17969, 17970, 17971, 17972, 17973, 17974, 17975, 17976, 17977, 17978, 17979, 17980, 17981, 17982, 17983, 17984, 17985, 17986, 17987, 17988, 17989, 17990, 17991, 17992, 17993, 17994, 17995, 17996, 17997, 17998, 17999, 18000, 18001, 18002, 18003, 18004, 18005, 18006, 18007, 18008, 18009, 18010, 18011, 18012, 18013, 18014, 18015, 18016, 18017, 18018, 18019, 18020, 18021, 18022, 18023, 18024, 18025, 18026, 18027, 18028, 18029, 18030, 18031, 18032, 18033, 18034, 18035, 18036, 18037, 18038, 18039, 18040, 18041, 18042, 18043, 18044, 18045, 18046, 18047, 18048, 18049, 18050, 18051, 18052, 18053, 18054, 18055, 18056, 18057, 18058, 18059, 18060, 18061, 18062, 18063, 18064, 18065, 18066, 18067, 18068, 18069, 18070, 18071, 18072, 18073, 18074, 18075, 18076, 18077, 18078, 18079, 18080, 18081, 18082, 18083, 18084, 18085, 18086, 18087, 18088, 18089, 18090, 18091, 18092, 18093, 18094, 18095, 18096, 18097, 18098, 18099, 18100, 18101, 18102, 18103, 18104, 18105, 18106, 18107, 18108, 18109, 18110, 18111, 18112, 18113, 18114, 18115, 18116, 18117, 18118, 18119, 18120, 18121, 18122, 18123, 18124, 18125, 18126, 18127, 18128, 18129, 18130, 18131, 18132, 18133, 18134, 18135, 18136, 18137, 18138, 18139, 18140, 18141, 18142, 18143, 18144, 18145, 18146, 18147, 18148, 18149, 18150, 18151, 18152, 18153, 18154, 18155, 18156, 18157, 18158, 18159, 18160, 18161, 18162, 18163, 18164, 18165, 18166, 18167, 18168, 18169, 18170, 18171, 18172, 18173, 18174, 18175, 18176, 18177, 18178, 18179, 18180, 18181, 18182, 18183, 18184, 18185, 18186, 18187, 18188, 18189, 18190, 18191, 18192, 18193, 18194, 18195, 18196, 18197, 18198, 18199, 18200, 18201, 18202, 18203, 18204, 18205, 18206, 18207, 18208, 18209, 18210, 18211, 18212, 18213, 18214, 18215, 18216, 18217, 18218, 18219, 18220, 18221, 18222, 18223, 18224, 18225, 18226, 18227, 18228, 18229, 18230, 18231, 18232, 18233, 18234, 18235, 18236, 18237, 18238, 18239, 18240, 18241, 18242, 18243, 18244, 18245, 18246, 18247, 18248, 18249, 18250, 18251, 18252, 18253, 18254, 18255, 18256, 18257, 18258, 18259, 18260, 18261, 18262, 18263, 18264, 18265, 18266, 18267, 18268, 18269, 18270, 18271, 18272, 18273, 18274, 18275, 18276, 18277, 18278, 18279, 18280, 18281, 18282, 18283, 18284, 18285, 18286, 18287, 18288, 18289, 18290, 18291, 18292, 18293, 18294, 18295, 18296, 18297, 18298, 18299, 18300, 18301, 18302, 18303, 18304, 18305, 18306, 18307, 18308, 18309, 18310, 18311, 18312, 18313, 18314, 18315, 18316, 18317, 18318, 18319, 18320, 18321, 18322, 18323, 18324, 18325, 18326, 18327, 18328, 18329, 18330, 18331, 18332, 18333, 18334, 18335, 18336, 18337, 18338, 18339, 18340, 18341, 18342, 18343, 18344, 18345, 18346, 18347, 18348, 18349, 18350, 18351, 18352, 18353, 18354, 18355, 18356, 18357, 18358, 18359, 18360, 18361, 18362, 18363, 18364, 18365, 18366, 18367, 18368, 18369, 18370, 18371, 18372, 18373, 18374, 18375, 18376, 18377, 18378, 18379, 18380, 18381, 18382, 18383, 18384, 18385, 18386, 18387, 18388, 18389, 18390, 18391, 18392, 18393, 18394, 18395, 18396, 18397, 18398, 18399, 18400, 18401, 18402, 18403, 18404, 18405, 18406, 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18550, 18551, 18552, 18553, 18554, 18555, 18556, 18557, 18558, 18559, 18560, 18561, 18562, 18563, 18564, 18565, 18566, 18567, 18568, 18569, 18570, 18571, 18572, 18573, 18574, 18575, 18576, 18577, 18578, 18579, 18580, 18581, 18582, 18583, 18584, 18585, 18586, 18587, 18588, 18589, 18590, 18591, 18592, 18593, 18594, 18595, 18596, 18597, 18598, 18599, 18600, 18601, 18602, 18603, 18604, 18605, 18606, 18607, 18608, 18609, 18610, 18611, 18612, 18613, 18614, 18615, 18616, 18617, 18618, 18619, 18620, 18621, 18622, 18623, 18624, 18625, 18626, 18627, 18628, 18629, 18630, 18631, 18632, 18633, 18634, 18635, 18636, 18637, 18638, 18639, 18640, 18641, 18642, 18643, 18644, 18645, 18646, 18647, 18648, 18649, 18650, 18651, 18652, 18653, 18654, 18655, 18656, 18657, 18658, 18659, 18660, 18661, 18662, 18663, 18664, 18665, 18666, 18667, 18668, 18669, 18670, 18671, 18672, 18673, 18674, 18675, 18676, 18677, 18678, 18679, 18680, 18681, 18682, 18683, 18684, 18685, 18686, 18687, 18688, 18689, 18690, 18691, 18692, 18693, 18694, 18695, 18696, 18697, 18698, 18699, 18700, 18701, 18702, 18703, 18704, 18705, 18706, 18707, 18708, 18709, 18710, 18711, 18712, 18713, 18714, 18715, 18716, 18717, 18718, 18719, 18720, 18721, 18722, 18723, 18724, 18725, 18726, 18727, 18728, 18729, 18730, 18731, 18732, 18733, 18734, 18735, 18736, 18737, 18738, 18739, 18740, 18741, 18742, 18743, 18744, 18745, 18746, 18747, 18748, 18749, 18750, 18751, 18752,							



GOTERM_MF_FAT	GO:0032553~ribonucleotide binding	81	14.80804388	2.E-02 18746, 228543, 14685, 26905, 13627, 19	476	1796	13288	1.E+00	1.E+00	2.E-01
SP_PIR_KEYWORDS	phorbol ester binding	3	0.548446069	2.E-02 18753, 18762, 18754	541	8	17854	1.E+01	1.E+00	1.E-01
INTERPRO	IPR000719:Protein kinase, core	24	4.387568556	2.E-02 11350, 13649, 270672, 18479, 545156, :	535	491	17763	2.E+00	1.E+00	4.E-01
GOTERM_BP_FAT	GO:0006468~protein amino acid phosphorylation	34	6.215722121	3.E-02 13649, 19247, 13665, 20416, 12912, 136	491	640	13588	1.E+00	1.E+00	3.E-01
UP_SEQ_FEATURE	binding site:ATP	28	5.118829982	3.E-02 13649, 22245, 103988, 545156, 13836, :	537	545	16021	2.E+00	1.E+00	6.E-01
INTERPRO	IPR015745:Protein kinase C	3	0.548446069	3.E-02 18753, 18762, 18754	535	9	17763	1.E+01	1.E+00	4.E-01
GOTERM_MF_FAT	GO:0004713~protein tyrosine kinase activity	12	2.193784278	3.E-02 13836, 11350, 13649, 14191, 20779, 138	476	164	13288	2.E+00	1.E+00	2.E-01
SMART	SM00133:S_TK_X	5	0.914076782	5.E-02 18753, 18762, 18754, 19108, 20112	248	53	9131	3.E+00	1.E+00	3.E-01
UP_SEQ_FEATURE	nucleotide phosphate-binding region:ATP	40	7.31261426	6.E-02 13649, 21915, 22245, 15929, 14450, 10:	537	907	16021	1.E+00	1.E+00	9.E-01
INTERPRO	IPR000961:AGC-kinase, C-terminal	5	0.914076782	7.E-02 18753, 18762, 18754, 19108, 20112	535	53	17763	3.E+00	1.E+00	7.E-01
GOTERM_MF_FAT	GO:0004697~protein kinase C activity	3	0.548446069	1.E-01 18753, 18762, 18754	476	15	13288	6.E+00	1.E+00	5.E-01
GOTERM_MF_FAT	GO:0004672~protein kinase activity	28	5.118829982	1.E-01 13649, 545156, 20020, 13836, 21813, 1:	476	583	13288	1.E+00	1.E+00	5.E-01
UP_SEQ_FEATURE	domain:AGC-kinase C-terminal	5	0.914076782	1.E-01 18753, 18762, 18754, 19108, 20112	537	53	16021	3.E+00	1.E+00	9.E-01
INTERPRO	IPR017892:Protein kinase, C-terminal	4	0.731261426	1.E-01 18753, 18762, 18754, 20112	535	40	17763	3.E+00	1.E+00	8.E-01
UP_SEQ_FEATURE	domain:Protein kinase	21	3.839122486	2.E-01 11350, 13649, 270672, 18479, 545156, :	537	476	16021	1.E+00	1.E+00	1.E+00
SP_PIR_KEYWORDS	atp-binding	45	8.226691042	2.E-01 18746, 13649, 21915, 27041, 22245, 15:	541	1287	17854	1.E+00	1.E+00	5.E-01
SP_PIR_KEYWORDS	serine/threonine-specific protein kinase	3	0.548446069	3.E-01 18753, 18762, 18754	541	40	17854	2.E+00	1.E+00	7.E-01
SMART	SM00220:S_TKc	9	1.645338208	4.E-01 270672, 18753, 18762, 18754, 19108, 1:	248	265	9131	1.E+00	1.E+00	9.E-01
GOTERM_MF_FAT	GO:0001882~nucleoside binding	57	10.42047532	5.E-01 18746, 66885, 18126, 20779, 72269, 27:	476	1558	13288	1.E+00	1.E+00	1.E+00
INTERPRO	IPR008271:Serine/threonine protein kinase, active site	12	2.193784278	5.E-01 270672, 18753, 21813, 18762, 18754, 1:	535	360	17763	1.E+00	1.E+00	1.E+00
GOTERM_MF_FAT	GO:0001883~purine nucleoside binding	56	10.23765996	5.E-01 18746, 66885, 18126, 20779, 270163, 1:	476	1548	13288	1.E+00	1.E+00	1.E+00
INTERPRO	IPR002290:Serine/threonine protein kinase	9	1.645338208	5.E-01 270672, 18753, 18762, 18754, 19108, 1:	535	265	17763	1.E+00	1.E+00	1.E+00
INTERPRO	IPR017442:Serine/threonine protein kinase-related	12	2.193784278	6.E-01 270672, 18753, 21813, 18762, 18754, 1:	535	374	17763	1.E+00	1.E+00	1.E+00
GOTERM_MF_FAT	GO:0030554~adenyl nucleotide binding	55	10.05484461	6.E-01 18746, 66885, 18126, 20779, 270163, 1:	476	1535	13288	1.E+00	1.E+00	1.E+00
SP_PIR_KEYWORDS	serine/threonine~protein kinase	12	2.193784278	6.E-01 270672, 18753, 21813, 18762, 18754, 1:	541	384	17854	1.E+00	1.E+00	9.E-01
KEGG_PATHWAY	mmu04530:Tight junction	9	1.645338208	7.E-01 18753, 18762, 20779, 18754, 19053, 22:	372	135	5738	1.E+00	1.E+00	9.E-01
GOTERM_MF_FAT	GO:0005524~ATP binding	50	9.140767824	7.E-01 18746, 20779, 270163, 19108, 11947, 2:	476	1443	13288	1.E+00	1.E+00	1.E+00
GOTERM_MF_FAT	GO:0032559~adenyl ribonucleotide binding	50	9.140767824	7.E-01 18746, 20779, 270163, 19108, 11947, 2:	476	1460	13288	1.E+00	1.E+00	1.E+00
GOTERM_MF_FAT	GO:0004674~protein serine/threonine kinase activity	14	2.559414991	7.E-01 270672, 18479, 545156, 21813, 18753, :	476	421	13288	9.E-01	1.E+00	1.E+00

Annotation Cluster 46	Enrichment Score: 2.0294292241304275										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
SP_PIR_KEYWORDS	membrane attack complex	5	0.914076782	4.E-06	12279, 230558, 69379, 15139, 110382	541	5	17854	3.E+01	2.E-03	5.E-05
SP_PIR_KEYWORDS	complement alternate pathway	6	1.096892139	6.E-06	12266, 12279, 230558, 69379, 15139, 110382	541	10	17854	2.E+01	2.E-03	7.E-05
GOTERM_CC_FAT	GO:0005579~membrane attack complex	5	0.914076782	6.E-06	12279, 230558, 69379, 15139, 110382	419	5	12504	3.E+01	2.E-03	6.E-05
GOTERM_BP_FAT	GO:0006957~complement activation, alternative pathway	6	1.096892139	1.E-05	12266, 12279, 230558, 69379, 15139, 110382	491	10	13588	2.E+01	3.E-02	5.E-04
SP_PIR_KEYWORDS	complement pathway	7	1.279707495	1.E-04	12266, 12258, 12279, 230558, 69379, 15139, 110382	541	26	17854	9.E+00	4.E-02	1.E-03
GOTERM_BP_FAT	GO:0006958~complement activation, classical pathway	7	1.279707495	6.E-04	12266, 12258, 12279, 230558, 69379, 15139, 110382	491	30	13588	6.E+00	7.E-01	2.E-02
SP_PIR_KEYWORDS	cytolysis	5	0.914076782	7.E-04	12279, 230558, 69379, 15139, 110382	541	14	17854	1.E+01	2.E-01	5.E-03
GOTERM_BP_FAT	GO:0002443~leukocyte mediated immunity	11	2.010968921	1.E-03	15170, 12266, 18753, 12258, 12279, 230558, 69379, 15139, 110382	491	89	13588	3.E+00	9.E-01	4.E-02
GOTERM_BP_FAT	GO:0002455~humoral immune response mediated by circulating immune complex	7	1.279707495	1.E-03	12266, 12258, 12279, 230558, 69379, 15139, 110382	491	35	13588	6.E+00	9.E-01	4.E-02
GOTERM_BP_FAT	GO:0002541~activation of plasma proteins involved in acute inflammation	7	1.279707495	2.E-03	12266, 12258, 12279, 230558, 69379, 15139, 110382	491	36	13588	5.E+00	1.E+00	5.E-02
GOTERM_BP_FAT	GO:0006956~complement activation	7	1.279707495	2.E-03	12266, 12258, 12279, 230558, 69379, 15139, 110382	491	36	13588	5.E+00	1.E+00	5.E-02
GOTERM_BP_FAT	GO:0002252~immune effector process	13	2.376599634	2.E-03	15170, 12266, 12258, 12279, 16423, 69379, 15139, 110382	491	126	13588	3.E+00	1.E+00	5.E-02
KEGG_PATHWAY	mmu04610:Complement and coagulation cascades	13	2.376599634	3.E-03	12266, 12258, 12279, 16644, 69379, 15139, 110382	372	75	5738	3.E+00	3.E-01	2.E-02
SMART	SM00457:MACPF	4	0.731261426	4.E-03	12279, 230558, 12274, 110382	248	12	9131	1.E+01	4.E-01	4.E-02
GOTERM_BP_FAT	GO:0002253~activation of immune response	10	1.828153565	4.E-03	15170, 12266, 12258, 12279, 230558, 69379, 15139, 110382	491	86	13588	3.E+00	1.E+00	9.E-02
INTERPRO	IPR001862:Membrane attack complex component/perforin/complement	4	0.731261426	5.E-03	12279, 230558, 12274, 110382	535	12	17763	1.E+01	1.E+00	1.E-01
GOTERM_BP_FAT	GO:0002449~lymphocyte mediated immunity	9	1.645338208	6.E-03	15170, 12266, 18753, 12258, 12279, 230558, 69379, 15139, 110382	491	76	13588	3.E+00	1.E+00	1.E-01
BIOCARTA	m_alternativePathway:Alternative Complement Pathway	5	0.914076782	6.E-03	12266, 12279, 15139, 12417, 12274	109	9	1171	6.E+00	7.E-01	9.E-02
KEGG_PATHWAY	mmu05020:Prion diseases	8	1.462522852	6.E-03	12279, 230558, 69379, 19108, 15139, 110382	372	35	5738	4.E+00	6.E-01	3.E-02
PIR_SUPERFAMILY	PIRSF002481:complement C9	3	0.548446069	6.E-03	12279, 230558, 110382	378	3	8136	2.E+01	9.E-01	4.E-01
GOTERM_BP_FAT	GO:0016064~immunoglobulin mediated immune response	8	1.462522852	7.E-03	12266, 18753, 12258, 12279, 230558, 69379, 15139, 110382	491	63	13588	4.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0009611~response to wounding	23	4.204753199	8.E-03	15170, 12266, 14674, 15930, 12258, 16423, 69379, 15139, 110382	491	347	13588	2.E+00	1.E+00	2.E-01
SMART	SM00192:LDLa	6	1.096892139	8.E-03	12279, 23359, 230558, 16835, 12274, 110382	248	46	9131	5.E+00	7.E-01	6.E-02
GOTERM_BP_FAT	GO:0019835~cytolysis	5	0.914076782	9.E-03	12279, 230558, 69379, 15139, 110382	491	23	13588	6.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0002526~acute inflammatory response	9	1.645338208	9.E-03	20848, 12266, 12258, 15930, 12279, 230558, 69379, 15139, 110382	491	81	13588	3.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0019724~B cell mediated immunity	8	1.462522852	9.E-03	12266, 18753, 12258, 12279, 230558, 69379, 15139, 110382	491	65	13588	3.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0051605~protein maturation by peptide bond cleavage	8	1.462522852	9.E-03	12266, 12258, 11487, 12279, 230558, 69379, 15139, 110382	491	65	13588	3.E+00	1.E+00	2.E-01



GOTERM_BP_FAT	GO:0002460~adaptive immune response based on somatic recomb	9	1.645338208	1.E-02	12266, 18753, 12258, 12279, 230558, 6	491	84	13588	3.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0002250~adaptive immune response	9	1.645338208	1.E-02	12266, 18753, 12258, 12279, 230558, 6	491	84	13588	3.E+00	1.E+00	2.E-01
INTERPRO	IPR002172:Low density lipoprotein-receptor, class A, cysteine-rich	6	1.096892139	1.E-02	12279, 22359, 230558, 16835, 12274, 1	535	46	17763	4.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0006959~humoral immune response	7	1.279707495	1.E-02	12266, 12258, 12279, 230558, 69379, 1	491	54	13588	4.E+00	1.E+00	2.E-01
KEGG_PATHWAY	mmu05322:Systemic lupus erythematosus	14	2.559414991	1.E-02	621893, 12266, 12279, 15078, 69379, 1	372	103	5738	2.E+00	9.E-01	6.E-02
UP_SEQ_FEATURE	domain:MACPF	3	0.548446069	2.E-02	12279, 230558, 110382	537	6	16021	1.E+01	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0048584~positive regulation of response to stimulus	14	2.559414991	2.E-02	15170, 12266, 15930, 12258, 12279, 16	491	186	13588	2.E+00	1.E+00	3.E-01
GOTERM_BP_FAT	GO:0050778~positive regulation of immune response	11	2.010968921	3.E-02	15170, 12266, 12258, 15930, 12279, 23	491	136	13588	2.E+00	1.E+00	3.E-01
BIOCARTA	m_classicPathway:Classical Complement Pathway	5	0.914076782	3.E-02	12266, 12279, 15139, 12417, 12274	109	13	1171	4.E+00	1.E+00	2.E-01
BIOCARTA	m_lectinPathway:Lectin Induced Complement Pathway	5	0.914076782	3.E-02	12266, 12279, 15139, 12417, 12274	109	13	1171	4.E+00	1.E+00	2.E-01
SP_PIR_KEYWORDS	innate immunity	7	1.279707495	3.E-02	12266, 12258, 12279, 230558, 69379, 1	541	75	17854	3.E+00	1.E+00	1.E-01
UP_SEQ_FEATURE	domain:EGF-like	7	1.279707495	3.E-02	11489, 12279, 20343, 230558, 18791, 2	537	68	16021	3.E+00	1.E+00	6.E-01
GOTERM_BP_FAT	GO:0006954~inflammatory response	15	2.742230347	3.E-02	12266, 15930, 12258, 12279, 16644, 69	491	225	13588	2.E+00	1.E+00	4.E-01
SP_PIR_KEYWORDS	plasma	4	0.731261426	3.E-02	12266, 12279, 238055, 15139	541	24	17854	6.E+00	1.E+00	1.E-01
GOTERM_CC_FAT	GO:0046930~pore complex	7	1.279707495	3.E-02	664868, 12279, 230558, 69379, 15139, 1	419	73	12504	3.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0016485~protein processing	8	1.462522852	4.E-02	12266, 12258, 11487, 12279, 230558, 6	491	90	13588	2.E+00	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0051604~protein maturation	8	1.462522852	6.E-02	12266, 12258, 11487, 12279, 230558, 6	491	96	13588	2.E+00	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0002684~positive regulation of immune system process	13	2.376599634	7.E-02	15170, 12266, 15930, 12258, 12279, 69	491	206	13588	2.E+00	1.E+00	6.E-01
BIOCARTA	m_compPathway:Complement Pathway	5	0.914076782	8.E-02	12266, 12279, 15139, 12417, 12274	109	18	1171	3.E+00	1.E+00	4.E-01
GOTERM_BP_FAT	GO:0045087~innate immune response	8	1.462522852	9.E-02	15170, 12266, 12258, 12279, 230558, 6	491	107	13588	2.E+00	1.E+00	7.E-01
UP_SEQ_FEATURE	domain:LDL-receptor class A	3	0.548446069	1.E-01	12279, 230558, 110382	537	17	16021	5.E+00	1.E+00	9.E-01
SP_PIR_KEYWORDS	immune response	9	1.645338208	2.E-01	12266, 208154, 12258, 12279, 230558, 6	541	184	17854	2.E+00	1.E+00	5.E-01
SMART	SM00209:TSP1	4	0.731261426	2.E-01	12279, 230558, 12274, 110382	248	59	9131	2.E+00	1.E+00	6.E-01
INTERPRO	IPR000884:Thrombospondin, type 1 repeat	4	0.731261426	3.E-01	12279, 230558, 12274, 110382	535	59	17763	2.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0006952~defense response	20	3.65630713	3.E-01	15170, 12266, 15930, 12258, 16644, 12	491	448	13588	1.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0006955~immune response	18	3.290676417	5.E-01	22324, 15170, 12266, 208154, 12258, 1	491	471	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0002697~regulation of immune effector process	3	0.548446069	8.E-01	15170, 12266, 12258	491	88	13588	9.E-01	1.E+00	1.E+00
GOTERM_CC_FAT	GO:0005887~integral to plasma membrane	13	2.376599634	9.E-01	208154, 12279, 16423, 69379, 15139, 1	419	531	12504	7.E-01	1.E+00	1.E+00
GOTERM_CC_FAT	GO:0031226~intrinsic to plasma membrane	13	2.376599634	1.E+00	208154, 12279, 16423, 69379, 15139, 1	419	552	12504	7.E-01	1.E+00	1.E+00



UP_SEQ_FEATURE	domain:DEP	4	0.731261426	2.E-02	19739, 218581, 211896, 76131	537	17	16021	7.E+00	1.E+00	5.E-01
INTERPRO	IPR011991:Winged helix repressor DNA-binding	10	1.828153565	8.E-02	277360, 13555, 242705, 56347, 13559, :	535	175	17763	2.E+00	1.E+00	7.E-01
Annotation Cluster 51											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
KEGG_PATHWAY	mmu04510:Focal adhesion	25	4.570383912	2.E-03	13649, 22324, 11855, 20416, 170758, 21	372	198	5738	2.E+00	3.E-01	1.E-02
KEGG_PATHWAY	mmu04662:B cell receptor signaling pathway	13	2.376599634	5.E-03	22324, 15170, 57257, 170758, 18709, 21	372	80	5738	3.E+00	5.E-01	3.E-02
KEGG_PATHWAY	mmu04664:Fc epsilon R1 signaling pathway	13	2.376599634	6.E-03	22324, 14389, 57257, 170758, 18709, 21	372	82	5738	2.E+00	6.E-01	3.E-02
KEGG_PATHWAY	mmu04650:Natural killer cell mediated cytotoxicity	16	2.925045704	1.E-02	22324, 15170, 19247, 57257, 18479, 20	372	122	5738	2.E+00	8.E-01	5.E-02
KEGG_PATHWAY	mmu04810:Regulation of actin cytoskeleton	22	4.021937843	4.E-02	14163, 13649, 22324, 14674, 12929, 57	372	217	5738	2.E+00	1.E+00	1.E-01
KEGG_PATHWAY	mmu04660:T cell receptor signaling pathway	13	2.376599634	8.E-02	22324, 15170, 57257, 18479, 11848, 18	372	118	5738	2.E+00	1.E+00	2.E-01
Annotation Cluster 52											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
SP_PIR_KEYWORDS	Flavoprotein	11	2.010968921	1.E-03	66885, 98256, 11409, 67273, 12952, 17	541	103	17854	4.E+00	3.E-01	7.E-03
SP_PIR_KEYWORDS	FAD	11	2.010968921	2.E-03	66885, 98256, 18126, 11409, 67273, 12	541	109	17854	3.E+00	5.E-01	1.E-02
UP_SEQ_FEATURE	nucleotide phosphate-binding region:FAD	6	1.096892139	4.E-02	66885, 18126, 11409, 13382, 18984, 20	537	58	16021	3.E+00	1.E+00	8.E-01
GOTERM_MF_FAT	GO:0050660--FAD binding	5	0.914076782	2.E-01	66885, 18126, 11409, 13382, 20775	476	71	13288	2.E+00	1.E+00	8.E-01
Annotation Cluster 53											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
KEGG_PATHWAY	mmu00020:Citrate cycle (TCA cycle)	10	1.828153565	1.E-04	68263, 17448, 235339, 18597, 78920, 11	372	31	5738	5.E+00	2.E-02	1.E-03
GOTERM_BP_FAT	GO:0006084--acetyl-CoA metabolic process	6	1.096892139	5.E-03	17448, 235339, 78920, 67834, 15929, 61	491	31	13588	5.E+00	1.E+00	1.E-01
SP_PIR_KEYWORDS	tricarboxylic acid cycle	4	0.731261426	2.E-02	17448, 78920, 67834, 15929	541	19	17854	7.E+00	1.E+00	8.E-02
GOTERM_BP_FAT	GO:0009109--coenzyme catabolic process	5	0.914076782	2.E-02	17448, 78920, 67834, 15929, 17969	491	29	13588	5.E+00	1.E+00	3.E-01
GOTERM_BP_FAT	GO:0051187--cofactor catabolic process	5	0.914076782	3.E-02	17448, 78920, 67834, 15929, 17969	491	32	13588	4.E+00	1.E+00	4.E-01
GOTERM_BP_FAT	GO:0006099--tricarboxylic acid cycle	4	0.731261426	5.E-02	17448, 78920, 67834, 15929	491	23	13588	5.E+00	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0046356--acetyl-CoA catabolic process	4	0.731261426	5.E-02	17448, 78920, 67834, 15929	491	24	13588	5.E+00	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0009060--aerobic respiration	4	0.731261426	7.E-02	17448, 78920, 67834, 15929	491	27	13588	4.E+00	1.E+00	6.E-01
Annotation Cluster 54											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
UP_SEQ_FEATURE	domain:SH3 1	6	1.096892139	4.E-03	22324, 14784, 57257, 12929, 17969, 54	537	33	16021	5.E+00	1.E+00	2.E-01
UP_SEQ_FEATURE	domain:SH3 2	6	1.096892139	5.E-03	22324, 14784, 57257, 12929, 17969, 54	537	34	16021	5.E+00	1.E+00	2.E-01
INTERPRO	IPR011511:Variant SH3	5	0.914076782	1.E-01	22324, 57257, 12929, 233071, 545156	535	59	17763	3.E+00	1.E+00	8.E-01
Annotation Cluster 55											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
INTERPRO	IPR002219:Protein kinase C, phorbol ester/diacylglycerol binding	9	1.645338208	1.E-04	22324, 18753, 78816, 18754, 17925, 70	535	52	17763	6.E+00	1.E-01	8.E-03
UP_SEQ_FEATURE	zinc finger region:Phorbol-ester/DAG-type 1	3	0.548446069	1.E-01	18753, 18754, 270163	537	19	16021	5.E+00	1.E+00	9.E-01
UP_SEQ_FEATURE	zinc finger region:Phorbol-ester/DAG-type 2	3	0.548446069	1.E-01	18753, 18754, 270163	537	19	16021	5.E+00	1.E+00	9.E-01
Annotation Cluster 56											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_CC_FAT	GO:0005626--insoluble fraction	29	5.301645338	1.E-02	13121, 14685, 19247, 12955, 11852, 66	419	528	12504	2.E+00	1.E+00	9.E-02
GOTERM_CC_FAT	GO:0000267--cell fraction	31	5.667276051	2.E-02	13121, 14685, 672195, 19247, 12955, 1	419	596	12504	2.E+00	1.E+00	1.E-01
GOTERM_CC_FAT	GO:0005624--membrane fraction	27	4.936014625	2.E-02	13121, 14685, 19247, 11852, 665032, 2	419	510	12504	2.E+00	1.E+00	2.E-01
Annotation Cluster 57											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_BP_FAT	GO:0009611--response to wounding	23	4.204753199	8.E-03	15170, 12266, 14674, 15930, 12258, 16	491	347	13588	2.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0007596--blood coagulation	8	1.462522852	1.E-02	14060, 14674, 12258, 16644, 12279, 74	491	70	13588	3.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0050817--coagulation	8	1.462522852	1.E-02	14060, 14674, 12258, 16644, 12279, 74	491	70	13588	3.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0007599--hemostasis	8	1.462522852	1.E-02	14060, 14674, 12258, 16644, 12279, 74	491	71	13588	3.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0042060--wound healing	10	1.828153565	2.E-02	14060, 14674, 21813, 12258, 16644, 12	491	112	13588	2.E+00	1.E+00	3.E-01
SP_PIR_KEYWORDS	blood coagulation	5	0.914076782	2.E-02	14060, 12258, 16644, 74145, 21789	541	37	17854	4.E+00	1.E+00	1.E-01
GOTERM_BP_FAT	GO:0050878--regulation of body fluid levels	8	1.462522852	4.E-02	14060, 14674, 12258, 16644, 12279, 74	491	89	13588	2.E+00	1.E+00	5.E-01
Annotation Cluster 58											
Enrichment Score: 1.7765197232735417											



[illegible]

Annotation Cluster 59	Enrichment Score: 1.7661347438113373										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
SMART	SM00515:elF5C	3	0.548446069	1.E-02	217869, 224045, 208643, 100047658	248	7	9131	2.E+01	9.E-01	1.E-01
INTERPRO	IPR003307:elF4-gamma/elF5/elF2-epsilon	3	0.548446069	2.E-02	217869, 224045, 208643, 100047658	535	7	17763	1.E+01	1.E+00	3.E-01
UP_SEQ_FEATURE	domain:W2	3	0.548446069	2.E-02	217869, 224045, 208643, 100047658	537	7	16021	1.E+01	1.E+00	6.E-01

Annotation Cluster 60		Enrichment Score: 1.758067532962539									
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_MF_FAT	GO:0009055~electron carrier activity	23	4.204753199	3.E-06	13121, 66694, 226646, 672195, 66885, 1	476	202	13288	3.E+00	2.E-03	7.E-05
SP_PIR_KEYWORDS	iron	25	4.570383912	5.E-05	13121, 226646, 672195, 12858, 18126, 1	541	321	17854	3.E+00	2.E-02	5.E-04
SP_PIR_KEYWORDS	heme	15	2.742230347	1.E-04	13121, 672195, 15930, 76279, 66445, 1	541	142	17854	3.E+00	4.E-02	1.E-03
SP_PIR_KEYWORDS	electron transfer	7	1.279707495	1.E-04	672195, 17705, 13087, 17706, 13074, 1	541	27	17854	9.E+00	5.E-02	1.E-03
SP_PIR_KEYWORDS	chromoprotein	8	1.462522852	2.E-04	672195, 15130, 13087, 13074, 13063, 1	541	40	17854	7.E+00	6.E-02	2.E-03
SP_PIR_KEYWORDS	metalloprotein	9	1.645338208	3.E-04	18746, 672195, 15130, 13087, 13074, 1	541	56	17854	5.E+00	9.E-02	2.E-03
GOTERM_MF_FAT	GO:0005506~iron ion binding	26	4.753199269	6.E-04	13121, 226646, 672195, 12858, 18126, 1	476	343	13288	2.E+00	3.E-01	9.E-03
UP_SEQ_FEATURE	metal ion-binding site:Iron (heme axial ligand)	11	2.010968921	2.E-03	13121, 18126, 672195, 76279, 13087, 6	537	99	16021	3.E+00	9.E-01	1.E-01
GOTERM_MF_FAT	GO:0046906~tetrapyrrole binding	13	2.376599634	8.E-03	13121, 672195, 15930, 76279, 65969, 6	476	151	13288	2.E+00	1.E+00	8.E-02
GOTERM_MF_FAT	GO:0020037~heme binding	12	2.193784278	1.E-02	13121, 672195, 15930, 76279, 66445, 1	476	144	13288	2.E+00	1.E+00	1.E-01
SP_PIR_KEYWORDS	microsome	7	1.279707495	8.E-02	13121, 76279, 13087, 13117, 94284, 13	541	100	17854	2.E+00	1.E+00	3.E-01
INTERPRO	IPR017973:Cytochrome P450, C-terminal region	6	1.096892139	1.E-01	13121, 76279, 13087, 13074, 13117, 13	535	81	17763	2.E+00	1.E+00	8.E-01
SP_PIR_KEYWORDS	Monoxygenase	7	1.279707495	1.E-01	13121, 98256, 76279, 13087, 13074, 13	541	108	17854	2.E+00	1.E+00	3.E-01
INTERPRO	IPR001128:Cytochrome P450	6	1.096892139	1.E-01	13121, 76279, 13087, 13074, 13117, 13	535	87	17763	2.E+00	1.E+00	8.E-01
INTERPRO	IPR017972:Cytochrome P450, conserved site	6	1.096892139	1.E-01	13121, 76279, 13087, 13074, 13117, 13	535	89	17763	2.E+00	1.E+00	9.E-01
COG_ONTOLOGY	Secondary metabolites biosynthesis, transport, and catabolism	6	1.096892139	1.E-01	13121, 76279, 13087, 13074, 13117, 13	52	109	2040	2.E+00	8.E-01	3.E-01
INTERPRO	IPR002401:Cytochrome P450, E-class, group I	5	0.914076782	2.E-01	76279, 13087, 13074, 13117, 13075	535	70	17763	2.E+00	1.E+00	9.E-01
GOTERM_CC_FAT	GO:0005792~microsome	9	1.645338208	2.E-01	13121, 13350, 76279, 238055, 13087, 1	419	176	12504	2.E+00	1.E+00	7.E-01
GOTERM_CC_FAT	GO:0042598~vesicular fraction	9	1.645338208	3.E-01	13121, 13350, 76279, 238055, 13087, 1	419	182	12504	1.E+00	1.E+00	8.E-01
GOTERM_MF_FAT	GO:0070330~aromatase activity	3	0.548446069	3.E-01	76279, 13087, 13075	476	34	13288	2.E+00	1.E+00	9.E-01
GOTERM_MF_FAT	GO:0016712~oxidoreductase activity, acting on paired donors, with	3	0.548446069	5.E-01	76279, 13087, 13075	476	44	13288	2.E+00	1.E+00	9.E-01
PIR_SUPERFAMILY	PIRSF000045:cyclochrome P450_CYP2D6	3	0.548446069	5.E-01	76279, 13087, 13074	378	36	8136	2.E+00	1.E+00	1.E+00
KEGG_PATHWAY	mmu00830:Retinol metabolism	4	0.731261426	8.E-01	13350, 13087, 13117, 94284, 394436	372	68	5738	9.E-01	1.E+00	1.E+00
GOTERM_CC_FAT	GO:0005783~endoplasmic reticulum	24	4.387568556	9.E-01	13121, 56348, 238055, 65969, 18205, 1	419	838	12504	9.E-01	1.E+00	1.E+00
SP_PIR_KEYWORDS	endoplasmic reticulum	16	2.925045704	9.E-01	13121, 76279, 56348, 18984, 10004345	541	678	17854	8.E-01	1.E+00	1.E+00

Annotation Category	Cluster 61 Term	Enrichment Score: 1.7113954013283899		Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
INTERPRO	IPR001078:2-oxoacid dehydrogenase acyltransferase, catalytic dom:			3	0.548446069		5.E-03 235339, 27402, 78920	535	4	17763	2.E+01	1.E+00	1.E-01
INTERPRO	IPR003016:2-oxo acid dehydrogenase, lipoyl-binding site			3	0.548446069		8.E-03 235339, 27402, 78920	535	5	17763	2.E+01	1.E+00	2.E-01
SP_PIR_KEYWORDS	lipoyl			3	0.548446069		9.E-03 235339, 27402, 78920	541	5	17854	2.E+01	1.E+00	4.E-02
GOTERM_MF_FAT	GO:0031405--lipic acid binding			3	0.548446069		1.E-02 235339, 27402, 78920	476	5	13288	2.E+01	1.E+00	1.E-01
INTERPRO	IPR000089:Biotin/lipoyl attachment			3	0.548446069		3.E-02 235339, 27402, 78920	535	9	17763	1.E+01	1.E+00	4.E-01
GOTERM_MF_FAT	GO:0031406-carboxylic acid binding			7	1.279707495		8.E-02 70316, 18126, 11409, 235339, 13350, 2	476	85	13288	2.E+00	1.E+00	5.E-01



SP_PIR_KEYWORDS	Acyltransferase		9	1.645338208	1.E-01	12753, 235339, 13350, 27402, 74145, 74146, 74147, 74148, 74149, 74150, 74151, 74152, 74153, 74154, 74155, 74156, 74157, 74158, 74159, 74160, 74161, 74162, 74163, 74164, 74165, 74166, 74167, 74168, 74169, 74170, 74171, 74172, 74173, 74174, 74175, 74176, 74177, 74178, 74179, 74180, 74181, 74182, 74183, 74184, 74185, 74186, 74187, 74188, 74189, 74190, 74191, 74192, 74193, 74194, 74195, 74196, 74197, 74198, 74199, 74200, 74201, 74202, 74203, 74204, 74205, 74206, 74207, 74208, 74209, 74210, 74211, 74212, 74213, 74214, 74215, 74216, 74217, 74218, 74219, 74220, 74221, 74222, 74223, 74224, 74225, 74226, 74227, 74228, 74229, 74230, 74231, 74232, 74233, 74234, 74235, 74236, 74237, 74238, 74239, 74240, 74241, 74242, 74243, 74244, 74245, 74246, 74247, 74248, 74249, 74250, 74251, 74252, 74253, 74254, 74255, 74256, 74257, 74258, 74259, 74260, 74261, 74262, 74263, 74264, 74265, 74266, 74267, 74268, 74269, 74270, 74271, 74272, 74273, 74274, 74275, 74276, 74277, 74278, 74279, 74280, 74281, 74282, 74283, 74284, 74285, 74286, 74287, 74288, 74289, 74290, 74291, 74292, 74293, 74294, 74295, 74296, 74297, 74298, 74299, 74300, 74301, 74302, 74303, 74304, 74305, 74306, 74307, 74308, 74309, 74310, 74311, 74312, 74313, 74314, 74315, 74316, 74317, 74318, 74319, 74320, 74321, 74322, 74323, 74324, 74325, 74326, 74327, 74328, 74329, 74330, 74331, 74332, 74333, 74334, 74335, 74336, 74337, 74338, 74339, 74340, 74341, 74342, 74343, 74344, 74345, 74346, 74347, 74348, 74349, 74350, 74351, 74352, 74353, 74354, 74355, 74356, 74357, 74358, 74359, 74360, 74361, 74362, 74363, 74364, 74365, 74366, 74367, 74368, 74369, 74370, 74371, 74372, 74373, 74374, 74375, 74376, 74377, 74378, 74379, 74380, 74381, 74382, 74383, 74384, 74385, 74386, 74387, 74388, 74389, 74390, 74391, 74392, 74393, 74394, 74395, 74396, 74397, 74398, 74399, 74400, 74401, 74402, 74403, 74404, 74405, 74406, 74407, 74408, 74409, 74410, 74411, 74412, 74413, 74414, 74415, 74416, 74417, 74418, 74419, 74420, 74421, 74422, 74423, 74424, 74425, 74426, 74427, 74428, 74429, 74430, 74431, 74432, 74433, 74434, 74435, 74436, 74437, 74438, 74439, 74440, 74441, 74442, 74443, 74444, 74445, 74446, 74447, 74448, 74449, 74450, 74451, 74452, 74453, 74454, 74455, 74456, 74457, 74458, 74459, 74460, 74461, 74462, 74463, 74464, 74465, 74466, 74467, 74468, 74469, 74470, 74471, 74472, 74473, 74474, 74475, 74476, 74477, 74478, 74479, 74480, 74481, 74482, 74483, 74484, 74485, 74486, 74487, 74488, 74489, 74490, 74491, 74492, 74493, 74494, 74495, 74496, 74497, 74498, 74499, 74500, 74501, 74502, 74503, 74504, 74505, 74506, 74507, 74508, 74509, 74510, 74511, 74512, 74513, 74514, 74515, 74516, 74517, 74518, 74519, 74520, 74521, 74522, 74523, 74524, 74525, 74526, 74527, 74528, 74529, 74530, 74531, 74532, 74533, 74534, 74535, 74536, 74537, 74538, 74539, 74540, 74541, 74542, 74543, 74544, 74545, 74546, 74547, 74548, 74549, 74550, 74551, 74552, 74553, 74554, 74555, 74556, 74557, 74558, 74559, 74560, 74561, 74562, 74563, 74564, 74565, 74566, 74567, 74568, 74569, 74570, 74571, 74572, 74573, 74574, 74575, 74576, 74577, 74578, 74579, 74580, 74581, 74582, 74583, 74584, 74585, 74586, 74587, 74588, 74589, 74590, 74591, 74592, 74593, 74594, 74595, 74596, 74597, 74598, 74599, 74600, 74601, 74602, 74603, 74604, 74605, 74606, 74607, 74608, 74609, 74610, 74611, 74612, 74613, 74614, 74615, 74616, 74617, 74618, 74619, 74620, 74621, 74622, 74623, 74624, 74625, 74626, 74627, 74628, 74629, 74630, 74631, 74632, 74633, 74634, 74635, 74636, 74637, 74638, 74639, 74640, 74641, 74642, 74643, 74644, 74645, 74646, 74647, 74648, 74649, 74650, 74651, 74652, 74653, 74654, 74655, 74656, 74657, 74658, 74659, 74660, 74661, 74662, 74663, 74664, 74665, 74666, 74667, 74668, 74669, 74670, 74671, 74672, 74673, 74674, 74675, 74676, 74677, 74678, 74679, 74680, 74681, 74682, 74683, 74684, 74685, 74686, 74687, 74688, 74689, 74690, 74691, 74692, 74693, 74694, 74695, 74696, 74697, 74698, 74699, 74700, 74701, 74702, 74703, 74704, 74705, 74706, 74707, 74708, 74709, 74710, 74711, 74712, 74713, 74714, 74715, 74716, 74
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SMART	SM00462:PTB	4	0.731261426	8.E-02 216148, 13131, 20416, 20418	248	38	9131	4.E+00	1.E+00	4.E-01
INTERPRO	IPR006020:Phosphotyrosine interaction region	4	0.731261426	1.E-01 216148, 13131, 20416, 20418	535	38	17763	3.E+00	1.E+00	8.E-01

Annotation Cluster 69	Enrichment Score: 1.4754032813017173										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_BP_FAT	GO:0046496--nicotinamide nucleotide metabolic process	5	0.914076782		1.E-02 98256, 21991, 17969, 103988, 14381	491	24	13588	6.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0006769--nicotinamide metabolic process	5	0.914076782		1.E-02 98256, 21991, 17969, 103988, 14381	491	24	13588	6.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0009820--alkaloid metabolic process	5	0.914076782		1.E-02 98256, 21991, 17969, 103988, 14381	491	24	13588	6.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0043603--cellular amide metabolic process	6	1.096892139		1.E-02 98256, 21991, 17969, 14600, 103988, 14381	491	39	13588	4.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0006739--NADP metabolic process	4	0.731261426		1.E-02 21991, 17969, 103988, 14381	491	14	13588	8.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0006732--coenzyme metabolic process	12	2.193784278		1.E-02 98256, 17448, 235339, 74147, 78920, 21991, 17969, 103988, 14381	491	143	13588	2.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0019362--pyridine nucleotide metabolic process	5	0.914076782		2.E-02 98256, 21991, 17969, 103988, 14381	491	28	13588	5.E+00	1.E+00	3.E-01
GOTERM_BP_FAT	GO:0006733--oxidoreduction coenzyme metabolic process	5	0.914076782		5.E-02 98256, 21991, 17969, 103988, 14381	491	38	13588	4.E+00	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0051186--cofactor metabolic process	12	2.193784278		7.E-02 98256, 17448, 235339, 74147, 78920, 21991, 17969, 103988, 14381	491	182	13588	2.E+00	1.E+00	6.E-01
GOTERM_BP_FAT	GO:0019748--secondary metabolic process	6	1.096892139		1.E-01 98256, 21991, 56847, 17969, 103988, 14381	491	69	13588	2.E+00	1.E+00	7.E-01
GOTERM_BP_FAT	GO:0006767--water-soluble vitamin metabolic process	3	0.548446069		3.E-01 98256, 17969, 14381	491	34	13588	2.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0006766--vitamin metabolic process	4	0.731261426		5.E-01 98256, 56847, 17969, 14381	491	69	13588	2.E+00	1.E+00	1.E+00

Annotation Cluster 70	Enrichment Score: 1.4683106148502776										
Category	Term: various cancer-related pathways	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
BIOCARTA	m_egfPathway:EGF Signaling Pathway	11	2.010968921		9.E-05 20848, 18708, 13649, 20846, 14784, 20416, 14625, 22852	109	28	1171	4.E+00	2.E-02	2.E-02
BIOCARTA	m_her2Pathway:Role of ERBB2 in Signal Transduction and Oncology	9	1.645338208		4.E-04 20848, 18708, 13649, 16195, 13867, 13645, 12912, 14784, 20662, 16476, 20416, 14625, 22852	109	22	1171	4.E+00	8.E-02	4.E-02
BIOCARTA	m_tffPathway:Trefoil Factors Initiate Mucosal Healing	9	1.645338208		6.E-04 18708, 13649, 672195, 13866, 14784, 20416, 14625, 22852	109	23	1171	4.E+00	1.E-01	4.E-02
BIOCARTA	m_metPathway:Signaling of Hepatocyte Growth Factor Receptor	10	1.828153565		2.E-03 20848, 18708, 20779, 19247, 14784, 20416, 14625, 22852	109	32	1171	3.E+00	3.E-01	7.E-02
BIOCARTA	m_il6Pathway:IL 6 signaling pathway	8	1.462522852		2.E-03 20848, 16195, 19247, 14784, 20662, 16476, 20416, 14625, 22852	109	21	1171	4.E+00	3.E-01	6.E-02
BIOCARTA	m_gleevecPathway:Inhibition of Cellular Proliferation by Gleevec	8	1.462522852		2.E-03 18708, 20846, 14784, 20662, 16476, 12912, 14784, 20662, 16476, 20416, 14625, 22852	109	22	1171	4.E+00	4.E-01	6.E-02
BIOCARTA	m_pdgfPathway:PDGF Signaling Pathway	9	1.645338208		3.E-03 20848, 18708, 20846, 14784, 20662, 16476, 20416, 14625, 22852	109	28	1171	3.E+00	4.E-01	6.E-02
BIOCARTA	m_TPOPathway:TPO Signaling Pathway	8	1.462522852		3.E-03 20848, 18708, 20846, 14784, 20662, 16476, 20416, 14625, 22852	109	23	1171	4.E+00	5.E-01	6.E-02
KEGG_PATHWAY	mmu05215:Prostate cancer	14	2.559414991		5.E-03 13649, 12912, 13645, 12914, 18709, 18708, 14784, 20662, 16476, 20416, 14625, 22852	372	90	5738	2.E+00	5.E-01	3.E-02
BIOCARTA	m_HBxPathway:Calcium Signaling by HBx of Hepatitis B virus	5	0.914076782		6.E-03 20779, 14784, 20662, 20416, 12912	109	9	1171	6.E+00	7.E-01	9.E-02
KEGG_PATHWAY	mmu05223:Non-small cell lung cancer	10	1.828153565		7.E-03 18709, 18708, 13649, 13555, 242705, 1171, 14784, 20662, 16476, 12929, 109	372	54	5738	3.E+00	7.E-01	4.E-02
BIOCARTA	m_pyk2Pathway:Links between Pyk2 and Map Kinases	8	1.462522852		9.E-03 20779, 14784, 20662, 16476, 12929, 18708, 14784, 20662, 16476, 20416, 14625, 22852	109	27	1171	3.E+00	8.E-01	1.E-01
BIOCARTA	m_igf1Pathway:IGF-1 Signaling Pathway	7	1.279707495		9.E-03 18708, 19247, 14784, 20662, 16476, 20416, 14625, 22852	109	21	1171	4.E+00	8.E-01	1.E-01
BIOCARTA	m_At1rPathway:Angiotensin II mediated activation of JNK Pathway	8	1.462522852		1.E-02 13649, 20779, 14784, 20662, 16476, 18708, 14784, 20662, 16476, 20416, 14625, 22852	109	28	1171	3.E+00	9.E-01	1.E-01
BIOCARTA	m_spryPathway:Sprouty regulation of tyrosine kinase signals	6	1.096892139		1.E-02 13649, 20779, 14784, 20662, 20416, 13645	109	16	1171	4.E+00	9.E-01	1.E-01
BIOCARTA	m_integrinPathway:Integrin Signaling Pathway	8	1.462522852		1.E-02 20779, 14784, 20662, 16476, 12929, 109	109	29	1171	3.E+00	9.E-01	1.E-01
BIOCARTA	m_il2rbPathway:IL-2 Receptor Beta Chain in T cell Activation	9	1.645338208		1.E-02 18708, 15170, 13555, 12702, 14784, 20416, 14625, 22852	109	36	1171	3.E+00	9.E-01	1.E-01
BIOCARTA	m_ghPathway:Growth Hormone Signaling Pathway	7	1.279707495		2.E-02 18708, 15170, 14784, 20662, 20416, 14625, 22852	109	25	1171	3.E+00	1.E+00	2.E-01
BIOCARTA	m_fcer1Pathway:Fc Epsilon Receptor I Signaling in Mast Cells	8	1.462522852		2.E-02 18708, 18783, 22324, 14784, 20662, 16476, 20416, 14625, 22852	109	32	1171	3.E+00	1.E+00	2.E-01
BIOCARTA	m_epoPathway:EPO Signaling Pathway	6	1.096892139		4.E-02 15170, 14784, 20662, 16476, 20416, 16452	109	21	1171	3.E+00	1.E+00	3.E-01
BIOCARTA	m_insulinPathway:Insulin Signaling Pathway	6	1.096892139		4.E-02 18708, 19247, 14784, 20662, 16476, 20416, 14625, 22852	109	22	1171	3.E+00	1.E+00	3.E-01
KEGG_PATHWAY	mmu05213:Endometrial cancer	8	1.462522852		5.E-02 18709, 18708, 13649, 13866, 14784, 20416, 14625, 22852	372	52	5738	2.E+00	1.E+00	1.E-01
BIOCARTA	m_il3Pathway:IL 3 signaling pathway	5	0.914076782		5.E-02 15170, 14784, 20662, 20416, 16452	109	16	1171	3.E+00	1.E+00	3.E-01
GOTERM_BP_FAT	GO:0007173~epidermal growth factor receptor signaling pathway	3	0.548446069		6.E-02 13649, 20779, 13645	491	11	13588	8.E+00	1.E+00	5.E-01
BIOCARTA	m_longevityPathway:The IGF-1 Receptor and Longevity	4	0.731261426		7.E-02 18708, 20416, 14600, 16000	109	11	1171	4.E+00	1.E+00	4.E-01
BIOCARTA	m_ngfPathway:Nerve growth factor pathway (NGF)	5	0.914076782		9.E-02 18708, 14784, 20662, 16476, 20416	109	19	1171	3.E+00	1.E+00	4.E-01
BIOCARTA	m_cblPathway:CBL mediated ligand-induced downregulation of EGF	4	0.731261426		9.E-02 13649, 20779, 14784, 13645	109	12	1171	4.E+00	1.E+00	4.E-01
KEGG_PATHWAY	mmu04912:GnRH signaling pathway	11	2.010968921		9.E-02 18783, 13649, 18753, 20779, 14784, 20416, 14625, 22852	372	97	5738	2.E+00	1.E+00	3.E-01
BIOCARTA	m_tcrPathway:T Cell Receptor Signaling Pathway	7	1.279707495		1.E-01 18708, 22324, 14784, 20662, 16476, 20416, 14625, 22852	109	36	1171	2.E+00	1.E+00	4.E-01
BIOCARTA	m_trkaPathway:Trka Receptor Signaling Pathway	4	0.731261426		1.E-01 18708, 14784, 20662, 20416	109	13	1171	3.E+00	1.E+00	4.E-01
BIOCARTA	m_bcrPathway:BCR Signaling Pathway	6	1.096892139		1.E-01 22324, 14784, 20662, 16476, 20416, 26476	109	29	1171	2.E+00	1.E+00	5.E-01
BIOCARTA	m_erk5Pathway:Role of Erk5 in Neuronal Survival	4	0.731261426		1.E-01 18708, 14784, 20416, 12912	109	14	1171	3.E+00	1.E+00	5.E-01
BIOCARTA	m_erkPathway:Erk1/Erk2 Mapk Signaling pathway	6	1.096892139		1.E-01 20848, 13649, 20779, 14784, 20662, 20416, 14625, 22852	109	31	1171	2.E+00	1.E+00	5.E-01
BIOCARTA	m_p38mapkPathway:p38 MAPK Signaling Pathway	6	1.096892139		2.E-01 20846, 14784, 12540, 20416, 12912, 26476	109	32	1171	2.E+00	1.E+00	5.E-01
KEGG_PATHWAY	mmu04320:Dorso-ventral axis formation	4	0.731261426		2.E-01 13649, 14784, 20662, 20663	372	22	5738	3.E+00	1.E+00	4.E-01
BIOCARTA	m_il2Pathway:IL 2 signaling pathway	5	0.914076782		2.E-01 14784, 20662, 16476, 16451, 20416	109	24	1171	2.E+00	1.E+00	5.E-01
BIOCARTA	m_igf1rPathway:Multiple antiapoptotic pathways from IGF-1R signal	4	0.731261426		3.E-01 18708, 14784, 20662, 20416	109	19	1171	2.E+00	1.E+00	7.E-01
BIOCARTA	m_ptenPathway:PTEN dependent cell cycle arrest and apoptosis	4	0.731261426		3.E-01 18708, 14784, 20662, 20416	109	20	1171	2.E+00	1.E+00	7.E-01
BIOCARTA	m_crebPathway:Transcription factor CREB and its extracellular signa	4	0.731261426		3.E-01 18708, 14784, 20662, 12912	109	21	1171	2.E+00	1.E+00	7.E-01



BIOCARTA	m_il4PathwayIL 4 signaling pathway	3	0.548446069	3.E-01	14784, 16451, 20416	109	12	1171	3.E+00	1.E+00	7.E-01
KEGG_PATHWAY	mmu04540:Gap junction	8	1.462522852	3.E-01	13649, 20779, 14784, 20662, 14678, 20416	372	86	5738	1.E+00	1.E+00	6.E-01
BIOCARTA	m_biopeptidesPathway:Bioactive Peptide Induced Signaling Pathway	5	0.914076782	3.E-01	20846, 14784, 20662, 20416, 16452	109	32	1171	2.E+00	1.E+00	8.E-01
BIOCARTA	m_ctla4Pathway:The Co-Stimulatory Signal During T-cell Activation	3	0.548446069	4.E-01	18708, 19247, 14784	109	16	1171	2.E+00	1.E+00	9.E-01
BIOCARTA	m_fasPathway:FAS signaling pathway ( CD95 )	4	0.731261426	5.E-01	16476, 18479, 11857, 26401	109	29	1171	1.E+00	1.E+00	9.E-01
BIOCARTA	m_tnfr1Pathway:TNFR1 Signaling Pathway	4	0.731261426	5.E-01	16476, 18479, 11857, 26401	109	30	1171	1.E+00	1.E+00	9.E-01
BIOCARTA	m_mapkPathway:MAPKinase Signaling Pathway	8	1.462522852	6.E-01	20846, 14784, 16476, 18479, 20416, 20417	109	80	1171	1.E+00	1.E+00	9.E-01

Annotation Cluster 71		Enrichment Score: 1.4078745646198654									
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Benferroni	Benjamini
INTERPRO	IPR000941:Enolase	3	0.548446069		5-E-03 433182, 13807, 13806, 13808, 1000442:	535	4	17763	2.E+01	1.E+00	1.E-01
GOTERM_CC_FAT	GO:0000015--phosphopyruvate hydratase complex	3	0.548446069		6-E-03 433182, 13807, 13806, 13808, 1000442:	419	4	12504	2.E+01	9.E-01	5.E-02
GOTERM_MF_FAT	GO:0004634--phosphopyruvate hydratase activity	3	0.548446069		7-E-03 433182, 13807, 13806, 13808, 1000442:	476	4	13288	2.E+01	1.E+00	7.E-02
PIR_SUPERFAMILY	PIRSF001400:Enolase	3	0.548446069		1.E-02 433182, 13807, 13806, 13808, 1000442:	378	4	8136	2.E+01	1.E+00	5.E-01
GOTERM_MF_FAT	GO:0016836--hydro-lyase activity	5	0.914076782		6.E-02 12350, 74147, 433182, 13807, 13806, 1:	476	42	13288	3.E+00	1.E+00	4.E-01
UP_SEQ_FEATURE	region of interest:Substrate binding	8	1.462522852		1.E-01 66885, 11409, 72269, 433182, 13807, 1:	537	125	16021	2.E+00	1.E+00	9.E-01
UP_SEQ_FEATURE	metal ion-binding site:Magnesium	6	1.096892139		3.E-01 18746, 433182, 110639, 13807, 13806, :	537	103	16021	2.E+00	1.E+00	1.E+00
KEGG_PATHWAY	mmu03018:RNA degradation	3	0.548446069		9.E-01 433182, 13807, 13806, 13808, 1000442:	372	60	5738	8.E-01	1.E+00	1.E+00

Annotation Cluster 72	Enrichment Score: 1.391346562569236											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	
GOTERM_MF_FAT	GO:0051287~NAD or NADH binding	8	1.46252852	8	9.E-04 226646, 100042746, 15929, 67834, 568,	476	44	13288	5.E+00	4.E-01	1.E-02	
GOTERM_MF_FAT	GO:0016620~oxidoreductase activity, acting on the aldehyde or oxc	4	0.731261426	8	8.E-02 100040053, 100042746, 14433, 14447, :	476	29	13288	4.E+00	1.E+00	5.E-01	
UP_SEQ_FEATURE	active site:Nucleophile	4	0.731261426	9	9.E-01 100040053, 100042746, 14433, 14447, :	537	168	16021	7.E-01	1.E+00	1.E+00	

Annotation Cluster 73		Enrichment Score: 1.3713460029473041										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold	Enrichment	Bonferroni	Benjamini
GOTERM_BP_FAT	GO:0043547--positive regulation of GTPase activity	4	0.731261426		1.E-02 71709, 11856, 19765, 19417	491	13	13588	9.E+00	1.E+00	2.E-01	
GOTERM_BP_FAT	GO:0051345--positive regulation of hydrolase activity	8	1.462522852		3.E-02 672195, 71709, 12279, 11856, 67469, 14	491	81	13588	3.E+00	1.E+00	4.E-01	
GOTERM_BP_FAT	GO:0032321--positive regulation of Rho GTPase activity	3	0.548446069		3.E-02 71709, 19765, 19417	491	8	13588	1.E+01	1.E+00	4.E-01	
GOTERM_BP_FAT	GO:0032320--positive regulation of Ras GTPase activity	3	0.548446069		5.E-02 71709, 19765, 19417	491	10	13588	8.E+00	1.E+00	5.E-01	
GOTERM_BP_FAT	GO:0032319--regulation of Rho GTPase activity	3	0.548446069		9.E-02 71709, 19765, 19417	491	14	13588	6.E+00	1.E+00	7.E-01	
GOTERM_BP_FAT	GO:0032318--regulation of Ras GTPase activity	6	1.096892139		2.E-01 71709, 228998, 19765, 19417, 212285, 1	491	80	13588	2.E+00	1.E+00	8.E-01	

Annotation Category	Enrichment Score: 1.3385513837398748	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
INTERPRO	IPR011765:Peptidase M16, N-terminal	3	0.548446069		1.E-02 73078, 67003, 22273	535	6	17763	2.E+01	1.E+00	2.E-01
INTERPRO	IPR001431:Peptidase M16, zinc-binding site	3	0.548446069		2.E-02 73078, 67003, 22273	535	7	17763	1.E+01	1.E+00	3.E-01
INTERPRO	IPR011237:Peptidase M16, core	3	0.548446069		2.E-02 73078, 67003, 22273	535	7	17763	1.E+01	1.E+00	3.E-01
INTERPRO	IPR007863:Peptidase M16, C-terminal	3	0.548446069		2.E-02 73078, 67003, 22273	535	7	17763	1.E+01	1.E+00	3.E-01
GOTERM_MF_FAT	GO:0004222-metalloendopeptidase activity	7	1.279707495		2.E-01 73078, 11489, 11487, 67003, 11491, 22273	476	114	13288	2.E+00	1.E+00	8.E-01
GOTERM_MF_FAT	GO:0008237-metallopeptidase activity	7	1.279707495		7.E-01 73078, 11489, 11487, 67003, 11491, 22273	476	187	13288	1.E+00	1.E+00	1.E+00

Annotation Cluster	Enrichment Score: 1.2627824150201667																		
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini								
GOTERM_MF_FAT	GO:0005158--insulin receptor binding	4	0.731261426	2.E-02	18708, 27261, 13449, 13448	476	17	13288	7.E+00	1.E+00	2.E-01								
SMART	SM00310:PTB	3	0.548446069	5.E-02	27261, 13449, 13448	248	13	9131	8.E+00	1.E+00	3.E-01								
INTERPRO	IPR002404:Insulin_receptor_substrate-1, PTB	3	0.548446069	6.E-02	27261, 13449, 13448	535	13	17763	8.E+00	1.E+00	6.E-01								
UP_SEQ_FEATURE	domain:IRS-type PTB	3	0.548446069	6.E-02	27261, 13449, 13448	537	12	16021	7.E+00	1.E+00	9.E-01								
GOTERM_MF_FAT	GO:0032403-protein complex binding	6	1.096892139	1.E-01	16854, 14685, 18708, 27261, 13449, 13448	476	78	13288	2.E+00	1.E+00	6.E-01								

Annotation Cluster 76 Category	Enrichment Score: 1.2370831766013215 Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
SP_PIR_KEYWORDS	GTP binding	7	1.279707495		6-E-04 14685, 19354, 14674, 14678, 11854, 12101	541	35	17854	7.E+00	2.E-01	4.E-03
SP_PIR_KEYWORDS	nucleotide binding	9	1.645338208		7-E-04 14685, 19354, 14674, 14678, 21877, 14679	541	64	17854	5.E+00	2.E-01	5.E-03
SP_PIR_KEYWORDS	P-loop	9	1.645338208		7-E-04 14685, 19354, 14674, 14678, 21877, 14679	541	65	17854	5.E+00	2.E-01	5.E-03
INTERPRO	IPR001019:Guanine nucleotide binding protein (G-protein), alpha subunit	4	0.731261426		1-E-02 14685, 14674, 14678, 14673	535	16	17763	8.E+00	1.E+00	2.E-01
PIR_SUPERFAMILY	PIRSF002400:GTP-binding regulatory protein Gs alpha chain	4	0.731261426		2-E-02 14685, 14674, 14678, 14673	378	14	8136	6.E+00	1.E+00	7.E-01
GOTERM_CC_FAT	GO:0005834-heterotrimeric G-protein complex	4	0.731261426		1-E-01 14685, 14674, 19739, 14673	419	35	12504	3.E+00	1.E+00	5.E-01



GOTERM_CC_FAT	GO:0019897~extrinsic to plasma membrane	5	0.914076782	1.E-01 14685, 14674, 11816, 19739, 14673	419	55	12504	3.E+00	1.E+00	5.E-01	
KEGG_PATHWAY	mmu04730:Long-term depression	6	1.096892139	5.E-01 18783, 14674, 19053, 14678, 14673, 160	372	72	5738	1.E+00	1.E+00	8.E-01	
UP_SEQ_FEATURE	lipid moiety-binding region:S-palmitoyl cysteine	7	1.279707495	5.E-01 228543, 14674, 11852, 14678, 14673, 1	537	175	16021	1.E+00	1.E+00	1.E+00	
GOTERM_CC_FAT	GO:0031225~anchored to membrane	8	1.462522852	5.E-01 19354, 14674, 11852, 104215, 109905, 1	419	207	12504	1.E+00	1.E+00	9.E-01	
SP_PIR_KEYWORDS	palmitate	7	1.279707495	6.E-01 228543, 14674, 11852, 14678, 14673, 1	541	206	17854	1.E+00	1.E+00	9.E-01	
SP_PIR_KEYWORDS	transducer	6	1.096892139	1.E+00 14685, 12765, 14674, 14678, 19739, 14	541	1467	17854	1.E-01	1.E+00	1.E+00	
GOTERM_BP_FAT	GO:0007186~G-protein coupled receptor protein signaling pathway	7	1.279707495	1.E+00 14685, 12765, 18126, 14674, 14678, 19	491	1877	13588	1.E-01	1.E+00	1.E+00	
Annotation Cluster 77	Enrichment Score: 1.2156610803000438										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
SMART	SM00516:SEC14	4	0.731261426		3.E-02 73167, 228359, 109904, 545156	248	26	9131	6.E+00	1.E+00	2.E-01
INTERPRO	IPR001251:Cellular retinaldehyde-binding/triple function, C-terminal	4	0.731261426		4.E-02 73167, 228359, 109904, 545156	535	26	17763	5.E+00	1.E+00	5.E-01
UP_SEQ_FEATURE	domain:CRAL-TRIO	3	0.548446069		2.E-01 73167, 228359, 545156	537	22	16021	4.E+00	1.E+00	1.E+00
Annotation Cluster 78	Enrichment Score: 1.2130490362902548										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_BP_FAT	GO:0009743~response to carbohydrate stimulus	5	0.914076782		1.E-02 21813, 230163, 224045, 217715, 10398	491	26	13588	5.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0009746~response to hexose stimulus	4	0.731261426		4.E-02 21813, 224045, 217715, 103988	491	22	13588	5.E+00	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0009749~response to glucose stimulus	4	0.731261426		4.E-02 21813, 224045, 217715, 103988	491	22	13588	5.E+00	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0034284~response to monosaccharide stimulus	4	0.731261426		4.E-02 21813, 224045, 217715, 103988	491	22	13588	5.E+00	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0009628~response to abiotic stimulus	8	1.462522852		8.E-01 14685, 12190, 21813, 12955, 11820, 22	491	251	13588	9.E-01	1.E+00	1.E+00
Annotation Cluster 79	Enrichment Score: 1.1662579011988976										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
SP_PIR_KEYWORDS	tryptophan catabolism	3	0.548446069		3.E-03 71562, 15930, 56720	541	3	17854	3.E+01	6.E-01	2.E-02
GOTERM_BP_FAT	GO:0019441~tryptophan catabolic process to kynurenine	3	0.548446069		7.E-03 71562, 15930, 56720	491	4	13588	2.E+01	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0042436~indole derivative catabolic process	3	0.548446069		1.E-02 71562, 15930, 56720	491	5	13588	2.E+01	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0006569~tryptophan catabolic process	3	0.548446069		1.E-02 71562, 15930, 56720	491	5	13588	2.E+01	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0046218~indolalkylamine catabolic process	3	0.548446069		1.E-02 71562, 15930, 56720	491	5	13588	2.E+01	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0006568~tryptophan metabolic process	3	0.548446069		2.E-02 71562, 15930, 56720	491	7	13588	1.E+01	1.E+00	3.E-01
KEGG_PATHWAY	mmu00380:Tryptophan metabolism	7	1.279707495		4.E-02 98256, 71562, 15107, 74147, 15930, 56	372	40	5738	3.E+00	1.E+00	1.E-01
GOTERM_BP_FAT	GO:0009074~aromatic amino acid family catabolic process	3	0.548446069		6.E-02 71562, 15930, 56720	491	11	13588	8.E+00	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0006586~indolalkylamine metabolic process	3	0.548446069		8.E-02 71562, 15930, 56720	491	13	13588	6.E+00	1.E+00	6.E-01
GOTERM_BP_FAT	GO:0042430~indole and derivative metabolic process	3	0.548446069		8.E-02 71562, 15930, 56720	491	13	13588	6.E+00	1.E+00	6.E-01
GOTERM_BP_FAT	GO:0042434~indole derivative metabolic process	3	0.548446069		8.E-02 71562, 15930, 56720	491	13	13588	6.E+00	1.E+00	6.E-01
GOTERM_BP_FAT	GO:0046700~heterocycle catabolic process	5	0.914076782		8.E-02 71562, 72269, 15930, 56720, 99586	491	46	13588	3.E+00	1.E+00	6.E-01
GOTERM_BP_FAT	GO:0019439~aromatic compound catabolic process	3	0.548446069		1.E-01 71562, 15930, 56720	491	15	13588	6.E+00	1.E+00	7.E-01
GOTERM_BP_FAT	GO:0042402~biogenic amine catabolic process	3	0.548446069		1.E-01 71562, 15930, 56720	491	15	13588	6.E+00	1.E+00	7.E-01
GOTERM_BP_FAT	GO:0042219~cellular amino acid derivative catabolic process	3	0.548446069		1.E-01 71562, 15930, 56720	491	18	13588	5.E+00	1.E+00	8.E-01
GOTERM_BP_FAT	GO:0016054~organic acid catabolic process	6	1.096892139		2.E-01 18126, 71562, 74147, 15930, 56720, 23	491	81	13588	2.E+00	1.E+00	8.E-01
GOTERM_BP_FAT	GO:0046395~carboxylic acid catabolic process	6	1.096892139		2.E-01 18126, 71562, 74147, 15930, 56720, 23	491	81	13588	2.E+00	1.E+00	8.E-01
GOTERM_BP_FAT	GO:0009072~aromatic amino acid family metabolic process	3	0.548446069		2.E-01 71562, 15930, 56720	491	21	13588	4.E+00	1.E+00	8.E-01
GOTERM_BP_FAT	GO:0009063~cellular amino acid catabolic process	4	0.731261426		3.E-01 18126, 71562, 15930, 56720	491	54	13588	2.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0009310~amine catabolic process	4	0.731261426		4.E-01 18126, 71562, 15930, 56720	491	65	13588	2.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0006576~biogenic amine metabolic process	4	0.731261426		6.E-01 71562, 15930, 56720, 18227	491	80	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0006575~cellular amino acid derivative metabolic process	6	1.096892139		6.E-01 71562, 15930, 56720, 18227, 14600, 14	491	141	13588	1.E+00	1.E+00	1.E+00
Annotation Cluster 80	Enrichment Score: 1.1534890107859834										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
SMART	SM00234:START	3	0.548446069		6.E-02 236920, 50768, 243362	248	15	9131	7.E+00	1.E+00	3.E-01
INTERPRO	IPR002913:Lipid-binding START	3	0.548446069		7.E-02 236920, 50768, 243362	535	15	17763	7.E+00	1.E+00	7.E-01
UP_SEQ_FEATURE	domain:START	3	0.548446069		8.E-02 236920, 50768, 243362	537	14	16021	6.E+00	1.E+00	9.E-01
Annotation Cluster 81	Enrichment Score: 1.0738400721267947										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_BP_FAT	GO:0051270~regulation of cell motion	9	1.645338208		4.E-02 18708, 14674, 73167, 74144, 11491, 11	491	107	13588	2.E+00	1.E+00	4.E-01
GOTERM_BP_FAT	GO:0030334~regulation of cell migration	8	1.462522852		5.E-02 18708, 14674, 73167, 74144, 11855, 20	491	92	13588	2.E+00	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0051272~positive regulation of cell motion	5	0.914076782		6.E-02 18708, 73167, 11491, 11855, 20339	491	41	13588	3.E+00	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0040012~regulation of locomotion	8	1.462522852		1.E-01 18708, 14674, 73167, 74144, 11855, 20	491	110	13588	2.E+00	1.E+00	7.E-01



GOTERM_BP_FAT	GO:0030335~positive regulation of cell migration	4	0.731261426	1.E-01 18708, 73167, 11855, 20339	491	37	13588	3.E+00	1.E+00	8.E-01	
GOTERM_BP_FAT	GO:0040017~positive regulation of locomotion	4	0.731261426	2.E-01 18708, 73167, 11855, 20339	491	44	13588	3.E+00	1.E+00	9.E-01	
Annotation Cluster 82	Enrichment Score: 1.0581660740417895										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
SP_PIR_KEYWORDS	lipid metabolism	10	1.828153565		2.E-02 66885, 15107, 11409, 74147, 22359, 659	541	136	17854	2.E+00	1.E+00	1.E-01
SP_PIR_KEYWORDS	fatty acid metabolism	6	1.096892139		4.E-02 66885, 15107, 11409, 74147, 67469, 230	541	61	17854	3.E+00	1.E+00	1.E-01
GOTERM_BP_FAT	GO:0006631~fatty acid metabolic process	12	2.193784278		7.E-02 70316, 66885, 15107, 11409, 74147, 223	491	184	13588	2.E+00	1.E+00	6.E-01
KEGG_PATHWAY	mmu00280:Valine, leucine and isoleucine degradation	7	1.279707495		7.E-02 66885, 15107, 11409, 74147, 73724, 130	372	46	5738	2.E+00	1.E+00	2.E-01
KEGG_PATHWAY	mmu00071:Fatty acid metabolism	6	1.096892139		2.E-01 66885, 15107, 11409, 74147, 13117, 230	372	45	5738	2.E+00	1.E+00	4.E-01
COG_ONTOLOGY	Lipid metabolism	3	0.548446069		6.E-01 66885, 15107, 11409	52	86	2040	1.E+00	1.E+00	8.E-01
Annotation Cluster 83	Enrichment Score: 1.0574725240145078										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
SMART	SM00088:PINT	3	0.548446069		7.E-02 13669, 16341, 56347	248	16	9131	7.E+00	1.E+00	3.E-01
INTERPRO	IPR000717:Proteasome component region PCI	3	0.548446069		8.E-02 13669, 16341, 56347	535	16	17763	6.E+00	1.E+00	7.E-01
UP_SEQ_FEATURE	domain:PCI	3	0.548446069		1.E-01 13669, 16341, 56347	537	18	16021	5.E+00	1.E+00	9.E-01
Annotation Cluster 84	Enrichment Score: 1.0400819133900352										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_BP_FAT	GO:0043467~regulation of generation of precursor metabolites and	3	0.548446069		8.E-02 14447, 103988, 208727	491	13	13588	6.E+00	1.E+00	6.E-01
GOTERM_BP_FAT	GO:0010906~regulation of glucose metabolic process	3	0.548446069		9.E-02 14447, 103988, 208727	491	14	13588	6.E+00	1.E+00	7.E-01
GOTERM_BP_FAT	GO:0006109~regulation of carbohydrate metabolic process	3	0.548446069		1.E-01 14447, 103988, 208727	491	15	13588	6.E+00	1.E+00	7.E-01
GOTERM_BP_FAT	GO:0010675~regulation of cellular carbohydrate metabolic process	3	0.548446069		1.E-01 14447, 103988, 208727	491	15	13588	6.E+00	1.E+00	7.E-01
Annotation Cluster 85	Enrichment Score: 1.032702425323715										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_CC_FAT	GO:0005851~eukaryotic translation initiation factor 2B complex	5	0.914076782		2.E-05 13667, 13665, 224045, 217715, 108067	419	6	12504	2.E+01	5.E-03	2.E-04
GOTERM_BP_FAT	GO:0010001~glial cell differentiation	7	1.279707495		7.E-03 13667, 13867, 224045, 217715, 16000, 1	491	48	13588	4.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0042552~myelination	6	1.096892139		1.E-02 13667, 13866, 224045, 12527, 217715, 1	491	37	13588	4.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0042063~gliogenesis	7	1.279707495		1.E-02 13667, 13867, 224045, 217715, 16000, 1	491	52	13588	4.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0007272~ensheathment of neurons	6	1.096892139		1.E-02 13667, 13866, 224045, 12527, 217715, 1	491	39	13588	4.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0008366~axon ensheathment	6	1.096892139		1.E-02 13667, 13866, 224045, 12527, 217715, 1	491	39	13588	4.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0014003~oligodendrocyte development	4	0.731261426		1.E-02 13667, 224045, 217715, 108067	491	14	13588	8.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0019228~regulation of action potential in neuron	6	1.096892139		2.E-02 13667, 13866, 224045, 12527, 217715, 1	491	45	13588	4.E+00	1.E+00	3.E-01
GOTERM_BP_FAT	GO:0048709~oligodendrocyte differentiation	4	0.731261426		3.E-02 13667, 224045, 217715, 108067	491	20	13588	6.E+00	1.E+00	4.E-01
GOTERM_BP_FAT	GO:0001508~regulation of action potential	6	1.096892139		4.E-02 13667, 13866, 224045, 12527, 217715, 1	491	54	13588	3.E+00	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0021782~glial cell development	4	0.731261426		5.E-02 13667, 224045, 217715, 108067	491	23	13588	5.E+00	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0046660~female sex differentiation	6	1.096892139		8.E-02 12190, 13667, 16847, 224045, 217715, 1	491	64	13588	3.E+00	1.E+00	6.E-01
GOTERM_BP_FAT	GO:0048608~reproductive structure development	9	1.645338208		1.E-01 12190, 13667, 20779, 16847, 224045, 2	491	130	13588	2.E+00	1.E+00	7.E-01
GOTERM_BP_FAT	GO:0019725~cellular homeostasis	18	3.290676417		1.E-01 13667, 104394, 11816, 11820, 13382, 10	491	343	13588	1.E+00	1.E+00	7.E-01
GOTERM_BP_FAT	GO:0008585~female gonad development	5	0.914076782		1.E-01 12190, 13667, 16847, 224045, 217715	491	53	13588	3.E+00	1.E+00	7.E-01
GOTERM_BP_FAT	GO:0042391~regulation of membrane potential	8	1.462522852		1.E-01 13667, 13866, 227197, 13382, 224045, 1	491	119	13588	2.E+00	1.E+00	8.E-01
GOTERM_BP_FAT	GO:0046545~development of primary female sexual characteristics	5	0.914076782		1.E-01 12190, 13667, 16847, 224045, 217715	491	57	13588	2.E+00	1.E+00	8.E-01
GOTERM_BP_FAT	GO:0048878~chemical homeostasis	18	3.290676417		2.E-01 13667, 19247, 11816, 11820, 238055, 1	491	365	13588	1.E+00	1.E+00	8.E-01
GOTERM_BP_FAT	GO:0022602~ovulation cycle process	4	0.731261426		2.E-01 13667, 16847, 224045, 217715	491	47	13588	2.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0042698~ovulation cycle	4	0.731261426		2.E-01 13667, 16847, 224045, 217715	491	48	13588	2.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0055082~cellular chemical homeostasis	13	2.376599634		3.E-01 13667, 11816, 11820, 13382, 103988, 1	491	268	13588	1.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0042592~homeostatic process	25	4.570383912		3.E-01 13667, 19247, 11816, 238055, 103988, 1	491	584	13588	1.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0001541~ovarian follicle development	3	0.548446069		3.E-01 13667, 224045, 217715	491	33	13588	3.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0003006~reproductive developmental process	12	2.193784278		4.E-01 12190, 13667, 20779, 18551, 16847, 20	491	264	13588	1.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0008406~gonad development	5	0.914076782		4.E-01 12190, 13667, 16847, 224045, 217715	491	88	13588	2.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0006873~cellular ion homeostasis	11	2.010968921		5.E-01 13667, 13866, 11816, 11820, 227197, 1	491	261	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0007548~sex differentiation	6	1.096892139		5.E-01 12190, 13667, 16847, 224045, 217715, 1	491	130	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0045137~development of primary sexual characteristics	5	0.914076782		5.E-01 12190, 13667, 16847, 224045, 217715	491	104	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0019226~transmission of nerve impulse	9	1.645338208		6.E-01 13667, 13866, 20909, 11820, 224045, 1	491	226	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0050801~ion homeostasis	11	2.010968921		6.E-01 13667, 13866, 11816, 11820, 227197, 1	491	293	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0032504~multicellular organism reproduction	14	2.559414991		7.E-01 12190, 13667, 26934, 19247, 238055, 1	491	409	13588	9.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0048609~reproductive process in a multicellular organism	14	2.559414991		7.E-01 12190, 13667, 26934, 19247, 238055, 1	491	409	13588	9.E-01	1.E+00	1.E+00



GOTERM_BP_FAT	GO:0050877~neurological system process	16	2.925045704	1.E+00	14685, 13667, 78405, 11820, 20909, 170	491	1681	13588	3.E-01	1.E+00	1.E+00
Annotation Cluster 86	Enrichment Score: 0.961764215478245										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
SMART	SM00091:PAS	6	1.096892139		2.E-03 11865, 12753, 18626, 17979, 18627, 186	248	32	9131	7.E+00	2.E-01	2.E-02
INTERPRO	IPR000014:PAS	6	1.096892139		2.E-03 11865, 12753, 18626, 17979, 18627, 186	535	32	17763	6.E+00	9.E-01	7.E-02
INTERPRO	IPR013767:PAS fold	3	0.548446069		2.E-01 11865, 12753, 17979	535	27	17763	4.E+00	1.E+00	9.E-01
UP_SEQ_FEATURE	DNA-binding region:Basic motif	7	1.279707495		4.E-01 11865, 12753, 16476, 18022, 12912, 179	537	154	16021	1.E+00	1.E+00	1.E+00
SMART	SM00353:HLH	3	0.548446069		8.E-01 11865, 12753, 17979	248	111	9131	1.E+00	1.E+00	1.E+00
INTERPRO	IPR001092:Basic helix-loop-helix dimerisation region bHLH	3	0.548446069		9.E-01 11865, 12753, 17979	535	111	17763	9.E-01	1.E+00	1.E+00
UP_SEQ_FEATURE	domain:Helix-loop-helix motif	3	0.548446069		9.E-01 11865, 12753, 17979	537	109	16021	8.E-01	1.E+00	1.E+00
Annotation Cluster 87	Enrichment Score: 0.9477785437914624										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_CC_FAT	GO:0030027~lamellipodium	6	1.096892139		6.E-02 12549, 14163, 170758, 224014, 106952,	419	63	12504	3.E+00	1.E+00	3.E-01
SP_PIR_KEYWORDS	cell projection	10	1.828153565		1.E-01 12549, 14163, 94190, 170758, 53972, 2	541	196	17854	2.E+00	1.E+00	4.E-01
GOTERM_CC_FAT	GO:0031252~cell leading edge	7	1.279707495		2.E-01 12549, 14163, 228359, 170758, 224014,	419	112	12504	2.E+00	1.E+00	6.E-01
Annotation Cluster 88	Enrichment Score: 0.9165760732563573										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
SMART	SM00140:NGF	4	0.731261426		8.E-05 18049, 12064, 78405, 18205	248	4	9131	4.E+01	1.E-02	1.E-03
INTERPRO	IPR019846:Nerve growth factor conserved site	4	0.731261426		1.E-04 18049, 12064, 78405, 18205	535	4	17763	3.E+01	9.E-02	7.E-03
INTERPRO	IPR002072:Nerve growth factor-related	4	0.731261426		1.E-04 18049, 12064, 78405, 18205	535	4	17763	3.E+01	9.E-02	7.E-03
SP_PIR_KEYWORDS	growth factor	8	1.462522852		9.E-02 18049, 14751, 12064, 78405, 14825, 13	541	127	17854	2.E+00	1.E+00	3.E-01
GOTERM_BP_FAT	GO:0043523~regulation of neuron apoptosis	6	1.096892139		2.E-01 18049, 12064, 13867, 18227, 18205, 11	491	80	13588	2.E+00	1.E+00	8.E-01
GOTERM_BP_FAT	GO:0051960~regulation of nervous system development	9	1.645338208		2.E-01 18049, 12064, 16392, 11853, 13645, 21	491	148	13588	2.E+00	1.E+00	8.E-01
GOTERM_MF_FAT	GO:0008083~growth factor activity	8	1.462522852		2.E-01 18049, 14751, 12064, 78405, 14825, 13	476	141	13288	2.E+00	1.E+00	8.E-01
GOTERM_BP_FAT	GO:0044057~regulation of system process	10	1.828153565		3.E-01 18049, 19247, 12064, 14678, 74318, 14	491	201	13588	1.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0045664~regulation of neuron differentiation	6	1.096892139		3.E-01 18049, 12064, 16392, 11853, 21844, 11	491	102	13588	2.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0050767~regulation of neurogenesis	7	1.279707495		3.E-01 18049, 12064, 16392, 11853, 21844, 18	491	132	13588	1.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0060284~regulation of cell development	8	1.462522852		3.E-01 18049, 12064, 16392, 11853, 21844, 20	491	159	13588	1.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0042490~mechanoreceptor differentiation	3	0.548446069		4.E-01 12064, 78405, 18205	491	36	13588	2.E+00	1.E+00	1.E+00
GOTERM_CC_FAT	GO:0005788~endoplasmic reticulum lumen	4	0.731261426		4.E-01 18049, 12064, 78405, 18205	419	72	12504	2.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0050769~positive regulation of neurogenesis	3	0.548446069		4.E-01 18049, 21844, 18205	491	41	13588	2.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0045597~positive regulation of cell differentiation	8	1.462522852		4.E-01 21813, 18049, 12702, 12064, 74318, 21	491	175	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0050804~regulation of synaptic transmission	5	0.914076782		5.E-01 18049, 12064, 14678, 19417, 18205	491	100	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0010720~positive regulation of cell development	3	0.548446069		5.E-01 18049, 21844, 18205	491	47	13588	2.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0051094~positive regulation of developmental process	9	1.645338208		5.E-01 21813, 18049, 12702, 12064, 11852, 74	491	214	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0051969~regulation of transmission of nerve impulse	5	0.914076782		5.E-01 18049, 12064, 14678, 19417, 18205	491	107	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0031644~regulation of neurological system process	5	0.914076782		6.E-01 18049, 12064, 14678, 19417, 18205	491	113	13588	1.E+00	1.E+00	1.E+00
GOTERM_CC_FAT	GO:0044432~endoplasmic reticulum part	5	0.914076782		1.E+00 13121, 18049, 12064, 78405, 18205	419	231	12504	6.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0050890~cognition	7	1.279707495		1.E+00 14685, 18049, 12064, 78405, 11820, 19	491	1480	13588	1.E-01	1.E+00	1.E+00
Annotation Cluster 89	Enrichment Score: 0.91461453360070111										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_BP_FAT	GO:0006606~protein import into nucleus	8	1.462522852		4.E-03 11865, 664868, 56338, 19384, 231103, :	491	56	13588	4.E+00	1.E+00	9.E-02
GOTERM_BP_FAT	GO:0051170~nuclear import	8	1.462522852		5.E-03 11865, 664868, 56338, 19384, 231103, :	491	58	13588	4.E+00	1.E+00	1.E-01
GOTERM_BP_FAT	GO:0034504~protein localization in nucleus	8	1.462522852		6.E-03 11865, 664868, 56338, 19384, 231103, :	491	61	13588	4.E+00	1.E+00	1.E-01
GOTERM_BP_FAT	GO:0006913~nucleocytoplasmic transport	9	1.645338208		2.E-02 11865, 664868, 56338, 19384, 11487, 2	491	96	13588	3.E+00	1.E+00	3.E-01
GOTERM_BP_FAT	GO:0051169~nuclear transport	9	1.645338208		3.E-02 11865, 664868, 56338, 19384, 11487, 2	491	98	13588	3.E+00	1.E+00	3.E-01
GOTERM_BP_FAT	GO:0017038~protein import	8	1.462522852		3.E-02 11865, 664868, 56338, 19384, 231103, :	491	82	13588	3.E+00	1.E+00	4.E-01
GOTERM_BP_FAT	GO:0033365~protein localization in organelle	8	1.462522852		6.E-02 11865, 664868, 56338, 19384, 231103, :	491	97	13588	2.E+00	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0000060~protein import into nucleus, translocation	3	0.548446069		1.E-01 11865, 231103, 16452	491	18	13588	5.E+00	1.E+00	8.E-01
GOTERM_BP_FAT	GO:0006605~protein targeting	8	1.462522852		2.E-01 11865, 664868, 56338, 19384, 231103, :	491	133	13588	2.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0046907~intracellular transport	19	3.473491773		3.E-01 11865, 11852, 56338, 19384, 22227, 22	491	431	13588	1.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0034613~cellular protein localization	10	1.828153565		8.E-01 11865, 664868, 56338, 19384, 231103, :	491	299	13588	9.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0070727~cellular macromolecule localization	10	1.828153565		8.E-01 11865, 664868, 56338, 19384, 231103, :	491	301	13588	9.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0006886~intracellular protein transport	9	1.645338208		8.E-01 11865, 664868, 56338, 19384, 231103, :	491	276	13588	9.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0008104~protein localization	23	4.204753199		9.E-01 11865, 56338, 11852, 11816, 19384, 23	491	753	13588	8.E-01	1.E+00	1.E+00



GOTERM_BP_FAT	GO:0015031~protein transport	19	3.473491773	9.E-01 11865, 11852, 56338, 19384, 238055, 20	491	651	13588	8.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0045184~establishment of protein localization	19	3.473491773	9.E-01 11865, 11852, 56338, 19384, 238055, 20	491	656	13588	8.E-01	1.E+00	1.E+00
SP_PIR_KEYWORDS	protein transport	8	1.462522852	1.E+00 664868, 11852, 13858, 19384, 228998, 6	541	461	17854	6.E-01	1.E+00	1.E+00
Annotation Cluster 90	Enrichment Score: 0.8967528470189441									
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni Benjamini
GOTERM_BP_FAT	GO:0030879~mammary gland development	9	1.645338208		1.E-02 12190, 21813, 20779, 11855, 15277, 12	491	86	13588	3.E+00	1.E+00 2.E-01
GOTERM_BP_FAT	GO:0048732~gland development	13	2.376599634		5.E-02 12190, 13649, 16392, 12929, 11855, 15	491	197	13588	2.E+00	1.E+00 5.E-01
GOTERM_BP_FAT	GO:0035239~tube morphogenesis	10	1.828153565		2.E-01 14674, 21813, 20779, 16911, 19713, 50	491	171	13588	2.E+00	1.E+00 8.E-01
GOTERM_BP_FAT	GO:0001763~morphogenesis of a branching structure	8	1.462522852		2.E-01 14674, 21813, 20779, 12702, 14784, 13	491	125	13588	2.E+00	1.E+00 8.E-01
GOTERM_BP_FAT	GO:0048754~branching morphogenesis of a tube	6	1.096892139		2.E-01 14674, 21813, 20779, 13645, 17979, 16	491	93	13588	2.E+00	1.E+00 9.E-01
GOTERM_BP_FAT	GO:0060443~mammary gland morphogenesis	3	0.548446069		3.E-01 21813, 20779, 17979	491	33	13588	3.E+00	1.E+00 9.E-01
GOTERM_BP_FAT	GO:0022612~gland morphogenesis	5	0.914076782		4.E-01 13649, 21813, 20779, 17979, 16000	491	84	13588	2.E+00	1.E+00 9.E-01
Annotation Cluster 91	Enrichment Score: 0.8233404773069987									
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni Benjamini
GOTERM_BP_FAT	GO:0031960~response to corticosteroid stimulus	4	0.731261426		5.E-02 20779, 11409, 230163, 94284, 394436	491	23	13588	5.E+00	1.E+00 5.E-01
GOTERM_BP_FAT	GO:0048545~response to steroid hormone stimulus	6	1.096892139		6.E-02 21813, 20779, 11409, 230163, 16847, 9	491	60	13588	3.E+00	1.E+00 6.E-01
GOTERM_BP_FAT	GO:0009991~response to extracellular stimulus	9	1.645338208		1.E-01 12190, 100040331, 66483, 18227, 1682	491	133	13588	2.E+00	1.E+00 7.E-01
GOTERM_BP_FAT	GO:0051384~response to glucocorticoid stimulus	3	0.548446069		1.E-01 11409, 230163, 94284, 394436	491	19	13588	4.E+00	1.E+00 8.E-01
GOTERM_BP_FAT	GO:0031667~response to nutrient levels	7	1.279707495		2.E-01 100048339, 12190, 19982, 21813, 1140	491	115	13588	2.E+00	1.E+00 9.E-01
GOTERM_BP_FAT	GO:0042594~response to starvation	3	0.548446069		3.E-01 11409, 230163, 94284, 394436	491	29	13588	3.E+00	1.E+00 9.E-01
GOTERM_BP_FAT	GO:0007584~response to nutrient	4	0.731261426		5.E-01 100048339, 12190, 19982, 21813, 1000	491	76	13588	1.E+00	1.E+00 1.E+00
Annotation Cluster 92	Enrichment Score: 0.818552905919452									
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni Benjamini
GOTERM_BP_FAT	GO:0034655~nucleobase, nucleoside, nucleotide and nucleic acid c	4	0.731261426		1.E-01 76654, 72269, 17969, 99586	491	36	13588	3.E+00	1.E+00 8.E-01
GOTERM_BP_FAT	GO:0034656~nucleobase, nucleoside and nucleotide catabolic proc	4	0.731261426		1.E-01 76654, 72269, 17969, 99586	491	36	13588	3.E+00	1.E+00 8.E-01
GOTERM_BP_FAT	GO:0009116~nucleoside metabolic process	5	0.914076782		1.E-01 76654, 72269, 110639, 72962, 99586	491	56	13588	2.E+00	1.E+00 8.E-01
GOTERM_BP_FAT	GO:0044270~nitrogen compound catabolic process	4	0.731261426		2.E-01 76654, 72269, 17969, 99586	491	42	13588	3.E+00	1.E+00 8.E-01
Annotation Cluster 93	Enrichment Score: 0.8167443967558107									
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni Benjamini
GOTERM_CC_FAT	GO:0030427~site of polarized growth	5	0.914076782		9.E-02 18479, 170758, 53972, 19417, 24001	419	51	12504	3.E+00	1.E+00 5.E-01
GOTERM_CC_FAT	GO:0030426~growth cone	5	0.914076782		9.E-02 18479, 170758, 53972, 19417, 24001	419	51	12504	3.E+00	1.E+00 5.E-01
GOTERM_CC_FAT	GO:0043005~neuron projection	10	1.828153565		4.E-01 94190, 11820, 13074, 16800, 18479, 17	419	245	12504	1.E+00	1.E+00 9.E-01
Annotation Cluster 94	Enrichment Score: 0.81568932402553									
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni Benjamini
UP_SEQ_FEATURE	repeat:6	7	1.279707495		3.E-02 16854, 20020, 13669, 20345, 13858, 11	537	71	16021	3.E+00	1.E+00 7.E-01
UP_SEQ_FEATURE	repeat:8	6	1.096892139		4.E-02 16854, 20020, 13669, 20345, 13858, 11	537	58	16021	3.E+00	1.E+00 8.E-01
UP_SEQ_FEATURE	repeat:5	7	1.279707495		6.E-02 16854, 20020, 13669, 20345, 13858, 11	537	84	16021	2.E+00	1.E+00 9.E-01
UP_SEQ_FEATURE	repeat:7	6	1.096892139		7.E-02 16854, 20020, 13669, 20345, 13858, 11	537	67	16021	3.E+00	1.E+00 9.E-01
UP_SEQ_FEATURE	repeat:4	7	1.279707495		1.E-01 16854, 20020, 13669, 20345, 13858, 11	537	101	16021	2.E+00	1.E+00 9.E-01
UP_SEQ_FEATURE	repeat:10	4	0.731261426		2.E-01 20020, 13669, 20345, 13858	537	46	16021	3.E+00	1.E+00 1.E+00
UP_SEQ_FEATURE	repeat:9	4	0.731261426		2.E-01 20020, 13669, 20345, 13858	537	46	16021	3.E+00	1.E+00 1.E+00
UP_SEQ_FEATURE	repeat:1	8	1.462522852		2.E-01 19944, 16854, 20020, 20345, 665032, 1	537	148	16021	2.E+00	1.E+00 1.E+00
UP_SEQ_FEATURE	repeat:2	8	1.462522852		2.E-01 19944, 16854, 13669, 20345, 665032, 1	537	151	16021	2.E+00	1.E+00 1.E+00
UP_SEQ_FEATURE	repeat:13	3	0.548446069		3.E-01 20020, 13669, 13858	537	34	16021	3.E+00	1.E+00 1.E+00
UP_SEQ_FEATURE	repeat:12	3	0.548446069		3.E-01 20020, 13669, 13858	537	35	16021	3.E+00	1.E+00 1.E+00
UP_SEQ_FEATURE	repeat:3	6	1.096892139		4.E-01 16854, 20020, 20345, 13858, 11816, 19	537	119	16021	2.E+00	1.E+00 1.E+00
UP_SEQ_FEATURE	repeat:11	3	0.548446069		4.E-01 20020, 13669, 13858	537	40	16021	2.E+00	1.E+00 1.E+00
Annotation Cluster 95	Enrichment Score: 0.7850546182502105									
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni Benjamini
UP_SEQ_FEATURE	repeat:LDL-receptor class B 6	3	0.548446069		3.E-02 22359, 16835, 13645	537	9	16021	1.E+01	1.E+00 7.E-01
GOTERM_BP_FAT	GO:0008203~cholesterol metabolic process	7	1.279707495		4.E-02 13121, 11816, 14137, 22359, 65969, 16	491	70	13588	3.E+00	1.E+00 4.E-01
UP_SEQ_FEATURE	repeat:LDL-receptor class B 5	3	0.548446069		6.E-02 22359, 16835, 13645	537	12	16021	7.E+00	1.E+00 9.E-01
GOTERM_BP_FAT	GO:0016125~sterol metabolic process	7	1.279707495		6.E-02 13121, 11816, 14137, 22359, 65969, 16	491	77	13588	3.E+00	1.E+00 5.E-01



SMART	SM00135:LY	3	0.548446069	6.E-02 22359, 16835, 13645	248	15	9131	7.E+00	1.E+00	3.E-01
SP_PIR_KEYWORDS	cholesterol metabolism	4	0.731261426	6.E-02 22359, 238055, 65969, 16835	541	30	17854	4.E+00	1.E+00	2.E-01
UP_SEQ_FEATURE	repeat:LDL-receptor class B 2	3	0.548446069	7.E-02 22359, 16835, 13645	537	13	16021	7.E+00	1.E+00	8.E-01
UP_SEQ_FEATURE	repeat:LDL-receptor class B 3	3	0.548446069	7.E-02 22359, 16835, 13645	537	13	16021	7.E+00	1.E+00	8.E-01
UP_SEQ_FEATURE	repeat:LDL-receptor class B 1	3	0.548446069	7.E-02 22359, 16835, 13645	537	13	16021	7.E+00	1.E+00	8.E-01
UP_SEQ_FEATURE	repeat:LDL-receptor class B 4	3	0.548446069	7.E-02 22359, 16835, 13645	537	13	16021	7.E+00	1.E+00	8.E-01
INTERPRO	IPR000033:Low-density lipoprotein receptor, YWTD repeat	3	0.548446069	7.E-02 22359, 16835, 13645	535	15	17763	7.E+00	1.E+00	7.E-01
SP_PIR_KEYWORDS	egf-like domain	12	2.193784278	8.E-02 11489, 12279, 20343, 22359, 65969, 23043	541	222	17854	2.E+00	1.E+00	2.E-01
GOTERM_CC_FAT	GO:0005905~coated pit	4	0.731261426	9.E-02 22359, 11820, 65969, 16835	419	32	12504	4.E+00	1.E+00	5.E-01
SP_PIR_KEYWORDS	steroid metabolism	4	0.731261426	1.E-01 22359, 65969, 54200, 16835	541	39	17854	3.E+00	1.E+00	3.E-01
INTERPRO	IPR006209:EGF	7	1.279707495	2.E-01 20343, 22359, 65969, 16835, 18791, 20343	535	128	17763	2.E+00	1.E+00	9.E-01
INTERPRO	IPR013032:EGF-like region, conserved site	13	2.376599634	2.E-01 12279, 22359, 65969, 18791, 13645, 13645	535	310	17763	1.E+00	1.E+00	1.E+00
UP_SEQ_FEATURE	domain:EGF-like 2, calcium-binding	4	0.731261426	3.E-01 22359, 65969, 16835, 13645	537	52	16021	2.E+00	1.E+00	1.E+00
INTERPRO	IPR011042:Six-bladed beta-propeller, TolB-like	3	0.548446069	3.E-01 22359, 16835, 13645	535	38	17763	3.E+00	1.E+00	1.E+00
INTERPRO	IPR013091:EGF calcium-binding	4	0.731261426	3.E-01 22359, 65969, 16835, 13645	535	69	17763	2.E+00	1.E+00	1.E+00
INTERPRO	IPR000742:EGF-like, type 3	8	1.462522852	4.E-01 11489, 20343, 22359, 65969, 16835, 18791, 20343	535	199	17763	1.E+00	1.E+00	1.E+00
SMART	SM00179:EGF_CA	4	0.731261426	4.E-01 22359, 65969, 16835, 13645	248	91	9131	2.E+00	1.E+00	9.E-01
SMART	SM00181:EGF	7	1.279707495	5.E-01 20343, 22359, 65969, 16835, 18791, 20343	248	203	9131	1.E+00	1.E+00	9.E-01
INTERPRO	IPR001881:EGF-like calcium-binding	4	0.731261426	5.E-01 22359, 65969, 16835, 13645	535	91	17763	1.E+00	1.E+00	1.E+00
INTERPRO	IPR018097:EGF-like calcium-binding, conserved site	4	0.731261426	5.E-01 22359, 65969, 16835, 13645	535	94	17763	1.E+00	1.E+00	1.E+00
INTERPRO	IPR000152:EGF-type aspartate/asparagine hydroxylation conserved	4	0.731261426	5.E-01 22359, 65969, 16835, 13645	535	94	17763	1.E+00	1.E+00	1.E+00
INTERPRO	IPR006210:EGF-like	7	1.279707495	6.E-01 20343, 22359, 65969, 16835, 18791, 20343	535	203	17763	1.E+00	1.E+00	1.E+00
UP_SEQ_FEATURE	domain:EGF-like 3	3	0.548446069	7.E-01 22359, 16835, 13645	537	66	16021	1.E+00	1.E+00	1.E+00
UP_SEQ_FEATURE	domain:EGF-like 1	3	0.548446069	9.E-01 22359, 65969, 16835	537	106	16021	8.E-01	1.E+00	1.E+00

Annotation Cluster 96		Enrichment Score: 0.779836742610819									
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
UP_SEQ_FEATURE	region of interest:Purine nucleotide binding	3	0.548446069	3.E-03	22227, 22229, 22228	537	3	16021	3.E+01	1.E+00	2.E-01
INTERPRO	IPR002030:Mitochondrial brown fat uncoupling protein	3	0.548446069	8.E-03	22227, 22229, 22228	535	5	17763	2.E+01	1.E+00	2.E-01
PIR_SUPERFAMILY	PIRSF002458:ADP/ATP carrier protein	3	0.548446069	4.E-01	22227, 22229, 22228	378	29	8136	2.E+00	1.E+00	1.E+00
UP_SEQ_FEATURE	repeat:Solcar 3	3	0.548446069	4.E-01	22227, 22229, 22228	537	44	16021	2.E+00	1.E+00	1.E+00
INTERPRO	IPR001993:Mitochondrial substrate carrier	3	0.548446069	4.E-01	22227, 22229, 22228	535	49	17763	2.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0006839~mitochondrial transport	3	0.548446069	5.E-01	22227, 22229, 22228	491	42	13588	2.E+00	1.E+00	1.E+00
INTERPRO	IPR018108:Mitochondrial substrate/solute carrier	3	0.548446069	5.E-01	22227, 22229, 22228	535	52	17763	2.E+00	1.E+00	1.E+00
UP_SEQ_FEATURE	repeat:Solcar 1	3	0.548446069	5.E-01	22227, 22229, 22228	537	47	16021	2.E+00	1.E+00	1.E+00
UP_SEQ_FEATURE	repeat:Solcar 2	3	0.548446069	5.E-01	22227, 22229, 22228	537	47	16021	2.E+00	1.E+00	1.E+00

Annotation Cluster 97		Enrichment Score: 0.7702453657851863									
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_BP_FAT	GO:0042326~negative regulation of phosphorylation	4	0.731261426		7.E-02 15170, 18753, 12577, 16476	491	27	13588	4.E+00	1.E+00	6.E-01
GOTERM_BP_FAT	GO:0045936~negative regulation of phosphate metabolic process	4	0.731261426		9.E-02 15170, 18753, 12577, 16476	491	29	13588	4.E+00	1.E+00	6.E-01
GOTERM_BP_FAT	GO:0010563~negative regulation of phosphorus metabolic process	4	0.731261426		9.E-02 15170, 18753, 12577, 16476	491	29	13588	4.E+00	1.E+00	6.E-01
GOTERM_BP_FAT	GO:0051248~negative regulation of protein metabolic process	6	1.096892139		2.E-01 15170, 18753, 12258, 16476, 19697, 224045	491	78	13588	2.E+00	1.E+00	8.E-01
GOTERM_BP_FAT	GO:0001933~negative regulation of protein amino acid phosphorylation	3	0.548446069		2.E-01 15170, 18753, 16476	491	23	13588	4.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0032269~negative regulation of cellular protein metabolic process	5	0.914076782		3.E-01 15170, 18753, 12258, 16476, 224045	491	72	13588	2.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0031400~negative regulation of protein modification process	3	0.548446069		4.E-01 15170, 18753, 16476	491	38	13588	2.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0048585~negative regulation of response to stimulus	4	0.731261426		4.E-01 15170, 18753, 12702, 12258	491	65	13588	2.E+00	1.E+00	1.E+00

Annotation Cluster 98		Enrichment Score: 0.7446905182761319									
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_BP_FAT	GO:0006090~pyruvate metabolic process	4	0.731261426		6.E-02 14751, 235339, 21991, 230163	491	25	13588	4.E+00	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0046364~monosaccharide biosynthetic process	4	0.731261426		1.E-01 14751, 21991, 230163, 14381	491	31	13588	4.E+00	1.E+00	7.E-01
GOTERM_BP_FAT	GO:0046165~alcohol biosynthetic process	4	0.731261426		1.E-01 14751, 21991, 230163, 14381	491	37	13588	3.E+00	1.E+00	8.E-01
GOTERM_BP_FAT	GO:0006094~gluconeogenesis	3	0.548446069		2.E-01 14751, 21991, 230163	491	20	13588	4.E+00	1.E+00	8.E-01
GOTERM_BP_FAT	GO:0019319~hexose biosynthetic process	3	0.548446069		2.E-01 14751, 21991, 230163	491	25	13588	3.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0034637~cellular carbohydrate biosynthetic process	4	0.731261426		3.E-01 14751, 21991, 230163, 14381	491	56	13588	2.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0016051~carbohydrate biosynthetic process	4	0.731261426		6.E-01 14751, 21991, 230163, 14381	491	83	13588	1.E+00	1.E+00	1.E+00

Annotation Cluster 99      Enrichment Score: 0.7367636283352474



Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
UP_SEQ_FEATURE	domain:N-terminal Ras-GEF	3	0.548446069	1.E-01	20662, 20663, 19417	537	17	16021	5.E+00	1.E+00	9.E-01
INTERPRO	IPR019804:Ras guanine-nucleotide exchange factor, conserved site	3	0.548446069	2.E-01	20662, 20663, 19417	535	24	17763	4.E+00	1.E+00	9.E-01
SMART	SM00147:RasGEF	3	0.548446069	2.E-01	20662, 20663, 19417	248	28	9131	4.E+00	1.E+00	6.E-01
UP_SEQ_FEATURE	domain:Ras-GEF	3	0.548446069	2.E-01	20662, 20663, 19417	537	24	16021	4.E+00	1.E+00	1.E+00
SMART	SM00229:RasGEFN	3	0.548446069	2.E-01	20662, 20663, 19417	248	30	9131	4.E+00	1.E+00	6.E-01
INTERPRO	IPR001895:Guanine-nucleotide dissociation stimulator CDC25	3	0.548446069	2.E-01	20662, 20663, 19417	535	28	17763	4.E+00	1.E+00	9.E-01
INTERPRO	IPR000651:Guanine nucleotide exchange factor for Ras-like GTPase:	3	0.548446069	2.E-01	20662, 20663, 19417	535	30	17763	3.E+00	1.E+00	1.E+00
INTERPRO	IPR008937:Ras guanine nucleotide exchange factor	3	0.548446069	2.E-01	20662, 20663, 19417	535	31	17763	3.E+00	1.E+00	1.E+00

Annotation Cluster 100		Enrichment Score: 0.7308282600690328									
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
SMART	SM00105:ArfGap	3	0.548446069		1.E-01 228998, 212285, 106952	248	23	9131	5.E+00	1.E+00	5.E-01
INTERPRO	IPR001164:Arf GTPase activating protein	3	0.548446069		2.E-01 228998, 212285, 106952	535	23	17763	4.E+00	1.E+00	9.E-01
UP_SEQ_FEATURE	domain:Arf-GAP	3	0.548446069		2.E-01 228998, 212285, 106952	537	21	16021	4.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0032318~regulation of Ras GTPase activity	6	1.096892139		2.E-01 71709, 228998, 19765, 19417, 212285, :	491	80	13588	2.E+00	1.E+00	8.E-01
GOTERM_MF_FAT	GO:0008060~ARF GTPase activator activity	3	0.548446069		2.E-01 228998, 212285, 106952	476	23	13288	4.E+00	1.E+00	7.E-01
GOTERM_BP_FAT	GO:0032312~regulation of ARF GTPase activity	3	0.548446069		2.E-01 228998, 212285, 106952	491	23	13588	4.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0032012~regulation of ARF protein signal transduction	3	0.548446069		4.E-01 228998, 212285, 106952	491	38	13588	2.E+00	1.E+00	1.E+00

Annotation Cluster	Enrichment Score: 0.7276805970639064																	
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold	Enrichment	Bonferroni	Benjamini						
INTERPRO	IPR016060:Complement control module	5	0.914076782	8.E-02	14060, 20343, 12274, 18791, 20339	535	54	17763	3.E+00	1.E+00	7.E-01							
SP_PIR_KEYWORDS	sushi	4	0.731261426	2.E-01	14060, 20343, 12274, 20339	541	46	17854	3.E+00	1.E+00	4.E-01							
SMART	SM00032:CCP	4	0.731261426	2.E-01	14060, 20343, 12274, 20339	248	53	9131	3.E+00	1.E+00	6.E-01							
INTERPRO	IPR000436:Sushi/SCR/CCP	4	0.731261426	2.E-01	14060, 20343, 12274, 20339	535	53	17763	3.E+00	1.E+00	9.E-01							
UP_SEQ_FEATURE	domain:Sushi_2	3	0.548446069	3.E-01	14060, 20343, 20339	537	33	16021	3.E+00	1.E+00	1.E+00							
UP_SEQ_FEATURE	domain:Sushi_1	3	0.548446069	3.E-01	14060, 20343, 20339	537	33	16021	3.E+00	1.E+00	1.E+00							

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_BP_FAT	GO:0042981~regulation of apoptosis	26	4.753199269	1.E-01	12190, 22029, 672195, 67184, 11816, 1:	491	553	13588	1.E+00	1.E+00	8.E-01
GOTERM_BP_FAT	GO:0043067~regulation of programmed cell death	26	4.753199269	2.E-01	12190, 22029, 672195, 67184, 11816, 1:	491	560	13588	1.E+00	1.E+00	8.E-01
GOTERM_BP_FAT	GO:0010941~regulation of cell death	26	4.753199269	2.E-01	12190, 22029, 672195, 67184, 11816, 1:	491	563	13588	1.E+00	1.E+00	8.E-01
GOTERM_BP_FAT	GO:0043065~positive regulation of apoptosis	13	2.376599634	2.E-01	12190, 672195, 15170, 67184, 15930, 1:	491	248	13588	1.E+00	1.E+00	8.E-01
GOTERM_BP_FAT	GO:0043068~positive regulation of programmed cell death	13	2.376599634	2.E-01	12190, 672195, 15170, 67184, 15930, 1:	491	250	13588	1.E+00	1.E+00	8.E-01
GOTERM_BP_FAT	GO:0010942~positive regulation of cell death	13	2.376599634	2.E-01	12190, 672195, 15170, 67184, 15930, 1:	491	252	13588	1.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0006917~induction of apoptosis	9	1.645338208	3.E-01	12190, 15170, 18753, 67184, 11816, 200	491	167	13588	1.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0012502~induction of programmed cell death	9	1.645338208	3.E-01	12190, 15170, 18753, 67184, 11816, 200	491	167	13588	1.E+00	1.E+00	9.E-01

Annotation Cluster	Enrichment Score: 0.6924509575479673												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini		
GOTERM_BP_FAT	GO:0008203~cholesterol metabolic process	7	1.279707495		4-E-02 13121, 11816, 14137, 22359, 65969, 161	491	70	13588	3.E+00	1.E+00	4.E-01		
GOTERM_BP_FAT	GO:0016125~sterol metabolic process	7	1.279707495		6-E-02 13121, 11816, 14137, 22359, 65969, 161	491	77	13588	3.E+00	1.E+00	5.E-01		
GOTERM_MF_FAT	GO:0008034~lipoprotein binding	3	0.548446069		2-E-01 11816, 22359, 16835	476	21	13288	4.E+00	1.E+00	7.E-01		
SP_PIR_KEYWORDS	lipid transport	4	0.731261426		2-E-01 11816, 22359, 238055, 16835	541	51	17854	3.E+00	1.E+00	5.E-01		
GOTERM_CC_FAT	GO:0034358~plasma lipoprotein particle	3	0.548446069		2-E-01 11816, 22359, 16835	419	27	12504	3.E+00	1.E+00	7.E-01		
GOTERM_CC_FAT	GO:0032994~protein-lipid complex	3	0.548446069		2-E-01 11816, 22359, 16835	419	27	12504	3.E+00	1.E+00	7.E-01		
GOTERM_BP_FAT	GO:0006869~lipid transport	4	0.731261426		8-E-01 11816, 22359, 238055, 16835	491	119	13588	9.E-01	1.E+00	1.E+00		
GOTERM_BP_FAT	GO:0010876~lipid localization	4	0.731261426		8-E-01 11816, 22359, 238055, 16835	491	128	13588	9.E-01	1.E+00	1.E+00		

Annotation Cluster 104	Enrichment Score: 0.6895334662836651											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold	Enrichment	Bonferroni	Benjamini
GOTERM_BP_FAT	GO:0006366~transcription from RNA polymerase II promoter	6	1.096892139		1.E-01 20848, 20020, 16911, 14884, 14885, 13117	491	74	13588	2.E+00	1.E+00	8.E-01	
GOTERM_BP_FAT	GO:0032774~RNA biosynthetic process	8	1.462522852		2.E-01 20848, 69890, 20020, 16911, 19075, 14884, 14885, 13117	491	126	13588	2.E+00	1.E+00	8.E-01	
GOTERM_BP_FAT	GO:0006351~transcription, DNA-dependent	7	1.279707495		3.E-01 20848, 69890, 20020, 16911, 14884, 14885, 13117	491	122	13588	2.E+00	1.E+00	9.E-01	
GOTERM_CC_FAT	GO:0016591~DNA-directed RNA polymerase II, holoenzyme	4	0.731261426		3.E-01 20020, 14884, 14885, 13117	419	56	12504	2.E+00	1.E+00	8.E-01	

Annotation Cluster 105      Enrichment Score: 0.6803067379245006







BiOARTA	m_arenrf2Pathway:Oxidative Stress Induced Gene Expression Via Nr	5	0.914076782	9.E-02 16476, 12912, 18984, 94284, 394436, 1	109	19	1171	3.E+00	1.E+00	4.E-01
SMART	SM00338:BRIZ	4	0.731261426	2.E-01 16476, 18022, 12912, 17135	248	54	9131	3.E+00	1.E+00	6.E-01
INTERPRO	IPR004827:Basic-leucine zipper (bZIP) transcription factor	4	0.731261426	2.E-01 16476, 18022, 12912, 17135	535	54	17763	2.E+00	1.E+00	9.E-01
INTERPRO	IPR011616:bZIP transcription factor, bZIP-1	3	0.548446069	2.E-01 16476, 18022, 12912	535	30	17763	3.E+00	1.E+00	1.E+00
UP_SEQ_FEATURE	DNA-binding region:Basic motif	7	1.279707495	4.E-01 11865, 12753, 16476, 18022, 12912, 17	537	154	16021	1.E+00	1.E+00	1.E+00
GOTERM_MF_FAT	GO:0043565~sequence-specific DNA binding	9	1.645338208	1.E+00 20848, 16392, 74318, 16476, 19697, 18	476	556	13288	5.E-01	1.E+00	1.E+00

Annotation Cluster 109	Enrichment Score: 0.6546755038754803										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_BP_FAT	GO:0042159~lipoprotein catabolic process	3	0.548446069		2.E-02 11816, 238055, 16835	491	6	13588	1.E+01	1.E+00	3.E-01
SP_PIR_KEYWORDS	vidl	3	0.548446069		4.E-02 11816, 22359, 238055	541	11	17854	9.E+00	1.E+00	2.E-01
SP_PIR_KEYWORDS	lipid transport	4	0.731261426		2.E-01 11816, 22359, 238055, 16835	541	51	17854	3.E+00	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0015918~sterol transport	3	0.548446069		2.E-01 11816, 238055, 16835	491	23	13588	4.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0030301~cholesterol transport	3	0.548446069		2.E-01 11816, 238055, 16835	491	23	13588	4.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0042632~cholesterol homeostasis	3	0.548446069		2.E-01 11816, 238055, 16835	491	26	13588	3.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0055092~sterol homeostasis	3	0.548446069		2.E-01 11816, 238055, 16835	491	26	13588	3.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0055088~lipid homeostasis	3	0.548446069		3.E-01 11816, 238055, 16835	491	34	13588	2.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0042157~lipoprotein metabolic process	3	0.548446069		8.E-01 11816, 238055, 16835	491	76	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0006869~lipid transport	4	0.731261426		8.E-01 11816, 22359, 238055, 16835	491	119	13588	9.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0010876~lipid localization	4	0.731261426		8.E-01 11816, 22359, 238055, 16835	491	128	13588	9.E-01	1.E+00	1.E+00

Annotation Cluster 110	Enrichment Score: 0.6393356511536122										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_MF_FAT	GO:0017016~Ras GTPase binding	5	0.914076782		1.E-01 117600, 13605, 16800, 109905, 19765	476	57	13288	2.E+00	1.E+00	6.E-01
GOTERM_MF_FAT	GO:0031267~small GTPase binding	5	0.914076782		2.E-01 117600, 13605, 16800, 109905, 19765	476	59	13288	2.E+00	1.E+00	7.E-01
GOTERM_MF_FAT	GO:0051020~GTPase binding	5	0.914076782		2.E-01 117600, 13605, 16800, 109905, 19765	476	62	13288	2.E+00	1.E+00	7.E-01
GOTERM_MF_FAT	GO:0017048~Rho GTPase binding	3	0.548446069		2.E-01 117600, 13605, 16800	476	24	13288	3.E+00	1.E+00	7.E-01
GOTERM_MF_FAT	GO:0019899~enzyme binding	8	1.462522852		7.E-01 20848, 117600, 21813, 11487, 13605, 11487	476	229	13288	1.E+00	1.E+00	1.E+00

Annotation Cluster 111	Enrichment Score: 0.6301005666614619										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_BP_FAT	GO:0043524~negative regulation of neuron apoptosis	5	0.914076782		1.E-01 18049, 12064, 13867, 18227, 11848	491	50	13588	3.E+00	1.E+00	7.E-01
GOTERM_BP_FAT	GO:0042981~regulation of apoptosis	26	4.753199269		1.E-01 12190, 22029, 672195, 67184, 11816, 11817	491	553	13588	1.E+00	1.E+00	8.E-01
GOTERM_BP_FAT	GO:0043067~regulation of programmed cell death	26	4.753199269		2.E-01 12190, 22029, 672195, 67184, 11816, 11817	491	560	13588	1.E+00	1.E+00	8.E-01
GOTERM_BP_FAT	GO:0043523~regulation of neuron apoptosis	6	1.096892139		2.E-01 18049, 12064, 13867, 18227, 18205, 11848	491	80	13588	2.E+00	1.E+00	8.E-01
GOTERM_BP_FAT	GO:0010941~regulation of cell death	26	4.753199269		2.E-01 12190, 22029, 672195, 67184, 11816, 11817	491	563	13588	1.E+00	1.E+00	8.E-01
GOTERM_BP_FAT	GO:0043066~negative regulation of apoptosis	10	1.828153565		5.E-01 18708, 18049, 19053, 12064, 13867, 15129	491	239	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0043069~negative regulation of programmed cell death	10	1.828153565		5.E-01 18708, 18049, 19053, 12064, 13867, 15129	491	244	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0060548~negative regulation of cell death	10	1.828153565		5.E-01 18708, 18049, 19053, 12064, 13867, 15129	491	245	13588	1.E+00	1.E+00	1.E+00

Annotation Cluster 112	Enrichment Score: 0.6263769406999816										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_BP_FAT	GO:0031589~cell-substrate adhesion	5	0.914076782		1.E-01 19944, 665032, 50768, 11856, 666642, :	491	57	13588	2.E+00	1.E+00	8.E-01
GOTERM_BP_FAT	GO:0007160~cell-matrix adhesion	4	0.731261426		3.E-01 50768, 11856, 19261, 11848	491	50	13588	2.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0007015~actin filament organization	4	0.731261426		3.E-01 11856, 16800, 19261, 11848	491	56	13588	2.E+00	1.E+00	9.E-01

Annotation Cluster 113		Enrichment Score: 0.6249899615268899									
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_BP_FAT	GO:0031349~positive regulation of defense response	5	0.914076782		1.E-01 12266, 15930, 16423, 19697, 106759	491	57	13588	2.E+00	1.E+00	8.E-01
GOTERM_BP_FAT	GO:0032101~regulation of response to external stimulus	7	1.279707495		2.E-01 12266, 21813, 12258, 15930, 74318, 16423	491	103	13588	2.E+00	1.E+00	8.E-01
GOTERM_BP_FAT	GO:0050729~positive regulation of inflammatory response	3	0.548446069		2.E-01 12266, 15930, 16423	491	24	13588	3.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0050727~regulation of inflammatory response	4	0.731261426		3.E-01 12266, 12258, 15930, 16423	491	57	13588	2.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0032103~positive regulation of response to external stimulus	3	0.548446069		4.E-01 12266, 15930, 16423	491	39	13588	2.E+00	1.E+00	1.E+00

Annotation Cluster 114	Enrichment Score: 0.6049764391064797										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_BP_FAT	GO:0006641~triglyceride metabolic process	4	0.731261426	1.E-01	19247, 13350, 238055, 67469	491	36	13588	3.E+00	1.E+00	8.E-01
GOTERM_BP_FAT	GO:0006639~acylglycerol metabolic process	4	0.731261426	2.E-01	19247, 13350, 238055, 67469	491	43	13588	3.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0006638~neutral lipid metabolic process	4	0.731261426	2.E-01	19247, 13350, 238055, 67469	491	45	13588	2.E+00	1.E+00	9.E-01



GOTERM_BP_FAT	GO:0006662~glycerol ether metabolic process	4	0.731261426	2.E-01	19247, 13350, 238055, 67469	491	45	13588	2.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0018904~organic ether metabolic process	4	0.731261426	2.E-01	19247, 13350, 238055, 67469	491	48	13588	2.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0046486~glycerolipid metabolic process	5	0.914076782	7.E-01	18708, 19247, 13350, 238055, 67469	491	129	13588	1.E+00	1.E+00	1.E+00
Annotation Cluster 115	Enrichment Score: 0.5890847186075064										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
INTERPRO	IPR003096:SM22/calponin	3	0.548446069	3.E-02	73341, 22324, 57257	535	10	17763	1.E+01	1.E+00	5.E-01
UP_SEQ_FEATURE	domain:CH	3	0.548446069	4.E-01	73341, 22324, 57257	537	39	16021	2.E+00	1.E+00	1.E+00
SMART	SM00033:CH	3	0.548446069	6.E-01	73341, 22324, 57257	248	68	9131	2.E+00	1.E+00	9.E-01
INTERPRO	IPR001715:Calponin-like actin-binding	3	0.548446069	6.E-01	73341, 22324, 57257	535	68	17763	1.E+00	1.E+00	1.E+00
Annotation Cluster 116	Enrichment Score: 0.5807037653751759										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_BP_FAT	GO:0022610~biological adhesion	25	4.570383912	2.E-01	69524, 11852, 665032, 11856, 16423, 20	491	562	13588	1.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0007155~cell adhesion	25	4.570383912	2.E-01	69524, 11852, 665032, 11856, 16423, 20	491	561	13588	1.E+00	1.E+00	9.E-01
SP_PIR_KEYWORDS	cell adhesion	14	2.559414991	4.E-01	11350, 69524, 11852, 11820, 16423, 17	541	380	17854	1.E+00	1.E+00	7.E-01
Annotation Cluster 117	Enrichment Score: 0.5618430591671122										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_BP_FAT	GO:0009156~ribonucleoside monophosphate biosynthetic process	3	0.548446069	1.E-01	110639, 14450, 99586	491	17	13588	5.E+00	1.E+00	7.E-01
GOTERM_BP_FAT	GO:0009161~ribonucleoside monophosphate metabolic process	3	0.548446069	1.E-01	110639, 14450, 99586	491	19	13588	4.E+00	1.E+00	8.E-01
GOTERM_BP_FAT	GO:0009124~nucleoside monophosphate biosynthetic process	3	0.548446069	5.E-01	110639, 14450, 99586	491	45	13588	2.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0009123~nucleoside monophosphate metabolic process	3	0.548446069	6.E-01	110639, 14450, 99586	491	59	13588	1.E+00	1.E+00	1.E+00
Annotation Cluster 118	Enrichment Score: 0.5541361890580664										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_BP_FAT	GO:0006935~chemotaxis	7	1.279707495	2.E-01	20310, 12765, 19354, 72962, 14158, 20	491	109	13588	2.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0042330~taxis	7	1.279707495	2.E-01	20310, 12765, 19354, 72962, 14158, 20	491	109	13588	2.E+00	1.E+00	9.E-01
SP_PIR_KEYWORDS	chemotaxis	4	0.731261426	3.E-01	20310, 12765, 20202, 20201	541	62	17854	2.E+00	1.E+00	6.E-01
GOTERM_BP_FAT	GO:0007626~locomotory behavior	11	2.010968921	4.E-01	20310, 12765, 19354, 78405, 72962, 14	491	239	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0007610~behavior	17	3.10786106	4.E-01	12765, 15930, 78405, 72962, 11820, 18	491	405	13588	1.E+00	1.E+00	1.E+00
Annotation Cluster 119	Enrichment Score: 0.5428490233928023										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_CC_FAT	GO:0030141~secretory granule	8	1.462522852	1.E-01	26934, 18551, 13035, 18791, 71326, 13	419	117	12504	2.E+00	1.E+00	5.E-01
GOTERM_CC_FAT	GO:0031988~membrane-bounded vesicle	18	3.290676417	2.E-01	13649, 26934, 14674, 19384, 65969, 13	419	420	12504	1.E+00	1.E+00	7.E-01
GOTERM_CC_FAT	GO:0016023~cytoplasmic membrane-bounded vesicle	17	3.10786106	3.E-01	13649, 26934, 14674, 19384, 65969, 13	419	414	12504	1.E+00	1.E+00	8.E-01
GOTERM_CC_FAT	GO:0031982~vesicle	19	3.473491773	5.E-01	13649, 26934, 14674, 19384, 11820, 65	419	519	12504	1.E+00	1.E+00	9.E-01
GOTERM_CC_FAT	GO:0031410~cytoplasmic vesicle	18	3.290676417	5.E-01	13649, 26934, 14674, 19384, 11820, 65	419	508	12504	1.E+00	1.E+00	9.E-01
Annotation Cluster 120	Enrichment Score: 0.5395023555933715										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_BP_FAT	GO:0009408~response to heat	4	0.731261426	1.E-01	12955, 224045, 217715, 15507	491	32	13588	3.E+00	1.E+00	7.E-01
GOTERM_BP_FAT	GO:0009266~response to temperature stimulus	4	0.731261426	3.E-01	12955, 224045, 217715, 15507	491	51	13588	2.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0009628~response to abiotic stimulus	8	1.462522852	8.E-01	14685, 12190, 21813, 12955, 11820, 22	491	251	13588	9.E-01	1.E+00	1.E+00
Annotation Cluster 121	Enrichment Score: 0.5331479341916965										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_BP_FAT	GO:0048011~nerve growth factor receptor signaling pathway	3	0.548446069	4.E-02	20779, 19247, 20662	491	9	13588	9.E+00	1.E+00	4.E-01
GOTERM_BP_FAT	GO:0009967~positive regulation of signal transduction	8	1.462522852	4.E-01	20779, 19247, 20662, 11491, 56847, 10	491	172	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0010647~positive regulation of cell communication	8	1.462522852	5.E-01	20779, 19247, 20662, 11491, 56847, 10	491	189	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0010740~positive regulation of protein kinase cascade	3	0.548446069	8.E-01	106759, 16452, 11848	491	88	13588	9.E-01	1.E+00	1.E+00
Annotation Cluster 122	Enrichment Score: 0.5285135509988										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_BP_FAT	GO:0048639~positive regulation of developmental growth	3	0.548446069	8.E-02	21813, 18049, 74318	491	13	13588	6.E+00	1.E+00	6.E-01
GOTERM_BP_FAT	GO:0045927~positive regulation of growth	4	0.731261426	3.E-01	21813, 18049, 74318, 12912	491	56	13588	2.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0048638~regulation of developmental growth	3	0.548446069	4.E-01	21813, 18049, 74318	491	37	13588	2.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0045597~positive regulation of cell differentiation	8	1.462522852	4.E-01	21813, 18049, 12702, 12064, 74318, 21	491	175	13588	1.E+00	1.E+00	1.E+00



GOTERM_BP_FAT	GO:0051094~positive regulation of developmental process	9	1.645338208	5.E-01	21813, 18049, 12702, 12064, 11852, 74:	491	214	13588	1.E+00	1.E+00	1.E+00
Annotation Cluster 123	Enrichment Score: 0.5269787786492612										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_BP_FAT	GO:0051345~positive regulation of hydrolase activity	8	1.462522852	3.E-02	672195, 71709, 12279, 11856, 67469, 14:	491	81	13588	3.E+00	1.E+00	4.E-01
GOTERM_BP_FAT	GO:0006919~activation of caspase activity	3	0.548446069	3.E-01	672195, 12279, 14852, 13063	491	33	13588	3.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0010952~positive regulation of peptidase activity	3	0.548446069	4.E-01	672195, 12279, 14852, 13063	491	36	13588	2.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0043280~positive regulation of caspase activity	3	0.548446069	4.E-01	672195, 12279, 14852, 13063	491	36	13588	2.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0052548~regulation of endopeptidase activity	3	0.548446069	5.E-01	672195, 12279, 14852, 13063	491	50	13588	2.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0043281~regulation of caspase activity	3	0.548446069	5.E-01	672195, 12279, 14852, 13063	491	50	13588	2.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0052547~regulation of peptidase activity	3	0.548446069	6.E-01	672195, 12279, 14852, 13063	491	51	13588	2.E+00	1.E+00	1.E+00
Annotation Cluster 124	Enrichment Score: 0.5252506053154805										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_BP_FAT	GO:0042551~neuron maturation	4	0.731261426	1.E-02	19713, 12577, 11820, 18227	491	13	13588	9.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0048469~cell maturation	8	1.462522852	2.E-02	12190, 19713, 12577, 11820, 18551, 18:	491	75	13588	3.E+00	1.E+00	3.E-01
GOTERM_BP_FAT	GO:0021700~developmental maturation	8	1.462522852	7.E-02	12190, 19713, 12577, 11820, 18551, 18:	491	101	13588	2.E+00	1.E+00	6.E-01
GOTERM_BP_FAT	GO:0048608~reproductive structure development	9	1.645338208	1.E-01	12190, 13667, 20779, 16847, 224045, 2:	491	130	13588	2.E+00	1.E+00	7.E-01
GOTERM_BP_FAT	GO:0008585~female gonad development	5	0.914076782	1.E-01	12190, 13667, 16847, 224045, 217715	491	53	13588	3.E+00	1.E+00	7.E-01
GOTERM_BP_FAT	GO:0046545~development of primary female sexual characteristics	5	0.914076782	1.E-01	12190, 13667, 16847, 224045, 217715	491	57	13588	2.E+00	1.E+00	8.E-01
GOTERM_BP_FAT	GO:0007292~female gamete generation	4	0.731261426	3.E-01	12190, 20779, 16847, 20112	491	56	13588	2.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0003006~reproductive developmental process	12	2.193784278	4.E-01	12190, 13667, 20779, 18551, 16847, 20:	491	264	13588	1.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0008406~gonad development	5	0.914076782	4.E-01	12190, 13667, 16847, 224045, 217715	491	88	13588	2.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0048477~oogenesis	3	0.548446069	4.E-01	12190, 20779, 20112	491	39	13588	2.E+00	1.E+00	1.E+00
GOTERM_CC_FAT	GO:0001669~acrosomal vesicle	3	0.548446069	4.E-01	26934, 18551, 13382	419	43	12504	2.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0045137~development of primary sexual characteristics	5	0.914076782	5.E-01	12190, 13667, 16847, 224045, 217715	491	104	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0007281~germ cell development	4	0.731261426	7.E-01	12190, 18551, 20112, 13382	491	101	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0032504~multicellular organism reproduction	14	2.559414991	7.E-01	12190, 13667, 26934, 19247, 238055, 1:	491	409	13588	9.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0048609~reproductive process in a multicellular organism	14	2.559414991	7.E-01	12190, 13667, 26934, 19247, 238055, 1:	491	409	13588	9.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0019953~sexual reproduction	10	1.828153565	9.E-01	20848, 12190, 26934, 20779, 238055, 1:	491	386	13588	7.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0048610~reproductive cellular process	4	0.731261426	1.E+00	12190, 18551, 20112, 13382	491	173	13588	6.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0007276~gamete generation	8	1.462522852	1.E+00	12190, 26934, 20779, 238055, 18551, 1:	491	331	13588	7.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0007283~spermatogenesis	5	0.914076782	1.E+00	12190, 26934, 238055, 18551, 13382	491	255	13588	5.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0048232~male gamete generation	5	0.914076782	1.E+00	12190, 26934, 238055, 18551, 13382	491	255	13588	5.E-01	1.E+00	1.E+00
Annotation Cluster 125	Enrichment Score: 0.5151475538273691										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_BP_FAT	GO:0042130~negative regulation of T cell proliferation	4	0.731261426	8.E-02	15170, 208154, 13866, 15930	491	28	13588	4.E+00	1.E+00	6.E-01
GOTERM_BP_FAT	GO:0070664~negative regulation of leukocyte proliferation	4	0.731261426	1.E-01	15170, 208154, 13866, 15930	491	35	13588	3.E+00	1.E+00	8.E-01
GOTERM_BP_FAT	GO:0032945~negative regulation of mononuclear cell proliferation	4	0.731261426	1.E-01	15170, 208154, 13866, 15930	491	35	13588	3.E+00	1.E+00	8.E-01
GOTERM_BP_FAT	GO:0050672~negative regulation of lymphocyte proliferation	4	0.731261426	1.E-01	15170, 208154, 13866, 15930	491	35	13588	3.E+00	1.E+00	8.E-01
GOTERM_BP_FAT	GO:0050868~negative regulation of T cell activation	4	0.731261426	2.E-01	15170, 208154, 13866, 15930	491	42	13588	3.E+00	1.E+00	8.E-01
GOTERM_BP_FAT	GO:0051250~negative regulation of lymphocyte activation	4	0.731261426	3.E-01	15170, 208154, 13866, 15930	491	52	13588	2.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0002764~immune response-regulating signal transduction	4	0.731261426	3.E-01	15170, 208154, 19697, 106759	491	52	13588	2.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0008285~negative regulation of cell proliferation	11	2.010968921	3.E-01	15170, 21813, 12064, 208154, 13866, 1:	491	224	13588	1.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0002683~negative regulation of immune system process	5	0.914076782	3.E-01	15170, 208154, 13866, 12258, 15930	491	76	13588	2.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0050866~negative regulation of cell activation	4	0.731261426	3.E-01	15170, 208154, 13866, 15930	491	53	13588	2.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0002695~negative regulation of leukocyte activation	4	0.731261426	3.E-01	15170, 208154, 13866, 15930	491	53	13588	2.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0032944~regulation of mononuclear cell proliferation	5	0.914076782	3.E-01	15170, 208154, 13866, 15930, 106759	491	80	13588	2.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0050670~regulation of lymphocyte proliferation	5	0.914076782	3.E-01	15170, 208154, 13866, 15930, 106759	491	80	13588	2.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0070663~regulation of leukocyte proliferation	5	0.914076782	3.E-01	15170, 208154, 13866, 15930, 106759	491	82	13588	2.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0042129~regulation of T cell proliferation	4	0.731261426	4.E-01	15170, 208154, 13866, 15930	491	59	13588	2.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0050863~regulation of T cell activation	5	0.914076782	5.E-01	15170, 21813, 208154, 13866, 15930	491	108	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0050864~regulation of B cell activation	3	0.548446069	6.E-01	15170, 208154, 106759	491	55	13588	2.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0051249~regulation of lymphocyte activation	6	1.096892139	6.E-01	15170, 21813, 208154, 13866, 15930, 1:	491	144	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0045619~regulation of lymphocyte differentiation	3	0.548446069	6.E-01	15170, 21813, 13866	491	58	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0002694~regulation of leukocyte activation	6	1.096892139	7.E-01	15170, 21813, 208154, 13866, 15930, 1:	491	154	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0050865~regulation of cell activation	6	1.096892139	7.E-01	15170, 21813, 208154, 13866, 15930, 1:	491	156	13588	1.E+00	1.E+00	1.E+00



Annotation Cluster 126	Enrichment Score: 0.5021255672601677												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini		
GOTERM_BP_FAT	GO:0031349~positive regulation of defense response	5	0.914076782		1.E-01 12266, 15930, 16423, 19697, 106759		491	57	13588	2.E+00	1.E+00	8.E-01	
GOTERM_BP_FAT	GO:0009617~response to bacterium	9	1.645338208		2.E-01 18126, 14191, 20846, 15930, 16423, 19697, 106759		491	157	13588	2.E+00	1.E+00	9.E-01	
GOTERM_BP_FAT	GO:0002237~response to molecule of bacterial origin	4	0.731261426		3.E-01 20846, 15930, 19697, 106759		491	49	13588	2.E+00	1.E+00	9.E-01	
GOTERM_BP_FAT	GO:0032496~response to lipopolysaccharide	3	0.548446069		4.E-01 20846, 15930, 106759		491	38	13588	2.E+00	1.E+00	1.E+00	
GOTERM_BP_FAT	GO:0001817~regulation of cytokine production	3	0.548446069		1.E+00 15930, 19697, 106759		491	139	13588	6.E-01	1.E+00	1.E+00	
Annotation Cluster 127	Enrichment Score: 0.5019948834818804												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini		
GOTERM_BP_FAT	GO:0050830~defense response to Gram-positive bacterium	3	0.548446069		2.E-01 14191, 13035, 17969		491	23	13588	4.E+00	1.E+00	9.E-01	
GOTERM_BP_FAT	GO:0009617~response to bacterium	9	1.645338208		2.E-01 18126, 14191, 20846, 15930, 16423, 19697, 106759		491	157	13588	2.E+00	1.E+00	9.E-01	
GOTERM_BP_FAT	GO:0042742~defense response to bacterium	4	0.731261426		8.E-01 18126, 14191, 13035, 17969		491	108	13588	1.E+00	1.E+00	1.E+00	
Annotation Cluster 128	Enrichment Score: 0.4980632098309933												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini		
GOTERM_CC_FAT	GO:0005925~focal adhesion	5	0.914076782		1.E-01 12549, 236920, 18479, 231532, 69581		419	57	12504	3.E+00	1.E+00	5.E-01	
GOTERM_CC_FAT	GO:0005924~cell-substrate adherens junction	5	0.914076782		1.E-01 12549, 236920, 18479, 231532, 69581		419	61	12504	2.E+00	1.E+00	6.E-01	
GOTERM_CC_FAT	GO:0030055~cell-substrate junction	5	0.914076782		2.E-01 12549, 236920, 18479, 231532, 69581		419	66	12504	2.E+00	1.E+00	6.E-01	
GOTERM_CC_FAT	GO:0005912~adherens junction	6	1.096892139		3.E-01 12549, 69524, 236920, 18479, 231532, 69581		419	106	12504	2.E+00	1.E+00	8.E-01	
GOTERM_CC_FAT	GO:0016323~basolateral plasma membrane	7	1.279707495		3.E-01 12549, 13649, 236920, 20909, 18479, 231532, 69581		419	141	12504	1.E+00	1.E+00	8.E-01	
GOTERM_CC_FAT	GO:0070161~anchoring junction	6	1.096892139		4.E-01 12549, 69524, 236920, 18479, 231532, 69581		419	123	12504	1.E+00	1.E+00	9.E-01	
GOTERM_CC_FAT	GO:0030054~cell junction	12	2.193784278		9.E-01 12549, 18762, 69524, 19247, 94190, 236920, 16800, 231532, 69581		419	470	12504	8.E-01	1.E+00	1.E+00	
SP_PIR_KEYWORDS	cell junction	8	1.462522852		1.E+00 12549, 69524, 94190, 236920, 16800, 231532, 69581		541	392	17854	7.E-01	1.E+00	1.E+00	
Annotation Cluster 129	Enrichment Score: 0.4932455842260168												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini		
UP_SEQ_FEATURE	domain:WW 2	3	0.548446069		2.E-01 223666, 75415, 22601		537	28	16021	3.E+00	1.E+00	1.E+00	
UP_SEQ_FEATURE	domain:WW 1	3	0.548446069		2.E-01 223666, 75415, 22601		537	28	16021	3.E+00	1.E+00	1.E+00	
SMART	SM00456:WW	3	0.548446069		4.E-01 223666, 75415, 22601		248	51	9131	2.E+00	1.E+00	9.E-01	
INTERPRO	IPR001202:WW/Rsp5/WWP	3	0.548446069		5.E-01 223666, 75415, 22601		535	51	17763	2.E+00	1.E+00	1.E+00	
Annotation Cluster 130	Enrichment Score: 0.47091335412602237												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini		
GOTERM_MF_FAT	GO:0005543~phospholipid binding	7	1.279707495		3.E-01 13131, 17972, 266781, 17969, 233071, 12306		476	119	13288	2.E+00	1.E+00	8.E-01	
GOTERM_MF_FAT	GO:0035091~phosphoinositide binding	5	0.914076782		3.E-01 17972, 266781, 17969, 233071, 12306		476	75	13288	2.E+00	1.E+00	8.E-01	
SMART	SM00312:PX	3	0.548446069		4.E-01 17972, 266781, 17969		248	47	9131	2.E+00	1.E+00	8.E-01	
UP_SEQ_FEATURE	domain:PX	3	0.548446069		4.E-01 17972, 266781, 17969		537	42	16021	2.E+00	1.E+00	1.E+00	
INTERPRO	IPR001683:Phox-like	3	0.548446069		4.E-01 17972, 266781, 17969		535	47	17763	2.E+00	1.E+00	1.E+00	
Annotation Cluster 131	Enrichment Score: 0.46680641849101695												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini		
GOTERM_BP_FAT	GO:0030705~cytoskeleton-dependent intracellular transport	4	0.731261426		1.E-01 17925, 11820, 59040, 214952		491	33	13588	3.E+00	1.E+00	7.E-01	
GOTERM_BP_FAT	GO:0010970~microtubule-based transport	3	0.548446069		1.E-01 11820, 59040, 214952		491	18	13588	5.E+00	1.E+00	8.E-01	
GOTERM_BP_FAT	GO:0007018~microtubule-based movement	3	0.548446069		9.E-01 11820, 59040, 214952		491	101	13588	8.E-01	1.E+00	1.E+00	
GOTERM_BP_FAT	GO:0007017~microtubule-based process	4	0.731261426		1.E+00 18762, 11820, 59040, 214952		491	211	13588	5.E-01	1.E+00	1.E+00	
Annotation Cluster 132	Enrichment Score: 0.451909090354547												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini		
GOTERM_BP_FAT	GO:0008361~regulation of cell size	8	1.462522852		1.E-01 104394, 18049, 67184, 72269, 68349, 11820, 59040, 214952		491	108	13588	2.E+00	1.E+00	7.E-01	
GOTERM_BP_FAT	GO:0032535~regulation of cellular component size	9	1.645338208		2.E-01 104394, 18049, 67184, 72269, 68349, 11820, 59040, 214952		491	161	13588	2.E+00	1.E+00	9.E-01	
GOTERM_BP_FAT	GO:0045926~negative regulation of growth	4	0.731261426		5.E-01 67184, 72269, 68349, 15929		491	71	13588	2.E+00	1.E+00	1.E+00	
GOTERM_BP_FAT	GO:0030308~negative regulation of cell growth	3	0.548446069		5.E-01 67184, 72269, 68349		491	47	13588	2.E+00	1.E+00	1.E+00	
GOTERM_BP_FAT	GO:0045792~negative regulation of cell size	3	0.548446069		6.E-01 67184, 72269, 68349		491	53	13588	2.E+00	1.E+00	1.E+00	
GOTERM_BP_FAT	GO:0001558~regulation of cell growth	4	0.731261426		6.E-01 18049, 67184, 72269, 68349		491	92	13588	1.E+00	1.E+00	1.E+00	
Annotation Cluster 133	Enrichment Score: 0.43610392587692987												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini		
GOTERM_MF_FAT	GO:0004402~histone acetyltransferase activity	3	0.548446069		2.E-01 12753, 17979, 12914		476	20	13288	4.E+00	1.E+00	7.E-01	



GOTERM_MF_FAT	GO:0004468~lysine N-acetyltransferase activity	3	0.548446069	2.E-01 12753, 17979, 12914	476	20	13288	4.E+00	1.E+00	7.E-01
GOTERM_MF_FAT	GO:0016407~acetyltransferase activity	4	0.731261426	4.E-01 12753, 235339, 17979, 12914	476	63	13288	2.E+00	1.E+00	9.E-01
GOTERM_MF_FAT	GO:0008080~N-acetyltransferase activity	3	0.548446069	5.E-01 12753, 17979, 12914	476	51	13288	2.E+00	1.E+00	1.E+00
UP_SEQ_FEATURE	compositionally biased region:Poly-Gln	5	0.914076782	6.E-01 12753, 76448, 17979, 545156, 12914	537	130	16021	1.E+00	1.E+00	1.E+00
GOTERM_MF_FAT	GO:0016410~N-acyltransferase activity	3	0.548446069	7.E-01 12753, 17979, 12914	476	67	13288	1.E+00	1.E+00	1.E+00

Annotation Cluster 134	Enrichment Score: 0.43522892913450223										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_BP_FAT	GO:0006446~regulation of translational initiation	3	0.548446069		2.E-01 13665, 224045, 73830	491	21	13588	4.E+00	1.E+00	8.E-01
GOTERM_BP_FAT	GO:0006417~regulation of translation	6	1.096892139		3.E-01 13684, 13665, 11820, 224045, 73830, 21	491	100	13588	2.E+00	1.E+00	9.E-01
SP_PIR_KEYWORDS	translation regulation	3	0.548446069		6.E-01 13684, 13665, 208643	541	63	17854	2.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0010608~posttranscriptional regulation of gene expression	6	1.096892139		6.E-01 13684, 13665, 11820, 224045, 73830, 21	491	148	13588	1.E+00	1.E+00	1.E+00

Annotation Cluster 135	Enrichment Score: 0.4260090027243418										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_BP_FAT	GO:0050766~positive regulation of phagocytosis	3	0.548446069		2.E-01 12266, 16423, 19261	491	23	13588	4.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0050764~regulation of phagocytosis	3	0.548446069		2.E-01 12266, 16423, 19261	491	25	13588	3.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0051130~positive regulation of cellular component organization	7	1.279707495		3.E-01 12266, 18049, 16423, 26401, 21844, 19261	491	122	13588	2.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0045807~positive regulation of endocytosis	3	0.548446069		3.E-01 12266, 16423, 19261	491	34	13588	2.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0051050~positive regulation of transport	6	1.096892139		5.E-01 12266, 19247, 16423, 12912, 103988, 11000	491	132	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0030100~regulation of endocytosis	3	0.548446069		6.E-01 12266, 16423, 19261	491	52	13588	2.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0060627~regulation of vesicle-mediated transport	3	0.548446069		8.E-01 12266, 16423, 19261	491	83	13588	1.E+00	1.E+00	1.E+00

Annotation Cluster 136	Enrichment Score: 0.42435099900681333										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_BP_FAT	GO:0016265~death	23	4.204753199	2.E-01	22029, 12765, 672195, 11852, 67184, 1,	491	519	13588	1.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0008219~cell death	22	4.021937843	3.E-01	22029, 12765, 672195, 11852, 67184, 1,	491	507	13588	1.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0006915~apoptosis	18	3.290676417	5.E-01	22029, 12765, 672195, 11852, 67184, 1,	491	465	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0012501~programmed cell death	18	3.290676417	5.E-01	22029, 12765, 672195, 11852, 67184, 1,	491	473	13588	1.E+00	1.E+00	1.E+00

Annotation Cluster 137	Enrichment Score: 0.4210211476118024										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
SP_PIR_KEYWORDS	EF hand	4	0.731261426		5.E-02 20692, 20202, 20200, 20201	541	28	17854	5.E+00	1.E+00	2.E-01
SP_PIR_KEYWORDS	calcium binding	5	0.914076782		5.E-02 20692, 20202, 20200, 20201, 12306	541	47	17854	4.E+00	1.E+00	2.E-01
PIR_SUPERFAMILY	PIRSF002353:S-100 protein	3	0.548446069		1.E-01 20202, 20200, 20201	378	12	8136	5.E+00	1.E+00	1.E+00
INTERPRO	IPR013787:S100/CaBP-9k-type, calcium binding, subdomain	3	0.548446069		1.E-01 20202, 20200, 20201	535	21	17763	5.E+00	1.E+00	8.E-01
INTERPRO	IPR001751:S100/CaBP-9k-type, calcium binding	3	0.548446069		2.E-01 20202, 20200, 20201	535	23	17763	4.E+00	1.E+00	9.E-01
INTERPRO	IPR011992:EF-Hand type	9	1.645338208		4.E-01 20848, 20846, 13858, 20692, 20202, 20	535	227	17763	1.E+00	1.E+00	1.E+00
INTERPRO	IPR018247:EF-HAND 1	8	1.462522852		4.E-01 70316, 13858, 20692, 20202, 20200, 20	535	211	17763	1.E+00	1.E+00	1.E+00
INTERPRO	IPR018248:EF hand	5	0.914076782		6.E-01 13858, 20202, 20200, 20201, 214952	535	132	17763	1.E+00	1.E+00	1.E+00
UP_SEQ_FEATURE	domain:EF-hand 2	6	1.096892139		6.E-01 13858, 20202, 20200, 20201, 59040, 21	537	160	16021	1.E+00	1.E+00	1.E+00
UP_SEQ_FEATURE	domain:EF-hand 1	6	1.096892139		6.E-01 13858, 20202, 20200, 20201, 59040, 21	537	161	16021	1.E+00	1.E+00	1.E+00
UP_SEQ_FEATURE	calcium-binding region:2	4	0.731261426		7.E-01 13858, 20200, 59040, 214952	537	110	16021	1.E+00	1.E+00	1.E+00
INTERPRO	IPR018249:EF-HAND 2	6	1.096892139		7.E-01 13858, 20202, 20200, 20201, 59040, 21	535	205	17763	1.E+00	1.E+00	1.E+00
UP_SEQ_FEATURE	calcium-binding region:1	4	0.731261426		8.E-01 13858, 20200, 59040, 214952	537	120	16021	1.E+00	1.E+00	1.E+00
SMART	SM00054:EFh	3	0.548446069		9.E-01 13858, 59040, 214952	248	137	9131	8.E-01	1.E+00	1.E+00
INTERPRO	IPR002048:Calcium-binding EF-hand	3	0.548446069		9.E-01 13858, 59040, 214952	535	137	17763	7.E-01	1.E+00	1.E+00
SP_PIR_KEYWORDS	calcium	13	2.376599634		1.E+00 238055, 65969, 214952, 21881, 18783, 1	541	731	17854	6.E-01	1.E+00	1.E+00
GOTERM_MF_FAT	GO:0005509~calcium ion binding	18	3.290676417		1.E+00 22359, 65969, 13645, 214952, 21881, 21	476	840	13288	6.E-01	1.E+00	1.E+00

Annotation Cluster 138	Enrichment Score: 0.4158348042827275										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_BP_FAT	GO:0035264~multicellular organism growth	4	0.731261426		2.E-01 19944, 12190, 665032, 17979, 666642, 1	491	39	13588	3.E+00	1.E+00	8.E-01
GOTERM_BP_FAT	GO:0048589~developmental growth	5	0.914076782		5.E-01 12190, 11820, 17979, 13075, 16000	491	100	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0040007~growth	7	1.279707495		7.E-01 19944, 12190, 19247, 665032, 11820, 11	491	193	13588	1.E+00	1.E+00	1.E+00

Annotation Cluster 139	Enrichment Score: 0.4115237229730565											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	
GOTERM_MF_FAT	GO:0008201~heparin binding	6	1.096892139	2.E-01	19944, 665032, 11816, 19934, 56348, 1	476	83	13288	2.E+00	1.E+00	7.E-01	



GOTERM_MF_FAT	GO:0005539--glycosaminoglycan binding	6	1.096892139	4.E-01 19944, 665032, 11816, 19934, 56348, 1:	476	114	13288	1.E+00	1.E+00	9.E-01
GOTERM_MF_FAT	GO:0030246--carbohydrate binding	13	2.376599634	4.E-01 19944, 665032, 19934, 11816, 56348, 1:	476	317	13288	1.E+00	1.E+00	9.E-01
SP_PIR_KEYWORDS	heparin-binding	3	0.548446069	5.E-01 11816, 19934, 11820, 100047372	541	53	17854	2.E+00	1.E+00	8.E-01
GOTERM_MF_FAT	GO:0030247--polysaccharide binding	6	1.096892139	5.E-01 19944, 665032, 11816, 19934, 56348, 1:	476	128	13288	1.E+00	1.E+00	1.E+00
GOTERM_MF_FAT	GO:0001871--pattern binding	6	1.096892139	5.E-01 19944, 665032, 11816, 19934, 56348, 1:	476	128	13288	1.E+00	1.E+00	1.E+00

[illegible]

Annotation Cluster 141		Enrichment Score: 0.3983388809904416									
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
KEGG_PATHWAY	mmu04150:mTOR signaling pathway	6	1.096892139	3.E-01	13684, 18709, 18708, 75705, 20112, 160	372	54	5738	2.E+00	1.E+00	5.E-01
KEGG_PATHWAY	mmu04914:Progesterone-mediated oocyte maturation	8	1.462522852	3.E-01	18709, 18708, 14678, 17222, 19108, 261	372	85	5738	1.E+00	1.E+00	6.E-01
KEGG_PATHWAY	mmu04960:Aldosterone-regulated sodium reabsorption	3	0.548446069	8.E-01	18709, 18708, 16000	372	42	5738	1.E+00	1.E+00	9.E-01

Annotation Cluster 142		Enrichment Score: 0.39392595018553594									
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_BP_FAT	GO:0051329~interphase of mitotic cell cycle	4	0.731261426		3.E-01 104394, 13559, 11820, 69581	491	49	13588	2.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0000082~G1/S transition of mitotic cell cycle	3	0.548446069		3.E-01 104394, 13559, 69581	491	28	13588	3.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0051325~interphase	4	0.731261426		3.E-01 104394, 13559, 11820, 69581	491	51	13588	2.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0000278~mitotic cell cycle	9	1.645338208		7.E-01 104394, 19384, 13559, 17222, 11820, 11821	491	244	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0022403~cell cycle phase	10	1.828153565		8.E-01 12190, 104394, 19384, 13559, 17222, 11820	491	328	13588	8.E-01	1.E+00	1.E+00

Annotation Cluster 143		Enrichment Score: 0.3904695970458693												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold	Enrichment	Bonferroni	Benjamini		
GOTERM_BP_FAT	GO:0032774~RNA biosynthetic process	8	1.462522852		2.E-01 20848, 69890, 20020, 16911, 19075, 141	491	126	13588	2.E+00	1.E+00	8.E-01			
SP_PIR_KEYWORDS	dna-directed rna polymerase	3	0.548446069		3.E-01 20020, 19075, 13117	541	33	17854	3.E+00	1.E+00	6.E-01			
GOTERM_MF_FAT	GO:0034062~RNA polymerase activity	3	0.548446069		4.E-01 20020, 19075, 13117	476	35	13288	2.E+00	1.E+00	9.E-01			
GOTERM_MF_FAT	GO:0003899~DNA-directed RNA polymerase activity	3	0.548446069		4.E-01 20020, 19075, 13117	476	35	13288	2.E+00	1.E+00	9.E-01			
GOTERM_MF_FAT	GO:0016779~nucleotidyltransferase activity	4	0.731261426		8.E-01 20020, 19075, 13117, 108067	476	127	13288	9.E-01	1.E+00	1.E+00			
KEGG_PATHWAY	mmu00230:Purine metabolism	7	1.279707495		9.E-01 18746, 20020, 110639, 19075, 14450, 1	372	157	5738	7.E-01	1.E+00	1.E+00			

Annotation Cluster 144 Category	Enrichment Score: 0.38981684013967155	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold	Enrichment	Bonferroni	Benjamini
Term												
GOTERM_BP_FAT	GO:0046887~positive regulation of hormone secretion	3	0.548446069	9.E-02	19247, 12912, 103988	491	14	13588	6.E+00	1.E+00	7.E-01	
GOTERM_BP_FAT	GO:0046883~regulation of hormone secretion	3	0.548446069	4.E-01	19247, 12912, 103988	491	36	13588	2.E+00	1.E+00	1.E+00	
GOTERM_BP_FAT	GO:0051050~positive regulation of transport	6	1.096892139	5.E-01	12266, 19247, 16423, 12912, 103988, 19247	491	132	13588	1.E+00	1.E+00	1.E+00	
GOTERM_BP_FAT	GO:0051047~positive regulation of secretion	3	0.548446069	6.E-01	19247, 12912, 103988	491	53	13588	2.E+00	1.E+00	1.E+00	
GOTERM_BP_FAT	GO:0051046~regulation of secretion	5	0.914076782	7.E-01	18049, 19247, 12912, 13645, 103988	491	125	13588	1.E+00	1.E+00	1.E+00	
GOTERM_BP_FAT	GO:0060341~regulation of cellular localization	6	1.096892139	7.E-01	18049, 19247, 12912, 13645, 103988, 2924	491	161	13588	1.E+00	1.E+00	1.E+00	

Annotation Cluster 145	Enrichment Score: 0.37099666842579276										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
SP_PIR_KEYWORDS	sh3-binding	8	1.462522852	2.E-03	0401, 11489, 13858, 11487, 228359, 1	541	57	17854	5.E+00	4.E-01	1.E-02



GOTERM_MF_FAT	GO:0004222~metalloendopeptidase activity	7	1.279707495	2.E-01 73078, 11489, 11487, 67003, 11491, 22:	476	114	13288	2.E+00	1.E+00	8.E-01
UP_SEQ_FEATURE	metal ion-binding site:Zinc; in inhibited form	3	0.548446069	3.E-01 11489, 11487, 11491	537	29	16021	3.E+00	1.E+00	1.E+00
SMART	SM00050:DISIN	3	0.548446069	3.E-01 11489, 11487, 11491	248	37	9131	3.E+00	1.E+00	7.E-01
INTERPRO	IPR001762:Blood coagulation inhibitor, Disintegrin	3	0.548446069	3.E-01 11489, 11487, 11491	535	37	17763	3.E+00	1.E+00	1.E+00
INTERPRO	IPR001818:Peptidase M10A and M12B, matrixin and adamalysin	3	0.548446069	3.E-01 11489, 11487, 11491	535	39	17763	3.E+00	1.E+00	1.E+00
UP_SEQ_FEATURE	metal ion-binding site:Zinc; catalytic	6	1.096892139	4.E-01 11489, 12350, 72269, 11487, 11491, 17:	537	118	16021	2.E+00	1.E+00	1.E+00
UP_SEQ_FEATURE	domain:Disintegrin	3	0.548446069	4.E-01 11489, 11487, 11491	537	38	16021	2.E+00	1.E+00	1.E+00
UP_SEQ_FEATURE	short sequence motif:Cysteine switch	3	0.548446069	4.E-01 11489, 11487, 11491	537	39	16021	2.E+00	1.E+00	1.E+00
UP_SEQ_FEATURE	domain:Peptidase M12B	3	0.548446069	4.E-01 11489, 11487, 11491	537	39	16021	2.E+00	1.E+00	1.E+00
INTERPRO	IPR018358:Disintegrin, conserved site	3	0.548446069	4.E-01 11489, 11487, 11491	535	46	17763	2.E+00	1.E+00	1.E+00
INTERPRO	IPR001590:Peptidase M12B, ADAM/reprolysin	3	0.548446069	5.E-01 11489, 11487, 11491	535	53	17763	2.E+00	1.E+00	1.E+00
INTERPRO	IPR006025:Peptidase M, neutral zinc metallopeptidases, zinc-binding	4	0.731261426	5.E-01 11489, 11487, 11491, 17380	535	87	17763	2.E+00	1.E+00	1.E+00
SP_PIR_KEYWORDS	zymogen	7	1.279707495	6.E-01 11489, 11487, 74145, 18551, 11491, 130	541	199	17854	1.E+00	1.E+00	9.E-01
SP_PIR_KEYWORDS	metalloprotease	5	0.914076782	6.E-01 73078, 11489, 11487, 11491, 17380	541	146	17854	1.E+00	1.E+00	9.E-01
UP_SEQ_FEATURE	compositionally biased region:Cys-rich	5	0.914076782	7.E-01 13836, 11489, 13866, 11487, 11491	537	134	16021	1.E+00	1.E+00	1.E+00
GOTERM_MF_FAT	GO:0008237~metallopeptidase activity	7	1.279707495	7.E-01 73078, 11489, 11487, 67003, 11491, 22:	476	187	13288	1.E+00	1.E+00	1.E+00
GOTERM_CC_FAT	GO:0031012~extracellular matrix	8	1.462522852	9.E-01 16854, 13801, 11489, 11487, 56348, 206	419	309	12504	8.E-01	1.E+00	1.E+00
GOTERM_CC_FAT	GO:0005578~proteinaceous extracellular matrix	7	1.279707495	9.E-01 16854, 13801, 11489, 11487, 20692, 114	419	297	12504	7.E-01	1.E+00	1.E+00
GOTERM_MF_FAT	GO:0004175~endopeptidase activity	10	1.828153565	1.E+00 73078, 11489, 11487, 67003, 18551, 114	476	421	13288	7.E-01	1.E+00	1.E+00
SP_PIR_KEYWORDS	extracellular matrix	3	0.548446069	1.E+00 13801, 20692, 12306	541	213	17854	5.E-01	1.E+00	1.E+00
SP_PIR_KEYWORDS	Protease	8	1.462522852	1.E+00 73078, 11489, 11487, 18551, 11491, 130	541	509	17854	5.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0006508~proteolysis	24	4.387568556	1.E+00 78294, 12266, 12258, 12279, 11491, 69:	491	1034	13588	6.E-01	1.E+00	1.E+00
GOTERM_MF_FAT	GO:0070011~peptidase activity, acting on L-amino acid peptides	10	1.828153565	1.E+00 73078, 11489, 11487, 67003, 18551, 114	476	603	13288	5.E-01	1.E+00	1.E+00
GOTERM_MF_FAT	GO:0008233~peptidase activity	10	1.828153565	1.E+00 73078, 11489, 11487, 67003, 18551, 114	476	629	13288	4.E-01	1.E+00	1.E+00

Annotation Cluster 146	Enrichment Score: 0.3317750552294683										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_MF_FAT	GO:0004896~cytokine receptor activity	5	0.914076782		1.E-01 12765, 16195, 16847, 16154, 14600	476	55	13288	3.E+00	1.E+00	6.E-01
UP_SEQ_FEATURE	short sequence motif:Box 1 motif	3	0.548446069		2.E-01 16195, 16847, 14600	537	25	16021	4.E+00	1.E+00	1.E+00
UP_SEQ_FEATURE	short sequence motif:WSXWS motif	3	0.548446069		3.E-01 16195, 16847, 14600	537	31	16021	3.E+00	1.E+00	1.E+00
INTERPRO	IPR008957:Fibronectin, type III-like fold	8	1.462522852		3.E-01 13836, 16195, 74145, 74144, 16847, 16:	535	187	17763	1.E+00	1.E+00	1.E+00
GOTERM_MF_FAT	GO:0019955~cytokine binding	5	0.914076782		4.E-01 12765, 16195, 16847, 16154, 14600	476	88	13288	2.E+00	1.E+00	9.E-01
SMART	SM00060:FN3	6	1.096892139		6.E-01 13836, 16195, 74144, 16847, 14600, 54:	248	191	9131	1.E+00	1.E+00	9.E-01
INTERPRO	IPR003961:Fibronectin, type III	6	1.096892139		7.E-01 13836, 16195, 74144, 16847, 14600, 54:	535	191	17763	1.E+00	1.E+00	1.E+00
UP_SEQ_FEATURE	domain:Fibronectin type-III 2	4	0.731261426		8.E-01 13836, 16195, 74144, 16847	537	120	16021	1.E+00	1.E+00	1.E+00
UP_SEQ_FEATURE	domain:Fibronectin type-III 1	4	0.731261426		8.E-01 13836, 16195, 74144, 16847	537	121	16021	1.E+00	1.E+00	1.E+00
GOTERM_MF_FAT	GO:0042277~peptide binding	3	0.548446069		1.E+00 12765, 16847, 14600	476	160	13288	5.E-01	1.E+00	1.E+00
KEGG_PATHWAY	mmu04060:Cytokine-cytokine receptor interaction	10	1.828153565		1.E+00 20310, 12765, 13649, 16195, 21813, 16:	372	244	5738	6.E-01	1.E+00	1.E+00

Annotation Cluster 147		Enrichment Score: 0.3311393034280652									
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_BP_FAT	GO:0001701~in utero embryonic development	13	2.376599634		3.E-01 12190, 13649, 14674, 238055, 13806, 1:	491	267	13588	1.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0043009~chordate embryonic development	17	3.10786106		5.E-01 12190, 13649, 14674, 16911, 238055, 1:	491	421	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0009792~embryonic development ending in birth or egg hatch	17	3.10786106		5.E-01 12190, 13649, 14674, 16911, 238055, 1:	491	425	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0048598~embryonic morphogenesis	11	2.010968921		8.E-01 13836, 21813, 12702, 16911, 19713, 14:	491	359	13588	8.E-01	1.E+00	1.E+00

Annotation Cluster 148	Enrichment Score: 0.3220705846068835										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_CC_FAT	GO:0031974~membrane-enclosed lumen	52	9.506398537		3.E-02 672195, 66885, 68263, 101206, 12912, :	419	1174	12504	1.E+00	1.E+00	2.E-01
GOTERM_CC_FAT	GO:0005667~transcription factor complex	14	2.559414991		5.E-02 11865, 12753, 104394, 16911, 12912, 1:	419	234	12504	2.E+00	1.E+00	3.E-01
GOTERM_CC_FAT	GO:0043233~organelle lumen	49	8.957952468		5.E-02 672195, 66885, 68263, 101206, 12912, :	419	1136	12504	1.E+00	1.E+00	3.E-01
GOTERM_CC_FAT	GO:0070013~intracellular organelle lumen	48	8.775137112		7.E-02 66885, 672195, 68263, 101206, 12912, :	419	1133	12504	1.E+00	1.E+00	4.E-01
GOTERM_CC_FAT	GO:0044451~nucleoplasm part	19	3.473491773		5.E-01 11865, 12753, 104394, 16911, 101206, :	419	513	12504	1.E+00	1.E+00	9.E-01
GOTERM_CC_FAT	GO:0005654~nucleoplasm	21	3.839122486		5.E-01 11865, 12753, 104394, 11546, 67184, 1:	419	599	12504	1.E+00	1.E+00	9.E-01
SP_PIR_KEYWORDS	activator	14	2.559414991		7.E-01 11865, 12753, 104394, 18022, 12912, 1:	541	484	17854	1.E+00	1.E+00	9.E-01
GOTERM_CC_FAT	GO:0031981~nuclear lumen	27	4.936014625		8.E-01 67184, 101206, 12912, 98386, 12914, 2:	419	883	12504	9.E-01	1.E+00	1.E+00
SP_PIR_KEYWORDS	transcription regulation	35	6.398537477		1.E+00 101206, 12952, 12953, 18227, 68910, 1:	541	1546	17854	7.E-01	1.E+00	1.E+00
SP_PIR_KEYWORDS	dna-binding	29	5.301645338		1.E+00 27041, 16392, 360198, 18227, 319191, 6	541	1404	17854	7.E-01	1.E+00	1.E+00
SP_PIR_KEYWORDS	Transcription	38	6.946983547		1.E+00 101206, 12952, 12953, 18227, 68910, 1:	541	1769	17854	7.E-01	1.E+00	1.E+00



[illegible][illegible]

Annotation Cluster 150 Category	Enrichment Score: 0.31078759734792255	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
Term											
SP_PIR_KEYWORDS	mitochondrion outer membrane	4	0.731261426	3.E-01	98256, 15275, 59040, 214952	541	69	17854	2.E+00	1.E+00	7.E-01
GOTERM_CC_FAT	GO:0005741-mitochondrial outer membrane	4	0.731261426	5.E-01	98256, 15275, 59040, 214952	419	80	12504	1.E+00	1.E+00	9.E-01
GOTERM_CC_FAT	GO:0031968-organelle outer membrane	4	0.731261426	6.E-01	98256, 15275, 59040, 214952	419	87	12504	1.E+00	1.E+00	9.E-01
GOTERM_CC_FAT	GO:0019867-outer membrane	4	0.731261426	6.E-01	98256, 15275, 59040, 214952	419	90	12504	1.E+00	1.E+00	9.E-01

Annotation Cluster	Enrichment Score: 0.3020331315335226																		
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold	Enrichment	Bonferroni	Benjamini							
GOTERM_BP_FAT	GO:0051091~positive regulation of transcription factor activity	3	0.548446069		3.E-01 19697, 106759, 12914	491	34	13588	2.E+00	1.E+00	9.E-01								
GOTERM_BP_FAT	GO:0043388~positive regulation of DNA binding	3	0.548446069		5.E-01 19697, 106759, 12914	491	42	13588	2.E+00	1.E+00	1.E+00								
GOTERM_BP_FAT	GO:0051099~positive regulation of binding	3	0.548446069		5.E-01 19697, 106759, 12914	491	45	13588	2.E+00	1.E+00	1.E+00								
GOTERM_BP_FAT	GO:0051101~regulation of DNA binding	4	0.731261426		5.E-01 19697, 106759, 16452, 12914	491	74	13588	1.E+00	1.E+00	1.E+00								
GOTERM_BP_FAT	GO:0051090~regulation of transcription factor activity	3	0.548446069		6.E-01 19697, 106759, 12914	491	59	13588	1.E+00	1.E+00	1.E+00								
GOTERM_BP_FAT	GO:0051098~regulation of binding	4	0.731261426		6.E-01 19697, 106759, 16452, 12914	491	90	13588	1.E+00	1.E+00	1.E+00								

Annotation Cluster 152		Enrichment Score: 0.3002545648440415									
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
UP_SEQ_FEATURE	domain:SAM	5	0.914076782	2.E-01	13836, 50768, 243362, 212285, 106952	537	68	16021	2.E+00	1.E+00	1.E+00
INTERPRO	IPR013761:Sterile alpha motif-type	3	0.548446069	6.E-01	13836, 212285, 106952	535	72	17763	1.E+00	1.E+00	1.E+00
SMART	SM00454:SAM	3	0.548446069	7.E-01	13836, 212285, 106952	248	87	9131	1.E+00	1.E+00	1.E+00
INTERPRO	IPR001660:Sterile alpha motif SAM	3	0.548446069	7.E-01	13836, 212285, 106952	535	87	17763	1.E+00	1.E+00	1.E+00

Annotation Cluster 153											
Enrichment Score: 0.2781345417533731											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_BP_FAT	GO:0032270~positive regulation of cellular protein metabolic process	5	0.914076782	5.E-01	14600, 224045, 208727, 16452, 56469	491	100	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0031401~positive regulation of protein modification process	4	0.731261426	5.E-01	14600, 208727, 16452, 56469	491	78	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0051247~positive regulation of protein metabolic process	5	0.914076782	6.E-01	14600, 224045, 208727, 16452, 56469	491	109	13588	1.E+00	1.E+00	1.E+00

[illegible]

Annotation Cluster 155		Enrichment Score: 0.2664815369801756									
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
UP_SEQ_FEATURE	domain:C2	4	0.731261426	4.E-01	18783, 18753, 18754, 109934	537	68	16021	2.E+00	1.E+00	1.E+00
SMART	SM00239:C2	5	0.914076782	5.E-01	18783, 18753, 18754, 109934, 214804	248	130	9131	1.E+00	1.E+00	9.E-01



INTERPRO	IPR000008:C2 calcium-dependent membrane targeting	5	0.914076782	6.E-01 18783, 18753, 18754, 109934, 214804	535	130	17763	1.E+00	1.E+00	1.E+00	
INTERPRO	IPR018029:C2 membrane targeting protein	3	0.548446069	8.E-01 18783, 18754, 109934	535	106	17763	9.E-01	1.E+00	1.E+00	
Annotation Cluster 156											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
UP_SEQ_FEATURE	domain:RRM	5	0.914076782		4.E-01 22384, 27979, 75705, 27041, 53356	537	99	16021	2.E+00	1.E+00	1.E+00
INTERPRO	IPR012677:Nucleotide-binding, alpha-beta plait	8	1.462522852		5.E-01 22384, 27979, 75705, 27041, 53356, 67	535	213	17763	1.E+00	1.E+00	1.E+00
SMART	SM00360:RRM	6	1.096892139		7.E-01 22384, 27979, 75705, 27041, 53356, 18	248	212	9131	1.E+00	1.E+00	1.E+00
INTERPRO	IPR000504:RNA recognition motif, RNP-1	6	1.096892139		8.E-01 22384, 27979, 75705, 27041, 53356, 18	535	212	17763	9.E-01	1.E+00	1.E+00
Annotation Cluster 157											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_BP_FAT	GO:0007528--neuromuscular junction development	3	0.548446069		2.E-01 13866, 11820, 18479	491	23	13588	4.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0048741--skeletal muscle fiber development	3	0.548446069		3.E-01 13866, 11820, 18479	491	32	13588	3.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0048747--muscle fiber development	3	0.548446069		4.E-01 13866, 11820, 18479	491	38	13588	2.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0007519--skeletal muscle tissue development	4	0.731261426		5.E-01 13866, 11820, 18479, 11848	491	72	13588	2.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0060538--skeletal muscle organ development	4	0.731261426		5.E-01 13866, 11820, 18479, 11848	491	74	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0050808--synapse organization	3	0.548446069		5.E-01 13866, 11820, 18479	491	49	13588	2.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0055002--striated muscle cell development	3	0.548446069		6.E-01 13866, 11820, 18479	491	54	13588	2.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0043062--extracellular structure organization	6	1.096892139		6.E-01 16854, 13866, 56348, 11820, 18479, 12	491	149	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0055001--muscle cell development	3	0.548446069		7.E-01 13866, 11820, 18479	491	61	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0042692--muscle cell differentiation	4	0.731261426		8.E-01 13866, 11820, 18479, 18205	491	117	13588	9.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0051146--striated muscle cell differentiation	3	0.548446069		8.E-01 13866, 11820, 18479	491	89	13588	9.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0014706--striated muscle tissue development	4	0.731261426		8.E-01 13866, 11820, 18479, 11848	491	127	13588	9.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0060537--muscle tissue development	4	0.731261426		9.E-01 13866, 11820, 18479, 11848	491	136	13588	8.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0007517--muscle organ development	5	0.914076782		9.E-01 12955, 13866, 11820, 18479, 11848	491	176	13588	8.E-01	1.E+00	1.E+00
Annotation Cluster 158											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_BP_FAT	GO:0030097--hemopoiesis	11	2.010968921		4.E-01 12190, 22324, 19934, 11491, 74734, 10	491	251	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0048534--hemopoietic or lymphoid organ development	12	2.193784278		4.E-01 12190, 22324, 19934, 12929, 11491, 74	491	281	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0002520--immune system development	12	2.193784278		5.E-01 12190, 22324, 19934, 12929, 11491, 74	491	295	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0030217--T cell differentiation	4	0.731261426		5.E-01 22324, 19934, 74734, 11491, 10004737	491	76	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0001775--cell activation	10	1.828153565		5.E-01 18708, 22324, 18753, 14674, 21813, 19	491	246	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0002521--leukocyte differentiation	6	1.096892139		6.E-01 18708, 22324, 21813, 19934, 74734, 11	491	142	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0030098--lymphocyte differentiation	5	0.914076782		6.E-01 18708, 22324, 19934, 74734, 11491, 10	491	114	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0045321--leukocyte activation	8	1.462522852		7.E-01 18708, 22324, 18753, 21813, 19934, 74	491	219	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0042113--B cell activation	3	0.548446069		8.E-01 18708, 18753, 11491	491	78	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0042110--T cell activation	4	0.731261426		8.E-01 22324, 19934, 74734, 11491, 10004737	491	116	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0046649--lymphocyte activation	6	1.096892139		8.E-01 18708, 22324, 18753, 19934, 74734, 11	491	191	13588	9.E-01	1.E+00	1.E+00
Annotation Cluster 159											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_CC_FAT	GO:0005720--nuclear heterochromatin	3	0.548446069		3.E-01 15078, 12417, 13436	419	35	12504	3.E+00	1.E+00	8.E-01
GOTERM_CC_FAT	GO:0000785--chromatin	7	1.279707495		5.E-01 319168, 621893, 319169, 15078, 12417,	419	165	12504	1.E+00	1.E+00	9.E-01
GOTERM_CC_FAT	GO:0000792--heterochromatin	3	0.548446069		5.E-01 15078, 12417, 13436	419	51	12504	2.E+00	1.E+00	9.E-01
GOTERM_CC_FAT	GO:0000790--nuclear chromatin	3	0.548446069		6.E-01 15078, 12417, 13436	419	55	12504	2.E+00	1.E+00	9.E-01
GOTERM_CC_FAT	GO:0044454--nuclear chromosome part	4	0.731261426		7.E-01 15078, 19075, 12417, 13436	419	103	12504	1.E+00	1.E+00	1.E+00
GOTERM_CC_FAT	GO:0044427--chromosomal part	10	1.828153565		7.E-01 319168, 621893, 319169, 19053, 15078,	419	318	12504	9.E-01	1.E+00	1.E+00
GOTERM_CC_FAT	GO:0000228--nuclear chromosome	4	0.731261426		8.E-01 15078, 19075, 12417, 13436	419	121	12504	1.E+00	1.E+00	1.E+00
GOTERM_CC_FAT	GO:0005694--chromosome	10	1.828153565		9.E-01 319168, 621893, 319169, 19053, 15078,	419	378	12504	8.E-01	1.E+00	1.E+00
Annotation Cluster 160											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
UP_SEQ_FEATURE	short sequence motif:Nuclear export signal	4	0.731261426		1.E-01 18626, 208727, 18627, 18628	537	36	16021	3.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0010551--regulation of specific transcription from RNA polymer	4	0.731261426		3.E-01 18626, 208727, 18627, 18628	491	51	13588	2.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0032583--regulation of gene-specific transcription	4	0.731261426		4.E-01 18626, 208727, 18627, 18628	491	67	13588	2.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0010605--negative regulation of macromolecule metabolic proc	18	3.290676417		7.E-01 12190, 15170, 67184, 56338, 12258, 24	491	506	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0045892--negative regulation of transcription, DNA-dependent	11	2.010968921		7.E-01 67184, 56338, 74318, 12577, 18626, 12	491	308	13588	1.E+00	1.E+00	1.E+00



GOTERM_BP_FAT	GO:0051253~negative regulation of RNA metabolic process	11	2.010968921	7.E-01	67184, 56338, 74318, 12577, 18626, 124	491	310	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0000122~negative regulation of transcription from RNA polym	8	1.462522852	7.E-01	56338, 74318, 12577, 18626, 208727, 11	491	231	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0045934~negative regulation of nucleobase, nucleoside, nucleo	13	2.376599634	8.E-01	12190, 67184, 56338, 24069, 72269, 74	491	397	13588	9.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0031327~negative regulation of cellular biosynthetic process	14	2.559414991	8.E-01	12190, 67184, 56338, 103988, 24069, 7	491	430	13588	9.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0051172~negative regulation of nitrogen compound metabolic	13	2.376599634	8.E-01	12190, 67184, 56338, 24069, 72269, 74	491	401	13588	9.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0009890~negative regulation of biosynthetic process	14	2.559414991	8.E-01	12190, 67184, 56338, 103988, 24069, 7	491	434	13588	9.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0010558~negative regulation of macromolecule biosynthetic pr	13	2.376599634	8.E-01	12190, 67184, 56338, 24069, 74318, 12	491	418	13588	9.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0016481~negative regulation of transcription	11	2.010968921	9.E-01	67184, 56338, 74318, 12577, 18626, 12	491	372	13588	8.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0010629~negative regulation of gene expression	11	2.010968921	9.E-01	67184, 56338, 74318, 12577, 18626, 12	491	410	13588	7.E-01	1.E+00	1.E+00
Annotation Cluster 161	Enrichment Score: 0.20507543871608505										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_MF_FAT	GO:0030246~carbohydrate binding	13	2.376599634		4.E-01 19944, 665032, 19934, 11816, 56348, 1		476	317	13288	1.E+00	9.E-01
SP_PIR_KEYWORDS	Lectin	6	1.096892139		6.E-01 83382, 16854, 20345, 20343, 20339, 12		541	167	17854	1.E+00	9.E-01
GOTERM_MF_FAT	GO:0005529~sugar binding	7	1.279707495		6.E-01 83382, 16854, 20345, 20343, 20339, 12		476	181	13288	1.E+00	1.E+00
KEGG_PATHWAY	mmu04514:Cell adhesion molecules (CAMs)	7	1.279707495		9.E-01 69524, 20345, 12490, 20343, 20339, 17		372	154	5738	7.E-01	1.E+00
Annotation Cluster 162	Enrichment Score: 0.2037855861541471										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_BP_FAT	GO:0034754~cellular hormone metabolic process	3	0.548446069		6.E-01 13074, 56847, 13075		491	52	13588	2.E+00	1.E+00
GOTERM_BP_FAT	GO:0042445~hormone metabolic process	4	0.731261426		6.E-01 19247, 13074, 56847, 13075		491	90	13588	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0010817~regulation of hormone levels	5	0.914076782		7.E-01 19247, 13350, 13074, 56847, 13075		491	128	13588	1.E+00	1.E+00
Annotation Cluster 163	Enrichment Score: 0.1877950018898824										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_CC_FAT	GO:0005923~tight junction	4	0.731261426		5.E-01 18762, 69524, 16800, 69847		419	76	12504	2.E+00	9.E-01
GOTERM_CC_FAT	GO:0070160~occluding junction	4	0.731261426		5.E-01 18762, 69524, 16800, 69847		419	76	12504	2.E+00	9.E-01
SP_PIR_KEYWORDS	Tight junction	3	0.548446069		6.E-01 69524, 16800, 69847		541	61	17854	2.E+00	9.E-01
GOTERM_CC_FAT	GO:0043296~apical junction complex	4	0.731261426		7.E-01 18762, 69524, 16800, 69847		419	101	12504	1.E+00	1.E+00
GOTERM_CC_FAT	GO:0016327~apicolateral plasma membrane	4	0.731261426		7.E-01 18762, 69524, 16800, 69847		419	103	12504	1.E+00	1.E+00
GOTERM_CC_FAT	GO:0005911~cell-cell junction	4	0.731261426		9.E-01 18762, 69524, 16800, 69847		419	173	12504	7.E-01	1.E+00
SP_PIR_KEYWORDS	cell junction	8	1.462522852		1.E+00 12549, 69524, 94190, 236920, 16800, 2		541	392	17854	7.E-01	1.E+00
Annotation Cluster 164	Enrichment Score: 0.1681973924397577										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_CC_FAT	GO:0030018~Z disc	3	0.548446069		5.E-01 12955, 208727, 15507		419	46	12504	2.E+00	9.E-01
GOTERM_CC_FAT	GO:0031674~I band	3	0.548446069		5.E-01 12955, 208727, 15507		419	53	12504	2.E+00	9.E-01
GOTERM_CC_FAT	GO:0030017~sarcomere	3	0.548446069		8.E-01 12955, 208727, 15507		419	80	12504	1.E+00	1.E+00
GOTERM_CC_FAT	GO:0044449~contractile fiber part	3	0.548446069		8.E-01 12955, 208727, 15507		419	86	12504	1.E+00	1.E+00
GOTERM_CC_FAT	GO:0030016~myofibril	3	0.548446069		8.E-01 12955, 208727, 15507		419	91	12504	1.E+00	1.E+00
GOTERM_CC_FAT	GO:0043292~contractile fiber	3	0.548446069		8.E-01 12955, 208727, 15507		419	95	12504	9.E-01	1.E+00
Annotation Cluster 165	Enrichment Score: 0.16176262097800198										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_CC_FAT	GO:0030141~secretory granule	8	1.462522852		1.E-01 26934, 18551, 13035, 18791, 71326, 13		419	117	12504	2.E+00	5.E-01
SP_PIR_KEYWORDS	zymogen	7	1.279707495		6.E-01 11489, 11487, 74145, 18551, 11491, 13		541	199	17854	1.E+00	9.E-01
SP_PIR_KEYWORDS	Serine protease	3	0.548446069		1.E+00 18551, 13035, 18791		541	164	17854	6.E-01	1.E+00
UP_SEQ_FEATURE	active site:Charge relay system	3	0.548446069		1.E+00 18551, 13035, 18791		537	198	16021	5.E-01	1.E+00
GOTERM_MF_FAT	GO:0004252~serine-type endopeptidase activity	3	0.548446069		1.E+00 18551, 13035, 18791		476	189	13288	4.E-01	1.E+00
SP_PIR_KEYWORDS	Protease	8	1.462522852		1.E+00 73078, 11489, 11487, 18551, 11491, 13		541	509	17854	5.E-01	1.E+00
GOTERM_MF_FAT	GO:0008236~serine-type peptidase activity	3	0.548446069		1.E+00 18551, 13035, 18791		476	212	13288	4.E-01	1.E+00
GOTERM_MF_FAT	GO:0017171~serine hydrolase activity	3	0.548446069		1.E+00 18551, 13035, 18791		476	213	13288	4.E-01	1.E+00
Annotation Cluster 166	Enrichment Score: 0.1589735933072159										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
UP_SEQ_FEATURE	domain:Ig-like V-type	8	1.462522852		6.E-02 83382, 69524, 208154, 16423, 71326, 1		537	104	16021	2.E+00	8.E-01
GOTERM_CC_FAT	GO:0009986~cell surface	11	2.010968921		6.E-01 16195, 21813, 208154, 11816, 11487, 1		419	305	12504	1.E+00	9.E-01
SMART	SM00409:IG	8	1.462522852		7.E-01 83382, 69524, 208154, 74144, 71326, 1		248	313	9131	9.E-01	1.E+00
SMART	SM00408:IGc2	5	0.914076782		7.E-01 83382, 69524, 74144, 12483, 545156		248	187	9131	1.E+00	1.E+00



SP_PIR_KEYWORDS	Immunoglobulin domain	12	2.193784278	8.E-01 83382, 16195, 69524, 208154, 74144, 16423, 11	541	443	17854	9.E-01	1.E+00	1.E+00
INTERPRO	IPR003598:Immunoglobulin subtype 2	5	0.914076782	8.E-01 83382, 69524, 74144, 12483, 545156	535	187	17763	9.E-01	1.E+00	1.E+00
INTERPRO	IPR003599:Immunoglobulin subtype	8	1.462522852	8.E-01 83382, 69524, 208154, 74144, 71326, 11	535	313	17763	8.E-01	1.E+00	1.E+00
UP_SEQ_FEATURE	domain:Ig-like C2-type 1	3	0.548446069	9.E-01 83382, 74144, 12483	537	130	16021	7.E-01	1.E+00	1.E+00
UP_SEQ_FEATURE	domain:Ig-like C2-type 2	3	0.548446069	9.E-01 83382, 74144, 12483	537	131	16021	7.E-01	1.E+00	1.E+00
INTERPRO	IPR013151:Immunoglobulin	3	0.548446069	1.E+00 83382, 208154, 12483	535	178	17763	6.E-01	1.E+00	1.E+00
INTERPRO	IPR013783:Immunoglobulin-like fold	12	2.193784278	1.E+00 83382, 16195, 69524, 208154, 74145, 71	535	644	17763	6.E-01	1.E+00	1.E+00
INTERPRO	IPR007110:Immunoglobulin-like	10	1.828153565	1.E+00 83382, 69524, 208154, 74144, 16423, 11	535	604	17763	5.E-01	1.E+00	1.E+00
INTERPRO	IPR013106:Immunoglobulin V-set	5	0.914076782	1.E+00 83382, 69524, 71326, 57781, 19261	535	364	17763	5.E-01	1.E+00	1.E+00

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_MF_FAT	GO:0019899~enzyme binding	8	1.462522852	7.E-01	20848, 117600, 21813, 11487, 13605, 11487	476	229	13288	1.E+00	1.E+00	1.E+00
GOTERM_MF_FAT	GO:0019901~protein kinase binding	3	0.548446069	7.E-01	20848, 21813, 11487	476	71	13288	1.E+00	1.E+00	1.E+00
GOTERM_MF_FAT	GO:0019900~kinase binding	3	0.548446069	8.E-01	20848, 21813, 11487	476	85	13288	1.E+00	1.E+00	1.E+00

[illegible]

Annotation Cluster 169	Enrichment Score: 0.11320776547683392										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_BP_FAT	GO:0001654~eye development	6	1.096892139	7.E-01	20848, 14685, 12955, 68193, 56847, 26401	491	157	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0048592~eye morphogenesis	3	0.548446069	7.E-01	20848, 14685, 56847	491	73	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0007423~sensory organ development	8	1.462522852	8.E-01	20848, 14685, 12955, 12064, 78405, 68193, 56847, 26401	491	257	13588	9.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0043010~camera-type eye development	4	0.731261426	9.E-01	12955, 68193, 56847, 26401	491	130	13588	9.E-01	1.E+00	1.E+00

Annotation Cluster 170		Enrichment Score: 0.11312151320092788									
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_BP_FAT	GO:0043414~biopolymer methylation	3	0.548446069	7.E-01	225363, 14852, 13436	491	71	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0032259~methylation	3	0.548446069	8.E-01	225363, 14852, 13436	491	79	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0006730~one-carbon metabolic process	4	0.731261426	8.E-01	225363, 12350, 14852, 13436	491	117	13588	9.E-01	1.E+00	1.E+00

Annotation Cluster 171	Enrichment Score: 0.11153669806769494										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_BP_FAT	GO:0007187~G-protein signaling, coupled to cyclic nucleotide seco	3	0.548446069		6.E-01 14685, 18126, 14678	491	60	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0019935~cyclic-nucleotide-mediated signaling	3	0.548446069		7.E-01 14685, 18126, 14678	491	66	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0019932~second-messenger-receptor signaling	4	0.731261426		8.E-01 14685, 18126, 14678, 103988	491	118	13588	9.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0007186~G-protein coupled receptor protein signaling pathway	7	1.279707495		1.E+00 14685, 12765, 18126, 14674, 14678, 19	491	1877	13588	1.E-01	1.E+00	1.E+00



Annotation Cluster 172	Enrichment Score: 0.09877295760260509											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	
GOTERM_BP_FAT	GO:0001892~embryonic placenta development	3	0.548446069		7.E-01 13649, 12702, 14784	491	61	13588	1.E+00	1.E+00	1.E+00	
GOTERM_BP_FAT	GO:0001890~placenta development	3	0.548446069		8.E-01 13649, 12702, 14784	491	87	13588	1.E+00	1.E+00	1.E+00	
GOTERM_BP_FAT	GO:0048568~embryonic organ development	6	1.096892139		9.E-01 13836, 13649, 21813, 12702, 14784, 561	491	241	13588	7.E-01	1.E+00	1.E+00	
Annotation Cluster 173	Enrichment Score: 0.09496594631205085											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	
GOTERM_BP_FAT	GO:0001649~osteoblast differentiation	3	0.548446069		5.E-01 78294, 208727, 16000	491	47	13588	2.E+00	1.E+00	1.E+00	
GOTERM_BP_FAT	GO:0001503~ossification	3	0.548446069		9.E-01 78294, 208727, 16000	491	106	13588	8.E-01	1.E+00	1.E+00	
GOTERM_BP_FAT	GO:0060348~bone development	3	0.548446069		9.E-01 78294, 208727, 16000	491	118	13588	7.E-01	1.E+00	1.E+00	
GOTERM_BP_FAT	GO:0001501~skeletal system development	6	1.096892139		1.E+00 16854, 78294, 13836, 21813, 208727, 16	491	285	13588	6.E-01	1.E+00	1.E+00	
Annotation Cluster 174	Enrichment Score: 0.08989696819488041											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	
GOTERM_BP_FAT	GO:0019226~transmission of nerve impulse	9	1.645338208		6.E-01 13667, 13866, 20909, 11820, 224045, 1	491	226	13588	1.E+00	1.E+00	1.E+00	
GOTERM_BP_FAT	GO:0007268~synaptic transmission	4	0.731261426		1.E+00 20909, 11820, 20418, 18205	491	178	13588	6.E-01	1.E+00	1.E+00	
GOTERM_BP_FAT	GO:0007267~cell-cell signaling	6	1.096892139		1.E+00 12064, 13350, 20909, 11820, 20418, 18	491	290	13588	6.E-01	1.E+00	1.E+00	
Annotation Cluster 175	Enrichment Score: 0.07377964156097344											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	
SP_PIR_KEYWORDS	metal-binding	86	15.72212066		3.E-01 18746, 228543, 226646, 22324, 672195,	541	2682	17854	1.E+00	1.E+00	7.E-01	
GOTERM_MF_FAT	GO:0046914~transition metal ion binding	82	14.99085923		9.E-01 226646, 22324, 672195, 65969, 16800, 1	476	2608	13288	9.E-01	1.E+00	1.E+00	
SP_PIR_KEYWORDS	zinc	46	8.409506399		1.E+00 22324, 16392, 16800, 18227, 68910, 12	541	1886	17854	8.E-01	1.E+00	1.E+00	
GOTERM_MF_FAT	GO:0046872~metal ion binding	109	19.92687386		1.E+00 18746, 226646, 22324, 16800, 18227, 1	476	3850	13288	8.E-01	1.E+00	1.E+00	
GOTERM_MF_FAT	GO:0043169~cation binding	109	19.92687386		1.E+00 18746, 226646, 22324, 16800, 18227, 1	476	3885	13288	8.E-01	1.E+00	1.E+00	
GOTERM_MF_FAT	GO:0008270~zinc ion binding	51	9.323583181		1.E+00 22324, 16800, 18227, 68910, 12914, 22	476	2105	13288	7.E-01	1.E+00	1.E+00	
GOTERM_MF_FAT	GO:0043167~ion binding	109	19.92687386		1.E+00 18746, 226646, 22324, 16800, 18227, 1	476	3934	13288	8.E-01	1.E+00	1.E+00	
Annotation Cluster 176	Enrichment Score: 0.067886754138957											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	
GOTERM_BP_FAT	GO:0006325~chromatin organization	11	2.010968921		7.E-01 319168, 621893, 319169, 15078, 74318,	491	315	13588	1.E+00	1.E+00	1.E+00	
GOTERM_BP_FAT	GO:0016568~chromatin modification	6	1.096892139		9.E-01 74318, 20220, 12417, 13436, 208727, 1	491	236	13588	7.E-01	1.E+00	1.E+00	
SP_PIR_KEYWORDS	repressor	8	1.462522852		1.E+00 74318, 20220, 12952, 12953, 12417, 13	541	391	17854	7.E-01	1.E+00	1.E+00	
Annotation Cluster 177	Enrichment Score: 0.06462329519985557											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	
SP_PIR_KEYWORDS	membrane	172	31.44424132		4.E-01 226646, 66377, 69524, 100041835, 243	541	5507	17854	1.E+00	1.E+00	7.E-01	
UP_SEQ_FEATURE	topological domain:Extracellular	35	6.398537477		1.E+00 12765, 13649, 69524, 16423, 20909, 71	537	2174	16021	5.E-01	1.E+00	1.E+00	
UP_SEQ_FEATURE	transmembrane region	81	14.80804388		1.E+00 12765, 100041273, 69524, 66377, 1000	537	4113	16021	6.E-01	1.E+00	1.E+00	
UP_SEQ_FEATURE	topological domain:Cytoplasmic	38	6.946983547		1.E+00 12765, 13649, 69524, 16423, 20909, 71	537	2780	16021	4.E-01	1.E+00	1.E+00	
SP_PIR_KEYWORDS	transmembrane	83	15.17367459		1.E+00 12765, 100041273, 69524, 66377, 1000	541	5237	17854	5.E-01	1.E+00	1.E+00	
GOTERM_CC_FAT	GO:0016021~integral to membrane	90	16.45338208		1.E+00 66377, 69524, 100041835, 56348, 2090	419	5709	12504	5.E-01	1.E+00	1.E+00	
GOTERM_CC_FAT	GO:0031224~intrinsic to membrane	98	17.91590494		1.E+00 69524, 66377, 100041835, 56348, 1770	419	5914	12504	5.E-01	1.E+00	1.E+00	
Annotation Cluster 178	Enrichment Score: 0.05573900724388254											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	
GOTERM_BP_FAT	GO:0009628~response to abiotic stimulus	8	1.462522852		8.E-01 14685, 12190, 21813, 12955, 11820, 22	491	251	13588	9.E-01	1.E+00	1.E+00	
GOTERM_BP_FAT	GO:0009416~response to light stimulus	3	0.548446069		9.E-01 14685, 12190, 11820	491	98	13588	8.E-01	1.E+00	1.E+00	
GOTERM_BP_FAT	GO:0009314~response to radiation	3	0.548446069		1.E+00 14685, 12190, 11820	491	143	13588	6.E-01	1.E+00	1.E+00	
Annotation Cluster 179	Enrichment Score: 0.050670920550533155											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	
GOTERM_BP_FAT	GO:0000278~mitotic cell cycle	9	1.645338208		7.E-01 104394, 19384, 13559, 17222, 11820, 1	491	244	13588	1.E+00	1.E+00	1.E+00	
GOTERM_BP_FAT	GO:0007049~cell cycle	20	3.65630713		8.E-01 12190, 26934, 104394, 56338, 19384, 2	491	611	13588	9.E-01	1.E+00	1.E+00	
GOTERM_BP_FAT	GO:0022403~cell cycle phase	10	1.828153565		8.E-01 12190, 104394, 19384, 13559, 17222, 1	491	328	13588	8.E-01	1.E+00	1.E+00	
GOTERM_BP_FAT	GO:0022402~cell cycle process	12	2.193784278		8.E-01 12190, 104394, 26934, 19384, 13559, 1	491	393	13588	8.E-01	1.E+00	1.E+00	
SP_PIR_KEYWORDS	cell division	6	1.096892139		9.E-01 26934, 19384, 17222, 12540, 16800, 23	541	256	17854	8.E-01	1.E+00	1.E+00	
GOTERM_BP_FAT	GO:0000087~M phase of mitotic cell cycle	5	0.914076782		9.E-01 19384, 17222, 16800, 68193, 20112	491	194	13588	7.E-01	1.E+00	1.E+00	



GOTERM_BP_FAT	GO:0051301~cell division	7	1.279707495	9.E-01	12190, 26934, 19384, 17222, 12540, 161	491	281	13588	7.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0000280~nuclear division	4	0.731261426	1.E+00	19384, 17222, 16800, 20112	491	190	13588	6.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0007067~mitosis	4	0.731261426	1.E+00	19384, 17222, 16800, 20112	491	190	13588	6.E-01	1.E+00	1.E+00
SP_PIR_KEYWORDS	mitosis	3	0.548446069	1.E+00	19384, 17222, 16800	541	179	17854	6.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0048285~organelle fission	4	0.731261426	1.E+00	19384, 17222, 16800, 20112	491	197	13588	6.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0000279~M phase	6	1.096892139	1.E+00	12190, 19384, 17222, 16800, 68193, 201	491	283	13588	6.E-01	1.E+00	1.E+00

Annotation Cluster 180	Enrichment Score: 0.03759199088505875										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_CC_FAT	GO:0005615~extracellular space	17	3.10786106	6.E-01	12266, 12258, 11816, 16644, 22359, 151	419	511	12504	1.E+00	1.E+00	9.E-01
GOTERM_CC_FAT	GO:0044421~extracellular region part	25	4.570383912	7.E-01	12258, 11816, 16644, 56348, 15139, 181	419	774	12504	1.E+00	1.E+00	1.E+00
SP_PIR_KEYWORDS	disulfide bond	68	12.43144424	8.E-01	12765, 69524, 12258, 16644, 65969, 711	541	2469	17854	9.E-01	1.E+00	1.E+00
UP_SEQ_FEATURE	disulfide bond	66	12.06581353	1.E+00	12765, 69524, 12258, 16644, 65969, 711	537	2379	16021	8.E-01	1.E+00	1.E+00
SP_PIR_KEYWORDS	Secreted	32	5.850091408	1.E+00	12258, 11816, 12279, 16644, 21789, 691	541	1420	17854	7.E-01	1.E+00	1.E+00
GOTERM_CC_FAT	GO:0005576~extracellular region	38	6.946983547	1.E+00	11816, 12258, 12279, 16644, 56348, 211	419	1680	12504	7.E-01	1.E+00	1.E+00
SP_PIR_KEYWORDS	signal	64	11.70018282	1.E+00	69524, 12258, 16644, 65969, 71326, 831	541	2970	17854	7.E-01	1.E+00	1.E+00
UP_SEQ_FEATURE	signal peptide	64	11.70018282	1.E+00	69524, 12258, 16644, 65969, 71326, 831	537	2963	16021	6.E-01	1.E+00	1.E+00
SP_PIR_KEYWORDS	glycoprotein	63	11.51736746	1.E+00	12765, 69524, 12258, 16644, 65969, 231	541	3600	17854	6.E-01	1.E+00	1.E+00
UP_SEQ_FEATURE	topological domain:Extracellular	35	6.398537477	1.E+00	12765, 13649, 69524, 16423, 20909, 711	537	2174	16021	5.E-01	1.E+00	1.E+00
UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	61	11.15173675	1.E+00	12765, 69524, 12258, 16644, 65969, 831	537	3444	16021	5.E-01	1.E+00	1.E+00
UP_SEQ_FEATURE	topological domain:Cytoplasmic	38	6.946983547	1.E+00	12765, 13649, 69524, 16423, 20909, 711	537	2780	16021	4.E-01	1.E+00	1.E+00

Annotation Cluster 181	Enrichment Score: 0.036693609676006635										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_MF_FAT	GO:0046983~protein dimerization activity	10	1.828153565	9.E-01	20848, 18126, 72269, 11487, 16476, 191	476	340	13288	8.E-01	1.E+00	1.E+00
GOTERM_MF_FAT	GO:0042803~protein homodimerization activity	5	0.914076782	9.E-01	18126, 72269, 11487, 19989, 14381	476	193	13288	7.E-01	1.E+00	1.E+00
GOTERM_MF_FAT	GO:0042802~identical protein binding	6	1.096892139	1.E+00	18126, 72269, 11487, 19989, 26401, 141	476	290	13288	6.E-01	1.E+00	1.E+00

Annotation Cluster 182	Enrichment Score: 0.030348668591472637										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_CC_FAT	GO:0005773~vacuole	5	0.914076782	9.E-01	14387, 65969, 230163, 13382, 16784	419	204	12504	7.E-01	1.E+00	1.E+00
SP_PIR_KEYWORDS	lysosome	3	0.548446069	9.E-01	14387, 65969, 16784	541	144	17854	7.E-01	1.E+00	1.E+00
GOTERM_CC_FAT	GO:0005764~lysosome	4	0.731261426	9.E-01	14387, 65969, 230163, 16784	419	178	12504	7.E-01	1.E+00	1.E+00
GOTERM_CC_FAT	GO:0000323~lytic vacuole	4	0.731261426	9.E-01	14387, 65969, 230163, 16784	419	179	12504	7.E-01	1.E+00	1.E+00

Annotation Cluster 183	Enrichment Score: 0.029856193802334195										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_BP_FAT	GO:0003001~generation of a signal involved in cell-cell signaling	3	0.548446069	8.E-01	12064, 13350, 20909	491	84	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0032940~secretion by cell	4	0.731261426	1.E+00	12064, 13350, 20909, 18551	491	186	13588	6.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0007267~cell-cell signaling	6	1.096892139	1.E+00	12064, 13350, 20909, 11820, 20418, 181	491	290	13588	6.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0046903~secretion	4	0.731261426	1.E+00	12064, 13350, 20909, 18551	491	221	13588	5.E-01	1.E+00	1.E+00

Annotation Cluster 184	Enrichment Score: 0.02687806678027869										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_BP_FAT	GO:0033554~cellular response to stress	12	2.193784278	9.E-01	12190, 57874, 11546, 19247, 13665, 141	491	404	13588	8.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0006281~DNA repair	6	1.096892139	9.E-01	12190, 11546, 14884, 12952, 12953, 141	491	222	13588	7.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0006974~response to DNA damage stimulus	7	1.279707495	9.E-01	12190, 11546, 19247, 14884, 12952, 121	491	287	13588	7.E-01	1.E+00	1.E+00
SP_PIR_KEYWORDS	dna repair	3	0.548446069	1.E+00	12190, 14884, 14885	541	173	17854	6.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0006259~DNA metabolic process	10	1.828153565	1.E+00	12190, 11546, 19075, 68240, 14884, 121	491	421	13588	7.E-01	1.E+00	1.E+00
SP_PIR_KEYWORDS	DNA damage	3	0.548446069	1.E+00	12190, 14884, 14885	541	194	17854	5.E-01	1.E+00	1.E+00

Annotation Cluster 185	Enrichment Score: 0.0221930143071203										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
SP_PIR_KEYWORDS	protein phosphatase	3	0.548446069	9.E-01	15170, 19053, 19247	541	120	17854	8.E-01	1.E+00	1.E+00
GOTERM_MF_FAT	GO:0004721~phosphoprotein phosphatase activity	3	0.548446069	1.E+00	15170, 19053, 19247	476	152	13288	6.E-01	1.E+00	1.E+00
GOTERM_MF_FAT	GO:0016791~phosphatase activity	3	0.548446069	1.E+00	15170, 19053, 19247	476	238	13288	4.E-01	1.E+00	1.E+00

Annotation Cluster 186	Enrichment Score: 0.01611141667563901										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini



UP_SEQ_FEATURE	repeatWD 4	5	0.914076782	9.E-01 27979, 76646, 54709, 66679, 67337	537	218	16021	7.E-01	1.E+00	1.E+00	
UP_SEQ_FEATURE	repeatWD 3	5	0.914076782	1.E+00 27979, 76646, 54709, 66679, 67337	537	231	16021	6.E-01	1.E+00	1.E+00	
INTERPRO	IPR019775:WD40 repeat, conserved site	5	0.914076782	1.E+00 27979, 76646, 54709, 66679, 67337	535	258	17763	6.E-01	1.E+00	1.E+00	
UP_SEQ_FEATURE	repeatWD 2	5	0.914076782	1.E+00 27979, 76646, 54709, 66679, 67337	537	235	16021	6.E-01	1.E+00	1.E+00	
UP_SEQ_FEATURE	repeatWD 1	5	0.914076782	1.E+00 27979, 76646, 54709, 66679, 67337	537	235	16021	6.E-01	1.E+00	1.E+00	
INTERPRO	IPR019782:WD40 repeat 2	4	0.731261426	1.E+00 76646, 54709, 66679, 67337	535	214	17763	6.E-01	1.E+00	1.E+00	
SP_PIR_KEYWORDS	wd repeat	5	0.914076782	1.E+00 27979, 76646, 54709, 66679, 67337	541	263	17854	6.E-01	1.E+00	1.E+00	
UP_SEQ_FEATURE	repeatWD 5	4	0.731261426	1.E+00 27979, 76646, 54709, 67337	537	202	16021	6.E-01	1.E+00	1.E+00	
INTERPRO	IPR017986:WD40 repeat, region	4	0.731261426	1.E+00 76646, 54709, 66679, 67337	535	228	17763	6.E-01	1.E+00	1.E+00	
SMART	SM00320:WD40	4	0.731261426	1.E+00 76646, 54709, 66679, 67337	248	259	9131	6.E-01	1.E+00	1.E+00	
INTERPRO	IPR019781:WD40 repeat, subgroup	4	0.731261426	1.E+00 76646, 54709, 66679, 67337	535	235	17763	6.E-01	1.E+00	1.E+00	
INTERPRO	IPR015943:WD40/YVTN repeat-like	5	0.914076782	1.E+00 27979, 76646, 54709, 66679, 67337	535	305	17763	5.E-01	1.E+00	1.E+00	
INTERPRO	IPR001680:WD40 repeat	4	0.731261426	1.E+00 76646, 54709, 66679, 67337	535	259	17763	5.E-01	1.E+00	1.E+00	
Annotation Cluster 187	Enrichment Score: 0.006621781694303422										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
SP_PIR_KEYWORDS	actin-binding	4	0.731261426		1.E+00 17925, 270163, 76448, 224014	541	226	17854	6.E-01	1.E+00	1.E+00
GOTERM_MF_FAT	GO:0008092~cytoskeletal protein binding	8	1.462522852		1.E+00 26934, 94190, 17925, 270163, 16800, 76448, 224014	476	414	13288	5.E-01	1.E+00	1.E+00
GOTERM_MF_FAT	GO:0003779~actin binding	5	0.914076782		1.E+00 94190, 17925, 270163, 76448, 224014	476	288	13288	5.E-01	1.E+00	1.E+00
Annotation Cluster 188	Enrichment Score: 0.0014806074235713042										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
SP_PIR_KEYWORDS	mrna processing	3	0.548446069		1.E+00 18458, 101943, 67337	541	240	17854	4.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0016071~mRNA metabolic process	5	0.914076782		1.E+00 16341, 11820, 18458, 101943, 67337	491	302	13588	5.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0006397~mRNA processing	4	0.731261426		1.E+00 11820, 18458, 101943, 67337	491	262	13588	4.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0006396~RNA processing	6	1.096892139		1.E+00 19896, 11820, 18458, 101943, 20044, 67337	491	437	13588	4.E-01	1.E+00	1.E+00
Annotation Cluster 189	Enrichment Score: 0.0012837232324015076										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
KEGG_PATHWAY	mmu04120:Ubiquitin mediated proteolysis	5	0.914076782		1.E+00 12702, 246710, 17222, 26401, 56469	372	136	5738	6.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0044265~cellular macromolecule catabolic process	12	2.193784278		1.E+00 78294, 19053, 12702, 16341, 11816, 11487, 12301, 17222, 56469	491	609	13588	5.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0009057~macromolecule catabolic process	13	2.376599634		1.E+00 78294, 11816, 238055, 11491, 16341, 11487, 12301, 17222, 56469	491	654	13588	6.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0051603~proteolysis involved in cellular protein catabolic process	8	1.462522852		1.E+00 78294, 19053, 12702, 11487, 12301, 17222, 56469	491	534	13588	4.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0044257~cellular protein catabolic process	8	1.462522852		1.E+00 78294, 19053, 12702, 11487, 12301, 17222, 56469	491	537	13588	4.E-01	1.E+00	1.E+00
SP_PIR_KEYWORDS	ubl conjugation pathway	5	0.914076782		1.E+00 78294, 12702, 12301, 17222, 56469	541	484	17854	3.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0030163~protein catabolic process	8	1.462522852		1.E+00 78294, 19053, 12702, 11487, 12301, 17222, 56469	491	556	13588	4.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0043632~modification-dependent macromolecule catabolic process	6	1.096892139		1.E+00 78294, 19053, 12702, 12301, 17222, 56469	491	508	13588	3.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0019941~modification-dependent protein catabolic process	6	1.096892139		1.E+00 78294, 19053, 12702, 12301, 17222, 56469	491	508	13588	3.E-01	1.E+00	1.E+00



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1.E-01  
1.E-01  
1.E-01  
2.E-01  
2.E-01  
8.E-01  
1.E+00  
1.E+00  
2.E+00  
2.E+00  
3.E+00  
4.E+00  
6.E+00  
6.E+00  
6.E+00  
6.E+00  
6.E+00  
7.E+00  
7.E+00  
8.E+00  
8.E+00  
8.E+00  
1.E+01  
1.E+01  
2.E+01  
2.E+01  
2.E+01



2.E+01  
2.E+01  
3.E+01  
3.E+01  
4.E+01  
4.E+01  
4.E+01  
4.E+01  
4.E+01  
5.E+01  
6.E+01  
6.E+01  
7.E+01  
7.E+01  
7.E+01

FDR

3.E-65  
2.E-64  
1.E-60  
9.E-45  
8.E-44  
4.E-43  
1.E-42  
2.E-42  
9.E-42  
3.E-39  
3.E-38  
1.E-37  
7.E-37  
3.E-36  
3.E-33  
4.E-33  
6.E-32  
1.E-31  
3.E-26  
3.E-25  
6.E-19  
3.E-16  
2.E-14  
5.E-04

FDR

7.E-51  
8.E-48  
3.E-43  
7.E-32



2.E-31  
2.E-31  
2.E-23  
4.E-19

FDR

6.E-62  
4.E-53  
5.E-50  
1.E-45  
3.E-45  
2.E-36  
8.E-23  
2.E-17  
4.E-06  
4.E-06

FDR

2.E-64  
1.E-60  
4.E-43  
3.E-39  
7.E-25  
7.E-25  
7.E-25  
9.E-23  
5.E-20  
4.E-18

FDR

6.E-40  
1.E-23  
8.E-22  
5.E-20  
8.E-15  
1.E-10

FDR

7.E-32  
2.E-31  
1.E-18  
3.E-17  
2.E-15  
3.E-15  
3.E-15  
2.E-14  
3.E-14  
1.E-12  
2.E-12  
4.E-12  
6.E-11  
1.E-10  
2.E-10  
2.E-08  
6.E-06



1.E-04

FDR

1.E-19  
7.E-19  
9.E-17  
9.E-17  
2.E-16  
2.E-16  
4.E-14  
8.E-13  
2.E-10  
2.E-09  
2.E-08  
8.E-08  
2.E-01  
2.E-01

FDR

6.E-20  
1.E-10  
2.E-10  
2.E-09  
3.E-07  
4.E-07  
1.E-02

FDR

3.E-10  
2.E-09  
2.E-06  
1.E-03  
5.E-02

FDR

2.E-09  
5.E-09  
2.E-08  
7.E-05  
1.E+01

FDR

3.E-10  
4.E-04  
1.E+00

FDR

3.E-07  
3.E-04  
3.E-04  
3.E-04



FDR

9.E-15  
6.E-14  
4.E-11  
2.E-07  
4.E-07  
1.E-04  
1.E-04  
2.E-04  
2.E-04  
9.E-04  
9.E-04  
6.E-03  
1.E-02  
1.E-02  
4.E-01  
5.E+00  
6.E+00  
2.E+01  
7.E+01  
1.E+02

FDR

[illegible]



6.E-03  
6.E-03  
3.E-02  
6.E-02  
1.E-01  
2.E-01  
2.E-01  
1.E+00  
2.E+00  
4.E+01  
7.E+01  
9.E+01  
9.E+01  
9.E+01  
9.E+01  
9.E+01  
1.E+02  
1.E+02  
1.E+02  
1.E+02  
1.E+02  
1.E+02

FDR

5.E-06  
1.E-04  
3.E+01

FDR

5.E-06  
1.E-01  
3.E-01

FDR

3.E-04  
3.E-03  
6.E-03  
5.E+00

FDR

1.E-03  
1.E-03  
1.E-03  
1.E-03  
3.E-02  
1.E+02

FDR

1.E-03  
2.E-03  
6.E-03  
5.E-02



2.E-01  
9.E-01  
2.E+01

FDR  
6.E-03  
3.E-02  
1.E+00

FDR  
4.E-01  
4.E-01  
9.E-01

FDR  
1.E-01  
2.E-01  
4.E+01

FDR  
3.E-03  
1.E-01  
2.E+00  
6.E+00  
5.E+01

FDR  
1.E-02  
9.E-02  
1.E+02

FDR  
1.E+00  
1.E+00  
1.E+00  
1.E+00

FDR  
2.E-01  
2.E-01  
6.E+01

FDR  
1.E-02  
4.E+00  
5.E+00  
8.E+00  
8.E+00

FDR



7.E-01  
1.E+00  
2.E+00  
5.E+00

FDR

6.E-01  
1.E+00  
1.E+00  
2.E+00  
2.E+00  
4.E+00  
2.E+01

FDR

1.E-03  
2.E-03  
5.E-01  
4.E+01  
6.E+01  
8.E+01  
9.E+01

FDR

1.E-01  
1.E-01  
1.E-01  
1.E-01  
2.E-01  
4.E-01  
7.E-01  
1.E+00  
2.E+00  
2.E+00  
1.E+01  
2.E+01  
4.E+01  
5.E+01  
8.E+01  
9.E+01  
9.E+01  
1.E+02  
1.E+02

FDR

4.E-01  
1.E+00  
9.E-01  
1.E+00  
2.E+00  
2.E+00  
2.E+00  
2.E+00  
2.E+00  
3.E+00



5.E+00  
5.E+00  
3.E+00  
9.E+00  
1.E+01  
1.E+01  
1.E+01  
2.E+01  
3.E+01  
7.E+01  
7.E+01  
1.E+02

FDR

2.E-01  
2.E-01  
8.E+00  
1.E+01  
3.E+01  
3.E+01  
7.E+01

FDR

1.E-01  
2.E-01  
2.E+00  
5.E+00  
5.E+00  
1.E+01  
2.E+01  
3.E+01  
3.E+01  
4.E+01  
5.E+01

FDR

7.E-02  
4.E+00  
5.E+00  
8.E+00  
8.E+00  
1.E+01  
4.E+01  
4.E+01

FDR

4.E+00  
4.E+00  
3.E+01

FDR

1.E+00  
1.E+00  
2.E+00



2.E+00  
4.E+00  
5.E+00  
8.E+00  
8.E+00  
1.E+01  
2.E+01  
4.E+01  
1.E+02

FDR

1.E-01  
1.E-01  
8.E-01  
6.E+00  
8.E+00  
8.E+00  
4.E+01  
8.E+01  
1.E+02

FDR

9.E-01  
3.E+00  
1.E+02

FDR

4.E-01  
8.E-01  
1.E+00  
1.E+00  
1.E+01  
8.E+00  
5.E+00  
2.E+01  
3.E+01  
3.E+01  
3.E+01  
4.E+01  
9.E+01

FDR

3.E-01  
2.E+00  
5.E+00  
5.E+00  
5.E+00  
2.E+01  
7.E+01  
9.E+01

FDR

7.E-01  
7.E-01



2.E+00  
3.E+00  
3.E+00  
2.E+01  
8.E+01  
8.E+01  
9.E+01

FDR

8.E+00  
7.E+00  
1.E+01

FDR

1.E-01  
5.E-01  
2.E+00  
3.E+00  
3.E+00  
4.E+00  
5.E+00  
5.E+00  
5.E+00  
5.E+00  
5.E+00  
6.E+00  
1.E+01  
1.E+01  
1.E+01  
9.E+01  
1.E+02  
1.E+02  
1.E+02  
1.E+02

FDR

2.E-07  
1.E-04  
1.E-04  
1.E-04  
8.E-02  
1.E-01  
4.E-01  
4.E-01  
6.E-01  
6.E-01  
1.E+00  
2.E+00  
3.E+00  
4.E+00  
2.E+01  
2.E+01  
1.E+01  
2.E+01  
2.E+01  
3.E+01



3.E+01  
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4.E+01  
4.E+01  
4.E+01  
4.E+01  
5.E+01  
7.E+01  
7.E+01  
8.E+01  
8.E+01  
8.E+01  
9.E+01  
1.E+02  
1.E+02  
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1.E+02  
1.E+02  
1.E+02  
1.E+02

FDR

6.E-03  
8.E-03  
8.E-03  
2.E-02  
1.E-01  
1.E+00  
9.E-01  
2.E+00  
2.E+00  
3.E+00  
3.E+00  
3.E+00  
3.E+00  
4.E+00  
6.E+00  
7.E+00  
1.E+01  
7.E+00  
7.E+00  
8.E+00  
1.E+01  
1.E+01  
9.E+00  
1.E+01  
1.E+01  
1.E+01  
1.E+01



2.E+01  
2.E+01  
2.E+01  
2.E+01  
2.E+01  
2.E+01  
3.E+01  
4.E+01  
3.E+01  
3.E+01  
3.E+01  
4.E+01  
4.E+01  
4.E+01  
4.E+01  
5.E+01  
6.E+01  
7.E+01  
6.E+01  
8.E+01  
9.E+01  
9.E+01  
9.E+01  
1.E+02  
1.E+02  
1.E+02  
1.E+02  
1.E+02  
1.E+02

FDR

2.E+00  
3.E+00  
3.E+00  
4.E+00  
2.E+01  
7.E+01  
1.E+02

FDR

3.E+00  
5.E+00  
9.E+01

FDR

4.E+00  
5.E+00  
5.E+00  
8.E+00  
1.E+01  
1.E+02

FDR

3.E+00  
6.E+00



3.E+01  
7.E+01

FDR

2.E+00  
6.E+00  
7.E+00  
1.E+01  
4.E+01  
6.E+01

FDR

2.E+00  
2.E+00  
5.E+01  
1.E+02

FDR

1.E-01  
8.E+00  
2.E+01  
3.E+01  
4.E+01  
6.E+01  
6.E+01  
7.E+01

FDR

7.E+00  
8.E+00  
8.E+01

FDR

2.E-01  
9.E+01  
9.E+01

FDR

1.E+01  
2.E+01  
3.E+01

FDR

1.E+01  
2.E+01  
2.E+01  
2.E+01  
3.E+01  
3.E+01  
5.E+01



FDR  
6.E-01  
1.E+00  
1.E+00  
3.E+00  
5.E+00  
1.E+01  
3.E+01  
3.E+01  
6.E+01  
6.E+01  
8.E+01  
9.E+01  
1.E+02  
1.E+02  
1.E+02

FDR  
2.E+01  
2.E+01  
3.E+01

FDR  
5.E-03  
6.E-02  
1.E-01  
2.E-01  
2.E-01  
4.E-01  
9.E-01  
3.E+00  
1.E+01  
2.E+01  
7.E+01  
8.E+01  
8.E+01  
9.E+01  
9.E+01  
6.E+01  
9.E+01  
1.E+02  
1.E+02  
1.E+02  
1.E+02  
1.E+02  
1.E+02  
1.E+02  
1.E+02

FDR  
8.E+00  
1.E+01  
1.E+01  
2.E+01  
4.E+01  
7.E+01



8.E+01

FDR  
6.E+00  
4.E+01  
4.E+01  
6.E+01

FDR  
2.E-01  
7.E+01  
1.E+02

FDR  
5.E-01  
8.E+00  
2.E+01  
2.E+01  
2.E+01  
6.E+01  
8.E+01  
9.E+01  
1.E+02

FDR  
4.E+00  
5.E+00  
2.E+01  
2.E+01  
3.E+01  
3.E+01  
8.E+01  
1.E+02  
1.E+02

FDR  
1.E+01  
4.E+01  
4.E+01  
5.E+01  
6.E+01

FDR  
1.E+01  
6.E+01  
6.E+01

FDR  
8.E+00  
2.E+01  
4.E+01  
6.E+01



6.E+01  
8.E+01

FDR

2.E+01  
2.E+01  
2.E+01  
2.E+01  
2.E+01  
2.E+01  
3.E+01  
6.E+01  
7.E+01  
8.E+01  
1.E+02  
1.E+02

FDR

1.E-01  
5.E-01  
8.E-01  
2.E+00  
2.E+00  
3.E+00  
3.E+00  
3.E+00  
4.E+00  
6.E+00  
7.E+00  
8.E+00  
1.E+01  
1.E+01  
1.E+01  
2.E+01  
2.E+01  
2.E+01  
2.E+01  
4.E+01  
4.E+01  
4.E+01  
5.E+01  
6.E+01  
6.E+01  
7.E+01  
7.E+01  
7.E+01  
8.E+01  
8.E+01  
8.E+01  
9.E+01  
9.E+01  
9.E+01  
9.E+01  
1.E+02  
1.E+02  
1.E+02



1.E+02  
1.E+02  
1.E+02  
1.E+02  
1.E+02  
1.E+02  
1.E+02

FDR

8.E+00  
8.E+00  
1.E+01  
2.E+01  
6.E+01  
9.E+01  
1.E+02  
1.E+02

FDR

1.E+00  
7.E+01  
1.E+02

FDR

2.E+01  
4.E+01  
4.E+01  
6.E+01  
8.E+01  
1.E+02

FDR

2.E+01  
2.E+01  
2.E+01  
2.E+01  
1.E+02  
1.E+02

FDR

3.E+01  
4.E+01  
6.E+01  
6.E+01  
9.E+01

FDR

8.E-01  
9.E-01  
1.E+00  
2.E+01  
3.E+01  
8.E+01



8.E+01  
1.E+02  
1.E+02  
1.E+02  
1.E+02  
1.E+02  
1.E+02

FDR

3.E+01  
5.E+01  
1.E+02

FDR

2.E+01  
5.E+01  
5.E+01  
5.E+01  
1.E+02

FDR

4.E+00  
1.E+01  
2.E+01  
2.E+01  
2.E+01  
3.E+01  
4.E+01  
6.E+01  
8.E+01  
8.E+01  
8.E+01  
8.E+01  
8.E+01  
9.E+01  
1.E+02  
1.E+02  
1.E+02  
1.E+02  
1.E+02  
1.E+02

FDR

5.E+01  
7.E+01  
7.E+01

FDR

5.E+01  
6.E+01  
7.E+01  
8.E+01



9.E+01  
1.E+02

FDR

3.E+01  
4.E+01  
7.E+01  
6.E+01  
9.E+01  
1.E+02

FDR

6.E+01  
7.E+01  
9.E+01

FDR

8.E+01  
8.E+01  
8.E+01  
8.E+01

FDR

[illegible]



1.E+02

FDR

2.E+00  
4.E+00  
1.E+02  
1.E+02  
1.E+02  
1.E+02  
1.E+02

FDR

6.E+01  
9.E+01  
9.E+01

FDR

9.E-02  
2.E-01  
2.E-01  
7.E+01  
1.E+02  
1.E+02  
1.E+02  
1.E+02  
1.E+02  
1.E+02  
1.E+02  
1.E+02  
1.E+02  
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1.E+02  
1.E+02  
1.E+02  
1.E+02  
1.E+02  
1.E+02  
1.E+02  
1.E+02

FDR

6.E+00  
8.E+00  
1.E+01  
3.E+01  
4.E+01  
4.E+01  
7.E+01  
9.E+01  
1.E+02  
1.E+02  
1.E+02  
1.E+02  
1.E+02  
1.E+02



1.E+02  
1.E+02  
1.E+02

FDR

2.E+01  
6.E+01  
1.E+02  
1.E+02  
1.E+02  
1.E+02  
1.E+02

FDR

6.E+01  
7.E+01  
9.E+01  
9.E+01  
1.E+02  
1.E+02  
1.E+02

FDR

9.E+01  
9.E+01  
9.E+01  
1.E+02

FDR

7.E+01  
7.E+01  
1.E+02

FDR

4.E+01  
5.E+01  
7.E+01  
7.E+01  
9.E+01  
1.E+02  
1.E+02  
1.E+02  
1.E+02  
1.E+02  
1.E+02  
1.E+02  
1.E+02

FDR

4.E+01  
5.E+01  
6.E+01  
7.E+01



5.E+01  
6.E+01  
7.E+01  
7.E+01  
7.E+01  
7.E+01  
7.E+01  
8.E+01  
1.E+02  
1.E+02  
1.E+02  
1.E+02  
1.E+02  
1.E+02  
1.E+02  
1.E+02  
1.E+02  
1.E+02  
1.E+02  
1.E+02

FDR

5.E+00  
1.E+01  
1.E+02  
1.E+02  
1.E+02  
1.E+02  
1.E+02  
1.E+02  
1.E+02  
1.E+02

FDR

7.E+01  
8.E+01  
8.E+01  
9.E+01  
1.E+02  
1.E+02  
1.E+02  
1.E+02

FDR

7.E+01  
8.E+01  
9.E+01  
1.E+02  
1.E+02  
1.E+02  
1.E+02



FDR  
9.E+01  
9.E+01  
9.E+01  
1.E+02  
9.E+01  
1.E+02  
1.E+02  
1.E+02

FDR  
8.E+01  
9.E+01  
9.E+01  
1.E+02  
1.E+02  
1.E+02  
1.E+02

FDR  
7.E+01  
9.E+01  
9.E+01  
1.E+02  
1.E+02  
1.E+02

FDR  
9.E+01  
9.E+01  
1.E+02  
1.E+02  
1.E+02  
1.E+02  
1.E+02  
1.E+02

FDR  
5.E+01  
7.E+01  
9.E+01  
1.E+02  
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TH/SH-PP1-David-Liver

Mus musculus (821)

Unknown (13)

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0006091~generation of precursor metabolites and energy	101	13.35978836	3.E-62	18746, 226646, 66377, 100041835, 17705	692	261	13588	8.E+00	8.E-59	8.E-59	6.E-59
GOTERM_BP_FAT	GO:0006412~translation	97	12.83068783	9.E-49	666899, 100048462, 13667, 13669, 10004	692	319	13588	6.E+00	2.E-45	1.E-45	2.E-45
GOTERM_BP_FAT	GO:0022900~electron transport chain	52	6.878306878	2.E-36	70316, 672195, 226646, 100041273, 6637	692	112	13588	9.E+00	6.E-33	2.E-33	4.E-33
GOTERM_BP_FAT	GO:0019320~hexose catabolic process	32	4.232804233	3.E-27	18746, 68263, 100042746, 15275, 15277,	692	52	13588	1.E+01	7.E-24	2.E-24	5.E-24
GOTERM_BP_FAT	GO:0006007~glucose catabolic process	32	4.232804233	3.E-27	18746, 68263, 100042746, 15275, 15277,	692	52	13588	1.E+01	7.E-24	2.E-24	5.E-24
GOTERM_BP_FAT	GO:0046365~monosaccharide catabolic process	32	4.232804233	1.E-26	18746, 68263, 100042746, 15275, 15277,	692	54	13588	1.E+01	4.E-23	7.E-24	2.E-23
GOTERM_BP_FAT	GO:0044275~cellular carbohydrate catabolic process	32	4.232804233	1.E-24	18746, 68263, 100042746, 15275, 15277,	692	60	13588	1.E+01	3.E-21	5.E-22	2.E-21
GOTERM_BP_FAT	GO:0006096~glycolysis	28	3.703703704	2.E-24	18746, 68263, 100042746, 15275, 15277,	692	44	13588	1.E+01	5.E-21	7.E-22	4.E-21
GOTERM_BP_FAT	GO:0046164~alcohol catabolic process	32	4.232804233	3.E-23	18746, 68263, 100042746, 15275, 15277,	692	65	13588	1.E+01	6.E-20	8.E-21	5.E-20
GOTERM_BP_FAT	GO:0055114~oxidation reduction	99	13.0952381	4.E-22	66885, 226646, 66377, 56348, 17705, 177	692	672	13588	3.E+00	1.E-18	1.E-19	8.E-19
GOTERM_BP_FAT	GO:0016310~phosphorylation	102	13.49206349	1.E-21	18747, 100041835, 13665, 17705, 17706,	692	718	13588	3.E+00	4.E-18	4.E-19	3.E-18
GOTERM_BP_FAT	GO:0007242~intracellular signaling cascade	116	15.34391534	2.E-20	12190, 22324, 192662, 14815, 16800, 170	692	915	13588	2.E+00	4.E-17	4.E-18	3.E-17
GOTERM_BP_FAT	GO:0006793~phosphorus metabolic process	111	14.68253968	6.E-20	18747, 100041835, 13665, 17705, 17706,	692	866	13588	3.E+00	2.E-16	1.E-17	1.E-16
GOTERM_BP_FAT	GO:0006796~phosphate metabolic process	111	14.68253968	6.E-20	18747, 100041835, 13665, 17705, 17706,	692	866	13588	3.E+00	2.E-16	1.E-17	1.E-16
GOTERM_BP_FAT	GO:0016052~carbohydrate catabolic process	32	4.232804233	8.E-20	18746, 68263, 100042746, 15275, 15277,	692	81	13588	8.E+00	2.E-16	1.E-17	1.E-16
GOTERM_BP_FAT	GO:0006119~oxidative phosphorylation	27	3.571428571	2.E-19	228033, 66416, 100041835, 66043, 17705	692	56	13588	9.E+00	5.E-16	4.E-17	4.E-16
GOTERM_BP_FAT	GO:0006006~glucose metabolic process	40	5.291005291	1.E-19	18746, 11911, 68263, 100042746, 11651,	692	140	13588	6.E+00	1.E-15	1.E-16	1.E-15
GOTERM_BP_FAT	GO:0019318~hexose metabolic process	40	5.291005291	8.E-16	18746, 11911, 68263, 100042746, 11651,	692	169	13588	5.E+00	2.E-12	1.E-13	1.E-12
GOTERM_BP_FAT	GO:0035023~regulation of Rho protein signal transduction	29	3.835978836	8.E-16	22324, 13605, 442801, 16800, 53972, 218	692	86	13588	7.E+00	2.E-12	1.E-13	1.E-12
GOTERM_BP_FAT	GO:0005996~monosaccharide metabolic process	41	5.423280423	1.E-14	18746, 11911, 68263, 18641, 11676, 1864	692	191	13588	4.E+00	3.E-11	1.E-12	2.E-11
GOTERM_BP_FAT	GO:0007264~small GTPase mediated signal transduction	48	6.349206349	1.E-14	228543, 192662, 170758, 80837, 14784, 1	692	258	13588	4.E+00	3.E-11	2.E-12	2.E-11
GOTERM_BP_FAT	GO:0006413~translational initiation	18	2.380952381	9.E-13	13684, 13667, 66235, 13669, 56347, 5335	692	38	13588	9.E+00	2.E-09	1.E-10	2.E-09
GOTERM_BP_FAT	GO:0006958~complement activation, classical pathway	16	2.116402116	3.E-12	17175, 12266, 50908, 12259, 14962, 1225	692	30	13588	1.E+01	6.E-09	3.E-10	5.E-09
GOTERM_BP_FAT	GO:0042773~ATP synthesis coupled electron transport	13	1.71957672	4.E-12	66416, 17719, 675851, 17705, 17706, 177	692	18	13588	1.E+01	9.E-09	4.E-10	7.E-09
GOTERM_BP_FAT	GO:0002541~activation of plasma proteins involved in acute inflammatory response	17	2.248677249	5.E-12	17175, 12266, 17174, 50908, 12259, 1496	692	36	13588	9.E+00	1.E-08	5.E-10	8.E-09
GOTERM_BP_FAT	GO:0006956~complement activation	17	2.248677249	5.E-12	17175, 12266, 17174, 50908, 12259, 1496	692	36	13588	9.E+00	1.E-08	5.E-10	8.E-09
GOTERM_BP_FAT	GO:0022904~respiratory electron transport chain	15	1.984126984	1.E-11	66416, 17719, 675851, 17705, 17706, 177	692	28	13588	1.E+01	3.E-08	1.E-09	2.E-08
GOTERM_BP_FAT	GO:0007049~cell cycle	73	9.656084656	2.E-11	12190, 12571, 19384, 243362, 59008, 168	692	611	13588	2.E+00	4.E-08	2.E-09	3.E-08
GOTERM_BP_FAT	GO:0045333~cellular respiration	20	2.645502646	4.E-11	66416, 17448, 17719, 675851, 17705, 177	692	59	13588	7.E+00	1.E-07	4.E-09	7.E-08
GOTERM_BP_FAT	GO:0002455~humoral immune response mediated by circulating immunoglobulin	16	2.116402116	4.E-11	17175, 12266, 50908, 12259, 14962, 1225	692	35	13588	9.E+00	1.E-07	4.E-09	7.E-08
GOTERM_BP_FAT	GO:0006468~protein amino acid phosphorylation	73	9.656084656	1.E-10	18747, 12571, 19247, 13665, 100048123,	692	640	13588	2.E+00	3.E-07	1.E-08	2.E-07
GOTERM_BP_FAT	GO:0000278~mitotic cell cycle	40	5.291005291	2.E-10	19384, 12649, 16800, 59008, 23834, 6714	692	244	13588	3.E+00	4.E-07	1.E-08	3.E-07
GOTERM_BP_FAT	GO:0051301~cell division	43	5.687830688	3.E-10	12190, 12571, 19384, 16800, 59008, 2383	692	281	13588	3.E+00	7.E-07	2.E-08	5.E-07
GOTERM_BP_FAT	GO:0046578~regulation of Ras protein signal transduction	33	4.365079365	5.E-10	22324, 13605, 442801, 16800, 53972, 218	692	181	13588	4.E+00	1.E-06	4.E-08	1.E-06
GOTERM_BP_FAT	GO:0007169~transmembrane receptor protein tyrosine kinase signaling pathway	34	4.497354497	6.E-10	13649, 19247, 20411, 11651, 18791, 1364	692	192	13588	3.E+00	2.E-06	5.E-08	1.E-06
GOTERM_BP_FAT	GO:0015985~energy coupled proton transport, down electrochemical gradient	15	1.984126984	1.E-09	228033, 100041835, 67126, 66043, 17705	692	37	13588	8.E+00	3.E-06	1.E-07	2.E-06
GOTERM_BP_FAT	GO:0015986~ATP synthesis coupled proton transport	15	1.984126984	1.E-09	228033, 100041835, 67126, 66043, 17705	692	37	13588	8.E+00	3.E-06	1.E-07	2.E-06
GOTERM_BP_FAT	GO:0002526~acute inflammatory response	21	2.777777778	3.E-09	12266, 17175, 17174, 50908, 12259, 1496	692	81	13588	5.E+00	6.E-06	2.E-07	5.E-06
GOTERM_BP_FAT	GO:0015980~energy derivation by oxidation of organic compounds	23	3.042328042	3.E-09	66416, 11651, 17705, 15929, 17706, 1772	692	98	13588	5.E+00	7.E-06	2.E-07	5.E-06
GOTERM_BP_FAT	GO:0042775~mitochondrial ATP synthesis coupled electron transport	10	1.322751323	3.E-09	67530, 17719, 675851, 67264, 17705, 177	692	14	13588	1.E+01	9.E-06	2.E-07	6.E-06
GOTERM_BP_FAT	GO:0006959~humoral immune response	17	2.248677249	6.E-09	17175, 12266, 17174, 50908, 12259, 1496	692	54	13588	6.E+00	1.E-05	4.E-07	1.E-05
GOTERM_BP_FAT	GO:0002253~activation of immune response	21	2.777777778	8.E-09	15170, 12266, 17175, 19264, 17174, 5090	692	86	13588	5.E+00	2.E-05	5.E-07	1.E-05
GOTERM_BP_FAT	GO:0034220~ion transmembrane transport	15	1.984126984	1.E-08	228033, 100041835, 67126, 66043, 17705	692	42	13588	7.E+00	2.E-05	6.E-07	2.E-05
GOTERM_BP_FAT	GO:0006260~DNA replication	28	3.703703704	1.E-08	12190, 50793, 68240, 23834, 17218, 1721	692	152	13588	4.E+00	3.E-05	7.E-07	2.E-05
GOTERM_BP_FAT	GO:0051605~protein maturation by peptide bond cleavage	18	2.380952381	2.E-08	17175, 12266, 17174, 50908, 12259, 1496	692	65	13588	5.E+00	4.E-05	1.E-06	3.E-05
GOTERM_BP_FAT	GO:0002252~immune effector process	25	3.306878307	2.E-08	17175, 19264, 17174, 12259, 12258, 1227	692	126	13588	4.E+00	4.E-05	1.E-06	3.E-05
GOTERM_BP_FAT	GO:0051174~regulation of phosphorus metabolic process	41	5.423280423	2.E-08	13649, 19264, 19247, 20416, 13645, 1870	692	301	13588	3.E+00	6.E-05	1.E-06	4.E-05
GOTERM_BP_FAT	GO:0019220~regulation of phosphate metabolic process	41	5.423280423	2.E-08	13649, 19264, 19247, 20416, 13645, 1870	692	301	13588	3.E+00	6.E-05	1.E-06	4.E-05
GOTERM_BP_FAT	GO:0007265~Ras protein signal transduction	17	2.248677249	2.E-08	117600, 14674, 16653, 192662, 18176, 69	692	59	13588	6.E+00	6.E-05	1.E-06	4.E-05
GOTERM_BP_FAT	GO:0042325~regulation of phosphorylation	40	5.291005291	2.E-08	13649, 19264, 19247, 20416, 13645, 1870	692	290	13588	3.E+00	6.E-05	1.E-06	4.E-05
GOTERM_BP_FAT	GO:0015992~proton transport	16	2.116402116	3.E-08	228033, 100041835, 67126, 66043, 17705	692	52	13588	6.E+00	6.E-05	1.E-06	5.E-05
GOTERM_BP_FAT	GO:0002460~adaptive immune response based on somatic recombination of immu	20	2.645502646	3.E-08	12266, 17175, 50908, 12259, 14962, 1225	692	84	13588	5.E+00	7.E-05	2.E-06	5.E-05
GOTERM_BP_FAT	GO:0002250~adaptive immune response	20	2.645502646	3.E-08	12266, 17175, 50908, 12259, 14962, 1225	692	84	13588	5.E+00	7.E-05	2.E-06	5.E-05
GOTERM_BP_FAT	GO:0006818~hydrogen transport	16	2.116402116	3.E-08	228033, 100041835, 67126, 66043, 17705	692	53	13588	6.E+00	9.E-05	2.E-06	6.E-05
GOTERM_BP_FAT	GO:0051726~regulation of cell cycle	33	4.365079365	4.E-08	12190, 19264, 19247, 245000, 11852, 126	692	214	13588	3.E+00	9.E-05	2.E-06	7.E-05
GOTERM_BP_FAT	GO:0000087~M phase of mitotic cell cycle	31	4.100529101	5.E-08	19384, 59008, 16800, 23834, 67141, 1822	692	194	13588	3.E+00	1.E-04	2.E-06	8.E-05
GOTERM_BP_FAT	GO:0051056~regulation of small GTPase mediated signal transduction	34	4.497354497	5.E-08	22324, 13605, 442801, 16800, 53972, 218	692	228	13588	3.E+00	1.E-04	2.E-06	9.E-05
GOTERM_BP_FAT	GO:0016064~immunoglobulin mediated immune response	17	2.248677249	7.E-08	17175, 12266, 50908, 12259, 14962, 1225	692	63	13588	5.E+00	2.E-04	3.E-06	1.E-04
GOTERM_BP_FAT	GO:0002443~leukocyte mediated immunity	20	2.645502646	8.E-08	15170, 12266, 17175, 50908, 12259, 1496	692	89	13588	4.E+00	2.E-04	4.E-06	1.E-04
GOTERM_BP_FAT	GO:0022403~cell cycle phase	42	5.555555556	9.E-08	12190, 19384, 12649, 16800, 59008, 2383	692	328	13588	3.E+00	2.E-04	4.E-06	2.E-04



GOTERM_BP_FAT	GO:0007067~mitosis	30	3.968253968	1.E-07	19384	59008	16800	23834	67141	1822	692	190	13588	3.E+00	3.E-04	5.E-06	2.E-04
GOTERM_BP_FAT	GO:0000280~nuclear division	30	3.968253968	1.E-07	19384	59008	16800	23834	67141	1822	692	190	13588	3.E+00	3.E-04	5.E-06	2.E-04
GOTERM_BP_FAT	GO:0022402~cell cycle process	47	6.216931217	1.E-07	12190	19384	12649	16800	59008	2383	692	393	13588	2.E+00	3.E-04	5.E-06	2.E-04
GOTERM_BP_FAT	GO:0019724~B cell mediated immunity	17	2.248677249	1.E-07	17175	12266	50908	12259	14962	1225	692	65	13588	5.E+00	3.E-04	5.E-06	2.E-04
GOTERM_BP_FAT	GO:0007167~enzyme linked receptor protein signaling pathway	37	4.894179894	1.E-07	13649	19247	20411	11651	18791	1364	692	273	13588	3.E+00	4.E-04	6.E-06	3.E-04
GOTERM_BP_FAT	GO:0002449~lymphocyte mediated immunity	18	2.380952381	2.E-07	15170	12266	17175	50908	12259	1496	692	76	13588	5.E+00	5.E-04	8.E-06	3.E-04
GOTERM_BP_FAT	GO:0048285~organelle fission	30	3.968253968	2.E-07	19384	59008	16800	23834	67141	1822	692	197	13588	3.E+00	6.E-04	9.E-06	4.E-04
GOTERM_BP_FAT	GO:0050778~positive regulation of immune response	24	3.174603175	3.E-07	15170	12266	17175	19264	17174	5090	692	136	13588	3.E+00	8.E-04	1.E-05	6.E-04
GOTERM_BP_FAT	GO:0002684~positive regulation of immune system process	30	3.968253968	6.E-07	17175	19264	17174	12259	12258	1227	692	206	13588	3.E+00	1.E-03	2.E-05	1.E-03
GOTERM_BP_FAT	GO:0048584~positive regulation of response to stimulus	28	3.703703704	8.E-07	17175	19264	17174	12259	12258	1227	692	186	13588	3.E+00	2.E-03	3.E-05	1.E-03
GOTERM_BP_FAT	GO:0007243~protein kinase cascade	32	4.232804233	1.E-06	19264	19247	11651	20416	13645	1636	692	236	13588	3.E+00	3.E-03	4.E-05	2.E-03
GOTERM_BP_FAT	GO:0051604~protein maturation	19	2.513227513	1.E-06	12266	17175	17174	50908	12259	1496	692	96	13588	4.E+00	3.E-03	5.E-05	2.E-03
GOTERM_BP_FAT	GO:0044093~positive regulation of molecular function	37	4.894179894	2.E-06	672195	18386	19264	19247	66593	122	692	306	13588	2.E+00	6.E-03	9.E-05	4.E-03
GOTERM_BP_FAT	GO:0016485~protein processing	18	2.380952381	2.E-06	17175	12266	17174	50908	12259	1496	692	90	13588	4.E+00	6.E-03	9.E-05	4.E-03
GOTERM_BP_FAT	GO:0009611~response to wounding	40	5.291005291	3.E-06	12475	17175	17174	12259	12258	1227	692	347	13588	2.E+00	7.E-03	1.E-04	5.E-03
GOTERM_BP_FAT	GO:0006270~DNA replication initiation	7	0.925925926	3.E-06	17218	17217	17220	17216	17215	1721	692	10	13588	1.E+01	7.E-03	1.E-04	5.E-03
GOTERM_BP_FAT	GO:0006957~complement activation, alternative pathway	7	0.925925926	3.E-06	12266	14962	12279	230558	69379	151	692	10	13588	1.E+01	7.E-03	1.E-04	5.E-03
GOTERM_BP_FAT	GO:0030029~actin filament-based process	26	3.439153439	3.E-06	94190	20411	11856	16800	20416	1707	692	176	13588	3.E+00	7.E-03	1.E-04	5.E-03
GOTERM_BP_FAT	GO:0030036~actin cytoskeleton organization	25	3.306878307	3.E-06	94190	20411	11856	16800	20416	1707	692	165	13588	3.E+00	8.E-03	1.E-04	5.E-03
GOTERM_BP_FAT	GO:0043085~positive regulation of catalytic activity	33	4.365079365	3.E-06	672195	18386	19264	19247	66593	122	692	261	13588	2.E+00	9.E-03	1.E-04	6.E-03
GOTERM_BP_FAT	GO:0006954~inflammatory response	30	3.968253968	4.E-06	12475	17175	17174	12259	12258	1664	692	225	13588	3.E+00	9.E-03	1.E-04	7.E-03
GOTERM_BP_FAT	GO:0031589~cell-substrate adhesion	14	1.851851852	4.E-06	19944	665032	12125	20411	12043	118	692	57	13588	5.E+00	1.E-02	1.E-04	7.E-03
GOTERM_BP_FAT	GO:0030879~mammary gland development	17	2.248677249	6.E-06	12190	12125	14815	11855	15277	1291	692	86	13588	4.E+00	1.E-02	2.E-04	1.E-02
GOTERM_BP_FAT	GO:0032268~regulation of cellular protein metabolic process	34	4.497354497	6.E-06	13684	13649	19264	12258	13665	1165	692	280	13588	2.E+00	1.E-02	2.E-04	1.E-02
GOTERM_BP_FAT	GO:0045087~innate immune response	19	2.513227513	7.E-06	15170	12266	17175	17174	50908	1225	692	107	13588	3.E+00	2.E-02	2.E-04	1.E-02
GOTERM_BP_FAT	GO:0000279~M phase	34	4.497354497	7.E-06	12190	19384	59008	16800	23834	6714	692	283	13588	2.E+00	2.E-02	2.E-04	1.E-02
GOTERM_BP_FAT	GO:0009725~response to hormone stimulus	24	3.174603175	1.E-05	19247	20411	232087	11651	11652	100	692	165	13588	3.E+00	3.E-02	3.E-04	2.E-02
GOTERM_BP_FAT	GO:0031399~regulation of protein modification process	24	3.174603175	1.E-05	13649	19264	67141	13645	15130	1270	692	165	13588	3.E+00	3.E-02	3.E-04	2.E-02
GOTERM_BP_FAT	GO:0046034~ATP metabolic process	17	2.248677249	1.E-05	228033	100041835	67126	66043	17705		692	90	13588	4.E+00	3.E-02	3.E-04	2.E-02
GOTERM_BP_FAT	GO:0006754~ATP biosynthetic process	16	2.116402116	1.E-05	228033	100041835	67126	66043	17705		692	82	13588	4.E+00	3.E-02	4.E-04	2.E-02
GOTERM_BP_FAT	GO:0043549~regulation of kinase activity	26	3.439153439	1.E-05	19264	19247	20416	13645	228775	218	692	192	13588	3.E+00	4.E-02	4.E-04	3.E-02
GOTERM_BP_FAT	GO:0009719~response to endogenous stimulus	25	3.306878307	2.E-05	19247	20411	232087	11651	11652	100	692	184	13588	3.E+00	5.E-02	6.E-04	4.E-02
GOTERM_BP_FAT	GO:0008283~cell proliferation	30	3.968253968	2.E-05	12190	19264	665032	26965	12234	129	692	247	13588	3.E+00	6.E-02	7.E-04	4.E-02
GOTERM_BP_FAT	GO:0051270~regulation of cell motion	18	2.380952381	3.E-05	14674	73167	12043	11491	11855	2233	692	107	13588	3.E+00	6.E-02	8.E-04	5.E-02
GOTERM_BP_FAT	GO:0051338~regulation of transferase activity	26	3.439153439	3.E-05	19264	19247	20416	13645	228775	218	692	199	13588	3.E+00	6.E-02	8.E-04	5.E-02
GOTERM_BP_FAT	GO:0032870~cellular response to hormone stimulus	13	1.71957672	3.E-05	19247	20411	11651	11652	100048123		692	58	13588	4.E+00	7.E-02	8.E-04	5.E-02
GOTERM_BP_FAT	GO:0033674~positive regulation of kinase activity	20	2.645502646	3.E-05	13131	19264	19247	14678	57257	2235	692	130	13588	3.E+00	7.E-02	9.E-04	5.E-02
GOTERM_BP_FAT	GO:0006120~mitochondrial electron transport, NADH to ubiquinone	5	0.661375661	3.E-05	17719	675851	67264	17717	13382	681	692	5	13588	2.E+01	8.E-02	9.E-04	6.E-02
GOTERM_BP_FAT	GO:0007160~cell-matrix adhesion	12	1.587301587	3.E-05	12125	50768	20411	12043	11856	1641	692	50	13588	5.E+00	8.E-02	9.E-04	6.E-02
GOTERM_BP_FAT	GO:0007044~cell-substrate junction assembly	7	0.925925926	4.E-05	50768	20411	16402	12043	11856	1641	692	14	13588	1.E+01	8.E-02	1.E-03	6.E-02
GOTERM_BP_FAT	GO:0006739~NADP metabolic process	7	0.925925926	4.E-05	19895	21991	21351	17969	66171	1039	692	14	13588	1.E+01	8.E-02	1.E-03	6.E-02
GOTERM_BP_FAT	GO:0007266~Rho protein signal transduction	9	1.19047619	4.E-05	80837	117600	57874	14674	12053	192	692	27	13588	7.E+00	1.E-01	1.E-03	7.E-02
GOTERM_BP_FAT	GO:0009260~ribonucleotide biosynthetic process	18	2.380952381	4.E-05	228033	100041835	67126	66043	17705		692	111	13588	3.E+00	1.E-01	1.E-03	8.E-02
GOTERM_BP_FAT	GO:0009205~purine ribonucleoside triphosphate metabolic process	17	2.248677249	5.E-05	228033	100041835	67126	66043	17705		692	101	13588	3.E+00	1.E-01	1.E-03	8.E-02
GOTERM_BP_FAT	GO:0051347~positive regulation of transferase activity	20	2.645502646	5.E-05	13131	19264	19247	14678	57257	2235	692	135	13588	3.E+00	1.E-01	1.E-03	9.E-02
GOTERM_BP_FAT	GO:0009199~ribonucleoside triphosphate metabolic process	17	2.248677249	5.E-05	228033	100041835	67126	66043	17705		692	102	13588	3.E+00	1.E-01	1.E-03	9.E-02
GOTERM_BP_FAT	GO:0009259~ribonucleotide metabolic process	19	2.513227513	6.E-05	228033	100041835	67126	66043	17705		692	125	13588	3.E+00	1.E-01	2.E-03	1.E-01
GOTERM_BP_FAT	GO:0009201~ribonucleoside triphosphate biosynthetic process	16	2.116402116	7.E-05	228033	100041835	67126	66043	17705		692	93	13588	3.E+00	1.E-01	2.E-03	1.E-01
GOTERM_BP_FAT	GO:0009206~purine ribonucleoside triphosphate biosynthetic process	16	2.116402116	7.E-05	228033	100041835	67126	66043	17705		692	93	13588	3.E+00	1.E-01	2.E-03	1.E-01
GOTERM_BP_FAT	GO:0009145~purine nucleoside triphosphate biosynthetic process	16	2.116402116	7.E-05	228033	100041835	67126	66043	17705		692	94	13588	3.E+00	2.E-01	2.E-03	1.E-01
GOTERM_BP_FAT	GO:0009142~nucleoside triphosphate biosynthetic process	16	2.116402116	8.E-05	228033	100041835	67126	66043	17705		692	95	13588	3.E+00	2.E-01	2.E-03	1.E-01
GOTERM_BP_FAT	GO:0043434~response to peptide hormone stimulus	16	2.116402116	8.E-05	12638	20411	12043	11651	11652	1000	692	95	13588	3.E+00	2.E-01	2.E-03	1.E-01
GOTERM_BP_FAT	GO:0009144~purine nucleoside triphosphate metabolic process	17	2.248677249	9.E-05	228033	100041835	67126	66043	17705		692	106	13588	3.E+00	2.E-01	2.E-03	2.E-01
GOTERM_BP_FAT	GO:0009152~purine ribonucleotide biosynthetic process	17	2.248677249	1.E-04	228033	100041835	67126	66043	17705		692	107	13588	3.E+00	2.E-01	2.E-03	2.E-01
GOTERM_BP_FAT	GO:0008360~regulation of cell shape	11	1.455026455	1.E-04	80837	14163	14674	104215	76117	146	692	47	13588	5.E+00	2.E-01	2.E-03	2.E-01
GOTERM_BP_FAT	GO:0009150~purine ribonucleotide metabolic process	18	2.380952381	1.E-04	228033	100041835	67126	66043	17705		692	119	13588	3.E+00	2.E-01	3.E-03	2.E-01
GOTERM_BP_FAT	GO:0001932~regulation of protein amino acid phosphorylation	18	2.380952381	1.E-04	15170	13649	19264	12043	13645	1216	692	121	13588	3.E+00	3.E-01	3.E-03	2.E-01
GOTERM_BP_FAT	GO:0048732~gland development	24	3.174603175	2.E-04	12190	13649	12125	16392	14815	1292	692	197	13588	2.E+00	3.E-01	4.E-03	3.E-01
GOTERM_BP_FAT	GO:0010033~response to organic substance	46	6.084656085	2.E-04	12475	19247	11816	20411	232087	116	692	505	13588	2.E+00	4.E-01	4.E-03	3.E-01
GOTERM_BP_FAT	GO:0008202~steroid metabolic process	21	2.777777778	2.E-04	12638	11816	66234	56348	14815	2235	692	161	13588	3.E+00	4.E-01	4.E-03	3.E-01
GOTERM_BP_FAT	GO:0045859~regulation of protein kinase activity	23	3.042328042	2.E-04	15170	13131	19264	19247	14678	2235	692	186	13588	2.E+00	4.E-01	4.E-03	3.E-01
GOTERM_BP_FAT	GO:0006259~DNA metabolic process	40	5.291005291	2.E-04	12190	245000	12649	68240	50793	238	692	421	13588	2.E+00	4.E-01	5.E-03	4.E-01
GOTERM_BP_FAT	GO:0030334~regulation of cell migration	15	1.984126984	2.E-04	14674	73167	12043	11855	22330	3847	692	92	13588	3.E+00	4.E-01	5.E-03	4.E-01
GOTERM_BP_FAT	GO:0006694~steroid biosynthetic process	13	1.71957672	2.E-04	12638	66234	56348	18194	16987	1549	692	71	13588	4.E+00	4.E-01	5.E-03	4



GOTERM_BP_FAT	GO:0006261~DNA-dependent DNA replication	9	1.19047619	2.E-04 17218 12190 17217, 17220, 17216, 1721	692	34	13588	5.E+00	4.E-01	5.E-03	4.E-01
GOTERM_BP_FAT	GO:0006952~defense response	41	5.423280423	4.E-04 12475, 19264 17175, 17174, 12259, 1225	692	448	13588	2.E+00	6.E-01	8.E-03	7.E-01
GOTERM_BP_FAT	GO:0040012~regulation of locomotion	16	2.116402116	4.E-04 14674, 73167, 12043, 11855, 22330, 3847	692	110	13588	3.E+00	7.E-01	9.E-03	8.E-01
GOTERM_BP_FAT	GO:0034329~cell junction assembly	7	0.925925926	5.E-04 50768, 20411, 16402, 12043, 11856, 1641	692	21	13588	7.E+00	7.E-01	1.E-02	8.E-01
GOTERM_BP_FAT	GO:0006800~oxygen and reactive oxygen species metabolic process	10	1.322751323	5.E-04 18126, 672195, 68349, 50493, 12043, 227	692	47	13588	4.E+00	7.E-01	1.E-02	9.E-01
GOTERM_BP_FAT	GO:0045860~positive regulation of protein kinase activity	17	2.248677249	5.E-04 13131, 19264 19247, 14678, 22359, 2041	692	124	13588	3.E+00	7.E-01	1.E-02	9.E-01
GOTERM_BP_FAT	GO:0000165~MAPKKK cascade	16	2.116402116	6.E-04 19264, 19247, 14678, 20416, 13645, 2240	692	114	13588	3.E+00	8.E-01	1.E-02	1.E+00
GOTERM_BP_FAT	GO:0043603~cellular amide metabolic process	9	1.19047619	6.E-04 19895, 21991, 21351, 17969, 66171, 1460	692	39	13588	5.E+00	8.E-01	1.E-02	1.E+00
GOTERM_BP_FAT	GO:0043523~regulation of neuron apoptosis	13	1.71957672	7.E-04 16653, 14815, 12043, 18227, 18176, 5880	692	80	13588	3.E+00	8.E-01	1.E-02	1.E+00
GOTERM_BP_FAT	GO:0042981~regulation of apoptosis	47	6.216931217	7.E-04 22029, 12190, 672195, 19264, 66593, 671	692	553	13588	2.E+00	8.E-01	1.E-02	1.E+00
GOTERM_BP_FAT	GO:0043524~negative regulation of neuron apoptosis	10	1.322751323	8.E-04 18049, 18211, 12048, 13867, 16653, 1546	692	50	13588	4.E+00	9.E-01	2.E-02	1.E+00
GOTERM_BP_FAT	GO:0043067~regulation of programmed cell death	47	6.216931217	9.E-04 22029, 12190, 672195, 19264, 66593, 671	692	560	13588	2.E+00	9.E-01	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0051272~positive regulation of cell motion	9	1.19047619	9.E-04 18708, 16367, 12053, 73167, 12043, 1149	692	41	13588	4.E+00	9.E-01	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0034330~cell junction organization	8	1.058201058	9.E-04 50768, 20411, 16402, 12043, 11856, 1254	692	32	13588	5.E+00	9.E-01	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0010941~regulation of cell death	47	6.216931217	1.E-03 22029, 12190, 672195, 19264, 66593, 671	692	563	13588	2.E+00	9.E-01	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0009820~alkaloid metabolic process	7	0.925925926	1.E-03 19895, 21991, 21351, 17969, 66171, 1039	692	24	13588	6.E+00	9.E-01	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0006769~nicotinamide metabolic process	7	0.925925926	1.E-03 19895, 21991, 21351, 17969, 66171, 1039	692	24	13588	6.E+00	9.E-01	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0046496~nicotinamide nucleotide metabolic process	7	0.925925926	1.E-03 19895, 21991, 21351, 17969, 66171, 1039	692	24	13588	6.E+00	9.E-01	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0042592~homeostatic process	48	6.349206349	1.E-03 13667, 19264 19247, 11816, 11651, 2380	692	584	13588	2.E+00	9.E-01	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0060396~growth hormone receptor signaling pathway	4	0.529100529	1.E-03 20848, 14600, 20850, 16452	692	5	13588	2.E+01	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0060416~response to growth hormone stimulus	4	0.529100529	1.E-03 20848, 14600, 20850, 16452	692	5	13588	2.E+01	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0022604~regulation of cell morphogenesis	14	1.851851852	1.E-03 14163, 14674, 14083, 76117, 21844, 1020	692	97	13588	3.E+00	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0006164~purine nucleotide biosynthetic process	17	2.248677249	2.E-03 228033, 100041835, 67126, 66043, 17705	692	137	13588	2.E+00	1.E+00	3.E-02	3.E+00
GOTERM_BP_FAT	GO:0008156~negative regulation of DNA replication	5	0.661375661	2.E-03 12190, 57441, 22130, 67177, 269582	692	11	13588	9.E+00	1.E+00	3.E-02	3.E+00
GOTERM_BP_FAT	GO:0006275~regulation of DNA replication	6	0.793650794	2.E-03 12190, 57441, 22130, 67177, 18538, 2695	692	18	13588	7.E+00	1.E+00	3.E-02	3.E+00
GOTERM_BP_FAT	GO:0043029~T cell homeostasis	6	0.793650794	2.E-03 12442, 12125, 11651, 12043, 19056, 2085	692	18	13588	7.E+00	1.E+00	3.E-02	3.E+00
GOTERM_BP_FAT	GO:0006122~mitochondrial electron transport, ubiquinol to cytochrome c	4	0.529100529	2.E-03 67530, 66594, 66576, 22273	692	6	13588	1.E+01	1.E+00	4.E-02	4.E+00
GOTERM_BP_FAT	GO:0051336~regulation of hydrolase activity	21	2.777777778	2.E-03 672195, 22324, 66593, 12279, 19218, 228	692	196	13588	2.E+00	1.E+00	4.E-02	4.E+00
GOTERM_BP_FAT	GO:0019362~pyridine nucleotide metabolic process	7	0.925925926	2.E-03 19895, 21991, 21351, 17969, 66171, 1039	692	28	13588	5.E+00	1.E+00	4.E-02	4.E+00
GOTERM_BP_FAT	GO:0043087~regulation of GTPase activity	13	1.71957672	3.E-03 22324, 228359, 57257, 11856, 14567, 145	692	93	13588	3.E+00	1.E+00	5.E-02	4.E+00
GOTERM_BP_FAT	GO:0031400~negative regulation of protein modification process	8	1.058201058	3.E-03 15170, 18753, 19264, 18750, 16476, 1256	692	38	13588	4.E+00	1.E+00	5.E-02	5.E+00
GOTERM_BP_FAT	GO:0051053~negative regulation of DNA metabolic process	6	0.793650794	3.E-03 12190, 57441, 22130, 67177, 12053, 2695	692	20	13588	6.E+00	1.E+00	5.E-02	5.E+00
GOTERM_BP_FAT	GO:0010563~negative regulation of phosphorus metabolic process	7	0.925925926	3.E-03 15170, 18753, 19264, 18750, 12577, 1647	692	29	13588	5.E+00	1.E+00	5.E-02	5.E+00
GOTERM_BP_FAT	GO:0045936~negative regulation of phosphate metabolic process	7	0.925925926	3.E-03 15170, 18753, 19264, 18750, 12577, 1647	692	29	13588	5.E+00	1.E+00	5.E-02	5.E+00
GOTERM_BP_FAT	GO:0006163~purine nucleotide metabolic process	18	2.380952381	3.E-03 228033, 100041835, 67126, 66043, 17705	692	160	13588	2.E+00	1.E+00	5.E-02	6.E+00
GOTERM_BP_FAT	GO:0009165~nucleotide biosynthetic process	19	2.513227513	3.E-03 228033, 100041835, 67126, 66043, 17705	692	174	13588	2.E+00	1.E+00	6.E-02	6.E+00
GOTERM_BP_FAT	GO:0034504~protein localization in nucleus	10	1.322751323	3.E-03 664868, 56338, 16646, 19384, 231103, 10	692	61	13588	3.E+00	1.E+00	6.E-02	6.E+00
GOTERM_BP_FAT	GO:0050796~regulation of insulin secretion	6	0.793650794	4.E-03 19015, 14661, 19247, 18641, 18642, 1039	692	22	13588	5.E+00	1.E+00	7.E-02	7.E+00
GOTERM_BP_FAT	GO:0046887~positive regulation of hormone secretion	5	0.661375661	4.E-03 14661, 19247, 18642, 12912, 103988	692	14	13588	7.E+00	1.E+00	7.E-02	7.E+00
GOTERM_BP_FAT	GO:0010906~regulation of glucose metabolic process	5	0.661375661	4.E-03 14447, 20411, 14815, 103988, 208727	692	14	13588	7.E+00	1.E+00	7.E-02	7.E+00
GOTERM_BP_FAT	GO:0034404~nucleobase, nucleoside and nucleotide biosynthetic process	19	2.513227513	4.E-03 228033, 100041835, 67126, 66043, 17705	692	179	13588	2.E+00	1.E+00	7.E-02	8.E+00
GOTERM_BP_FAT	GO:0034654~nucleobase, nucleoside, nucleotide and nucleic acid biosynthetic proc	19	2.513227513	4.E-03 228033, 100041835, 67126, 66043, 17705	692	179	13588	2.E+00	1.E+00	7.E-02	8.E+00
GOTERM_BP_FAT	GO:0048534~hemopoietic or lymphoid organ development	26	3.439153439	5.E-03 12190, 22324, 19264, 12571, 19934, 1870	692	281	13588	2.E+00	1.E+00	8.E-02	8.E+00
GOTERM_BP_FAT	GO:0007010~cytoskeleton organization	29	3.835978836	5.E-03 94190, 20411, 11856, 16800, 20416, 6714	692	326	13588	2.E+00	1.E+00	8.E-02	8.E+00
GOTERM_BP_FAT	GO:0032774~RNA biosynthetic process	15	1.984126984	5.E-03 69890, 22130, 16911, 74197, 68153, 1062	692	126	13588	2.E+00	1.E+00	8.E-02	8.E+00
GOTERM_BP_FAT	GO:0007229~integrin-mediated signaling pathway	11	1.455026455	5.E-03 22324, 11487, 14083, 16402, 14389, 5725	692	76	13588	3.E+00	1.E+00	8.E-02	8.E+00
GOTERM_BP_FAT	GO:0050730~regulation of peptidyl-tyrosine phosphorylation	9	1.19047619	5.E-03 15170, 13649, 18753, 19264, 18754, 1875	692	53	13588	3.E+00	1.E+00	8.E-02	8.E+00
GOTERM_BP_FAT	GO:0031960~response to corticosteroid stimulus	6	0.793650794	5.E-03 20779, 11409, 26395, 12043, 230163, 942	692	23	13588	5.E+00	1.E+00	8.E-02	9.E+00
GOTERM_BP_FAT	GO:0032869~cellular response to insulin stimulus	8	1.058201058	6.E-03 18709, 18708, 16367, 20411, 104215, 116	692	43	13588	4.E+00	1.E+00	9.E-02	9.E+00
GOTERM_BP_FAT	GO:0010675~regulation of cellular carbohydrate metabolic process	5	0.661375661	6.E-03 14447, 20411, 14815, 103988, 208727	692	15	13588	7.E+00	1.E+00	9.E-02	1.E+01
GOTERM_BP_FAT	GO:0006109~regulation of carbohydrate metabolic process	5	0.661375661	6.E-03 14447, 20411, 14815, 103988, 208727	692	15	13588	7.E+00	1.E+00	9.E-02	1.E+01
GOTERM_BP_FAT	GO:0031570~DNA integrity checkpoint	7	0.925925926	6.E-03 19247, 245000, 67177, 12649, 12443, 269	692	33	13588	4.E+00	1.E+00	9.E-02	1.E+01
GOTERM_BP_FAT	GO:0051248~negative regulation of protein metabolic process	11	1.455026455	6.E-03 15170, 18753, 19264, 12258, 18750, 1647	692	78	13588	3.E+00	1.E+00	9.E-02	1.E+01
GOTERM_BP_FAT	GO:0043550~regulation of lipid kinase activity	4	0.529100529	6.E-03 19645, 16367, 57257, 12540	692	8	13588	1.E+01	1.E+00	9.E-02	1.E+01
GOTERM_BP_FAT	GO:0006098~pentose-phosphate shunt	4	0.529100529	6.E-03 19895, 21991, 21351, 66171	692	8	13588	1.E+01	1.E+00	9.E-02	1.E+01
GOTERM_BP_FAT	GO:0048041~focal adhesion formation	4	0.529100529	6.E-03 50768, 20411, 12043, 11856	692	8	13588	1.E+01	1.E+00	9.E-02	1.E+01
GOTERM_BP_FAT	GO:0042127~regulation of cell proliferation	42	5.555555556	6.E-03 13649, 19264, 11855, 58801, 13645, 1812	692	538	13588	2.E+00	1.E+00	9.E-02	1.E+01
GOTERM_BP_FAT	GO:0040017~positive regulation of locomotion	8	1.058201058	6.E-03 18708, 16367, 73167, 18750, 12043, 1185	692	44	13588	4.E+00	1.E+00	9.E-02	1.E+01
GOTERM_BP_FAT	GO:0006606~protein import into nucleus	9	1.19047619	7.E-03 664868, 56338, 16646, 19384, 231103, 10	692	56	13588	3.E+00	1.E+00	1.E-01	1.E+01
GOTERM_BP_FAT	GO:0019221~cytokine-mediated signaling pathway	9	1.19047619	7.E-03 20848, 15170, 16195, 20846, 12015, 1298	692	56	13588	3.E+00	1.E+00	1.E-01	1.E+01
GOTERM_BP_FAT	GO:0006635~fatty acid beta-oxidation	5	0.661375661	7.E-03 19015, 74147, 13177, 11364, 231086	692	16	13588	6.E+00	1.E+00	1.E-01	1.E+01
GOTERM_BP_FAT	GO:0006090~pyruvate metabolic process	6	0.793650794	8.E-03 11911, 14751, 235339, 21991, 230163, 14	692	25	13588	5.E+00	1.E+00	1.E-01	1.E+01
GOTERM_BP_FAT	GO:0019748~secondary metabolic process	10	1.322751323	8.E-03 19895, 12043, 21991, 21351, 56847, 1796	692	69	13588	3.E+00	1.E+00	1.E-01	1.E+01
GOTERM_BP_FAT	GO:0002520~immune system development	26	3.439153439	9.E-03 12190, 22324, 19264, 12571, 19934, 1870	692	295	13588	2.E+00	1.E+00	1.E-01	1.E+01
GOTERM_BP_FAT	GO:0051170~nuclear import	9	1.19047619	9.E-03 664868, 56338, 16646, 19384, 231103, 10	692	58	13588	3.E+00	1.E+00	1.E-01	1.E+01



GOTERM_BP_FAT	GO:0019216~regulation of lipid metabolic process	9	1.19047619	9.E-03 19645	16367	11816	20411	57257	2380	692	58	13588	3.E+00	1.E+00	1.E-01	1.E+01
GOTERM_BP_FAT	GO:0048011~nerve growth factor receptor signaling pathway	4	0.529100529	9.E-03 20779	19247	20662	110157			692	9	13588	9.E+00	1.E+00	1.E-01	1.E+01
GOTERM_BP_FAT	GO:0048009~insulin-like growth factor receptor signaling pathway	4	0.529100529	9.E-03 18708	16367	11651	16000			692	9	13588	9.E+00	1.E+00	1.E-01	1.E+01
GOTERM_BP_FAT	GO:0043068~positive regulation of programmed cell death	23	3.042328042	9.E-03 12190	15170	672195	19264	66593	671	692	250	13588	2.E+00	1.E+00	1.E-01	1.E+01
GOTERM_BP_FAT	GO:0046883~regulation of hormone secretion	7	0.925925926	9.E-03 19015	14661	19247	18641	18642	1291	692	36	13588	4.E+00	1.E+00	1.E-01	1.E+01
GOTERM_BP_FAT	GO:0002791~regulation of peptide secretion	6	0.793650794	9.E-03 19015	14661	19247	18641	18642	1039	692	26	13588	5.E+00	1.E+00	1.E-01	1.E+01
GOTERM_BP_FAT	GO:0006351~transcription, DNA-dependent	14	1.851851852	9.E-03 69890	22130	16911	74197	68153	1062	692	122	13588	2.E+00	1.E+00	1.E-01	1.E+01
GOTERM_BP_FAT	GO:0030097~hemopoiesis	23	3.042328042	9.E-03 12190	22324	19264	12571	19934	1870	692	251	13588	2.E+00	1.E+00	1.E-01	1.E+01
GOTERM_BP_FAT	GO:0048599~oocyte development	5	0.661375661	9.E-03 12190	12043	12531	20112	67141		692	17	13588	6.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0007346~regulation of mitotic cell cycle	12	1.587301587	9.E-03 12190	67177	52563	12443	12043	1254	692	96	13588	2.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0001701~in utero embryonic development	24	3.174603175	1.E-02 12190	13649	238055	11651	15139	218	692	267	13588	2.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0010942~positive regulation of cell death	23	3.042328042	1.E-02 12190	15170	672195	19264	66593	671	692	252	13588	2.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0006955~immune response	37	4.894179894	1.E-02 12475	22324	19264	17175	17174	1225	692	471	13588	2.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0043405~regulation of MAP kinase activity	11	1.455026455	1.E-02 15170	19264	228775	19247	26408	263	692	84	13588	3.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0018212~peptidyl-tyrosine modification	7	0.925925926	1.E-02 12229	20779	14158	16451	13645	2085	692	37	13588	4.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0030335~positive regulation of cell migration	7	0.925925926	1.E-02 18708	16367	73167	12043	11855	2033	692	37	13588	4.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0018108~peptidyl-tyrosine phosphorylation	7	0.925925926	1.E-02 12229	20779	14158	16451	13645	2085	692	37	13588	4.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0048870~cell motility	25	3.306878307	1.E-02 117600	13649	16392	238055	18791	18	692	284	13588	2.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0051674~localization of cell	25	3.306878307	1.E-02 117600	13649	16392	238055	18791	18	692	284	13588	2.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0008284~positive regulation of cell proliferation	25	3.306878307	1.E-02 13649	19264	11855	13645	21813	1636	692	284	13588	2.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0032269~negative regulation of cellular protein metabolic process	10	1.322751323	1.E-02 15170	18753	19264	12258	18750	1647	692	72	13588	3.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0048545~response to steroid hormone stimulus	9	1.19047619	1.E-02 21813	20779	11409	12638	26395	1204	692	60	13588	3.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0042326~negative regulation of phosphorylation	6	0.793650794	1.E-02 15170	18753	19264	18750	12577	1647	692	27	13588	4.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0051329~interphase of mitotic cell cycle	8	1.058201058	1.E-02 19645	12649	12443	12043	16412	1905	692	49	13588	3.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0009994~oocyte differentiation	5	0.661375661	1.E-02 12190	12043	12531	20112	67141		692	18	13588	5.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0006733~oxidoreduction coenzyme metabolic process	7	0.925925926	1.E-02 19895	21991	21351	17969	66171	1039	692	38	13588	4.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0001556~oocyte maturation	4	0.529100529	1.E-02 12190	12531	20112	67141			692	10	13588	8.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0035020~regulation of Rac protein signal transduction	4	0.529100529	1.E-02 16653	18176	19417	106952			692	10	13588	8.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0046626~regulation of insulin receptor signaling pathway	4	0.529100529	1.E-02 18753	20779	12702	18750			692	10	13588	8.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0000082~G1/S transition of mitotic cell cycle	6	0.793650794	1.E-02 19645	12443	12043	16412	19055	6958	692	28	13588	4.E+00	1.E+00	2.E-01	2.E+01
GOTERM_BP_FAT	GO:0008286~insulin receptor signaling pathway	6	0.793650794	1.E-02 18709	18708	16367	20411	11651	3847	692	28	13588	4.E+00	1.E+00	2.E-01	2.E+01
GOTERM_BP_FAT	GO:0006979~response to oxidative stress	11	1.455026455	1.E-02 226646	19053	56338	11816	26395	264	692	87	13588	2.E+00	1.E+00	2.E-01	2.E+01
GOTERM_BP_FAT	GO:0000187~activation of MAPK activity	8	1.058201058	1.E-02 19264	19247	26408	26395	20416	2640	692	50	13588	3.E+00	1.E+00	2.E-01	2.E+01
GOTERM_BP_FAT	GO:0001568~blood vessel development	22	2.91005291	1.E-02 19317	14674	11852	11816	14083	1165	692	244	13588	2.E+00	1.E+00	2.E-01	2.E+01
GOTERM_BP_FAT	GO:0043086~negative regulation of catalytic activity	12	1.587301587	1.E-02 18386	15170	19645	19264	228775	146	692	101	13588	2.E+00	1.E+00	2.E-01	2.E+01
GOTERM_BP_FAT	GO:0051384~response to glucocorticoid stimulus	5	0.661375661	1.E-02 11409	26395	12043	230163	94284	394	692	19	13588	5.E+00	1.E+00	2.E-01	2.E+01
GOTERM_BP_FAT	GO:0033673~negative regulation of kinase activity	8	1.058201058	1.E-02 15170	19645	19264	228775	18750	125	692	51	13588	3.E+00	1.E+00	2.E-01	2.E+01
GOTERM_BP_FAT	GO:0006469~negative regulation of protein kinase activity	8	1.058201058	1.E-02 15170	19645	19264	228775	18750	125	692	51	13588	3.E+00	1.E+00	2.E-01	2.E+01
GOTERM_BP_FAT	GO:0051325~interphase	8	1.058201058	1.E-02 19645	12649	12443	12043	16412	1905	692	51	13588	3.E+00	1.E+00	2.E-01	2.E+01
GOTERM_BP_FAT	GO:0006732~coenzyme metabolic process	15	1.984126984	1.E-02 17448	19895	15929	67834	14782	6617	692	143	13588	2.E+00	1.E+00	2.E-01	2.E+01
GOTERM_BP_FAT	GO:0060397~JAK-STAT cascade involved in growth hormone signaling pathway	3	0.396825397	1.E-02 20848	20850	16452				692	4	13588	1.E+01	1.E+00	2.E-01	2.E+01
GOTERM_BP_FAT	GO:0048608~reproductive structure development	14	1.851851852	2.E-02 12190	13667	12125	12043	11622	2077	692	130	13588	2.E+00	1.E+00	2.E-01	2.E+01
GOTERM_BP_FAT	GO:0043065~positive regulation of apoptosis	22	2.91005291	2.E-02 12190	15170	672195	19264	66593	671	692	248	13588	2.E+00	1.E+00	2.E-01	2.E+01
GOTERM_BP_FAT	GO:0000075~cell cycle checkpoint	8	1.058201058	2.E-02 19247	245000	67177	12649	12443	681	692	52	13588	3.E+00	1.E+00	2.E-01	2.E+01
GOTERM_BP_FAT	GO:0032880~regulation of protein localization	11	1.455026455	2.E-02 18747	19247	14570	20411	104215	192	692	90	13588	2.E+00	1.E+00	2.E-01	2.E+01
GOTERM_BP_FAT	GO:0016125~sterol metabolic process	10	1.322751323	2.E-02 15490	12638	11816	66234	14137	2235	692	77	13588	3.E+00	1.E+00	2.E-01	2.E+01
GOTERM_BP_FAT	GO:0006268~DNA unwinding during replication	4	0.529100529	2.E-02 17217	17220	17216	17219			692	11	13588	7.E+00	1.E+00	2.E-01	2.E+01
GOTERM_BP_FAT	GO:0002260~lymphocyte homeostasis	6	0.793650794	2.E-02 12442	12125	11651	12043	19056	2085	692	30	13588	4.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0001944~vasculature development	22	2.91005291	2.E-02 19317	14674	11852	11816	14083	1165	692	250	13588	2.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0002698~negative regulation of immune effector process	5	0.661375661	2.E-02 15170	19264	12258	12053	19056		692	20	13588	5.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0006094~gluconeogenesis	5	0.661375661	2.E-02 11911	14751	21991	230163	14120		692	20	13588	5.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0042743~hydrogen peroxide metabolic process	5	0.661375661	2.E-02 672195	50493	13063	17969	13077	130	692	20	13588	5.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0051050~positive regulation of transport	14	1.851851852	2.E-02 18747	12266	19247	20411	68092	1642	692	132	13588	2.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0051348~negative regulation of transferase activity	8	1.058201058	2.E-02 15170	19645	19264	228775	18750	125	692	53	13588	3.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0006605~protein targeting	14	1.851851852	2.E-02 16646	56338	19384	54401	108989	162	692	133	13588	2.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0009991~response to extracellular stimulus	14	1.851851852	2.E-02 12190	14962	11651	12043	100040331		692	133	13588	2.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0006084~acetyl-CoA metabolic process	6	0.793650794	2.E-02 17448	235339	78920	67834	15929	687	692	31	13588	4.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0046364~monosaccharide biosynthetic process	6	0.793650794	2.E-02 11911	14751	21991	230163	14381	141	692	31	13588	4.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0048878~chemical homeostasis	29	3.835978836	2.E-02 13667	19264	19247	11816	238055	186	692	365	13588	2.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0043066~negative regulation of apoptosis	21	2.777777778	2.E-02 16653	13628	11651	12043	18176	1822	692	239	13588	2.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0032508~DNA duplex unwinding	4	0.529100529	2.E-02 17217	17220	17216	17219			692	12	13588	7.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0016477~cell migration	21	2.777777778	2.E-02 117600	13649	13131	14083	16392	143	692	240	13588	2.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0045786~negative regulation of cell cycle	7	0.925925926	2.E-02 57441	19645	11852	12043	12568	1257	692	43	13588	3.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0050864~regulation of B cell activation	8	1.058201058	2.E-02 15170	19264	12015	208154	12053	106	692	55	13588	3.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0030155~regulation of cell adhesion	11	1.455026455	2.E-02 18708	22324	13131	20779	11487	1205	692	94	13588	2.E+00	1.E+00	2.E-01	3.E+01



GOTERM_BP_FAT	GO:0006928~cell motion	29	3.835978836	2.E-02 117600, 13649, 16392, 238055, 18227, 18	692	367	13588	2.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0051345~positive regulation of hydrolase activity	10	1.322751323	2.E-02 672195, 71709, 66593, 12279, 19218, 118	692	81	13588	2.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0007015~actin filament organization	8	1.058201058	2.E-02 13800, 20411, 12043, 11856, 16800, 2237	692	56	13588	3.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0017038~protein import	10	1.322751323	2.E-02 11632, 664868, 56338, 16646, 19384, 231	692	82	13588	2.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0016265~death	38	5.026455026	2.E-02 22029, 12765, 672195, 66593, 67184, 118	692	519	13588	1.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0006913~nucleocytoplasmic transport	11	1.455026455	2.E-02 664868, 56338, 16646, 19384, 11487, 231	692	96	13588	2.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0043069~negative regulation of programmed cell death	21	2.777777778	2.E-02 16653, 13628, 11651, 12043, 18176, 1822	692	244	13588	2.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0060548~negative regulation of cell death	21	2.777777778	3.E-02 16653, 13628, 11651, 12043, 18176, 1822	692	245	13588	2.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0008203~cholesterol metabolic process	9	1.19047619	3.E-02 15490, 12638, 11816, 14137, 22359, 6596	692	70	13588	3.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0033365~protein localization in organelle	11	1.455026455	3.E-02 11632, 664868, 56338, 16646, 19384, 231	692	97	13588	2.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0006631~fatty acid metabolic process	17	2.248677249	3.E-02 70316, 66885, 19317, 15107, 66234, 2222	692	184	13588	2.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0006805~xenobiotic metabolic process	4	0.529100529	3.E-02 11632, 11622, 13077, 94284, 394436	692	13	13588	6.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0043547~positive regulation of GTPase activity	4	0.529100529	3.E-02 71709, 11856, 19765, 19417	692	13	13588	6.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0032392~DNA geometric change	4	0.529100529	3.E-02 17217, 17220, 17216, 17219	692	13	13588	6.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0002820~negative regulation of adaptive immune response	4	0.529100529	3.E-02 15170, 19264, 12053, 19056	692	13	13588	6.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0002823~negative regulation of adaptive immune response based on somatic r	4	0.529100529	3.E-02 15170, 19264, 12053, 19056	692	13	13588	6.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0043467~regulation of generation of precursor metabolites and energy	4	0.529100529	3.E-02 14447, 20411, 103988, 208727	692	13	13588	6.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0008219~cell death	37	4.894179894	3.E-02 22029, 12765, 672195, 66593, 67184, 118	692	507	13588	1.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0022612~gland morphogenesis	10	1.322751323	3.E-02 13649, 21813, 20779, 12043, 14815, 2085	692	84	13588	2.E+00	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0051052~regulation of DNA metabolic process	8	1.058201058	3.E-02 12190, 57441, 19264, 22130, 67177, 1205	692	58	13588	3.E+00	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0051169~nuclear transport	11	1.455026455	3.E-02 664868, 56338, 16646, 19384, 11487, 231	692	98	13588	2.E+00	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0042060~wound healing	12	1.587301587	3.E-02 19015, 14060, 14674, 21813, 12258, 9957	692	112	13588	2.E+00	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0019835~cytolysis	5	0.661375661	3.E-02 12279, 230558, 69379, 15139, 110382	692	23	13588	4.E+00	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0001933~negative regulation of protein amino acid phosphorylation	5	0.661375661	3.E-02 15170, 18753, 19264, 18750, 16476	692	23	13588	4.E+00	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0050830~defense response to Gram-positive bacterium	5	0.661375661	3.E-02 14191, 13035, 17969, 15162, 16803	692	23	13588	4.E+00	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0009062~fatty acid catabolic process	5	0.661375661	3.E-02 19015, 74147, 13177, 11364, 231086	692	23	13588	4.E+00	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0007599~hemostasis	9	1.19047619	3.E-02 14060, 14674, 12258, 99571, 16644, 1227	692	71	13588	2.E+00	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0019725~cellular homeostasis	27	3.571428571	3.E-02 13667, 19264, 11816, 14782, 103988, 214	692	343	13588	2.E+00	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0048872~homeostasis of number of cells	12	1.587301587	3.E-02 19645, 12442, 12125, 20085, 12053, 1165	692	113	13588	2.E+00	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0002521~leukocyte differentiation	14	1.851851852	3.E-02 22324, 19264, 19934, 12043, 11491, 7473	692	142	13588	2.E+00	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0043406~positive regulation of MAP kinase activity	8	1.058201058	3.E-02 19264, 19247, 26408, 26395, 20416, 2640	692	59	13588	3.E+00	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0032868~response to insulin stimulus	8	1.058201058	3.E-02 18709, 18708, 16367, 20411, 104215, 116	692	59	13588	3.E+00	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0030098~lymphocyte differentiation	12	1.587301587	3.E-02 22324, 19264, 19934, 12043, 11491, 7473	692	114	13588	2.E+00	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0032270~positive regulation of cellular protein metabolic process	11	1.455026455	3.E-02 18750, 12567, 11651, 12043, 216080, 146	692	100	13588	2.E+00	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0045834~positive regulation of lipid metabolic process	5	0.661375661	3.E-02 16367, 11816, 20411, 57257, 12540	692	24	13588	4.E+00	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0050729~positive regulation of inflammatory response	5	0.661375661	3.E-02 12266, 18750, 16423, 16803, 20850	692	24	13588	4.E+00	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0019395~fatty acid oxidation	5	0.661375661	3.E-02 19015, 74147, 13177, 11364, 231086	692	24	13588	4.E+00	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0034440~lipid oxidation	5	0.661375661	3.E-02 19015, 74147, 13177, 11364, 231086	692	24	13588	4.E+00	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0032319~regulation of Rho GTPase activity	4	0.529100529	3.E-02 71709, 12053, 19765, 19417	692	14	13588	6.E+00	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0006366~transcription from RNA polymerase II promoter	9	1.19047619	3.E-02 20848, 11622, 20020, 16911, 74197, 6815	692	74	13588	2.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0042159~lipoprotein catabolic process	3	0.396825397	3.E-02 11816, 238055, 16835	692	6	13588	1.E+01	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0043552~positive regulation of phosphoinositide 3-kinase activity	3	0.396825397	3.E-02 16367, 57257, 12540	692	6	13588	1.E+01	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0043551~regulation of phosphoinositide 3-kinase activity	3	0.396825397	3.E-02 16367, 57257, 12540	692	6	13588	1.E+01	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0000302~response to reactive oxygen species	6	0.793650794	3.E-02 19053, 26462, 22229, 50493, 12043, 2222	692	36	13588	3.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0044271~nitrogen compound biosynthetic process	24	3.174603175	3.E-02 228033, 100041835, 232087, 66043, 1770	692	302	13588	2.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0007162~negative regulation of cell adhesion	5	0.661375661	4.E-02 18708, 13131, 11487, 12053, 11947	692	25	13588	4.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0008637~apoptotic mitochondrial changes	5	0.661375661	4.E-02 12048, 11651, 12043, 58801, 26401	692	25	13588	4.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0019319~hexose biosynthetic process	5	0.661375661	4.E-02 11911, 14751, 21991, 230163, 14120	692	25	13588	4.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0044092~negative regulation of molecular function	13	1.71957672	4.E-02 15170, 18386, 19264, 14678, 67141, 2287	692	132	13588	2.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0050878~regulation of body fluid levels	10	1.322751323	4.E-02 14060, 14674, 12258, 99571, 16644, 1227	692	89	13588	2.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0002237~response to molecule of bacterial origin	7	0.925925926	4.E-02 12475, 20846, 17087, 19697, 16803, 1067	692	49	13588	3.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0040008~regulation of growth	21	2.777777778	4.E-02 19247, 67184, 11816, 12125, 14083, 6834	692	256	13588	2.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0050871~positive regulation of B cell activation	6	0.793650794	4.E-02 19264, 12015, 12053, 106759, 20850, 125	692	37	13588	3.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0046165~alcohol biosynthetic process	6	0.793650794	4.E-02 11911, 14751, 21991, 230163, 14381, 141	692	37	13588	3.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0030217~cell differentiation	9	1.19047619	4.E-02 22324, 19264, 19934, 12043, 74734, 1149	692	76	13588	2.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0050777~negative regulation of immune response	5	0.661375661	4.E-02 15170, 19264, 12258, 12053, 19056	692	26	13588	4.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0009743~response to carbohydrate stimulus	5	0.661375661	4.E-02 21813, 230163, 18641, 224045, 103988	692	26	13588	4.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0046660~female sex differentiation	8	1.058201058	4.E-02 12190, 13667, 12048, 12043, 16847, 2240	692	64	13588	2.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0051186~cofactor metabolic process	16	2.116402116	4.E-02 17448, 19895, 15929, 67834, 14782, 6617	692	182	13588	2.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0009410~response to xenobiotic stimulus	4	0.529100529	4.E-02 11632, 11622, 13077, 94284, 394436	692	16	13588	5.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0045577~regulation of B cell differentiation	4	0.529100529	4.E-02 15170, 19264, 12015, 20850	692	16	13588	5.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0032024~positive regulation of insulin secretion	3	0.396825397	5.E-02 14661, 18642, 103988	692	7	13588	8.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0046825~regulation of protein export from nucleus	3	0.396825397	5.E-02 18747, 19247, 12568	692	7	13588	8.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0046627~negative regulation of insulin receptor signaling pathway	3	0.396825397	5.E-02 18753, 12702, 18750	692	7	13588	8.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0000910~cytokinesis	5	0.661375661	5.E-02 12190, 26934, 20877, 233406, 19200	692	27	13588	4.E+00	1.E+00	4.E-01	6.E+01



GOTERM_BP_FAT	GO:0001775~cell activation	20	2.645502646	5.E-02 22324 14674 19264 19934 12043 1149	692	246	13588	2.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0001776~leukocyte homeostasis	6	0.793650794	5.E-02 12442 12125 11651 12043 19056 2085	692	39	13588	3.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0048477~oogenesis	6	0.793650794	5.E-02 12190 20779 12043 12531 20112 6714	692	39	13588	3.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0048585~negative regulation of response to stimulus	8	1.058201058	5.E-02 15170 18753 19264 12702 12258 1205	692	65	13588	2.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0003006~reproductive developmental process	21	2.777777778	5.E-02 12190 13667 12125 11651 12043 1338	692	264	13588	2.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0032944~regulation of mononuclear cell proliferation	9	1.19047619	5.E-02 15170 19264 208154 13866 18761 120	692	80	13588	2.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0050670~regulation of lymphocyte proliferation	9	1.19047619	5.E-02 15170 19264 208154 13866 18761 120	692	80	13588	2.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0051247~positive regulation of protein metabolic process	11	1.455026455	5.E-02 18750 12567 11651 12043 216080 146	692	109	13588	2.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0006915~apoptosis	33	4.365079365	5.E-02 22029 12765 672195 66593 67184 118	692	465	13588	1.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0042593~glucose homeostasis	6	0.793650794	5.E-02 20848 12015 19247 231103 18642 103	692	40	13588	3.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0033500~carbohydrate homeostasis	6	0.793650794	5.E-02 20848 12015 19247 231103 18642 103	692	40	13588	3.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0008585~female gonad development	7	0.925925926	5.E-02 12190 13667 12048 12043 16847 2240	692	53	13588	3.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0007259~JAK-STAT cascade	5	0.661375661	5.E-02 20848 12568 20850 16452 56469	692	28	13588	4.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0055082~cellular chemical homeostasis	21	2.777777778	6.E-02 13667 19317 19264 11816 19218 1204	692	268	13588	2.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0070663~regulation of leukocyte proliferation	9	1.19047619	6.E-02 15170 19264 208154 13866 18761 120	692	82	13588	2.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0009109~coenzyme catabolic process	5	0.661375661	6.E-02 17448 78920 67834 15929 17969	692	29	13588	3.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0033032~regulation of myeloid cell apoptosis	3	0.396825397	6.E-02 12043 11491 20850	692	8	13588	7.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0032321~positive regulation of Rho GTPase activity	3	0.396825397	6.E-02 71709 19765 19417	692	8	13588	7.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0050732~negative regulation of peptidyl-tyrosine phosphorylation	3	0.396825397	6.E-02 15170 18753 19264	692	8	13588	7.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0060674~placenta blood vessel development	4	0.529100529	6.E-02 12702 26395 11651 18194	692	18	13588	4.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0012501~programmed cell death	33	4.365079365	6.E-02 22029 12765 672195 66593 67184 118	692	473	13588	1.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0016126~sterol biosynthetic process	5	0.661375661	6.E-02 15490 12638 66234 14137 18194	692	30	13588	3.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0000077~DNA damage checkpoint	5	0.661375661	6.E-02 19247 245000 12649 12443 12534	692	30	13588	3.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0044242~cellular lipid catabolic process	7	0.925925926	6.E-02 19015 18783 74147 13177 238055 113	692	56	13588	2.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0007292~female gamete generation	7	0.925925926	6.E-02 12190 20779 12043 12531 16847 2011	692	56	13588	2.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0034637~cellular carbohydrate biosynthetic process	7	0.925925926	6.E-02 11911 14751 11651 21991 230163 143	692	56	13588	2.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0007596~blood coagulation	8	1.058201058	6.E-02 14060 14674 12258 99571 16644 1227	692	70	13588	2.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0050817~coagulation	8	1.058201058	6.E-02 14060 14674 12258 99571 16644 1227	692	70	13588	2.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0008285~negative regulation of cell proliferation	18	2.380952381	6.E-02 15170 208154 12043 58801 19015 218	692	224	13588	2.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0050900~leukocyte migration	6	0.793650794	7.E-02 20310 20345 12490 18750 20202 1680	692	43	13588	3.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0031667~response to nutrient levels	11	1.455026455	7.E-02 12190 14962 12043 11651 100040331	692	115	13588	2.E+00	1.E+00	5.E-01	7.E+01
GOTERM_BP_FAT	GO:0050804~regulation of synaptic transmission	10	1.322751323	7.E-02 18747 18049 16653 14678 15461 1256	692	100	13588	2.E+00	1.E+00	5.E-01	7.E+01
GOTERM_BP_FAT	GO:0050727~regulation of inflammatory response	7	0.925925926	7.E-02 12266 12258 12053 18750 16423 1680	692	57	13588	2.E+00	1.E+00	5.E-01	7.E+01
GOTERM_BP_FAT	GO:0031349~positive regulation of defense response	7	0.925925926	7.E-02 12266 18750 16423 19697 16803 1067	692	57	13588	2.E+00	1.E+00	5.E-01	7.E+01
GOTERM_BP_FAT	GO:0046545~development of primary female sexual characteristics	7	0.925925926	7.E-02 12190 13667 12048 12043 16847 2240	692	57	13588	2.E+00	1.E+00	5.E-01	7.E+01
GOTERM_BP_FAT	GO:0021700~developmental maturation	10	1.322751323	7.E-02 19015 12190 12229 11651 12577 1253	692	101	13588	2.E+00	1.E+00	5.E-01	7.E+01
GOTERM_BP_FAT	GO:0051051~negative regulation of transport	8	1.058201058	7.E-02 19247 14678 104215 18750 12043 186	692	72	13588	2.E+00	1.E+00	5.E-01	7.E+01
GOTERM_BP_FAT	GO:0045619~regulation of lymphocyte differentiation	7	0.925925926	7.E-02 15170 21813 19264 12015 13866 1205	692	58	13588	2.E+00	1.E+00	5.E-01	7.E+01
GOTERM_BP_FAT	GO:0010907~positive regulation of glucose metabolic process	3	0.396825397	7.E-02 14447 20411 103988	692	9	13588	7.E+00	1.E+00	5.E-01	7.E+01
GOTERM_BP_FAT	GO:0033598~mammary gland epithelial cell proliferation	3	0.396825397	7.E-02 12443 12234 21943	692	9	13588	7.E+00	1.E+00	5.E-01	7.E+01
GOTERM_BP_FAT	GO:0001890~placenta development	9	1.19047619	7.E-02 19015 13649 15516 12702 13857 1478	692	87	13588	2.E+00	1.E+00	5.E-01	7.E+01
GOTERM_BP_FAT	GO:0034621~cellular macromolecular complex subunit organization	19	2.513227513	8.E-02 13800 13669 22130 56195 15078 1408	692	245	13588	2.E+00	1.E+00	5.E-01	7.E+01
GOTERM_BP_FAT	GO:0046907~intracellular transport	30	3.968253968	8.E-02 16646 11852 19384 22227 22229 2222	692	431	13588	1.E+00	1.E+00	5.E-01	7.E+01
GOTERM_BP_FAT	GO:0010564~regulation of cell cycle process	8	1.058201058	8.E-02 12190 67177 52563 56371 12540 6714	692	73	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0051271~negative regulation of cell motion	5	0.661375661	8.E-02 74144 12043 20130 106952 12576	692	32	13588	3.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0051187~cofactor catabolic process	5	0.661375661	8.E-02 17448 78920 67834 15929 17969	692	32	13588	3.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0030888~regulation of B cell proliferation	5	0.661375661	8.E-02 19264 208154 12053 106759 12575	692	32	13588	3.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0043648~dicarboxylic acid metabolic process	4	0.529100529	8.E-02 17448 18478 14600 20850	692	20	13588	4.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0002697~regulation of immune effector process	9	1.19047619	8.E-02 15170 12266 19264 12258 12053 1905	692	88	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0032101~regulation of response to external stimulus	10	1.322751323	8.E-02 12266 21813 12258 12053 74318 1875	692	103	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0048514~blood vessel morphogenesis	16	2.116402116	8.E-02 19317 14674 11852 11816 14083 2380	692	198	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0035295~tube development	20	2.645502646	8.E-02 14674 13800 12638 16911 12125 1481	692	264	13588	1.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0030183~B cell differentiation	6	0.793650794	8.E-02 18708 19264 18211 12053 12043 1149	692	46	13588	3.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0006917~induction of apoptosis	14	1.851851852	8.E-02 12190 15170 66593 67184 11816 1227	692	167	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0012502~induction of programmed cell death	14	1.851851852	8.E-02 12190 15170 66593 67184 11816 1227	692	167	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0043933~macromolecular complex subunit organization	26	3.439153439	8.E-02 22130 13669 56195 11816 74197 5594	692	367	13588	1.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0060443~mammary gland morphogenesis	5	0.661375661	8.E-02 21813 20779 14815 17979 12234	692	33	13588	3.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0030705~cytoskeleton-dependent intracellular transport	5	0.661375661	8.E-02 17925 13426 59040 22376 214952	692	33	13588	3.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0006919~activation of caspase activity	5	0.661375661	8.E-02 672195 66593 12279 14852 13063 268	692	33	13588	3.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0040014~regulation of multicellular organism growth	8	1.058201058	9.E-02 20848 19247 11816 12043 12912 1460	692	75	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0048469~cell maturation	8	1.058201058	9.E-02 12190 12229 12577 12531 18227 2011	692	75	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0006446~regulation of translational initiation	4	0.529100529	9.E-02 13665 68092 224045 73830	692	21	13588	4.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0044057~regulation of system process	16	2.116402116	9.E-02 18747 19247 16653 14678 18176 1216	692	201	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0043009~chordate embryonic development	29	3.835978836	9.E-02 12190 13649 11651 238055 15139 138	692	421	13588	1.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0032320~positive regulation of Ras GTPase activity	3	0.396825397	9.E-02 71709 19765 19417	692	10	13588	6.E+00	1.E+00	5.E-01	8.E+01



GOTERM_BP_FAT	GO:0033143~regulation of steroid hormone receptor signaling pathway	3	0.396825397	9.E-02 20779, 16000, 11848	692	10	13588	6.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0030104~water homeostasis	3	0.396825397	9.E-02 19218, 16000, 11750	692	10	13588	6.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0010676~positive regulation of cellular carbohydrate metabolic process	3	0.396825397	9.E-02 14447, 20411, 103988	692	10	13588	6.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0045913~positive regulation of carbohydrate metabolic process	3	0.396825397	9.E-02 14447, 20411, 103988	692	10	13588	6.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0043255~regulation of carbohydrate biosynthetic process	3	0.396825397	9.E-02 20411, 14815, 103988	692	10	13588	6.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0022602~ovulation cycle process	6	0.793650794	9.E-02 13667, 12048, 12043, 16847, 224045, 208	692	47	13588	3.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0030258~lipid modification	6	0.793650794	9.E-02 19015, 18708, 74147, 13177, 11364, 2310	692	47	13588	3.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0022618~ribonucleoprotein complex assembly	5	0.661375661	9.E-02 13669, 56195, 68193, 55944, 20044	692	34	13588	3.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0045321~leukocyte activation	17	2.248677249	9.E-02 22324, 19264, 19934, 12043, 11491, 7473	692	219	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0051969~regulation of transmission of nerve impulse	10	1.322751323	9.E-02 18747, 18049, 16653, 14678, 15461, 1256	692	107	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0048167~regulation of synaptic plasticity	6	0.793650794	1.E-01 16653, 15461, 12568, 18176, 22628, 1941	692	48	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0042698~ovulation cycle	6	0.793650794	1.E-01 13667, 12048, 12043, 16847, 224045, 208	692	48	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0045580~regulation of T cell differentiation	6	0.793650794	1.E-01 21813, 19264, 12015, 13866, 12053, 2085	692	48	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0010035~response to inorganic substance	9	1.19047619	1.E-01 19053, 12443, 26462, 22229, 50493, 1204	692	92	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0035239~tube morphogenesis	14	1.851851852	1.E-01 14674, 13800, 16911, 12125, 14815, 1204	692	171	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0009792~embryonic development ending in birth or egg hatching	29	3.835978836	1.E-01 12190, 13649, 11651, 238055, 15139, 138	692	425	13588	1.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0010627~regulation of protein kinase cascade	13	1.71957672	1.E-01 15170, 19264, 11652, 100048123, 12234,	692	155	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0034284~response to monosaccharide stimulus	4	0.529100529	1.E-01 21813, 18641, 224045, 103988	692	22	13588	4.E+00	1.E+00	6.E-01	8.E+01
GOTERM_BP_FAT	GO:0009746~response to hexose stimulus	4	0.529100529	1.E-01 21813, 18641, 224045, 103988	692	22	13588	4.E+00	1.E+00	6.E-01	8.E+01
GOTERM_BP_FAT	GO:0009749~response to glucose stimulus	4	0.529100529	1.E-01 21813, 18641, 224045, 103988	692	22	13588	4.E+00	1.E+00	6.E-01	8.E+01
GOTERM_BP_FAT	GO:0019218~regulation of steroid metabolic process	4	0.529100529	1.E-01 11816, 238055, 14815, 20850	692	22	13588	4.E+00	1.E+00	6.E-01	8.E+01
GOTERM_BP_FAT	GO:0048538~thymus development	4	0.529100529	1.E-01 12442, 12125, 12043, 12929	692	22	13588	4.E+00	1.E+00	6.E-01	8.E+01
GOTERM_BP_FAT	GO:0030890~positive regulation of B cell proliferation	4	0.529100529	1.E-01 19264, 12053, 106759, 12575	692	22	13588	4.E+00	1.E+00	6.E-01	8.E+01
GOTERM_BP_FAT	GO:0002053~positive regulation of mesenchymal cell proliferation	4	0.529100529	1.E-01 21813, 16367, 11855, 384783	692	22	13588	4.E+00	1.E+00	6.E-01	8.E+01
GOTERM_BP_FAT	GO:0018105~peptidyl-serine phosphorylation	4	0.529100529	1.E-01 11651, 12043, 12568, 20112	692	22	13588	4.E+00	1.E+00	6.E-01	8.E+01
GOTERM_BP_FAT	GO:0001732~formation of translation initiation complex	2	0.264550265	1.E-01 13669, 55944	692	2	13588	2.E+01	1.E+00	6.E-01	8.E+01
GOTERM_BP_FAT	GO:0032613~interleukin-10 production	2	0.264550265	1.E-01 18753, 14381	692	2	13588	2.E+01	1.E+00	6.E-01	8.E+01
GOTERM_BP_FAT	GO:0032615~interleukin-12 production	2	0.264550265	1.E-01 18753, 14381	692	2	13588	2.E+01	1.E+00	6.E-01	8.E+01
GOTERM_BP_FAT	GO:0031953~negative regulation of protein amino acid autophosphorylation	2	0.264550265	1.E-01 19264, 16476	692	2	13588	2.E+01	1.E+00	6.E-01	8.E+01
GOTERM_BP_FAT	GO:0031952~regulation of protein amino acid autophosphorylation	2	0.264550265	1.E-01 19264, 16476	692	2	13588	2.E+01	1.E+00	6.E-01	8.E+01
GOTERM_BP_FAT	GO:0048729~tissue morphogenesis	18	2.380952381	1.E-01 13649, 18747, 13800, 16911, 14815, 1204	692	238	13588	1.E+00	1.E+00	6.E-01	8.E+01
GOTERM_CC_FAT	GO:0070460~respiratory chain	52	6.878306878	2.E-57 70316, 672195, 226646, 100041273, 6637	548	65	12504	2.E+01	6.E-55	6.E-55	2.E-54
GOTERM_CC_FAT	GO:0005840~ribosome	66	8.73015873	9.E-41 666899, 100048462, 20103, 100044516, 1	548	192	12504	8.E+00	3.E-38	2.E-38	1.E-37
GOTERM_CC_FAT	GO:0019866~organelle inner membrane	80	10.58201058	4.E-39 226646, 100041273, 66377, 100041835, 2	548	312	12504	6.E+00	1.E-36	5.E-37	6.E-36
GOTERM_CC_FAT	GO:0005743~mitochondrial inner membrane	78	10.31746032	5.E-39 226646, 100041273, 66377, 100041835, 2	548	296	12504	6.E+00	2.E-36	4.E-37	7.E-36
GOTERM_CC_FAT	GO:0031966~mitochondrial membrane	85	11.24338624	7.E-38 226646, 100041273, 66377, 100041835, 2	548	368	12504	5.E+00	2.E-35	5.E-36	9.E-35
GOTERM_CC_FAT	GO:0044429~mitochondrial part	100	13.22751323	4.E-37 66885, 226646, 66377, 100041835, 17705	548	524	12504	4.E+00	1.E-34	2.E-35	5.E-34
GOTERM_CC_FAT	GO:0005740~mitochondrial envelope	86	11.37566138	1.E-36 226646, 100041273, 66377, 100041835, 2	548	391	12504	5.E+00	4.E-34	6.E-35	2.E-33
GOTERM_CC_FAT	GO:0031967~organelle envelope	98	12.96296296	2.E-34 226646, 66377, 100041835, 17705, 14270	548	540	12504	4.E+00	6.E-32	7.E-33	2.E-31
GOTERM_CC_FAT	GO:0031975~envelope	98	12.96296296	2.E-34 226646, 66377, 100041835, 17705, 14270	548	542	12504	4.E+00	8.E-32	9.E-33	3.E-31
GOTERM_CC_FAT	GO:0005739~mitochondrion	148	19.57671958	3.E-28 18746, 18747, 226646, 66885, 66377, 100	548	1322	12504	3.E+00	9.E-26	9.E-27	4.E-25
GOTERM_CC_FAT	GO:0030529~ribonucleoprotein complex	71	9.391534392	2.E-20 666899, 100048462, 20103, 56195, 10004	548	462	12504	4.E+00	6.E-18	5.E-19	2.E-17
GOTERM_CC_FAT	GO:0045259~proton-transporting ATP synthase complex	16	2.116402116	1.E-17 228033, 100041835, 67126, 66043, 17705	548	19	12504	2.E+01	4.E-15	3.E-16	2.E-14
GOTERM_CC_FAT	GO:0031090~organelle membrane	92	12.16931217	2.E-17 226646, 66377, 100041835, 17705, 14270	548	809	12504	3.E+00	5.E-15	4.E-16	2.E-14
GOTERM_CC_FAT	GO:0044455~mitochondrial membrane part	20	2.645502646	6.E-14 226646, 67184, 67126, 68349, 17705, 177	548	49	12504	9.E+00	2.E-11	1.E-12	8.E-11
GOTERM_CC_FAT	GO:0005852~eukaryotic translation initiation factor 3 complex	11	1.455026455	1.E-12 27979, 66085, 13669, 16341, 53356, 5634	548	12	12504	2.E+01	5.E-10	3.E-11	2.E-09
GOTERM_CC_FAT	GO:0005829~cytosol	62	8.201058201	1.E-11 100048462, 269378, 18747, 672195, 2010	548	549	12504	3.E+00	4.E-09	3.E-10	2.E-08
GOTERM_CC_FAT	GO:0043228~non-membrane-bounded organelle	144	19.04761905	2.E-11 666899, 100048462, 22130, 13669, 10004	548	1919	12504	2.E+00	6.E-09	4.E-10	2.E-08
GOTERM_CC_FAT	GO:0043232~intracellular non-membrane-bounded organelle	144	19.04761905	2.E-11 666899, 100048462, 22130, 13669, 10004	548	1919	12504	2.E+00	6.E-09	4.E-10	2.E-08
GOTERM_CC_FAT	GO:0022626~cytosolic ribosome	12	1.587301587	2.E-11 100048462, 19944, 100042832, 20103, 19	548	18	12504	2.E+01	8.E-09	5.E-10	3.E-08
GOTERM_CC_FAT	GO:0033279~ribosomal subunit	20	2.645502646	3.E-11 100048462, 20103, 100039355, 10004339	548	66	12504	7.E+00	9.E-09	5.E-10	4.E-08
GOTERM_CC_FAT	GO:0044445~cytosolic part	19	2.513227513	1.E-10 100048462, 20103, 100043391, 18641, 18	548	63	12504	7.E+00	4.E-08	2.E-09	1.E-07
GOTERM_CC_FAT	GO:0016469~proton-transporting two-sector ATPase complex	16	2.116402116	1.E-10 228033, 100041835, 67126, 66043, 17705	548	42	12504	9.E+00	4.E-08	2.E-09	2.E-07
GOTERM_CC_FAT	GO:0045263~proton-transporting ATP synthase complex, coupling factor F(o)	10	1.322751323	3.E-10 228033, 100041835, 17705, 17706, 27425	548	13	12504	2.E+01	1.E-07	5.E-09	5.E-07
GOTERM_CC_FAT	GO:0005746~mitochondrial respiratory chain	10	1.322751323	2.E-09 226646, 67184, 67264, 68349, 12862, 227	548	15	12504	2.E+01	7.E-07	3.E-08	3.E-06
GOTERM_CC_FAT	GO:0005753~mitochondrial proton-transporting ATP synthase complex	7	0.925925926	5.E-08 11950, 100042348, 67126, 17705, 27425,	548	7	12504	2.E+01	2.E-05	6.E-07	6.E-05
GOTERM_CC_FAT	GO:0033177~proton-transporting two-sector ATPase complex, proton-transporting	10	1.322751323	2.E-07 228033, 100041835, 17705, 17706, 27425	548	22	12504	1.E+01	6.E-05	2.E-06	2.E-04
GOTERM_CC_FAT	GO:0015935~small ribosomal subunit	11	1.455026455	2.E-07 20103, 100039355, 677113, 20102, 20088	548	29	12504	9.E+00	7.E-05	3.E-06	3.E-04
GOTERM_CC_FAT	GO:0030964~NADH dehydrogenase complex	6	0.793650794	9.E-07 226646, 67264, 68349, 227197, 17993, 17	548	6	12504	2.E+01	3.E-04	1.E-05	1.E-03
GOTERM_CC_FAT	GO:0005747~mitochondrial respiratory chain complex I	6	0.793650794	9.E-07 226646, 67264, 68349, 227197, 17993, 17	548	6	12504	2.E+01	3.E-04	1.E-05	1.E-03
GOTERM_CC_FAT	GO:0045261~proton-transporting ATP synthase complex, catalytic core F(1)	6	0.793650794	9.E-07 66043, 67126, 11947, 11949, 100047429,	548	6	12504	2.E+01	3.E-04	1.E-05	1.E-03
GOTERM_CC_FAT	GO:0045271~respiratory chain complex I	6	0.793650794	9.E-07 226646, 67264, 68349, 227197, 17993, 17	548	6	12504	2.E+01	3.E-04	1.E-05	1.E-03
GOTERM_CC_FAT	GO:0000276~mitochondrial proton-transporting ATP synthase complex, coupling fa	6	0.793650794	9.E-07 11950, 100042348, 17705, 27425, 17706,	548	6	12504	2.E+01	3.E-04	1.E-05	1.E-03
GOTERM_CC_FAT	GO:0022625~cytosolic large ribosomal subunit	6	0.793650794	3.E-06 100048462, 20005, 110954, 100042832, 1	548	7	12504	2.E+01	1.E-03	4.E-05	4.E-03
GOTERM_CC_FAT	GO:0005579~membrane attack complex	5	0.661375661	2.E-05 12279, 230558, 69379, 15139, 110382	548	5	12504	2.E+01	6.E-03	2.E-04	2.E-02



GOTERM_CC_FAT	GO:0000808~origin recognition complex	5	0.661375661	2.E-05	18393, 17216	50793, 26428	56452	548	5	12504	2.E+01	6.E-03	2.E-04	2.E-02
GOTERM_CC_FAT	GO:0031980~mitochondrial lumen	21	2.777777778	3.E-05	672195, 66885, 68263	15107, 17448	133	548	163	12504	3.E+00	1.E-02	3.E-04	4.E-02
GOTERM_CC_FAT	GO:0005759~mitochondrial matrix	21	2.777777778	3.E-05	672195, 66885, 68263	15107, 17448	133	548	163	12504	3.E+00	1.E-02	3.E-04	4.E-02
GOTERM_CC_FAT	GO:0030027~lamellipodium	12	1.587301587	8.E-05	14163, 13800	14083, 11651, 11652	1000	548	63	12504	4.E+00	3.E-02	9.E-04	1.E-01
GOTERM_CC_FAT	GO:0015934~large ribosomal subunit	9	1.19047619	2.E-04	100048462, 100042832	19921, 10004339		548	39	12504	5.E+00	8.E-02	2.E-03	3.E-01
GOTERM_CC_FAT	GO:0005664~nuclear origin of replication recognition complex	4	0.529100529	3.E-04	18393, 17216	50793, 56452		548	4	12504	2.E+01	1.E-01	3.E-03	4.E-01
GOTERM_CC_FAT	GO:0000307~cyclin-dependent protein kinase holoenzyme complex	5	0.661375661	4.E-04	12443, 12567, 12566	18538, 12575		548	9	12504	1.E+01	1.E-01	4.E-03	5.E-01
GOTERM_CC_FAT	GO:0033178~proton-transporting two-sector ATPase complex, catalytic domain	6	0.793650794	6.E-04	66043, 67126	11947, 11949, 100047429		548	17	12504	8.E+00	2.E-01	6.E-03	9.E-01
GOTERM_CC_FAT	GO:0031252~cell leading edge	14	1.851851852	1.E-03	14163, 13800	14083, 228359, 11651, 116		548	112	12504	3.E+00	3.E-01	1.E-02	2.E+00
GOTERM_CC_FAT	GO:0005924~cell-substrate adherens junction	10	1.322751323	1.E-03	12549, 19264	13800, 236920, 20411, 140		548	61	12504	4.E+00	3.E-01	1.E-02	2.E+00
GOTERM_CC_FAT	GO:0022627~cytosolic small ribosomal subunit	4	0.529100529	2.E-03	20103, 20085, 677113, 20088, 20068			548	6	12504	2.E+01	4.E-01	1.E-02	2.E+00
GOTERM_CC_FAT	GO:0000267~cell fraction	43	5.687830688	2.E-03	672195, 19247, 12955, 665032, 238055, 1			548	596	12504	2.E+00	4.E-01	1.E-02	2.E+00
GOTERM_CC_FAT	GO:0005626~insoluble fraction	39	5.158730159	2.E-03	18386, 19247, 11852, 12955, 665032, 238			548	528	12504	2.E+00	4.E-01	1.E-02	2.E+00
GOTERM_CC_FAT	GO:0030055~cell-substrate junction	10	1.322751323	2.E-03	12549, 19264	13800, 236920, 20411, 140		548	66	12504	3.E+00	5.E-01	2.E-02	3.E+00
GOTERM_CC_FAT	GO:0005819~spindle	13	1.71957672	3.E-03	26934, 20871, 20878, 11651, 20877, 1680			548	109	12504	3.E+00	6.E-01	2.E-02	4.E+00
GOTERM_CC_FAT	GO:0005925~focal adhesion	9	1.19047619	3.E-03	12549, 19264	13800, 236920, 14083, 184		548	57	12504	4.E+00	7.E-01	2.E-02	4.E+00
GOTERM_CC_FAT	GO:0042470~melanosome	11	1.455026455	4.E-03	269378, 14674, 22631, 15516, 54401, 193			548	85	12504	3.E+00	7.E-01	3.E-02	5.E+00
GOTERM_CC_FAT	GO:0048770~pigment granule	11	1.455026455	4.E-03	269378, 14674, 22631, 15516, 54401, 193			548	85	12504	3.E+00	7.E-01	3.E-02	5.E+00
GOTERM_CC_FAT	GO:0005624~membrane fraction	36	4.761904762	5.E-03	18386, 19247, 11852, 665032, 238055, 14			548	510	12504	2.E+00	8.E-01	4.E-02	7.E+00
GOTERM_CC_FAT	GO:0005945~6-phosphofructokinase complex	3	0.396825397	6.E-03	56421, 18641, 18642			548	3	12504	2.E+01	8.E-01	4.E-02	7.E+00
GOTERM_CC_FAT	GO:0042641~actomyosin	6	0.793650794	6.E-03	13800, 19247, 20411, 12306, 208727, 192			548	27	12504	5.E+00	9.E-01	4.E-02	7.E+00
GOTERM_CC_FAT	GO:0000015~phosphopyruvate hydratase complex	3	0.396825397	1.E-02	433182, 13807, 13806, 13808, 100044223			548	4	12504	2.E+01	1.E+00	7.E-02	1.E+01
GOTERM_CC_FAT	GO:0005853~eukaryotic translation elongation factor 1 complex	3	0.396825397	1.E-02	13628, 66656, 55949			548	4	12504	2.E+01	1.E+00	7.E-02	1.E+01
GOTERM_CC_FAT	GO:0031974~membrane-enclosed lumen	68	8.994708995	1.E-02	11911, 18747, 672195, 66885, 68263, 221			548	1174	12504	1.E+00	1.E+00	9.E-02	2.E+01
GOTERM_CC_FAT	GO:0046930~pore complex	9	1.19047619	1.E-02	664868, 16646, 12279, 230558, 69379, 15			548	73	12504	3.E+00	1.E+00	9.E-02	2.E+01
GOTERM_CC_FAT	GO:0044454~nuclear chromosome part	11	1.455026455	1.E-02	18393, 19891, 17216, 245000, 15078, 507			548	103	12504	2.E+00	1.E+00	9.E-02	2.E+01
GOTERM_CC_FAT	GO:0001725~stress fiber	5	0.661375661	2.E-02	13800, 19247, 20411, 12306, 19200			548	23	12504	5.E+00	1.E+00	1.E-01	2.E+01
GOTERM_CC_FAT	GO:0005912~adherens junction	11	1.455026455	2.E-02	12549, 19264, 69524, 13800, 236920, 204			548	106	12504	2.E+00	1.E+00	1.E-01	2.E+01
GOTERM_CC_FAT	GO:0032432~actin filament bundle	5	0.661375661	2.E-02	13800, 19247, 20411, 12306, 19200			548	24	12504	5.E+00	1.E+00	1.E-01	2.E+01
GOTERM_CC_FAT	GO:0005657~replication fork	5	0.661375661	2.E-02	19891, 12649, 19075, 18538, 68275			548	24	12504	5.E+00	1.E+00	1.E-01	2.E+01
GOTERM_CC_FAT	GO:0030427~site of polarized growth	7	0.925925926	2.E-02	18479, 12568, 170758, 53972, 66440, 194			548	51	12504	3.E+00	1.E+00	1.E-01	3.E+01
GOTERM_CC_FAT	GO:0030426~growth cone	7	0.925925926	2.E-02	18479, 12568, 170758, 53972, 66440, 194			548	51	12504	3.E+00	1.E+00	1.E-01	3.E+01
GOTERM_CC_FAT	GO:0005851~eukaryotic translation initiation factor 2B complex	3	0.396825397	3.E-02	13667, 13665, 224045			548	6	12504	1.E+01	1.E+00	1.E-01	3.E+01
GOTERM_CC_FAT	GO:0043233~organelle lumen	64	8.465608466	3.E-02	11911, 18747, 672195, 66885, 68263, 221			548	1136	12504	1.E+00	1.E+00	2.E-01	3.E+01
GOTERM_CC_FAT	GO:0016591~DNA-directed RNA polymerase II, holoenzyme	7	0.925925926	3.E-02	20020, 74197, 68153, 21343, 14884, 1488			548	56	12504	3.E+00	1.E+00	2.E-01	4.E+01
GOTERM_CC_FAT	GO:0015629~actin cytoskeleton	16	2.116402116	4.E-02	19247, 13800, 94190, 20411, 11856, 1715			548	205	12504	2.E+00	1.E+00	2.E-01	4.E+01
GOTERM_CC_FAT	GO:0005635~nuclear envelope	13	1.71957672	4.E-02	16646, 12043, 54151, 108989, 98386, 162			548	153	12504	2.E+00	1.E+00	2.E-01	4.E+01
GOTERM_CC_FAT	GO:0070013~intracellular organelle lumen	63	8.333333333	4.E-02	11911, 18747, 672195, 66885, 68263, 221			548	1133	12504	1.E+00	1.E+00	2.E-01	4.E+01
GOTERM_CC_FAT	GO:0000228~nuclear chromosome	11	1.455026455	4.E-02	18393, 19891, 17216, 245000, 15078, 507			548	121	12504	2.E+00	1.E+00	2.E-01	4.E+01
GOTERM_CC_FAT	GO:0070161~anchoring junction	11	1.455026455	4.E-02	12549, 19264, 69524, 13800, 236920, 204			548	123	12504	2.E+00	1.E+00	2.E-01	5.E+01
GOTERM_CC_FAT	GO:0005667~transcription factor complex	17	2.248677249	5.E-02	11911, 16911, 74197, 68153, 14281, 1291			548	234	12504	2.E+00	1.E+00	2.E-01	5.E+01
GOTERM_CC_FAT	GO:0030894~replisome	3	0.396825397	6.E-02	19891, 19075, 68275			548	9	12504	8.E+00	1.E+00	3.E-01	5.E+01
GOTERM_CC_FAT	GO:0043601~nuclear replisome	3	0.396825397	6.E-02	19891, 19075, 68275			548	9	12504	8.E+00	1.E+00	3.E-01	5.E+01
GOTERM_CC_FAT	GO:0005741~mitochondrial outer membrane	8	1.058201058	6.E-02	12015, 12048, 15275, 12043, 58801, 1097			548	80	12504	2.E+00	1.E+00	3.E-01	6.E+01
GOTERM_CC_FAT	GO:0044427~chromosomal part	21	2.777777778	7.E-02	19891, 245000, 15078, 12649, 20871, 507			548	318	12504	2.E+00	1.E+00	3.E-01	6.E+01
GOTERM_CC_FAT	GO:0005625~soluble fraction	9	1.19047619	7.E-02	672195, 12955, 11852, 18641, 18642, 130			548	99	12504	2.E+00	1.E+00	3.E-01	6.E+01
GOTERM_CC_FAT	GO:0043596~nuclear replication fork	3	0.396825397	7.E-02	19891, 19075, 68275			548	10	12504	7.E+00	1.E+00	3.E-01	6.E+01
GOTERM_CC_FAT	GO:0030175~filopodium	4	0.529100529	7.E-02	13800, 12568, 224014, 24001			548	22	12504	4.E+00	1.E+00	3.E-01	6.E+01
GOTERM_CC_FAT	GO:0031594~neuromuscular junction	4	0.529100529	7.E-02	18747, 16412, 12568, 208727			548	22	12504	4.E+00	1.E+00	3.E-01	6.E+01
GOTERM_CC_FAT	GO:0043235~receptor complex	8	1.058201058	7.E-02	15170, 12475, 21813, 16402, 12978, 1641			548	83	12504	2.E+00	1.E+00	3.E-01	6.E+01
GOTERM_CC_FAT	GO:0005680~anaphase-promoting complex	3	0.396825397	8.E-02	52563, 66440, 668450, 68999			548	11	12504	6.E+00	1.E+00	3.E-01	7.E+01
GOTERM_CC_FAT	GO:0017177~alpha-glucosidase II complex	2	0.264550265	9.E-02	19089, 14376			548	2	12504	2.E+01	1.E+00	3.E-01	7.E+01
GOTERM_CC_FAT	GO:0031968~organelle outer membrane	8	1.058201058	9.E-02	12015, 12048, 15275, 12043, 58801, 1097			548	87	12504	2.E+00	1.E+00	3.E-01	7.E+01
GOTERM_CC_FAT	GO:0016323~basolateral plasma membrane	11	1.455026455	9.E-02	12549, 13649, 19264, 13800, 236920, 204			548	141	12504	2.E+00	1.E+00	3.E-01	7.E+01
GOTERM_CC_FAT	GO:0019867~outer membrane	8	1.058201058	1.E-01	12015, 12048, 15275, 12043, 58801, 1097			548	90	12504	2.E+00	1.E+00	4.E-01	8.E+01
GOTERM_MF_FAT	GO:0003735~structural constituent of ribosome	62	8.201058201	1.E-40	666899, 100048462, 20103, 100044516, 1			651	151	13288	8.E+00	8.E-38	8.E-38	2.E-37
GOTERM_MF_FAT	GO:0030695~GTPase regulator activity	73	9.656084656	2.E-25	13667, 22324, 228482, 94190, 192662, 24			651	361	13288	4.E+00	1.E-22	7.E-23	3.E-22
GOTERM_MF_FAT	GO:0050136~NADH dehydrogenase (quinone) activity	22	2.91005291	4.E-25	226646, 100041273, 66416, 67184, 17721			651	24	13288	2.E+01	2.E-22	8.E-23	6.E-22
GOTERM_MF_FAT	GO:0003954~NADH dehydrogenase activity	22	2.91005291	4.E-25	226646, 100041273, 66416, 67184, 17721			651	24	13288	2.E+01	2.E-22	8.E-23	6.E-22
GOTERM_MF_FAT	GO:0008137~NADH dehydrogenase (ubiquinone) activity	22	2.91005291	4.E-25	226646, 100041273, 66416, 67184, 17721			651	24	13288	2.E+01	2.E-22	8.E-23	6.E-22
GOTERM_MF_FAT	GO:0060589~nucleoside-triphosphatase regulator activity	73	9.656084656	6.E-25	13667, 22324, 228482, 94190, 192662, 24			651	367	13288	4.E+00	4.E-22	9.E-23	9.E-22
GOTERM_MF_FAT	GO:0016655~oxidoreductase activity, acting on NADH or NADPH, quinone or simila	22	2.91005291	5.E-23	226646, 100041273, 66416, 67184, 17721			651	27	13288	2.E+01	3.E-20	6.E-21	7.E-20
GOTERM_MF_FAT	GO:0016651~oxidoreductase activity, acting on NADH or NADPH	28	3.703703704	2.E-22	226646, 100041273, 66416, 67184, 14782			651	51	13288	1.E+01	1.E-19	2.E-20	3.E-19
GOTERM_MF_FAT	GO:0005096~GTPase activator activity	47	6.216931217	6.E-20	117600, 94190, 228482, 192662, 243362,			651	192	13288	5.E+00	4.E-17	6.E-18	9.E-17
GOTERM_MF_FAT	GO:0008047~enzyme activator activity	52	6.878306878	9.E-19	94190, 228482, 243362, 192662, 14270, 2			651	249	13288	4.E+00	5.E-16	7.E-17	1.E-15



GOTERM_MF_FAT	GO:0008135~translation factor activity, nucleic acid binding	33	4.365079365	2.E-18	13684	13667	66235	13669	56347	5335	651	98	13288	7.E+00	1.E-15	1.E-16	2.E-15
GOTERM_MF_FAT	GO:0003743~translation initiation factor activity	26	3.439153439	3.E-17	13684	13667	66235	13669	56347	5335	651	62	13288	9.E+00	2.E-14	2.E-15	4.E-14
GOTERM_MF_FAT	GO:0015078~hydrogen ion transmembrane transporter activity	27	3.571428571	6.E-15	228033	100041835	66043	17705	17706		651	82	13288	7.E+00	4.E-12	4.E-13	1.E-11
GOTERM_MF_FAT	GO:0005198~structural molecule activity	65	8.597883598	8.E-15	666899	100048462	20103	100044516	1		651	450	13288	3.E+00	5.E-12	4.E-13	1.E-11
GOTERM_MF_FAT	GO:0005089~Rho guanyl-nucleotide exchange factor activity	25	3.306878307	1.E-14	22324	13605	16800	442801	53972	218	651	71	13288	7.E+00	9.E-12	7.E-13	2.E-11
GOTERM_MF_FAT	GO:0005083~small GTPase regulator activity	43	5.687830688	3.E-14	117600	22324	192662	13605	11856	44	651	223	13288	4.E+00	2.E-11	1.E-12	4.E-11
GOTERM_MF_FAT	GO:0015077~monovalent inorganic cation transmembrane transporter activity	27	3.571428571	3.E-14	228033	100041835	66043	17705	17706		651	87	13288	6.E+00	2.E-11	1.E-12	5.E-11
GOTERM_MF_FAT	GO:0000166~nucleotide binding	178	23.54497354	7.E-13	18746	18747	226646	66885	56195	269	651	2183	13288	2.E+00	4.E-10	3.E-11	1.E-09
GOTERM_MF_FAT	GO:0005088~Ras guanyl-nucleotide exchange factor activity	25	3.306878307	7.E-13	22324	13605	16800	442801	53972	218	651	83	13288	6.E+00	4.E-10	3.E-11	1.E-09
GOTERM_MF_FAT	GO:0017076~purine nucleotide binding	158	20.8994709	1.E-12	18746	18747	66885	26905	71819	1000	651	1871	13288	2.E+00	9.E-10	5.E-11	2.E-09
GOTERM_MF_FAT	GO:0032555~purine ribonucleotide binding	149	19.70899471	3.E-11	18746	18747	26905	71819	100048123		651	1796	13288	2.E+00	2.E-08	1.E-09	5.E-08
GOTERM_MF_FAT	GO:0032553~ribonucleotide binding	149	19.70899471	3.E-11	18746	18747	26905	71819	100048123		651	1796	13288	2.E+00	2.E-08	1.E-09	5.E-08
GOTERM_MF_FAT	GO:0022890~inorganic cation transmembrane transporter activity	27	3.571428571	4.E-10	228033	100041835	66043	17705	17706		651	127	13288	4.E+00	2.E-07	1.E-08	6.E-07
GOTERM_MF_FAT	GO:0005085~guanyl-nucleotide exchange factor activity	29	3.835978836	5.E-10	22324	13667	13605	442801	16800	539	651	147	13288	4.E+00	3.E-07	1.E-08	7.E-07
GOTERM_MF_FAT	GO:0004672~protein kinase activity	63	8.333333333	5.E-09	18747	12571	100048123	228775	20779		651	583	13288	2.E+00	3.E-06	2.E-07	8.E-06
GOTERM_MF_FAT	GO:0005100~Rho GTPase activator activity	10	1.322751323	5.E-08	117600	71709	17925	50768	228359	76	651	18	13288	1.E+01	3.E-05	1.E-06	7.E-05
GOTERM_MF_FAT	GO:0001882~nucleoside binding	123	16.26984127	6.E-08	18746	18747	66885	71819	100048123		651	1558	13288	2.E+00	3.E-05	1.E-06	8.E-05
GOTERM_MF_FAT	GO:0001883~purine nucleoside binding	122	16.13756614	7.E-08	18746	18747	66885	71819	100048123		651	1548	13288	2.E+00	4.E-05	2.E-06	1.E-04
GOTERM_MF_FAT	GO:0030554~adenyl nucleotide binding	121	16.00529101	8.E-08	18746	18747	66885	71819	100048123		651	1535	13288	2.E+00	5.E-05	2.E-06	1.E-04
GOTERM_MF_FAT	GO:0019992~diacylglycerol binding	16	2.116402116	1.E-07	22324	26934	70719	57257	16800	1875	651	59	13288	6.E+00	6.E-05	2.E-06	1.E-04
GOTERM_MF_FAT	GO:0005524~ATP binding	112	14.81481481	6.E-07	18746	18747	71819	18641	100048123		651	1443	13288	2.E+00	4.E-04	1.E-05	9.E-04
GOTERM_MF_FAT	GO:0019843~rRNA binding	10	1.322751323	1.E-06	26961	100042832	20102	268449	10004		651	24	13288	9.E+00	6.E-04	2.E-05	2.E-03
GOTERM_MF_FAT	GO:0032559~adenyl ribonucleotide binding	112	14.81481481	1.E-06	18746	18747	71819	18641	100048123		651	1460	13288	7.E+00	7.E-04	2.E-05	2.E-03
GOTERM_MF_FAT	GO:0003924~GTPase activity	21	2.777777777	4.E-06	14674	16653	26905	13627	19384	1467	651	128	13288	3.E+00	2.E-03	8.E-05	6.E-03
GOTERM_MF_FAT	GO:0009055~electron carrier activity	27	3.571428571	6.E-06	226646	66885	672195	14782	109731	6	651	202	13288	3.E+00	4.E-03	1.E-04	9.E-03
GOTERM_MF_FAT	GO:0004129~cytochrome-c oxidase activity	9	1.19047619	8.E-06	12868	12858	333182	17705	17706	128	651	23	13288	8.E+00	5.E-03	2.E-04	1.E-02
GOTERM_MF_FAT	GO:0016676~oxidoreductase activity, acting on heme group of donors, oxygen as e	9	1.19047619	8.E-06	12868	12858	333182	17705	17706	128	651	23	13288	8.E+00	5.E-03	2.E-04	1.E-02
GOTERM_MF_FAT	GO:0016675~oxidoreductase activity, acting on heme group of donors	9	1.19047619	8.E-06	12868	12858	333182	17705	17706	128	651	23	13288	8.E+00	5.E-03	2.E-04	1.E-02
GOTERM_MF_FAT	GO:0015002~heme-copper terminal oxidase activity	9	1.19047619	8.E-06	12868	12858	333182	17705	17706	128	651	23	13288	8.E+00	5.E-03	2.E-04	1.E-02
GOTERM_MF_FAT	GO:0004674~protein serine/threonine kinase activity	43	5.687830688	9.E-06	18747	107951	12571	245000	12649	11	651	421	13288	2.E+00	5.E-03	2.E-04	1.E-02
GOTERM_MF_FAT	GO:0050662~coenzyme binding	23	3.042328042	1.E-05	226646	66885	100042746	15929	56847		651	160	13288	3.E+00	7.E-03	2.E-04	2.E-02
GOTERM_MF_FAT	GO:0005525~GTP binding	38	5.026455026	1.E-05	228543	11852	26905	19384	13627	136	651	354	13288	2.E+00	7.E-03	2.E-04	2.E-02
GOTERM_MF_FAT	GO:0004715~non-membrane spanning protein tyrosine kinase activity	11	1.455026455	2.E-05	14191	12229	20779	22390	22612	1408	651	40	13288	6.E+00	1.E-02	3.E-04	2.E-02
GOTERM_MF_FAT	GO:0032561~guanyl ribonucleotide binding	38	5.026455026	2.E-05	228543	11852	26905	19384	13627	136	651	363	13288	2.E+00	1.E-02	3.E-04	3.E-02
GOTERM_MF_FAT	GO:0019001~guanyl nucleotide binding	38	5.026455026	2.E-05	228543	11852	26905	19384	13627	136	651	363	13288	2.E+00	1.E-02	3.E-04	3.E-02
GOTERM_MF_FAT	GO:0019904~protein domain specific binding	25	3.306878307	2.E-05	11856	19261	12549	22631	16367	2077	651	192	13288	3.E+00	1.E-02	4.E-04	3.E-02
GOTERM_MF_FAT	GO:0005092~GDP-dissociation inhibitor activity	5	0.661375661	3.E-05	14570	192662	14567	11857	14569		651	5	13288	2.E+01	2.E-02	4.E-04	4.E-02
GOTERM_MF_FAT	GO:0048037~cofactor binding	27	3.571428571	4.E-05	70316	66885	226646	100042746	15929		651	226	13288	2.E+00	3.E-02	7.E-04	7.E-02
GOTERM_MF_FAT	GO:0033764~steroid dehydrogenase activity, acting on the CH-OH group of donor	8	1.058201058	8.E-05	15490	100043456	56348	15493	15492		651	23	13288	7.E+00	5.E-02	1.E-03	1.E-01
GOTERM_MF_FAT	GO:0046933~hydrogen ion transporting ATP synthase activity, rotational mechanis	6	0.793650794	1.E-04	66043	67126	11947	11949	100047429		651	11	13288	1.E+01	6.E-02	1.E-03	1.E-01
GOTERM_MF_FAT	GO:0005158~insulin receptor binding	7	0.925925926	1.E-04	18708	16367	20411	13449	13448	3847	651	17	13288	8.E+00	6.E-02	1.E-03	2.E-01
GOTERM_MF_FAT	GO:0017124~SH3 domain binding	14	1.851851852	1.E-04	20401	15170	19317	13800	228359	118	651	79	13288	4.E+00	7.E-02	2.E-03	2.E-01
GOTERM_MF_FAT	GO:0008289~lipid binding	34	4.497354497	2.E-04	22324	228033	100041835	11816	14815		651	345	13288	2.E+00	1.E-01	2.E-03	3.E-01
GOTERM_MF_FAT	GO:0019200~carbohydrate kinase activity	7	0.925925926	3.E-04	56421	15275	15277	18641	18642	1039	651	20	13288	7.E+00	2.E-01	4.E-03	4.E-01
GOTERM_MF_FAT	GO:0032403~protein complex binding	13	1.71957672	4.E-04	245000	20411	16412	384783	16419	16	651	78	13288	3.E+00	2.E-01	5.E-03	6.E-01
GOTERM_MF_FAT	GO:0016229~steroid dehydrogenase activity	8	1.058201058	4.E-04	15490	100043456	56348	15493	15492		651	29	13288	6.E+00	2.E-01	5.E-03	6.E-01
GOTERM_MF_FAT	GO:0046961~proton-transporting ATPase activity, rotational mechanism	6	0.793650794	5.E-04	66043	67126	11947	11949	100047429		651	15	13288	8.E+00	3.E-01	7.E-03	8.E-01
GOTERM_MF_FAT	GO:0030675~Rac GTPase activator activity	5	0.661375661	6.E-04	228359	76117	19765	233071	106952		651	9	13288	1.E+01	3.E-01	7.E-03	9.E-01
GOTERM_MF_FAT	GO:0003854~3-beta-hydroxy-delta5-steroid dehydrogenase activity	5	0.661375661	6.E-04	100043456	15493	15492	18194	15497		651	9	13288	1.E+01	3.E-01	7.E-03	9.E-01
GOTERM_MF_FAT	GO:0000287~magnesium ion binding	36	4.761904762	9.E-04	228543	18746	232087	15929	18641	18	651	409	13288	2.E+00	4.E-01	1.E-02	1.E+00
GOTERM_MF_FAT	GO:0004713~protein tyrosine kinase activity	19	2.513227513	1.E-03	13649	12229	14083	15162	13836	1419	651	164	13288	2.E+00	5.E-01	1.E-02	2.E+00
GOTERM_MF_FAT	GO:0005099~Ras GTPase activator activity	11	1.455026455	1.E-03	117600	71709	17925	50768	228359	76	651	65	13288	3.E+00	5.E-01	1.E-02	2.E+00
GOTERM_MF_FAT	GO:0016679~oxidoreductase activity, acting on diphenols and related substances a	4	0.529100529	2.E-03	66694	67530	66594	66576			651	6	13288	1.E+01	7.E-01	2.E-02	3.E+00
GOTERM_MF_FAT	GO:0016681~oxidoreductase activity, acting on diphenols and related substances a	4	0.529100529	2.E-03	66694	67530	66594	66576			651	6	13288	1.E+01	7.E-01	2.E-02	3.E+00
GOTERM_MF_FAT	GO:0004396~hexokinase activity	4	0.529100529	2.E-03	15275	15277	103988	212032			651	6	13288	1.E+01	7.E-01	2.E-02	3.E+00
GOTERM_MF_FAT	GO:0008121~ubiquinol-cytochrome-c reductase activity	4	0.529100529	2.E-03	66694	67530	66594	66576			651	6	13288	1.E+01	7.E-01	2.E-02	3.E+00
GOTERM_MF_FAT	GO:0016668~oxidoreductase activity, acting on sulfur group of donors: NAD or NAD	4	0.529100529	2.E-03	26462	50493	14782	13382			651	6	13288	1.E+01	7.E-01	2.E-02	3.E+00
GOTERM_MF_FAT	GO:0016860~intramolecular oxidoreductase activity	8	1.058201058	2.E-03	14751	74147	19895	13177	21991	1549	651	38	13288	4.E+00	7.E-01	2.E-02	3.E+00
GOTERM_MF_FAT	GO:0019901~protein kinase binding	11	1.455026455	2.E-03	20848	21813	19264	228775	16367	114	651	71	13288	3.E+00	8.E-01	2.E-02	3.E+00
GOTERM_MF_FAT	GO:0019900~kinase binding	12	1.587301587	3.E-03	20848	19645	21813	19264	228775	163	651	85	13288	3.E+00	8.E-01	3.E-02	4.E+00
GOTERM_MF_FAT	GO:0005159~insulin-like growth factor receptor binding	4	0.529100529	4.E-03	18708	16367	22628	16000			651	7	13288	1.E+01	9.E-01	4.E-02	5.E+00
GOTERM_MF_FAT	GO:0016863~intramolecular oxidoreductase activity, transposing C=C bonds	5	0.661375661	4.E-03	74147	13177	15493	15492	15497		651	14	13288	7.E+00	9.E-01	4.E-02	6.E+00
GOTERM_MF_FAT	GO:0004697~protein kinase C activity	5	0.661375661	5.E-03	18751	18753	18754	18761	18750		651	15	13288	7.E+00	1.E+00	5.E-02	7.E+00
GOTERM_MF_FAT	GO:0051287~NAD or NADH binding	8	1.058201058	5.E-03	226646	100042746	15929	67834	56847		651	44	13288	4.E+00	1.E+00	5.E-02	7.E+00
GOTERM_MF_F																	



GOTERM_MF_FAT	GO:0003872~6-phosphofructokinase activity	3	0.396825397	7.E-03 56421, 18641, 18642	651	3	13288	2.E+01	1.E+00	7.E-02	1.E+01
GOTERM_MF_FAT	GO:0004739~pyruvate dehydrogenase (acetyl-transferring) activity	3	0.396825397	7.E-03 68263, 18597, 18598	651	3	13288	2.E+01	1.E+00	7.E-02	1.E+01
GOTERM_MF_FAT	GO:0004738~pyruvate dehydrogenase activity	3	0.396825397	7.E-03 68263, 18597, 18598	651	3	13288	2.E+01	1.E+00	7.E-02	1.E+01
GOTERM_MF_FAT	GO:0005094~Rho GDP-dissociation inhibitor activity	3	0.396825397	7.E-03 14570, 192662, 11857	651	3	13288	2.E+01	1.E+00	7.E-02	1.E+01
GOTERM_MF_FAT	GO:0016624~oxidoreductase activity, acting on the aldehyde or oxo group of dono	4	0.529100529	8.E-03 68263, 18597, 18598, 18293	651	9	13288	9.E+00	1.E+00	7.E-02	1.E+01
GOTERM_MF_FAT	GO:0019899~enzyme binding	21	2.777777778	9.E-03 117600, 19264, 20411, 26965, 12649, 136	651	229	13288	2.E+00	1.E+00	8.E-02	1.E+01
GOTERM_MF_FAT	GO:0004459~L-lactate dehydrogenase activity	3	0.396825397	1.E-02 16828, 16833, 16832	651	4	13288	2.E+01	1.E+00	1.E-01	2.E+01
GOTERM_MF_FAT	GO:0016802~trialkylsulfonium hydrolase activity	3	0.396825397	1.E-02 269378, 229709, 74340	651	4	13288	2.E+01	1.E+00	1.E-01	2.E+01
GOTERM_MF_FAT	GO:0004013~adenosylhomocysteine activity	3	0.396825397	1.E-02 269378, 229709, 74340	651	4	13288	2.E+01	1.E+00	1.E-01	2.E+01
GOTERM_MF_FAT	GO:0004769~steroid delta-isomerase activity	3	0.396825397	1.E-02 15493, 15492, 15497	651	4	13288	2.E+01	1.E+00	1.E-01	2.E+01
GOTERM_MF_FAT	GO:0004634~phosphopyruvate hydratase activity	3	0.396825397	1.E-02 433182, 13807, 13806, 13808, 100044223	651	4	13288	2.E+01	1.E+00	1.E-01	2.E+01
GOTERM_MF_FAT	GO:0004693~cyclin-dependent protein kinase activity	6	0.793650794	1.E-02 107951, 12571, 12567, 12566, 12568, 125	651	30	13288	4.E+00	1.E+00	1.E-01	2.E+01
GOTERM_MF_FAT	GO:0005506~iron ion binding	27	3.571428571	2.E-02 226646, 672195, 66234, 12858, 18126, 15	651	343	13288	2.E+00	1.E+00	1.E-01	2.E+01
GOTERM_MF_FAT	GO:0008353~RNA polymerase II carboxy-terminal domain kinase activity	4	0.529100529	2.E-02 107951, 14884, 14885, 12534	651	12	13288	7.E+00	1.E+00	2.E-01	2.E+01
GOTERM_MF_FAT	GO:0030676~Rac guanyl-nucleotide exchange factor activity	3	0.396825397	2.E-02 22324, 57257, 16800	651	5	13288	1.E+01	1.E+00	2.E-01	3.E+01
GOTERM_MF_FAT	GO:0004457~lactate dehydrogenase activity	3	0.396825397	2.E-02 16828, 16833, 16832	651	5	13288	1.E+01	1.E+00	2.E-01	3.E+01
GOTERM_MF_FAT	GO:0004332~fructose-bisphosphate aldolase activity	3	0.396825397	2.E-02 230163, 11676, 11674	651	5	13288	1.E+01	1.E+00	2.E-01	3.E+01
GOTERM_MF_FAT	GO:0031405~lipoic acid binding	3	0.396825397	2.E-02 235339, 27402, 78920	651	5	13288	1.E+01	1.E+00	2.E-01	3.E+01
GOTERM_MF_FAT	GO:0050660~FAD binding	9	1.19047619	2.E-02 66885, 18126, 11409, 26462, 50493, 1478	651	71	13288	3.E+00	1.E+00	2.E-01	3.E+01
GOTERM_MF_FAT	GO:0051539~4 iron, 4 sulfur cluster binding	5	0.661375661	2.E-02 226646, 17995, 227197, 225887, 75406	651	23	13288	4.E+00	1.E+00	2.E-01	3.E+01
GOTERM_MF_FAT	GO:0042169~SH2 domain binding	4	0.529100529	3.E-02 15170, 13131, 16367, 11487	651	14	13288	6.E+00	1.E+00	2.E-01	3.E+01
GOTERM_MF_FAT	GO:0004861~cyclin-dependent protein kinase inhibitor activity	3	0.396825397	3.E-02 12577, 12575, 12576	651	6	13288	1.E+01	1.E+00	2.E-01	4.E+01
GOTERM_MF_FAT	GO:0016538~cyclin-dependent protein kinase regulator activity	4	0.529100529	3.E-02 12443, 12577, 12575, 12576	651	15	13288	5.E+00	1.E+00	2.E-01	4.E+01
GOTERM_MF_FAT	GO:0051536~iron-sulfur cluster binding	7	0.925925926	3.E-02 66694, 226646, 17995, 227197, 225887, 7	651	50	13288	3.E+00	1.E+00	2.E-01	4.E+01
GOTERM_MF_FAT	GO:0051540~metal cluster binding	7	0.925925926	3.E-02 66694, 226646, 17995, 227197, 225887, 7	651	50	13288	3.E+00	1.E+00	2.E-01	4.E+01
GOTERM_MF_FAT	GO:0016832~aldehyde-lyase activity	3	0.396825397	4.E-02 230163, 11676, 11674	651	7	13288	9.E+00	1.E+00	3.E-01	5.E+01
GOTERM_MF_FAT	GO:0008443~phosphofructokinase activity	3	0.396825397	4.E-02 56421, 18641, 18642	651	7	13288	9.E+00	1.E+00	3.E-01	5.E+01
GOTERM_MF_FAT	GO:0005070~SH3/SH2 adaptor activity	4	0.529100529	5.E-02 14784, 20411, 12928, 107746	651	17	13288	5.E+00	1.E+00	3.E-01	5.E+01
GOTERM_MF_FAT	GO:0004896~cytokine receptor activity	7	0.925925926	5.E-02 12765, 16195, 13857, 12984, 16847, 1615	651	55	13288	3.E+00	1.E+00	3.E-01	5.E+01
GOTERM_MF_FAT	GO:0001530~lipopolysaccharide binding	3	0.396825397	5.E-02 12475, 17087, 16803	651	8	13288	8.E+00	1.E+00	4.E-01	6.E+01
GOTERM_MF_FAT	GO:0031406~carboxylic acid binding	9	1.19047619	6.E-02 70316, 19015, 18126, 11409, 235339, 133	651	85	13288	2.E+00	1.E+00	4.E-01	6.E+01
GOTERM_MF_FAT	GO:0003746~translation elongation factor activity	5	0.661375661	6.E-02 13627, 13628, 13629, 66656, 55949	651	31	13288	3.E+00	1.E+00	4.E-01	6.E+01
GOTERM_MF_FAT	GO:0019207~kinase regulator activity	8	1.058201058	7.E-02 18709, 18708, 18126, 228775, 12443, 125	651	73	13288	2.E+00	1.E+00	4.E-01	6.E+01
GOTERM_MF_FAT	GO:0016861~intramolecular oxidoreductase activity, interconverting aldoses and kel	3	0.396825397	7.E-02 14751, 19895, 21991	651	9	13288	7.E+00	1.E+00	4.E-01	7.E+01
GOTERM_MF_FAT	GO:0016801~hydrolase activity, acting on ether bonds	3	0.396825397	7.E-02 269378, 229709, 74340	651	9	13288	7.E+00	1.E+00	4.E-01	7.E+01
GOTERM_MF_FAT	GO:0030291~protein serine/threonine kinase inhibitor activity	3	0.396825397	7.E-02 12577, 12575, 12576	651	9	13288	7.E+00	1.E+00	4.E-01	7.E+01
GOTERM_MF_FAT	GO:0004721~phosphoprotein phosphatase activity	13	1.71957672	7.E-02 15170, 19264, 19247, 19253, 19053, 2639	651	152	13288	2.E+00	1.E+00	4.E-01	7.E+01
GOTERM_MF_FAT	GO:0004860~protein kinase inhibitor activity	4	0.529100529	7.E-02 228775, 12577, 12575, 12576	651	20	13288	4.E+00	1.E+00	4.E-01	7.E+01
GOTERM_MF_FAT	GO:0030674~protein binding, bridging	5	0.661375661	8.E-02 99571, 14784, 20411, 12928, 107746	651	33	13288	3.E+00	1.E+00	4.E-01	7.E+01
GOTERM_MF_FAT	GO:0003697~single-stranded DNA binding	5	0.661375661	8.E-02 12190, 17217, 17220, 17219, 21681	651	33	13288	3.E+00	1.E+00	4.E-01	7.E+01
GOTERM_MF_FAT	GO:0043566~structure-specific DNA binding	8	1.058201058	8.E-02 12190, 17217, 17220, 12053, 17219, 2168	651	76	13288	2.E+00	1.E+00	4.E-01	7.E+01
GOTERM_MF_FAT	GO:0050661~NADP or NADPH binding	4	0.529100529	8.E-02 18126, 26462, 50493, 14782	651	21	13288	4.E+00	1.E+00	4.E-01	7.E+01
GOTERM_MF_FAT	GO:0003723~RNA binding	42	5.555555556	8.E-02 230257, 13684, 107951, 66235, 23983, 26	651	672	13288	1.E+00	1.E+00	4.E-01	7.E+01
GOTERM_MF_FAT	GO:0019210~kinase inhibitor activity	4	0.529100529	9.E-02 228775, 12577, 12575, 12576	651	22	13288	4.E+00	1.E+00	5.E-01	8.E+01
GOTERM_MF_FAT	GO:0017077~oxidative phosphorylation uncoupler activity	2	0.264550265	1.E-01 22227, 22229	651	2	13288	2.E+01	1.E+00	5.E-01	8.E+01
GOTERM_MF_FAT	GO:0005093~Rab GDP-dissociation inhibitor activity	2	0.264550265	1.E-01 14567, 14569	651	2	13288	2.E+01	1.E+00	5.E-01	8.E+01
GOTERM_MF_FAT	GO:0004478~methionine adenosyltransferase activity	2	0.264550265	1.E-01 232087, 11720	651	2	13288	2.E+01	1.E+00	5.E-01	8.E+01
GOTERM_MF_FAT	GO:0004743~pyruvate kinase activity	2	0.264550265	1.E-01 18746, 18770	651	2	13288	2.E+01	1.E+00	5.E-01	8.E+01
GOTERM_MF_FAT	GO:0045309~protein phosphorylated amino acid binding	3	0.396825397	1.E-01 15170, 12928, 19261	651	11	13288	6.E+00	1.E+00	5.E-01	8.E+01
BIOCARTA	m_gleevecPathway:Inhibition of Cellular Proliferation by Gleevec	15	1.984126984	3.E-07 12929, 11651, 14281, 18708, 12015, 2084	182	22	1171	4.E+00	6.E-05	6.E-05	4.E-04
BIOCARTA	m_metPathway:Signaling of Hepatocyte Growth Factor Receptor	18	2.380952381	6.E-07 19247, 14083, 12929, 12928, 18479, 1641	182	32	1171	4.E+00	1.E-04	6.E-05	7.E-04
BIOCARTA	m_egfPathway:EGF Signaling Pathway	16	2.116402116	2.E-06 13649, 14281, 20416, 13645, 20848, 1875	182	28	1171	4.E+00	5.E-04	2.E-04	3.E-03
BIOCARTA	m_tffPathway:Trefoil Factors Initiate Mucosal Healing	14	1.851851852	5.E-06 672195, 13649, 14083, 11651, 16412, 204	182	23	1171	4.E+00	1.E-03	3.E-04	7.E-03
BIOCARTA	m_TPOPathway:TPO Signaling Pathway	14	1.851851852	5.E-06 14281, 20416, 20848, 18751, 18708, 2084	182	23	1171	4.E+00	1.E-03	3.E-04	7.E-03
BIOCARTA	m_RacCycDPathway:Influence of Ras and Rho proteins on G1 to S Transition	14	1.851851852	1.E-05 12571, 11651, 18479, 11848, 18708, 1964	182	24	1171	4.E+00	2.E-03	4.E-04	1.E-02
BIOCARTA	m_compPathway:Complement Pathway	12	1.587301587	1.E-05 17175, 12266, 17174, 50908, 12259, 1496	182	18	1171	4.E+00	2.E-03	4.E-04	1.E-02
BIOCARTA	m_il2rbPathway:IL-2 Receptor Beta Chain in T cell Activation	17	2.248677249	2.E-05 15170, 12929, 12043, 11651, 14281, 2041	182	36	1171	3.E+00	5.E-03	8.E-04	3.E-02
BIOCARTA	m_il6Pathway:IL 6 signaling pathway	12	1.587301587	8.E-05 20848, 16195, 19247, 14784, 20662, 2639	182	21	1171	4.E+00	2.E-02	2.E-03	1.E-01
BIOCARTA	m_igf1Pathway:IGF-1 Signaling Pathway	12	1.587301587	8.E-05 18708, 19247, 16367, 14784, 20662, 2639	182	21	1171	4.E+00	2.E-02	2.E-03	1.E-01
BIOCARTA	m_epoPathway:EPO Signaling Pathway	12	1.587301587	8.E-05 15170, 13857, 14784, 20662, 26395, 1546	182	21	1171	4.E+00	2.E-02	2.E-03	1.E-01
BIOCARTA	m_pdgPathway:PDGF Signaling Pathway	14	1.851851852	8.E-05 14281, 20416, 20848, 18751, 18708, 2084	182	28	1171	3.E+00	2.E-02	2.E-03	1.E-01
BIOCARTA	m_fcer1Pathway:Fc Epsilon Receptor I Signaling in Mast Cells	15	1.984126984	1.E-04 22324, 12229, 14281, 20416, 18751, 1878	182	32	1171	3.E+00	2.E-02	2.E-03	1.E-01
BIOCARTA	m_ghPathway:Growth Hormone Signaling Pathway	13	1.71957672	1.E-04 15170, 20416, 18751, 18708, 16367, 1478	182	25	1171	3.E+00	2.E-02	2.E-03	1.E-01
BIOCARTA	m_integrinPathway:Integrin Signaling Pathway	14	1.851851852	1.E-04 14083, 12929, 16412, 20416, 11848, 2077	182	29	1171	3.E+00	3.E-02	2.E-03	2.E-01
BIOCARTA	m_her2Pathway:Role of ERBB2 in Signal Transduction and Oncology	12	1.587301587	1.E-04 20848, 18708, 13649, 16195, 13867, 1386	182	22	1171	4.E+00	3.E-02	2.E-03	2.E-01



BIOCARTA	m_igf1rPathway:Multiple antiapoptotic pathways from IGF-1R signaling lead to BAD	11	1.455026455	2E-04	18708	18747	12015	16367	14784	2066	182	19	1171	4E+00	3E-02	3E-03	2E-01
BIOCARTA	m_il3Pathway:IL 3 signaling pathway	10	1.322751323	2E-04	15170	14784	20662	26395	15461	1428	182	16	1171	4E+00	4E-02	3E-03	2E-01
BIOCARTA	m_classicPathway:Classical Complement Pathway	9	1.19047619	2E-04	12266	50908	12259	12279	15139	1241	182	13	1171	4E+00	4E-02	3E-03	2E-01
BIOCARTA	m_Atl1rPathway:Angiotensin II mediated activation of JNK Pathway via Pyk2 depend	13	1.71957672	4E-04	13649	14083	18479	20416	18751	2077	182	28	1171	3E+00	9E-02	5E-03	5E-01
BIOCARTA	m_bcrPathway:BCR Signaling Pathway	13	1.71957672	6E-04	22324	12229	14281	20416	18751	1478	182	29	1171	3E+00	1E-01	7E-03	8E-01
BIOCARTA	m_insulinPathway:Insulin Signaling Pathway	11	1.455026455	7E-04	18708	19247	16367	14784	20662	2639	182	22	1171	3E+00	1E-01	9E-03	9E-01
BIOCARTA	m_ecmPathway:Erk and PI-3 Kinase Are Necessary for Collagen Binding in Corneal E	10	1.322751323	9E-04	18708	20779	14083	26395	15461	1185	182	19	1171	3E+00	2E-01	1E-02	1E+00
BIOCARTA	m_spryPathway:Sprouty regulation of tyrosine kinase signals	9	1.19047619	1E-03	13649	20779	14784	20662	26395	1546	182	16	1171	4E+00	2E-01	1E-02	2E+00
BIOCARTA	m_pyk2Pathway:Links between Pyk2 and Map Kinases	12	1.587301587	1E-03	18751	20779	14784	20662	26395	1546	182	27	1171	3E+00	2E-01	1E-02	2E+00
BIOCARTA	m_trkaPathway:Trka Receptor Signaling Pathway	8	1.058201058	1E-03	18751	18708	18211	14784	20662	1546	182	13	1171	4E+00	3E-01	1E-02	2E+00
BIOCARTA	m_lectinPathway:Lectin Induced Complement Pathway	8	1.058201058	1E-03	17175	12266	17174	12279	15139	1241	182	13	1171	4E+00	3E-01	1E-02	2E+00
BIOCARTA	m_rasPathway:Ras Signaling Pathway	10	1.322751323	1E-03	18708	12015	12048	26395	15461	1165	182	20	1171	3E+00	3E-01	1E-02	2E+00
BIOCARTA	m_tcrPathway:T Cell Receptor Signaling Pathway	14	1.851851852	2E-03	22324	14281	20416	18751	18708	1478	182	36	1171	3E+00	3E-01	1E-02	2E+00
BIOCARTA	m_rbPathway:RB Tumor Suppressor/Checkpoint Signaling in response to DNA dam	7	0.925925926	3E-03	19645	22390	12649	12567	12532	1256	182	11	1171	4E+00	5E-01	3E-02	4E+00
BIOCARTA	m_il22bpathway:IL22 Soluble Receptor Signaling Pathway	6	0.793650794	3E-03	20848	20846	12702	16451	16154	2085	182	8	1171	5E+00	5E-01	3E-02	4E+00
BIOCARTA	m_ngfPathway:Nerve growth factor pathway (NGF)	9	1.19047619	5E-03	18708	14784	20662	26395	15461	1647	182	19	1171	3E+00	6E-01	4E-02	6E+00
BIOCARTA	m_HBxPathway:Calcium Signaling by HBx of Hepatitis B virus	6	0.793650794	6E-03	20779	14784	20662	15461	20416	1291	182	9	1171	4E+00	8E-01	5E-02	8E+00
BIOCARTA	m_alternativePathway:Alternative Complement Pathway	6	0.793650794	6E-03	12266	14962	12279	15139	12417	1227	182	9	1171	4E+00	8E-01	5E-02	8E+00
BIOCARTA	m_il2Pathway:IL 2 signaling pathway	10	1.322751323	7E-03	14784	20662	26395	15461	16476	1645	182	24	1171	3E+00	8E-01	5E-02	8E+00
BIOCARTA	m_ptenPathway:PTEN dependent cell cycle arrest and apoptosis	9	1.19047619	7E-03	18708	14784	20662	14083	18607	1165	182	20	1171	3E+00	8E-01	5E-02	8E+00
BIOCARTA	m_chemicalPathway:Apoptotic Signaling in Response to DNA Damage	9	1.19047619	7E-03	18751	672195	20846	12015	12048	140	182	20	1171	3E+00	8E-01	5E-02	8E+00
BIOCARTA	m_g1Pathway:Cell Cycle: G1/S Check Point	10	1.322751323	9E-03	19645	12571	245000	12443	12567	125	182	25	1171	3E+00	9E-01	6E-02	1E+01
BIOCARTA	m_gpcrPathway:Signaling Pathway from G-Protein Families	10	1.322751323	9E-03	18751	18747	26395	15461	16476	1428	182	25	1171	3E+00	9E-01	6E-02	1E+01
BIOCARTA	m_cardiacegfPathway:Role of EGF Receptor Transactivation by GPCRs in Cardiac Hy	8	1.058201058	9E-03	18751	13649	11489	15461	16476	1428	182	17	1171	3E+00	9E-01	6E-02	1E+01
BIOCARTA	m_erk5Pathway:Role of Erk5 in Neuronal Survival	7	0.925925926	1E-02	18708	18211	14784	15461	11651	2041	182	14	1171	3E+00	9E-01	8E-02	2E+01
BIOCARTA	m_badPathway:Regulation of BAD phosphorylation	8	1.058201058	1E-02	18708	18747	12015	12048	12984	1165	182	18	1171	3E+00	9E-01	8E-02	2E+01
BIOCARTA	m_srcRPTPPathway:Activation of Src by Protein-tyrosine phosphatase alpha	5	0.661375661	1E-02	18751	20779	14784	12532	12534		182	7	1171	5E+00	9E-01	8E-02	2E+01
BIOCARTA	m_mcmPathway:CDK Regulation of DNA Replication	5	0.661375661	1E-02	17217	26429	12566	23834	12576		182	7	1171	5E+00	9E-01	8E-02	2E+01
BIOCARTA	m_eifPathway:Eukaryotic protein translation	5	0.661375661	1E-02	13669	217869	13664	13629	67204	100	182	7	1171	5E+00	9E-01	8E-02	2E+01
BIOCARTA	m_cellcyclePathway:Cyclins and Cell Cycle Regulation	9	1.19047619	2E-02	19645	12571	12443	12567	12566	1253	182	23	1171	3E+00	1E+00	1E-01	2E+01
BIOCARTA	m_longevityPathway:The IGF-1 Receptor and Longevity	6	0.793650794	2E-02	18708	15461	11651	20416	14600	1600	182	11	1171	4E+00	1E+00	1E-01	2E+01
BIOCARTA	m_biopeptidesPathway:Bioactive Peptide Induced Signaling Pathway	11	1.455026455	2E-02	18751	20846	14784	20662	26395	1546	182	32	1171	2E+00	1E+00	1E-01	2E+01
BIOCARTA	m_eif4Pathway:Regulation of eIF4e and p70 S6 Kinase	8	1.058201058	2E-02	13684	18751	18708	16367	18607	1165	182	20	1171	3E+00	1E+00	1E-01	3E+01
BIOCARTA	m_igf1mtorpathway:Skeletal muscle hypertrophy is regulated via AKT/mTOR pathwa	8	1.058201058	2E-02	13684	18708	26905	13665	67204	1860	182	20	1171	3E+00	1E+00	1E-01	3E+01
BIOCARTA	m_nkcellspPathway:Ras-Independent pathway in NK cell-mediated cytotoxicity	7	0.925925926	3E-02	18708	15170	22324	26395	16412	1847	182	16	1171	3E+00	1E+00	1E-01	3E+01
BIOCARTA	m_p53Pathway:p53 Signaling Pathway	7	0.925925926	3E-02	19645	12443	12567	12043	12566	1853	182	16	1171	3E+00	1E+00	1E-01	3E+01
BIOCARTA	m_cblPathway:CBL mediated ligand-induced downregulation of EGF receptors	6	0.793650794	3E-02	18751	13649	20779	14784	12978	1364	182	12	1171	3E+00	1E+00	1E-01	3E+01
BIOCARTA	m_crebPathway:Transcription factor CREB and its extracellular signals	8	1.058201058	3E-02	18751	18708	18747	14784	20662	1546	182	21	1171	2E+00	1E+00	2E-01	3E+01
BIOCARTA	m_erkPPathway:Erk1/Erk2 Mapk Signaling pathway	10	1.322751323	4E-02	20848	13649	20779	14784	20662	2639	182	31	1171	2E+00	1E+00	2E-01	4E+01
BIOCARTA	m_telPathway:Telomeres, Telomerase, Cellular Aging, and Immortality	7	0.925925926	5E-02	13649	20020	19645	16653	18750	1165	182	18	1171	3E+00	1E+00	2E-01	5E+01
BIOCARTA	m_ErbB3Pathway:Neuroregulin receptor degradation protein-1 Controls ErbB3 rece	4	0.529100529	5E-02	13649	13867	216080	13645			182	6	1171	4E+00	1E+00	2E-01	5E+01
BIOCARTA	m_jresPathway:Internal Ribosome entry pathway	4	0.529100529	5E-02	13684	13669	19205	13681			182	6	1171	4E+00	1E+00	2E-01	5E+01
BIOCARTA	m_mCalpainPathway:mCalpain and friends in Cell motility	6	0.793650794	5E-02	18747	13649	14083	15461	16412	1364	182	14	1171	3E+00	1E+00	2E-01	5E+01
BIOCARTA	m_hcmvPathway:Human Cytomegalovirus and Map Kinase Pathways	6	0.793650794	5E-02	18708	19645	26395	11651	12912	2640	182	14	1171	3E+00	1E+00	2E-01	5E+01
BIOCARTA	m_cdMacPathway:Cadmium induces DNA synthesis and proliferation in macrophagi	6	0.793650794	5E-02	18751	26395	15461	16476	14281	1101	182	14	1171	3E+00	1E+00	2E-01	5E+01
BIOCARTA	m_dreampathway:Repression of Pain Sensation by the Transcriptional Regulator DR	5	0.661375661	5E-02	18747	20020	16476	14281	12912		182	10	1171	3E+00	1E+00	2E-01	5E+01
BIOCARTA	m_rhoPathway:Rho cell motility signaling pathway	7	0.925925926	6E-02	20779	94190	11856	11855	171207	168	182	19	1171	2E+00	1E+00	2E-01	5E+01
BIOCARTA	m_arenrf2Pathway:Oxidative Stress Induced Gene Expression Via Nrf2	7	0.925925926	6E-02	18751	11911	16476	14281	12912	9428	182	19	1171	2E+00	1E+00	2E-01	5E+01
BIOCARTA	m_keratinocytePathway:Keratinocyte Differentiation	11	1.455026455	7E-02	18751	13649	18753	26408	26395	1546	182	39	1171	2E+00	1E+00	3E-01	6E+01
BIOCARTA	m_plcPathway:Phospholipase C Signaling Pathway	4	0.529100529	8E-02	18751	18708	22324	11651			182	7	1171	4E+00	1E+00	3E-01	6E+01
BIOCARTA	m_cdc25Pathway:cdc25 and chk1 Regulatory Pathway in response to DNA damage	4	0.529100529	8E-02	22390	12649	12532	12534			182	7	1171	4E+00	1E+00	3E-01	6E+01
BIOCARTA	m_agrPathway:Agurin in Postsynaptic Differentiation	8	1.058201058	9E-02	73341	13649	20779	14083	16476	1254	182	26	1171	2E+00	1E+00	3E-01	7E+01
BIOCARTA	m_uclapainPathway:uClapain and friends in Cell spread	5	0.661375661	1E-01	20779	14083	16412	16416	11848		182	12	1171	3E+00	1E+00	4E-01	7E+01
BIOCARTA	m_il4Pathway:IL 4 signaling pathway	5	0.661375661	1E-01	16367	14784	11651	16451	20416		182	12	1171	3E+00	1E+00	4E-01	7E+01
KEGG_PATHWAY	mmu03010:Ribosome	64	8.465608466	2E-46	666899	100048462	20103	100044516	1		525	89	5738	8E+00	3E-44	3E-44	3E-43
KEGG_PATHWAY	mmu00190:Oxidative phosphorylation	71	9.391534392	9E-40	70316	226646	100041273	66377	10004		525	130	5738	6E+00	1E-37	7E-38	1E-36
KEGG_PATHWAY	mmu05012:Parkinson's disease	68	8.994708995	1E-35	70316	672195	226646	100041273	6637		525	133	5738	6E+00	2E-33	6E-34	1E-32
KEGG_PATHWAY	mmu05010:Alzheimer's disease	73	9.656084656	9E-30	70316	226646	672195	100041273	6637		525	182	5738	4E+00	1E-27	4E-28	1E-26
KEGG_PATHWAY	mmu04110:Cell cycle	58	7.671957672	8E-27	12571	50793	59008	12914	17218	1721	525	128	5738	5E+00	1E-24	2E-25	9E-24
KEGG_PATHWAY	mmu05016:Huntington's disease	67	8.862433862	1E-24	70316	672195	226646	100041273	6637		525	183	5738	4E+00	2E-22	4E-23	2E-21
KEGG_PATHWAY	mmu04722:Neurotrophin signaling pathway	46	6.084656085	4E-16	11911	19247	192662	11651	11652	100	525	130	5738	4E+00	7E-14	1E-14	5E-13
KEGG_PATHWAY	mmu04914:Progesterone-mediated oocyte maturation	36	4.761904762	2E-15	18747	11651	59008	11652	100048123		525	85	5738	5E+00	3E-13	3E-14	2E-12
KEGG_PATHWAY	mmu04114:Oocyte meiosis	41	5.423280423	1E-14	18747	26965	59008	103583	67141	122	525	115	5738	4E+00	2E-12	2E-13	2E-11
KEGG_PATHWAY	mmu00010:Glycolysis / Gluconeogenesis	30	3.968253968	2E-13	18746	68263	100042746	15275	15277		525	68	5738	5E+00	2E-11	2E-12	2E-10
KEGG_PATHWAY	mmu05220:Chronic myeloid leukemia	31	4.100529101	7E-13	19247	12571	11651	11652	100048123		525	76	5738	4E+00	1E-10	1E-11	8E-10



KEGG_PATHWAY	mmu04012:ErbB signaling pathway	32	4.232804233	7.E-12	13649	11651	11652	100048123	20416	525	87	5738	4.E+00	1.E-09	9.E-11	8.E-09	
KEGG_PATHWAY	mmu05212:Pancreatic cancer	28	3.703703704	4.E-11	12190	13649	12571	11651	11652	1000	525	72	5738	4.E+00	7.E-09	5.E-10	5.E-08
KEGG_PATHWAY	mmu00030:Pentose phosphate pathway	17	2.248677249	4.E-11	19895	72157	18641	18642	11676	6617	525	26	5738	7.E+00	7.E-09	5.E-10	5.E-08
KEGG_PATHWAY	mmu05223:Non-small cell lung cancer	24	3.174603175	6.E-11	13649	12571	11651	11652	100048123		525	54	5738	5.E+00	9.E-09	6.E-10	7.E-08
KEGG_PATHWAY	mmu04062:Chemokine signaling pathway	47	6.216931217	6.E-11	22324	18747	12765	100048123	22376		525	182	5738	3.E+00	1.E-08	6.E-10	7.E-08
KEGG_PATHWAY	mmu05214:Glioma	26	3.439153439	8.E-11	13649	12571	11651	11652	100048123		525	64	5738	4.E+00	1.E-08	7.E-10	1.E-07
KEGG_PATHWAY	mmu05215:Prostate cancer	30	3.968253968	6.E-10	13649	11911	11651	11652	100048123		525	90	5738	4.E+00	9.E-08	5.E-09	7.E-07
KEGG_PATHWAY	mmu04662:B cell receptor signaling pathway	28	3.703703704	7.E-10	22324	11651	11652	100048123	170758		525	80	5738	4.E+00	1.E-07	6.E-09	8.E-07
KEGG_PATHWAY	mmu04510:Focal adhesion	47	6.216931217	1.E-09	22324	100048123	170758	18709	18708		525	198	5738	3.E+00	2.E-07	1.E-08	2.E-06
KEGG_PATHWAY	mmu04370:VEGF signaling pathway	25	3.306878307	3.E-08	11651	11652	100048123	170758	18709		525	76	5738	4.E+00	4.E-06	2.E-07	3.E-05
KEGG_PATHWAY	mmu04910:Insulin signaling pathway	35	4.62962963	4.E-08	13684	18747	20411	11651	15275	1165	525	138	5738	3.E+00	7.E-06	3.E-07	5.E-05
KEGG_PATHWAY	mmu05200:Pathways in cancer	60	7.936507937	9.E-08	12190	672195	12571	100048123	17075		525	323	5738	2.E+00	1.E-05	6.E-07	1.E-04
KEGG_PATHWAY	mmu04610:Complement and coagulation cascades	24	3.174603175	1.E-07	12266	17175	17174	50908	12259	1496	525	75	5738	3.E+00	2.E-05	6.E-07	1.E-04
KEGG_PATHWAY	mmu05211:Renal cell carcinoma	23	3.042328042	1.E-07	19247	11651	11652	100048123	12914		525	70	5738	4.E+00	2.E-05	7.E-07	1.E-04
KEGG_PATHWAY	mmu05213:Endometrial cancer	19	2.513227513	3.E-07	13649	16653	11651	11652	100048123		525	52	5738	4.E+00	5.E-05	2.E-06	4.E-04
KEGG_PATHWAY	mmu04010:MAPK signaling pathway	51	6.746031746	3.E-07	18747	11911	12475	100048123	170758		525	265	5738	2.E+00	5.E-05	2.E-06	4.E-04
KEGG_PATHWAY	mmu04650:Natural killer cell mediated cytotoxicity	30	3.968253968	1.E-06	22324	19247	20416	170758	20418	187	525	122	5738	3.E+00	2.E-04	5.E-06	1.E-03
KEGG_PATHWAY	mmu05221:Acute myeloid leukemia	19	2.513227513	2.E-06	16653	11651	11652	100048123	18176		525	57	5738	4.E+00	2.E-04	8.E-06	2.E-03
KEGG_PATHWAY	mmu04660:T cell receptor signaling pathway	29	3.835978836	2.E-06	22324	19264	11651	11652	100048123		525	118	5738	3.E+00	2.E-04	8.E-06	2.E-03
KEGG_PATHWAY	mmu04720:Long-term potentiation	21	2.777777778	2.E-06	18747	11911	16653	18176	12914	1875	525	70	5738	3.E+00	4.E-04	1.E-05	3.E-03
KEGG_PATHWAY	mmu04664:Fc epsilon RI signaling pathway	23	3.042328042	2.E-06	22324	12229	16653	14389	11651	5725	525	82	5738	3.E+00	4.E-04	1.E-05	3.E-03
KEGG_PATHWAY	mmu05210:Colorectal cancer	22	2.91005291	2.E-05	672195	13649	16653	11651	12043	116	525	86	5738	3.E+00	3.E-03	1.E-04	2.E-02
KEGG_PATHWAY	mmu04810:Regulation of actin cytoskeleton	40	5.291005291	2.E-05	12475	13649	22324	170758	13645	218	525	217	5738	2.E+00	4.E-03	1.E-04	3.E-02
KEGG_PATHWAY	mmu05020:Prion diseases	13	1.71957672	3.E-05	18747	12259	12279	69379	15139	2639	525	35	5738	4.E+00	5.E-03	2.E-04	4.E-02
KEGG_PATHWAY	mmu05218:Melanoma	19	2.513227513	5.E-05	13649	12571	16653	11651	11652	1000	525	71	5738	3.E+00	7.E-03	2.E-04	5.E-02
KEGG_PATHWAY	mmu04666:Fc gamma R-mediated phagocytosis	23	3.042328042	5.E-05	22324	19264	14389	11651	12929	5725	525	98	5738	3.E+00	8.E-03	2.E-04	6.E-02
KEGG_PATHWAY	mmu05222:Small cell lung cancer	21	2.777777778	6.E-05	22029	672195	12571	14083	11651	120	525	85	5738	3.E+00	9.E-03	2.E-04	7.E-02
KEGG_PATHWAY	mmu04210:Apoptosis	20	2.645502646	2.E-04	672195	18747	11651	12043	11652	100	525	87	5738	3.E+00	4.E-02	1.E-03	3.E-01
KEGG_PATHWAY	mmu05219:Bladder cancer	13	1.71957672	3.E-04	13649	16653	18176	13645	19645	1386	525	42	5738	3.E+00	4.E-02	1.E-03	3.E-01
KEGG_PATHWAY	mmu04120:Ubiquitin mediated proteolysis	26	3.439153439	5.E-04	56550	218793	26965	246710	59008	10	525	136	5738	2.E+00	7.E-02	2.E-03	6.E-01
KEGG_PATHWAY	mmu00620:Pyruvate metabolism	12	1.587301587	8.E-04	18746	16828	18770	68263	17448	2353	525	41	5738	3.E+00	1.E-01	3.E-03	1.E+00
KEGG_PATHWAY	mmu03030:DNA replication	11	1.455026455	8.E-04	17218	19891	17217	17220	17216	1721	525	35	5738	3.E+00	1.E-01	3.E-03	1.E+00
KEGG_PATHWAY	mmu04912:GnRH signaling pathway	20	2.645502646	1.E-03	18747	13649	11911	16653	18176	1875	525	97	5738	2.E+00	1.E-01	4.E-03	1.E+00
KEGG_PATHWAY	mmu04115:p53 signaling pathway	16	2.116402116	1.E-03	672195	12571	245000	12649	58801	12	525	69	5738	3.E+00	2.E-01	4.E-03	1.E+00
KEGG_PATHWAY	mmu04930:Type II diabetes mellitus	13	1.71957672	1.E-03	18746	15275	15277	384783	103988	21	525	49	5738	3.E+00	2.E-01	4.E-03	1.E+00
KEGG_PATHWAY	mmu00020:Citrate cycle (TCA cycle)	10	1.322751323	1.E-03	68263	17448	235339	18597	78920	185	525	31	5738	4.E+00	2.E-01	4.E-03	2.E+00
KEGG_PATHWAY	mmu00051:Fructose and mannose metabolism	11	1.455026455	1.E-03	56421	15275	21991	230163	15277	186	525	37	5738	3.E+00	2.E-01	4.E-03	2.E+00
KEGG_PATHWAY	mmu04260:Cardiac muscle contraction	17	2.248677249	2.E-03	66694	17705	17706	66445	66142	1771	525	78	5738	2.E+00	2.E-01	5.E-03	2.E+00
KEGG_PATHWAY	mmu00150:Androgen and estrogen metabolism	10	1.322751323	2.E-03	15490	100043456	56348	54200	15493		525	33	5738	3.E+00	3.E-01	7.E-03	3.E+00
KEGG_PATHWAY	mmu04630:JAK-STAT signaling pathway	26	3.439153439	3.E-03	19247	11651	11652	100048123	12914		525	152	5738	2.E+00	3.E-01	8.E-03	3.E+00
KEGG_PATHWAY	mmu04360:Axon guidance	23	3.042328042	3.E-03	117600	16653	14083	11854	14678	142	525	131	5738	2.E+00	4.E-01	1.E-02	4.E+00
KEGG_PATHWAY	mmu04540:Gap junction	17	2.248677249	4.E-03	18747	13649	16653	14678	18176	1364	525	86	5738	2.E+00	5.E-01	1.E-02	5.E+00
KEGG_PATHWAY	mmu04670:Leukocyte transendothelial migration	21	2.777777778	5.E-03	22324	69524	19247	14083	14678	1797	525	119	5738	2.E+00	6.E-01	1.E-02	6.E+00
KEGG_PATHWAY	mmu00140:Steroid hormone biosynthesis	11	1.455026455	6.E-03	56348	15490	100043456	15493	54200		525	45	5738	3.E+00	6.E-01	2.E-02	7.E+00
KEGG_PATHWAY	mmu04520:Adherens junction	15	1.984126984	8.E-03	13649	15170	20411	22330	170758	129	525	76	5738	2.E+00	7.E-01	2.E-02	9.E+00
KEGG_PATHWAY	mmu00270:Cysteine and methionine metabolism	9	1.19047619	8.E-03	269378	16828	232087	13436	16833	16	525	33	5738	3.E+00	7.E-01	2.E-02	9.E+00
KEGG_PATHWAY	mmu04150:mTOR signaling pathway	12	1.587301587	8.E-03	13684	11651	11652	100048123	18709		525	54	5738	2.E+00	7.E-01	2.E-02	1.E+01
KEGG_PATHWAY	mmu00052:Galactose metabolism	8	1.058201058	9.E-03	56421	15275	72157	15277	18641	1864	525	27	5738	3.E+00	8.E-01	2.E-02	1.E+01
KEGG_PATHWAY	mmu05322:Systemic lupus erythematosus	18	2.380952381	1.E-02	12266	50908	12259	15078	12279	6937	525	103	5738	2.E+00	8.E-01	3.E-02	1.E+01
KEGG_PATHWAY	mmu04960:Aldosterone-regulated sodium reabsorption	10	1.322751323	1.E-02	18709	18751	18708	16367	16653	1107	525	42	5738	3.E+00	8.E-01	3.E-02	1.E+01
KEGG_PATHWAY	mmu04730:Long-term depression	14	1.851851852	1.E-02	14674	16653	14678	18176	18751	1878	525	72	5738	2.E+00	9.E-01	3.E-02	1.E+01
KEGG_PATHWAY	mmu05216:Thyroid cancer	8	1.058201058	1.E-02	18211	16653	12443	26395	15461	1089	525	29	5738	3.E+00	9.E-01	3.E-02	2.E+01
KEGG_PATHWAY	mmu00100:Steroid biosynthesis	6	0.793650794	2.E-02	15490	66234	14137	18194	16987	2077	525	17	5738	4.E+00	9.E-01	4.E-02	2.E+01
KEGG_PATHWAY	mmu04310:Wnt signaling pathway	22	2.91005291	3.E-02	18747	26965	103583	21402	170758	12	525	149	5738	2.E+00	1.E+00	7.E-02	3.E+01
KEGG_PATHWAY	mmu05014:Amyotrophic lateral sclerosis (ALS)	11	1.455026455	3.E-02	672195	12015	12048	26408	12043	190	525	57	5738	2.E+00	1.E+00	7.E-02	3.E+01
KEGG_PATHWAY	mmu04920:Adipocytokine signaling pathway	12	1.587301587	4.E-02	19247	11651	11652	100048123	384783		525	67	5738	2.E+00	1.E+00	9.E-02	4.E+01
KEGG_PATHWAY	mmu04320:Dorso-ventral axis formation	6	0.793650794	4.E-02	13649	16653	14784	20662	20663	2639	525	22	5738	3.E+00	1.E+00	1.E-01	4.E+01
KEGG_PATHWAY	mmu00640:Propanoate metabolism	7	0.925925926	5.E-02	16828	74147	73724	68738	16833	1683	525	30	5738	3.E+00	1.E+00	1.E-01	5.E+01



T/C/SC-PPI-David-Lung

Mus musculus (655)
Unknown (2)

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0006006~glucose metabolic process	54	8.477237049	5E-37	18746, 68263, 18679, 11676, 56012, 1167	572	140	13588	9.E+00	1.E-33	1.E-33	9.E-34
GOTERM_BP_FAT	GO:0019318~hexose metabolic process	55	8.63422292	3E-33	18746, 68263, 18679, 11676, 56012, 1167	572	169	13588	8.E+00	8.E-30	4.E-30	5.E-30
GOTERM_BP_FAT	GO:0019320~hexose catabolic process	34	5.337519623	5.E-33	18746, 68263, 100042746, 15275, 15277,	572	52	13588	2.E+01	1.E-29	5.E-30	1.E-29
GOTERM_BP_FAT	GO:0006007~glucose catabolic process	34	5.337519623	5.E-33	18746, 68263, 100042746, 15275, 15277,	572	52	13588	2.E+01	1.E-29	5.E-30	1.E-29
GOTERM_BP_FAT	GO:0046365~monosaccharide catabolic process	34	5.337519623	3.E-32	18746, 68263, 100042746, 15275, 15277,	572	54	13588	1.E+01	9.E-29	2.E-29	6.E-29
GOTERM_BP_FAT	GO:0005996~monosaccharide metabolic process	56	8.791208791	3.E-31	18746, 68263, 18679, 11676, 56012, 1167	572	191	13588	7.E+00	8.E-28	2.E-28	5.E-28
GOTERM_BP_FAT	GO:0044275~cellular carbohydrate catabolic process	34	5.337519623	4.E-30	18746, 68263, 100042746, 15275, 15277,	572	60	13588	1.E+01	1.E-26	2.E-27	8.E-27
GOTERM_BP_FAT	GO:0046164~alcohol catabolic process	35	5.494505495	6.E-30	18746, 68263, 100042746, 15275, 15277,	572	65	13588	1.E+01	2.E-26	2.E-27	1.E-26
GOTERM_BP_FAT	GO:0006096~glycolysis	30	4.709576138	8.E-30	18746, 68263, 100042746, 15275, 15277,	572	44	13588	2.E+01	2.E-26	3.E-27	1.E-26
GOTERM_BP_FAT	GO:0016052~carbohydrate catabolic process	34	5.337519623	1.E-24	18746, 68263, 100042746, 15275, 15277,	572	81	13588	1.E+01	3.E-21	4.E-22	2.E-21
GOTERM_BP_FAT	GO:0007242~intracellular signaling cascade	109	17.11145997	1.E-23	22324, 19744, 192662, 16800, 170758, 16	572	915	13588	3.E+00	3.E-20	3.E-21	2.E-20
GOTERM_BP_FAT	GO:0006091~generation of precursor metabolites and energy	49	7.692307692	2.E-18	18746, 672195, 68263, 18679, 11676, 560	572	261	13588	4.E+00	6.E-15	5.E-16	4.E-15
GOTERM_BP_FAT	GO:0035023~regulation of Rho protein signal transduction	29	4.552590267	5.E-18	22324, 13605, 16800, 442801, 53972, 218	572	86	13588	8.E+00	1.E-14	1.E-15	8.E-15
GOTERM_BP_FAT	GO:0000278~mitotic cell cycle	41	6.436420722	1.E-13	19384, 12454, 12236, 16800, 59008, 5615	572	244	13588	4.E+00	3.E-10	2.E-11	2.E-10
GOTERM_BP_FAT	GO:0007264~small GTPase mediated signal transduction	42	6.593406593	1.E-13	228543, 117600, 19744, 232906, 11852, 1	572	258	13588	4.E+00	4.E-10	3.E-11	3.E-10
GOTERM_BP_FAT	GO:0007067~mitosis	35	5.494505495	6.E-13	19384, 12454, 12236, 59008, 16800, 5615	572	190	13588	4.E+00	2.E-09	1.E-10	1.E-09
GOTERM_BP_FAT	GO:0000280~nuclear division	35	5.494505495	6.E-13	19384, 12454, 12236, 59008, 16800, 5615	572	190	13588	4.E+00	2.E-09	1.E-10	1.E-09
GOTERM_BP_FAT	GO:0051301~cell division	43	6.750392465	6.E-13	19384, 12454, 12236, 16800, 59008, 5615	572	281	13588	4.E+00	2.E-09	1.E-10	1.E-09
GOTERM_BP_FAT	GO:0000087~M phase of mitotic cell cycle	35	5.494505495	1.E-12	19384, 12454, 12236, 59008, 16800, 5615	572	194	13588	4.E+00	3.E-09	2.E-10	2.E-09
GOTERM_BP_FAT	GO:0048285~organelle fission	35	5.494505495	2.E-12	19384, 12454, 12236, 59008, 16800, 5615	572	197	13588	4.E+00	5.E-09	3.E-10	3.E-09
GOTERM_BP_FAT	GO:0030029~actin filament-based process	33	5.180533752	2.E-12	22323, 215280, 227753, 94190, 11856, 16	572	176	13588	4.E+00	5.E-09	3.E-10	3.E-09
GOTERM_BP_FAT	GO:0046578~regulation of Ras protein signal transduction	32	5.023547881	2.E-11	22324, 13605, 442801, 16800, 53972, 218	572	181	13588	4.E+00	6.E-08	3.E-09	4.E-08
GOTERM_BP_FAT	GO:0007049~cell cycle	64	10.04709576	3.E-11	19384, 16952, 243362, 22778, 59008, 168	572	611	13588	2.E+00	8.E-08	4.E-09	5.E-08
GOTERM_BP_FAT	GO:0030036~actin cytoskeleton organization	30	4.709576138	5.E-11	22323, 227753, 94190, 11856, 16800, 204	572	165	13588	4.E+00	1.E-07	6.E-09	8.E-08
GOTERM_BP_FAT	GO:0045321~leukocyte activation	34	5.337519623	2.E-10	22324, 22778, 16803, 22376, 58240, 1205	572	219	13588	4.E+00	4.E-07	2.E-08	3.E-07
GOTERM_BP_FAT	GO:0001775~cell activation	36	5.651491366	2.E-10	22324, 22778, 16803, 22376, 58240, 1205	572	246	13588	3.E+00	6.E-07	3.E-08	4.E-07
GOTERM_BP_FAT	GO:0022402~cell cycle process	46	7.221350078	9.E-10	19384, 12454, 12236, 16800, 59008, 5615	572	393	13588	3.E+00	2.E-06	1.E-07	2.E-06
GOTERM_BP_FAT	GO:0022403~cell cycle phase	41	6.436420722	1.E-09	19384, 12454, 12236, 16800, 59008, 5615	572	328	13588	3.E+00	3.E-06	1.E-07	2.E-06
GOTERM_BP_FAT	GO:0051056~regulation of small GTPase mediated signal transducti	33	5.180533752	2.E-09	22324, 13605, 442801, 16800, 53972, 218	572	228	13588	3.E+00	5.E-06	2.E-07	3.E-06
GOTERM_BP_FAT	GO:0046649~lymphocyte activation	29	4.552590267	7.E-09	22324, 22778, 22376, 58240, 16408, 1205	572	191	13588	4.E+00	2.E-05	7.E-07	1.E-05
GOTERM_BP_FAT	GO:0000279~M phase	36	5.651491366	1.E-08	19384, 12454, 12236, 16800, 59008, 5615	572	283	13588	3.E+00	3.E-05	9.E-07	2.E-05
GOTERM_BP_FAT	GO:0042110~T cell activation	22	3.453689168	1.E-08	22324, 16414, 12043, 22778, 74734, 1081	572	116	13588	5.E+00	4.E-05	1.E-06	2.E-05
GOTERM_BP_FAT	GO:0043603~cellular amide metabolic process	13	2.040816327	4.E-08	18416, 19895, 17970, 109900, 11847, 103	572	39	13588	8.E+00	1.E-04	3.E-06	7.E-05
GOTERM_BP_FAT	GO:0016310~phosphorylation	63	9.89010989	5.E-08	13665, 72508, 12912, 16818, 18708, 2392	572	718	13588	2.E+00	1.E-04	4.E-06	8.E-05
GOTERM_BP_FAT	GO:0042325~regulation of phosphorylation	35	5.494505495	6.E-08	13649, 20416, 15163, 18709, 56717, 1859	572	290	13588	3.E+00	2.E-04	5.E-06	1.E-04
GOTERM_BP_FAT	GO:0044093~positive regulation of molecular function	36	5.651491366	7.E-08	672195, 66593, 11856, 17869, 20416, 129	572	306	13588	3.E+00	2.E-04	6.E-06	1.E-04
GOTERM_BP_FAT	GO:0006796~phosphate metabolic process	71	11.14599686	8.E-08	218294, 13665, 72508, 12912, 23920, 187	572	866	13588	2.E+00	2.E-04	6.E-06	1.E-04
GOTERM_BP_FAT	GO:0006793~phosphorus metabolic process	71	11.14599686	8.E-08	218294, 13665, 72508, 12912, 23920, 187	572	866	13588	2.E+00	2.E-04	6.E-06	1.E-04
GOTERM_BP_FAT	GO:0010033~response to organic substance	49	7.692307692	1.E-07	12475, 16803, 12912, 14645, 12010, 1590	572	505	13588	2.E+00	3.E-04	8.E-06	2.E-04
GOTERM_BP_FAT	GO:0031399~regulation of protein modification process	25	3.924646782	1.E-07	13649, 67141, 15163, 18596, 56717, 1270	572	165	13588	4.E+00	3.E-04	8.E-06	2.E-04
GOTERM_BP_FAT	GO:0001932~regulation of protein amino acid phosphorylation	21	3.296703297	1.E-07	13649, 15170, 11806, 21899, 19088, 1204	572	121	13588	4.E+00	4.E-04	1.E-05	3.E-04
GOTERM_BP_FAT	GO:0051174~regulation of phosphorus metabolic process	35	5.494505495	1.E-07	13649, 20416, 15163, 18709, 56717, 1859	572	301	13588	3.E+00	4.E-04	1.E-05	3.E-04
GOTERM_BP_FAT	GO:0019220~regulation of phosphate metabolic process	35	5.494505495	1.E-07	13649, 20416, 15163, 18709, 56717, 1859	572	301	13588	3.E+00	4.E-04	1.E-05	3.E-04
GOTERM_BP_FAT	GO:0051336~regulation of hydrolase activity	27	4.238618524	2.E-07	22324, 672195, 66593, 17869, 11856, 145	572	196	13588	3.E+00	5.E-04	1.E-05	4.E-04
GOTERM_BP_FAT	GO:0006468~protein amino acid phosphorylation	56	8.791208791	3.E-07	13665, 72508, 12912, 16818, 18708, 2392	572	640	13588	2.E+00	9.E-04	2.E-05	6.E-04
GOTERM_BP_FAT	GO:0007169~transmembrane receptor protein tyrosine kinase signa	26	4.081632653	5.E-07	13649, 13685, 14178, 11651, 21844, 1870	572	192	13588	3.E+00	1.E-03	3.E-05	9.E-04
GOTERM_BP_FAT	GO:0006739~NADP metabolic process	8	1.25588697	6.E-07	19895, 17970, 21991, 21351, 17969, 6617	572	14	13588	1.E+01	2.E-03	4.E-05	1.E-03
GOTERM_BP_FAT	GO:0030097~hemopoiesis	30	4.709576138	8.E-07	22324, 22778, 15163, 15902, 58240, 1205	572	251	13588	3.E+00	2.E-03	5.E-05	1.E-03
GOTERM_BP_FAT	GO:0032268~regulation of cellular protein metabolic process	32	5.023547881	8.E-07	13684, 13649, 13685, 13665, 11651, 6714	572	280	13588	3.E+00	2.E-03	5.E-05	1.E-03
GOTERM_BP_FAT	GO:0048534~hemopoietic or lymphoid organ development	32	5.023547881	9.E-07	22324, 22778, 15163, 15902, 58240, 1205	572	281	13588	3.E+00	2.E-03	5.E-05	2.E-03
GOTERM_BP_FAT	GO:0007010~cytoskeleton organization	35	5.494505495	1.E-06	22323, 227753, 94190, 11856, 16800, 204	572	326	13588	3.E+00	3.E-03	6.E-05	2.E-03
GOTERM_BP_FAT	GO:0009725~response to hormone stimulus	23	3.610675039	2.E-06	13685, 12842, 109900, 232087, 11651, 12	572	165	13588	3.E+00	4.E-03	9.E-05	3.E-03
GOTERM_BP_FAT	GO:0043085~positive regulation of catalytic activity	30	4.709576138	2.E-06	672195, 66593, 11856, 17869, 20416, 168	572	261	13588	3.E+00	5.E-03	1.E-04	3.E-03
GOTERM_BP_FAT	GO:0002684~positive regulation of immune system process	22	4.081632653	2.E-06	14972, 15018, 22778, 16396, 16803, 1201	572	206	13588	3.E+00	5.E-03	1.E-04	3.E-03
GOTERM_BP_FAT	GO:0010627~regulation of protein kinase cascade	26	3.453689168	2.E-06	15170, 21899, 21898, 12234, 224014, 151	572	155	13588	3.E+00	6.E-03	1.E-04	4.E-03
GOTERM_BP_FAT	GO:0002520~immune system development	32	5.023547881	3.E-06	22324, 22778, 15163, 15902, 58240, 1205	572	295	13588	3.E+00	7.E-03	1.E-04	4.E-03
GOTERM_BP_FAT	GO:0008360~regulation of cell shape	12	1.883830455	3.E-06	80837, 14163, 14674, 232906, 77579, 104	572	47	13588	6.E+00	8.E-03	2.E-04	5.E-03
GOTERM_BP_FAT	GO:0051726~regulation of cell cycle	26	4.081632653	4.E-06	11852, 17869, 56150, 67141, 12234, 1699	572	214	13588	3.E+00	1.E-02	2.E-04	7.E-03
GOTERM_BP_FAT	GO:0007265~Ras protein signal transduction	13	2.040816327	5.E-06	117600, 14674, 192662, 69581, 11848, 80	572	59	13588	5.E+00	1.E-02	3.E-04	9.E-03
GOTERM_BP_FAT	GO:0030098~lymphocyte differentiation	18	2.825745683	5.E-06	22324, 12043, 20375, 74734, 22778, 1081	572	114	13588	4.E+00	1.E-02	3.E-04	9.E-03



GOTERM_BP_FAT	GO:0040402~glucan metabolic process	10	1.569858713	6.E-06	18682, 110095, 16195, 102093, 110094, 1	572	33	13588	7.E+00	2.E-02	3.E-04	1.E-02
GOTERM_BP_FAT	GO:0006073~cellular glucan metabolic process	10	1.569858713	6.E-06	18682, 110095, 16195, 102093, 110094, 1	572	33	13588	7.E+00	2.E-02	3.E-04	1.E-02
GOTERM_BP_FAT	GO:0005977~glycogen metabolic process	10	1.569858713	6.E-06	18682, 110095, 16195, 102093, 110094, 1	572	33	13588	7.E+00	2.E-02	3.E-04	1.E-02
GOTERM_BP_FAT	GO:0009719~response to endogenous stimulus	23	3.610675039	1.E-05	13685, 12842, 109900, 232087, 11651, 12	572	184	13588	3.E+00	3.E-02	5.E-04	2.E-02
GOTERM_BP_FAT	GO:0048584~positive regulation of response to stimulus	23	3.610675039	1.E-05	19370, 14972, 15170, 11657, 15018, 2700	572	186	13588	3.E+00	3.E-02	5.E-04	2.E-02
GOTERM_BP_FAT	GO:0007167~enzyme linked receptor protein signaling pathway	29	4.552590267	1.E-05	13649, 13685, 14178, 11651, 21844, 1870	572	273	13588	3.E+00	3.E-02	6.E-04	2.E-02
GOTERM_BP_FAT	GO:0001568~blood vessel development	27	4.238618524	1.E-05	12831, 11852, 11816, 238055, 11651, 204	572	244	13588	3.E+00	3.E-02	6.E-04	2.E-02
GOTERM_BP_FAT	GO:0050778~positive regulation of immune response	19	2.982731554	2.E-05	19370, 14972, 15170, 15018, 27007, 2189	572	136	13588	3.E+00	4.E-02	7.E-04	3.E-02
GOTERM_BP_FAT	GO:0008283~cell proliferation	27	4.238618524	2.E-05	26965, 12234, 12914, 16408, 12445, 1201	572	247	13588	3.E+00	4.E-02	7.E-04	3.E-02
GOTERM_BP_FAT	GO:0006112~energy reserve metabolic process	10	1.569858713	2.E-05	18682, 110095, 16195, 102093, 110094, 1	572	37	13588	6.E+00	5.E-02	7.E-04	3.E-02
GOTERM_BP_FAT	GO:0007015~actin filament organization	12	1.883830455	2.E-05	227753, 100044475, 18826, 17973, 11464	572	56	13588	5.E+00	5.E-02	7.E-04	3.E-02
GOTERM_BP_FAT	GO:0001944~vasculature development	27	4.238618524	2.E-05	12831, 11852, 11816, 238055, 11651, 204	572	250	13588	3.E+00	5.E-02	8.E-04	3.E-02
GOTERM_BP_FAT	GO:0002757~immune response-activating signal transduction	11	1.726844584	2.E-05	14127, 15170, 17874, 18803, 16818, 1617	572	48	13588	5.E+00	7.E-02	1.E-03	4.E-02
GOTERM_BP_FAT	GO:0002521~leukocyte differentiation	19	2.982731554	3.E-05	22324, 12043, 20375, 74734, 22778, 1081	572	142	13588	3.E+00	7.E-02	1.E-03	5.E-02
GOTERM_BP_FAT	GO:0042592~homeostatic process	47	7.37833595	3.E-05	11816, 11651, 238055, 14782, 12815, 103	572	584	13588	2.E+00	8.E-02	1.E-03	5.E-02
GOTERM_BP_FAT	GO:0001836~release of cytochrome c from mitochondria	7	1.098901099	3.E-05	12048, 12028, 12122, 12018, 12043, 1786	572	16	13588	1.E+01	8.E-02	1.E-03	5.E-02
GOTERM_BP_FAT	GO:0031960~response to corticosteroid stimulus	8	1.25588697	3.E-05	20779, 12842, 18670, 109900, 26395, 120	572	23	13588	8.E+00	8.E-02	1.E-03	5.E-02
GOTERM_BP_FAT	GO:0043434~response to peptide hormone stimulus	15	2.354788069	4.E-05	13685, 12842, 109900, 12043, 11651, 384	572	95	13588	4.E+00	1.E-01	2.E-03	7.E-02
GOTERM_BP_FAT	GO:0046496~nicotinamide nucleotide metabolic process	8	1.25588697	4.E-05	19895, 17970, 21991, 21351, 17969, 6617	572	24	13588	8.E+00	1.E-01	2.E-03	7.E-02
GOTERM_BP_FAT	GO:0009820~alkaloid metabolic process	8	1.25588697	4.E-05	19895, 17970, 21991, 21351, 17969, 6617	572	24	13588	8.E+00	1.E-01	2.E-03	7.E-02
GOTERM_BP_FAT	GO:0006769~nicotinamide metabolic process	8	1.25588697	4.E-05	19895, 17970, 21991, 21351, 17969, 6617	572	24	13588	8.E+00	1.E-01	2.E-03	7.E-02
GOTERM_BP_FAT	GO:0043009~chordate embryonic development	37	5.808477237	4.E-05	22323, 13649, 18107, 232906, 11651, 238	572	421	13588	2.E+00	1.E-01	2.E-03	7.E-02
GOTERM_BP_FAT	GO:0043067~regulation of programmed cell death	45	7.064364207	5.E-05	22029, 672195, 11657, 66593, 11816, 149	572	560	13588	2.E+00	1.E-01	2.E-03	8.E-02
GOTERM_BP_FAT	GO:0002764~immune response-regulating signal transduction	11	1.726844584	5.E-05	14127, 15170, 17874, 18803, 16818, 1617	572	52	13588	5.E+00	1.E-01	2.E-03	9.E-02
GOTERM_BP_FAT	GO:0009792~embryonic development ending in birth or egg hatch	37	5.808477237	5.E-05	22323, 13649, 18107, 232906, 11651, 238	572	425	13588	2.E+00	1.E-01	2.E-03	9.E-02
GOTERM_BP_FAT	GO:0010941~regulation of cell death	45	7.064364207	5.E-05	22029, 672195, 11657, 66593, 11816, 149	572	563	13588	2.E+00	1.E-01	2.E-03	1.E-01
GOTERM_BP_FAT	GO:0008637~apoptotic mitochondrial changes	8	1.25588697	6.E-05	12048, 12028, 12122, 12018, 11651, 1204	572	25	13588	8.E+00	1.E-01	2.E-03	1.E-01
GOTERM_BP_FAT	GO:0015980~energy derivation by oxidation of organic compound	15	2.354788069	6.E-05	17448, 102093, 18534, 11651, 13382, 186	572	98	13588	4.E+00	1.E-01	2.E-03	1.E-01
GOTERM_BP_FAT	GO:0007243~protein kinase cascade	25	3.924646782	6.E-05	72508, 11651, 20416, 12703, 16367, 1478	572	236	13588	3.E+00	1.E-01	2.E-03	1.E-01
GOTERM_BP_FAT	GO:0044264~cellular polysaccharide metabolic process	10	1.569858713	6.E-05	18682, 110095, 16195, 102093, 110094, 1	572	43	13588	6.E+00	2.E-01	2.E-03	1.E-01
GOTERM_BP_FAT	GO:0042981~regulation of apoptosis	44	6.907378336	7.E-05	22029, 672195, 11657, 66593, 11816, 149	572	553	13588	2.E+00	2.E-01	2.E-03	1.E-01
GOTERM_BP_FAT	GO:0048872~homeostasis of number of cells	16	2.51177394	8.E-05	12043, 20375, 11651, 12183, 15902, 1516	572	113	13588	3.E+00	2.E-01	2.E-03	1.E-01
GOTERM_BP_FAT	GO:0050798~activated T cell proliferation	5	0.784929356	1.E-04	16408, 16411, 16414, 14360, 16409	572	7	13588	2.E+01	2.E-01	3.E-03	2.E-01
GOTERM_BP_FAT	GO:0034637~cellular carbohydrate biosynthetic process	11	1.726844584	1.E-04	18682, 14751, 234779, 18534, 11651, 219	572	56	13588	5.E+00	2.E-01	3.E-03	2.E-01
GOTERM_BP_FAT	GO:0009617~response to bacterium	19	2.982731554	1.E-04	14972, 12475, 239081, 21898, 13035, 168	572	157	13588	3.E+00	3.E-01	3.E-03	2.E-01
GOTERM_BP_FAT	GO:0018108~peptidyl-tyrosine phosphorylation	9	1.412872841	1.E-04	11350, 16818, 12229, 20779, 18413, 1436	572	37	13588	6.E+00	3.E-01	4.E-03	2.E-01
GOTERM_BP_FAT	GO:0018212~peptidyl-tyrosine modification	9	1.412872841	1.E-04	11350, 16818, 12229, 20779, 18413, 1436	572	37	13588	6.E+00	3.E-01	4.E-03	2.E-01
GOTERM_BP_FAT	GO:0007623~circadian rhythm	9	1.412872841	1.E-04	11865, 12753, 11657, 232087, 12952, 186	572	37	13588	6.E+00	3.E-01	4.E-03	2.E-01
GOTERM_BP_FAT	GO:0019362~pyridine nucleotide metabolic process	8	1.25588697	1.E-04	19895, 17970, 21991, 21351, 17969, 6617	572	28	13588	7.E+00	3.E-01	4.E-03	2.E-01
GOTERM_BP_FAT	GO:0019748~secondary metabolic process	12	1.883830455	1.E-04	19895, 17970, 19378, 12043, 21991, 2135	572	69	13588	4.E+00	3.E-01	4.E-03	2.E-01
GOTERM_BP_FAT	GO:0043087~regulation of GTPase activity	14	2.197802198	1.E-04	22324, 228359, 57257, 11856, 14567, 145	572	93	13588	4.E+00	3.E-01	4.E-03	2.E-01
GOTERM_BP_FAT	GO:0051345~positive regulation of hydrolase activity	13	2.040816327	1.E-04	672195, 66593, 17869, 11856, 16818, 717	572	81	13588	4.E+00	3.E-01	4.E-03	2.E-01
GOTERM_BP_FAT	GO:0051240~positive regulation of multicellular organismal process	19	2.982731554	2.E-04	19370, 12475, 11657, 15018, 27007, 2189	572	163	13588	3.E+00	4.E-01	5.E-03	3.E-01
GOTERM_BP_FAT	GO:0002237~response to molecule of bacterial origin	10	1.569858713	2.E-04	17874, 12475, 16179, 17087, 234779, 264	572	49	13588	5.E+00	4.E-01	5.E-03	3.E-01
GOTERM_BP_FAT	GO:0043122~regulation of I-kappaB kinase/NF-kappaB cascade	9	1.412872841	2.E-04	16994, 17874, 21899, 21898, 56722, 1921	572	40	13588	5.E+00	5.E-01	6.E-03	4.E-01
GOTERM_BP_FAT	GO:0001819~positive regulation of cytokine production	11	1.726844584	2.E-04	12051, 19370, 14127, 17874, 12475, 1501	572	62	13588	4.E+00	5.E-01	7.E-03	4.E-01
GOTERM_BP_FAT	GO:0002253~activation of immune response	13	2.040816327	2.E-04	15170, 27007, 21898, 16818, 17874, 1880	572	86	13588	4.E+00	5.E-01	7.E-03	4.E-01
GOTERM_BP_FAT	GO:0002429~immune response-activating cell surface receptor sign	9	1.412872841	3.E-04	14127, 15170, 18803, 16818, 234779, 270	572	41	13588	5.E+00	5.E-01	7.E-03	5.E-01
GOTERM_BP_FAT	GO:0032760~positive regulation of tumor necrosis factor productio	6	0.941915228	3.E-04	14127, 17874, 12475, 21898, 24088, 1680	572	15	13588	1.E+01	5.E-01	8.E-03	5.E-01
GOTERM_BP_FAT	GO:0051338~regulation of transferase activity	21	3.296703297	3.E-04	15170, 11806, 14678, 21899, 21898, 5725	572	199	13588	3.E+00	5.E-01	8.E-03	5.E-01
GOTERM_BP_FAT	GO:0046651~lymphocyte proliferation	9	1.412872841	3.E-04	16408, 12445, 16197, 16411, 12028, 1204	572	42	13588	5.E+00	6.E-01	8.E-03	5.E-01
GOTERM_BP_FAT	GO:0030217~T cell differentiation	12	1.883830455	3.E-04	12051, 22324, 16818, 18771, 16197, 1204	572	76	13588	4.E+00	6.E-01	9.E-03	6.E-01
GOTERM_BP_FAT	GO:0043065~positive regulation of apoptosis	24	3.767660911	3.E-04	672195, 66593, 14939, 11816, 17869, 568	572	248	13588	2.E+00	6.E-01	9.E-03	6.E-01
GOTERM_BP_FAT	GO:0050730~regulation of peptidyl-tyrosine phosphorylation	10	1.569858713	3.E-04	18596, 56717, 15170, 13649, 12703, 1841	572	53	13588	4.E+00	6.E-01	9.E-03	6.E-01
GOTERM_BP_FAT	GO:0019627~urea metabolic process	5	0.784929356	3.E-04	227231, 18416, 217214, 109900, 11847	572	9	13588	1.E+01	6.E-01	9.E-03	6.E-01
GOTERM_BP_FAT	GO:0048009~insulin-like growth factor receptor signaling pathway	5	0.784929356	3.E-04	18708, 16367, 11651, 16001, 16000	572	9	13588	1.E+01	6.E-01	9.E-03	6.E-01
GOTERM_BP_FAT	GO:0006525~arginine metabolic process	5	0.784929356	3.E-04	18126, 18416, 217214, 109900, 11847	572	9	13588	1.E+01	6.E-01	9.E-03	6.E-01
GOTERM_BP_FAT	GO:0000050~urea cycle	5	0.784929356	3.E-04	227231, 18416, 217214, 109900, 11847	572	9	13588	1.E+01	6.E-01	9.E-03	6.E-01
GOTERM_BP_FAT	GO:0042127~regulation of cell proliferation	41	6.436420722	3.E-04	13649, 14178, 16952, 17869, 11855, 1639	572	538	13588	2.E+00	6.E-01	9.E-03	6.E-01
GOTERM_BP_FAT	GO:0009611~response to wounding	30	4.709576138	3.E-04	12475, 11651, 16803, 21937, 18126, 1406	572	347	13588	2.E+00	6.E-01	9.E-03	6.E-01
GOTERM_BP_FAT	GO:0002009~morphogenesis of an epithelium	19	2.982731554	4.E-04	22323, 13649, 232906, 16911, 19378, 120	572	173	13588	3.E+00	6.E-01	9.E-03	6.E-01
GOTERM_BP_FAT	GO:0043068~positive regulation of programmed cell death	24	3.767660911	4.E-04	672195, 66593, 14939, 11816, 17869, 568	572	250	13588	2.E+00	6.E-01	9.E-03	6.E-01
GOTERM_BP_FAT	GO:0032869~cellular response to insulin stimulus	9	1.412872841	4.E-04	18709, 18708, 13685, 16367, 16334, 1042	572	43	13588	5.E+00	6.E-01	9.E-03	6.E-01
GOTERM_BP_FAT	GO:0032943~mononuclear cell proliferation	9	1.412872841	4.E-04	16408, 12445, 16197, 16411, 12028, 1204	572	43	13588	5.E+00	6.E-01	9.E-03	6.E-01
GOTERM_BP_FAT	GO:0070661~leukocyte proliferation	9	1.412872841	4.E-04	16408, 12445, 16197, 16411, 12028, 1204	572	43	13588	5.E+00	6.E-01	9.E-03	6.E-01



GOTERM_BP_FAT	GO:0006919~activation of caspase activity	8	1.25588697	4.E-04	16818, 672195, 66593, 12028, 12018, 178	572	33	13588	6.E+00	6.E-01	9.E-03	7.E-01
GOTERM_BP_FAT	GO:0008219~cell death	39	6.12244898	4.E-04	22029, 12765, 672195, 66593, 11852, 149	572	507	13588	2.E+00	7.E-01	1.E-02	7.E-01
GOTERM_BP_FAT	GO:0046777~protein amino acid autophosphorylation	11	1.726844584	4.E-04	56717, 13649, 16818, 23920, 16179, 2261	572	66	13588	4.E+00	7.E-01	1.E-02	7.E-01
GOTERM_BP_FAT	GO:0010942~positive regulation of cell death	24	3.767660911	4.E-04	672195, 66593, 14939, 11816, 17869, 568	572	252	13588	2.E+00	7.E-01	1.E-02	7.E-01
GOTERM_BP_FAT	GO:0002768~immune response-regulating cell surface receptor sigi	9	1.412872841	4.E-04	14127, 15170, 18803, 16818, 234779, 270	572	44	13588	5.E+00	7.E-01	1.E-02	8.E-01
GOTERM_BP_FAT	GO:0048729~tissue morphogenesis	23	3.610675039	5.E-04	22323, 13649, 14178, 232906, 16911, 193	572	238	13588	2.E+00	7.E-01	1.E-02	8.E-01
GOTERM_BP_FAT	GO:0030334~regulation of cell migration	13	2.040816327	5.E-04	21687, 14674, 73167, 12043, 11855, 3847	572	92	13588	3.E+00	7.E-01	1.E-02	8.E-01
GOTERM_BP_FAT	GO:0043549~regulation of kinase activity	20	3.139717425	5.E-04	15170, 14678, 21899, 21898, 57257, 2041	572	192	13588	2.E+00	7.E-01	1.E-02	8.E-01
GOTERM_BP_FAT	GO:0043604~amide biosynthetic process	5	0.784929356	5.E-04	227231, 18416, 217214, 109900, 11847	572	10	13588	1.E+01	8.E-01	1.E-02	9.E-01
GOTERM_BP_FAT	GO:0051270~regulation of cell motion	14	2.197802198	5.E-04	21687, 14674, 73167, 12043, 11855, 3847	572	107	13588	3.E+00	8.E-01	1.E-02	1.E+00
GOTERM_BP_FAT	GO:0051347~positive regulation of transferase activity	16	2.51177394	5.E-04	11806, 14678, 21899, 21898, 57257, 2041	572	135	13588	3.E+00	8.E-01	1.E-02	1.E+00
GOTERM_BP_FAT	GO:0016265~death	39	6.12244898	6.E-04	22029, 12765, 672195, 66593, 11852, 149	572	519	13588	2.E+00	8.E-01	1.E-02	1.E+00
GOTERM_BP_FAT	GO:0043069~negative regulation of programmed cell death	23	3.610675039	6.E-04	11657, 13628, 11651, 17869, 12043, 1081	572	244	13588	2.E+00	8.E-01	1.E-02	1.E+00
GOTERM_BP_FAT	GO:0043280~positive regulation of caspase activity	8	1.25588697	6.E-04	16818, 672195, 66593, 12028, 12018, 178	572	36	13588	5.E+00	8.E-01	1.E-02	1.E+00
GOTERM_BP_FAT	GO:0010952~positive regulation of peptidase activity	8	1.25588697	6.E-04	16818, 672195, 66593, 12028, 12018, 178	572	36	13588	5.E+00	8.E-01	1.E-02	1.E+00
GOTERM_BP_FAT	GO:0032870~cellular response to hormone stimulus	10	1.569858713	6.E-04	18709, 18708, 13685, 16367, 16334, 1042	572	58	13588	4.E+00	8.E-01	1.E-02	1.E+00
GOTERM_BP_FAT	GO:0060548~negative regulation of cell death	23	3.610675039	7.E-04	11657, 13628, 11651, 17869, 12043, 1081	572	245	13588	2.E+00	8.E-01	1.E-02	1.E+00
GOTERM_BP_FAT	GO:0048514~blood vessel morphogenesis	20	3.139717425	7.E-04	19317, 14674, 11852, 11816, 238055, 204	572	198	13588	2.E+00	9.E-01	1.E-02	1.E+00
GOTERM_BP_FAT	GO:0070391~response to lipoteichoic acid	4	0.627943485	7.E-04	12475, 21898, 24088, 16803	572	5	13588	2.E+01	9.E-01	1.E-02	1.E+00
GOTERM_BP_FAT	GO:0051094~positive regulation of developmental process	21	3.296703297	7.E-04	11852, 16414, 12043, 22778, 108138, 218	572	214	13588	2.E+00	9.E-01	2.E-02	1.E+00
GOTERM_BP_FAT	GO:0032868~response to insulin stimulus	10	1.569858713	7.E-04	18709, 18708, 56717, 13685, 16367, 1633	572	59	13588	4.E+00	9.E-01	2.E-02	1.E+00
GOTERM_BP_FAT	GO:0022604~regulation of cell morphogenesis	13	2.040816327	7.E-04	14163, 14674, 232906, 76117, 21844, 102	572	97	13588	3.E+00	9.E-01	2.E-02	1.E+00
GOTERM_BP_FAT	GO:0007266~Rho protein signal transduction	7	1.098901099	7.E-04	80837, 117600, 14674, 192662, 12540, 14	572	27	13588	6.E+00	9.E-01	2.E-02	1.E+00
GOTERM_BP_FAT	GO:0032680~regulation of tumor necrosis factor production	7	1.098901099	7.E-04	12051, 14127, 17874, 12475, 21898, 2408	572	27	13588	6.E+00	9.E-01	2.E-02	1.E+00
GOTERM_BP_FAT	GO:0030335~positive regulation of cell migration	8	1.25588697	8.E-04	18708, 16367, 73167, 12043, 11855, 2033	572	37	13588	5.E+00	9.E-01	2.E-02	1.E+00
GOTERM_BP_FAT	GO:0006955~immune response	36	5.651491366	8.E-04	14972, 12475, 22324, 15018, 16803, 1201	572	471	13588	2.E+00	9.E-01	2.E-02	1.E+00
GOTERM_BP_FAT	GO:0001914~regulation of T cell mediated cytotoxicity	5	0.784929356	8.E-04	14972, 15018, 16197, 19056, 12010	572	11	13588	1.E+01	9.E-01	2.E-02	1.E+00
GOTERM_BP_FAT	GO:0048511~rhythmic process	13	2.040816327	8.E-04	11865, 12753, 11657, 232087, 12043, 129	572	98	13588	3.E+00	9.E-01	2.E-02	1.E+00
GOTERM_BP_FAT	GO:0006733~oxidoreductase coenzyme metabolic process	8	1.25588697	9.E-04	19895, 17970, 21991, 21351, 17969, 6617	572	38	13588	5.E+00	9.E-01	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0032496~response to lipopolysaccharide	8	1.25588697	9.E-04	17874, 12475, 16179, 17087, 234779, 264	572	38	13588	5.E+00	9.E-01	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0008286~insulin receptor signaling pathway	7	1.098901099	9.E-04	18709, 18708, 13685, 16367, 16334, 1165	572	28	13588	6.E+00	9.E-01	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0042098~T cell proliferation	7	1.098901099	9.E-04	16408, 12445, 16411, 12028, 16414, 1436	572	28	13588	6.E+00	9.E-01	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0045428~regulation of nitric oxide biosynthetic process	6	0.941915228	9.E-04	19370, 21898, 27007, 11847, 16414, 3790	572	19	13588	8.E+00	9.E-01	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0051384~response to glucocorticoid stimulus	6	0.941915228	9.E-04	18670, 109900, 26395, 12043, 230163, 94	572	19	13588	8.E+00	9.E-01	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0030879~mammary gland development	12	1.883830455	9.E-04	15438, 20779, 16367, 15405, 11855, 1600	572	86	13588	3.E+00	9.E-01	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0008284~positive regulation of cell proliferation	25	3.924646782	9.E-04	13649, 14178, 17869, 11855, 15163, 1640	572	284	13588	2.E+00	9.E-01	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0009967~positive regulation of signal transduction	18	2.825745683	9.E-04	21899, 21898, 56847, 15163, 11848, 1699	572	172	13588	2.E+00	9.E-01	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0009894~regulation of catabolic process	9	1.412872841	1.E-03	11865, 56717, 17999, 14447, 282663, 116	572	50	13588	4.E+00	9.E-01	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0052548~regulation of endopeptidase activity	9	1.412872841	1.E-03	16818, 672195, 12015, 66593, 12028, 120	572	50	13588	4.E+00	9.E-01	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0043281~regulation of caspase activity	9	1.412872841	1.E-03	16818, 672195, 12015, 66593, 12028, 120	572	50	13588	4.E+00	9.E-01	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0045454~cell redox homeostasis	10	1.569858713	1.E-03	18453, 12304, 93692, 26462, 50493, 1482	572	62	13588	4.E+00	9.E-01	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0010740~positive regulation of protein kinase cascade	12	1.883830455	1.E-03	16994, 17874, 21899, 21898, 18413, 5672	572	88	13588	3.E+00	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0033674~positive regulation of kinase activity	15	2.354788069	1.E-03	14678, 21899, 21898, 57257, 20416, 2240	572	130	13588	3.E+00	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0045597~positive regulation of cell differentiation	18	2.825745683	1.E-03	12043, 22778, 108138, 21844, 15902, 118	572	175	13588	2.E+00	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0043066~negative regulation of apoptosis	22	3.453689168	1.E-03	11657, 13628, 11651, 17869, 12043, 1081	572	239	13588	2.E+00	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0052547~regulation of peptidase activity	9	1.412872841	1.E-03	16818, 672195, 12015, 66593, 12028, 120	572	51	13588	4.E+00	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0006915~apoptosis	35	5.494505495	1.E-03	22029, 12765, 672195, 66593, 11852, 149	572	465	13588	2.E+00	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0042157~lipoprotein metabolic process	11	1.726844584	1.E-03	18108, 18107, 108672, 17777, 11814, 118	572	76	13588	3.E+00	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0010604~positive regulation of macromolecule metabolic proce	44	6.907378336	1.E-03	17536, 22130, 11651, 17869, 22778, 1639	572	633	13588	2.E+00	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0046907~intracellular transport	33	5.180533752	1.E-03	215280, 269589, 11852, 19384, 12953, 17	572	431	13588	2.E+00	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0043551~regulation of phosphoinositide 3-kinase activity	4	0.627943485	1.E-03	18048, 16367, 57257, 12540	572	6	13588	2.E+01	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0043552~positive regulation of phosphoinositide 3-kinase activ	4	0.627943485	1.E-03	18048, 16367, 57257, 12540	572	6	13588	2.E+01	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0031341~regulation of cell killing	7	1.098901099	1.E-03	19370, 14972, 15018, 16197, 27007, 3790	572	30	13588	6.E+00	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0002260~lymphocyte homeostasis	7	1.098901099	1.E-03	12442, 12028, 12018, 11651, 12043, 1905	572	30	13588	6.E+00	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0001910~regulation of leukocyte mediated cytotoxicity	7	1.098901099	1.E-03	19370, 14972, 15018, 16197, 27007, 3790	572	30	13588	6.E+00	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0051272~positive regulation of cell motion	8	1.25588697	1.E-03	18708, 16367, 73167, 12043, 11855, 2033	572	41	13588	5.E+00	1.E+00	3.E-02	3.E+00
GOTERM_BP_FAT	GO:0042113~B cell activation	11	1.726844584	2.E-03	12051, 18708, 16197, 11486, 234779, 120	572	78	13588	1.E+00	3.E+00	3.E-02	3.E+00
GOTERM_BP_FAT	GO:0012501~programmed cell death	35	5.494505495	2.E-03	22029, 12765, 672195, 66593, 11852, 149	572	473	13588	2.E+00	1.E+00	3.E-02	3.E+00
GOTERM_BP_FAT	GO:0048732~gland development	19	2.982731554	2.E-03	13649, 14178, 11806, 12043, 22778, 1185	572	197	13588	2.E+00	1.E+00	3.E-02	3.E+00
GOTERM_BP_FAT	GO:0043408~regulation of MAPKKK cascade	12	1.883830455	2.E-03	15170, 17874, 16179, 24064, 16334, 1478	572	93	13588	3.E+00	1.E+00	3.E-02	3.E+00
GOTERM_BP_FAT	GO:0045087~innate immune response	13	2.040816327	2.E-03	15170, 239081, 21899, 21898, 16803, 178	572	107	13588	3.E+00	1.E+00	3.E-02	3.E+00
GOTERM_BP_FAT	GO:0033554~cellular response to stress	31	4.866562009	2.E-03	80905, 11657, 13665, 12952, 12953, 1205	572	404	13588	2.E+00	1.E+00	3.E-02	3.E+00
GOTERM_BP_FAT	GO:0045582~positive regulation of T cell differentiation	7	1.098901099	2.E-03	16818, 12015, 16197, 11486, 22778, 1619	572	32	13588	5.E+00	1.E+00	3.E-02	3.E+00
GOTERM_BP_FAT	GO:0050900~leukocyte migration	8	1.25588697	2.E-03	20310, 14127, 20345, 12490, 16414, 2020	572	43	13588	4.E+00	1.E+00	3.E-02	3.E+00
GOTERM_BP_FAT	GO:0048870~cell motility	24	3.767660911	2.E-03	117600, 13649, 100044475, 11806, 17973	572	284	13588	2.E+00	1.E+00	3.E-02	4.E+00



GOTERM_BP_FAT	GO:0051674~localization of cell	24	3.767660911	2.E-03 117600. 13649. 100044475. 11806. 17973	572	284	13588	2.E+00	1.E+00	3.E-02	4.E+00
GOTERM_BP_FAT	GO:0001817~regulation of cytokine production	15	2.354788069	2.E-03 19370. 12475. 15018. 11807. 21899. 2700	572	139	13588	3.E+00	1.E+00	4.E-02	4.E+00
GOTERM_BP_FAT	GO:0002218~activation of innate immune response	5	0.784929356	2.E-03 17874. 16179. 21898. 27007. 24088	572	14	13588	8.E+00	1.E+00	4.E-02	4.E+00
GOTERM_BP_FAT	GO:0040017~positive regulation of locomotion	8	1.25588697	2.E-03 18708. 16367. 73167. 12043. 11855. 2033	572	44	13588	4.E+00	1.E+00	4.E-02	4.E+00
GOTERM_BP_FAT	GO:0002819~regulation of adaptive immune response	9	1.412872841	2.E-03 14972. 14127. 15170. 15018. 16197. 1148	572	56	13588	4.E+00	1.E+00	4.E-02	4.E+00
GOTERM_BP_FAT	GO:0019221~cytokine-mediated signaling pathway	9	1.412872841	2.E-03 15170. 17874. 16195. 12703. 12983. 1201	572	56	13588	4.E+00	1.E+00	4.E-02	4.E+00
GOTERM_BP_FAT	GO:0002822~regulation of adaptive immune response based on so	9	1.412872841	2.E-03 14972. 14127. 15170. 15018. 16197. 1148	572	56	13588	4.E+00	1.E+00	4.E-02	4.E+00
GOTERM_BP_FAT	GO:0040012~regulation of locomotion	13	2.040816327	2.E-03 21687. 14674. 73167. 12043. 11855. 3847	572	110	13588	3.E+00	1.E+00	4.E-02	4.E+00
GOTERM_BP_FAT	GO:0030705~cytoskeleton-dependent intracellular transport	7	1.098901099	2.E-03 245049. 215280. 17925. 77579. 59040. 22	572	33	13588	5.E+00	1.E+00	4.E-02	4.E+00
GOTERM_BP_FAT	GO:0043123~positive regulation of I-kappaB kinase/NF-kappaB cas	7	1.098901099	2.E-03 16994. 17874. 21899. 21898. 56722. 1921	572	33	13588	5.E+00	1.E+00	4.E-02	4.E+00
GOTERM_BP_FAT	GO:0050830~defense response to Gram-positive bacterium	6	0.941915228	2.E-03 17874. 14191. 13035. 17969. 24088. 1680	572	23	13588	6.E+00	1.E+00	4.E-02	4.E+00
GOTERM_BP_FAT	GO:0060562~epithelial tube morphogenesis	13	2.040816327	2.E-03 22323. 232906. 16911. 12043. 12234. 240	572	111	13588	3.E+00	1.E+00	4.E-02	4.E+00
GOTERM_BP_FAT	GO:0016051~carbohydrate biosynthetic process	11	1.726844584	2.E-03 18682. 14751. 234779. 18534. 11651. 219	572	83	13588	3.E+00	1.E+00	4.E-02	4.E+00
GOTERM_BP_FAT	GO:0031349~positive regulation of defense response	9	1.412872841	2.E-03 19370. 14127. 17874. 16179. 21898. 2700	572	57	13588	4.E+00	1.E+00	4.E-02	4.E+00
GOTERM_BP_FAT	GO:0060429~epithelium development	23	3.610675039	3.E-03 22323. 13649. 16456. 232906. 16911. 193	572	271	13588	2.E+00	1.E+00	4.E-02	4.E+00
GOTERM_BP_FAT	GO:0002703~regulation of leukocyte mediated immunity	10	1.569858713	3.E-03 19370. 14972. 14127. 15170. 15018. 1619	572	70	13588	3.E+00	1.E+00	4.E-02	4.E+00
GOTERM_BP_FAT	GO:0030031~cell projection assembly	10	1.569858713	3.E-03 19354. 100044475. 77579. 30938. 17973.	572	70	13588	3.E+00	1.E+00	4.E-02	4.E+00
GOTERM_BP_FAT	GO:0010647~positive regulation of cell communication	18	2.825745683	3.E-03 21899. 21898. 56847. 15163. 11848. 1699	572	189	13588	2.E+00	1.E+00	4.E-02	5.E+00
GOTERM_BP_FAT	GO:0045621~positive regulation of lymphocyte differentiation	7	1.098901099	3.E-03 16818. 12015. 16197. 11486. 22778. 1619	572	34	13588	5.E+00	1.E+00	4.E-02	5.E+00
GOTERM_BP_FAT	GO:0016477~cell migration	21	3.296703297	3.E-03 117600. 13649. 100044475. 11806. 17973	572	240	13588	2.E+00	1.E+00	4.E-02	5.E+00
GOTERM_BP_FAT	GO:0030183~B cell differentiation	8	1.25588697	3.E-03 12051. 18708. 11486. 234779. 12028. 120	572	46	13588	4.E+00	1.E+00	4.E-02	5.E+00
GOTERM_BP_FAT	GO:0002699~positive regulation of immune effector process	8	1.25588697	3.E-03 19370. 14972. 14127. 15018. 27007. 3790	572	46	13588	4.E+00	1.E+00	4.E-02	5.E+00
GOTERM_BP_FAT	GO:0002696~positive regulation of leukocyte activation	12	1.883830455	3.E-03 19370. 21898. 22778. 16408. 16818. 1787	572	99	13588	3.E+00	1.E+00	4.E-02	5.E+00
GOTERM_BP_FAT	GO:0030048~actin filament-based movement	5	0.784929356	3.E-03 245049. 215280. 17925. 77579. 22376	572	15	13588	8.E+00	1.E+00	4.E-02	5.E+00
GOTERM_BP_FAT	GO:0045429~positive regulation of nitric oxide biosynthetic proces	5	0.784929356	3.E-03 19370. 21898. 27007. 16414. 379043. 240	572	15	13588	8.E+00	1.E+00	4.E-02	5.E+00
GOTERM_BP_FAT	GO:0045576~mast cell activation	5	0.784929356	3.E-03 23880. 14127. 21898. 74734. 16822	572	15	13588	8.E+00	1.E+00	4.E-02	5.E+00
GOTERM_BP_FAT	GO:0002274~myeloid leukocyte activation	7	1.098901099	3.E-03 23880. 14127. 21898. 20375. 74734. 1682	572	35	13588	5.E+00	1.E+00	5.E-02	5.E+00
GOTERM_BP_FAT	GO:0051051~negative regulation of transport	10	1.569858713	3.E-03 16994. 11486. 17999. 14678. 104215. 184	572	72	13588	3.E+00	1.E+00	5.E-02	5.E+00
GOTERM_BP_FAT	GO:0006800~oxygen and reactive oxygen species metabolic proces	8	1.25588697	3.E-03 18126. 672195. 17970. 50493. 12043. 130	572	47	13588	4.E+00	1.E+00	5.E-02	6.E+00
GOTERM_BP_FAT	GO:0050867~positive regulation of cell activation	12	1.883830455	3.E-03 19370. 21898. 22778. 16408. 16818. 1787	572	101	13588	3.E+00	1.E+00	5.E-02	6.E+00
GOTERM_BP_FAT	GO:0006090~pyruvate metabolic process	6	0.941915228	3.E-03 14751. 235339. 18534. 21991. 230163. 74	572	25	13588	6.E+00	1.E+00	5.E-02	6.E+00
GOTERM_BP_FAT	GO:0031032~actomyosin structure organization	6	0.941915228	3.E-03 26934. 77579. 11464. 71994. 16412. 1145	572	25	13588	6.E+00	1.E+00	5.E-02	6.E+00
GOTERM_BP_FAT	GO:0048545~response to steroid hormone stimulus	9	1.412872841	3.E-03 20779. 12842. 18670. 109900. 26395. 120	572	60	13588	4.E+00	1.E+00	5.E-02	6.E+00
GOTERM_BP_FAT	GO:0031328~positive regulation of cellular biosynthetic process	38	5.965463108	3.E-03 17536. 22130. 17869. 22778. 12912. 1039	572	552	13588	2.E+00	1.E+00	5.E-02	6.E+00
GOTERM_BP_FAT	GO:0046902~regulation of mitochondrial membrane permeability	4	0.627943485	4.E-03 12028. 12122. 12018. 12043	572	8	13588	1.E+01	1.E+00	5.E-02	6.E+00
GOTERM_BP_FAT	GO:0043550~regulation of lipid kinase activity	4	0.627943485	4.E-03 18048. 16367. 57257. 12540	572	8	13588	1.E+01	1.E+00	5.E-02	6.E+00
GOTERM_BP_FAT	GO:0006098~pentose-phosphate shunt	4	0.627943485	4.E-03 19895. 21991. 21351. 66171	572	8	13588	1.E+01	1.E+00	5.E-02	6.E+00
GOTERM_BP_FAT	GO:0045089~positive regulation of innate immune response	7	1.098901099	4.E-03 19370. 17874. 16179. 21898. 27007. 3790	572	36	13588	5.E+00	1.E+00	5.E-02	6.E+00
GOTERM_BP_FAT	GO:0030218~erythrocyte differentiation	8	1.25588697	4.E-03 18771. 21349. 20375. 12183. 14381. 1590	572	48	13588	4.E+00	1.E+00	5.E-02	6.E+00
GOTERM_BP_FAT	GO:0010959~regulation of metal ion transport	8	1.25588697	4.E-03 17999. 234779. 14678. 12028. 12018. 116	572	48	13588	4.E+00	1.E+00	5.E-02	6.E+00
GOTERM_BP_FAT	GO:0051050~positive regulation of transport	14	2.197802198	4.E-03 68092. 11651. 12912. 103988. 16994. 141	572	132	13588	3.E+00	1.E+00	5.E-02	6.E+00
GOTERM_BP_FAT	GO:0043507~positive regulation of JUN kinase activity	5	0.784929356	4.E-03 16179. 16334. 21899. 20963. 224014	572	16	13588	7.E+00	1.E+00	5.E-02	6.E+00
GOTERM_BP_FAT	GO:0001906~cell killing	5	0.784929356	4.E-03 15170. 11657. 11891. 13035. 17969	572	16	13588	7.E+00	1.E+00	5.E-02	6.E+00
GOTERM_BP_FAT	GO:0002697~regulation of immune effector process	11	1.726844584	4.E-03 19370. 14972. 14127. 15170. 15018. 1619	572	88	13588	3.E+00	1.E+00	5.E-02	7.E+00
GOTERM_BP_FAT	GO:0034613~cellular protein localization	24	3.767660911	4.E-03 11865. 269589. 19894. 19384. 380714. 12	572	299	13588	2.E+00	1.E+00	5.E-02	7.E+00
GOTERM_BP_FAT	GO:0009891~positive regulation of biosynthetic process	38	5.965463108	4.E-03 17536. 22130. 17869. 22778. 12912. 1039	572	557	13588	2.E+00	1.E+00	5.E-02	7.E+00
GOTERM_BP_FAT	GO:0046165~alcohol biosynthetic process	7	1.098901099	4.E-03 14751. 234779. 18534. 21991. 230163. 14	572	37	13588	4.E+00	1.E+00	6.E-02	7.E+00
GOTERM_BP_FAT	GO:0043269~regulation of ion transport	9	1.412872841	4.E-03 16994. 17999. 234779. 14678. 12028. 120	572	62	13588	3.E+00	1.E+00	6.E-02	7.E+00
GOTERM_BP_FAT	GO:0070727~cellular macromolecule localization	24	3.767660911	4.E-03 11865. 269589. 19894. 19384. 380714. 12	572	301	13588	2.E+00	1.E+00	6.E-02	7.E+00
GOTERM_BP_FAT	GO:0001701~in utero embryonic development	22	3.453689168	4.E-03 13649. 14674. 18107. 11651. 238055. 138	572	267	13588	2.E+00	1.E+00	6.E-02	8.E+00
GOTERM_BP_FAT	GO:0006952~defense response	32	5.023547881	5.E-03 14972. 12475. 15018. 11651. 16803. 1201	572	448	13588	2.E+00	1.E+00	6.E-02	8.E+00
GOTERM_BP_FAT	GO:0006917~induction of apoptosis	16	2.51177394	5.E-03 382985. 15170. 66593. 11816. 14939. 178	572	167	13588	2.E+00	1.E+00	6.E-02	8.E+00
GOTERM_BP_FAT	GO:0012502~induction of programmed cell death	16	2.51177394	5.E-03 382985. 15170. 66593. 11816. 14939. 178	572	167	13588	2.E+00	1.E+00	6.E-02	8.E+00
GOTERM_BP_FAT	GO:0007160~cell-matrix adhesion	8	1.25588697	5.E-03 21687. 50768. 12043. 16414. 11856. 1641	572	50	13588	4.E+00	1.E+00	6.E-02	8.E+00
GOTERM_BP_FAT	GO:0009156~ribonucleoside monophosphate biosynthetic process	5	0.784929356	5.E-03 11486. 11717. 56749. 11566. 99586	572	17	13588	7.E+00	1.E+00	6.E-02	8.E+00
GOTERM_BP_FAT	GO:0002474~antigen processing and presentation of peptide antig	5	0.784929356	5.E-03 15007. 14972. 14127. 15018. 12010	572	17	13588	7.E+00	1.E+00	6.E-02	8.E+00
GOTERM_BP_FAT	GO:0060537~muscle tissue development	14	2.197802198	5.E-03 15430. 18479. 16412. 20467. 11848. 1543	572	136	13588	2.E+00	1.E+00	6.E-02	8.E+00
GOTERM_BP_FAT	GO:0060326~cell chemotaxis	6	0.941915228	5.E-03 20310. 14127. 16414. 20202. 16803. 1640	572	27	13588	5.E+00	1.E+00	6.E-02	8.E+00
GOTERM_BP_FAT	GO:0030595~leukocyte chemotaxis	6	0.941915228	5.E-03 20310. 14127. 16414. 20202. 16803. 1640	572	27	13588	5.E+00	1.E+00	6.E-02	8.E+00
GOTERM_BP_FAT	GO:0048598~embryonic morphogenesis	27	4.238618524	5.E-03 22323. 232906. 17869. 56847. 15402. 138	572	359	13588	2.E+00	1.E+00	6.E-02	9.E+00
GOTERM_BP_FAT	GO:0010035~response to inorganic substance	11	1.726844584	5.E-03 18669. 11657. 18671. 12842. 19053. 2646	572	92	13588	3.E+00	1.E+00	7.E-02	9.E+00
GOTERM_BP_FAT	GO:0010551~regulation of specific transcription from RNA polymer	8	1.25588697	5.E-03 18771. 21349. 17869. 22778. 18626. 2087	572	51	13588	4.E+00	1.E+00	7.E-02	9.E+00
GOTERM_BP_FAT	GO:0034101~erythrocyte homeostasis	8	1.25588697	5.E-03 18771. 21349. 20375. 12183. 14381. 1590	572	51	13588	4.E+00	1.E+00	7.E-02	9.E+00
GOTERM_BP_FAT	GO:0010648~negative regulation of cell communication	17	2.668759812	5.E-03 15170. 69121. 380714. 66042. 14678. 204	572	186	13588	2.E+00	1.E+00	7.E-02	9.E+00
GOTERM_BP_FAT	GO:0016331~morphogenesis of embryonic epithelium	10	1.569858713	5.E-03 22323. 16911. 232906. 19713. 50768. 186	572	78	13588	3.E+00	1.E+00	7.E-02	9.E+00



GOTERM_BP_FAT	GO:0001776~leukocyte homeostasis	7	1.098901099	5.E-03 12442, 12028, 12018, 11651, 12043, 1905	572	39	13588	4.E+00	1.E+00	7.E-02	9.E+00
GOTERM_BP_FAT	GO:0009119~ribonucleoside metabolic process	7	1.098901099	5.E-03 22017, 11486, 72269, 232087, 56749, 222	572	39	13588	4.E+00	1.E+00	7.E-02	9.E+00
GOTERM_BP_FAT	GO:0002694~regulation of leukocyte activation	15	2.354788069	5.E-03 19370, 15170, 21898, 22778, 16396, 1640	572	154	13588	2.E+00	1.E+00	7.E-02	9.E+00
GOTERM_BP_FAT	GO:0042742~defense response to bacterium	12	1.883830455	6.E-03 12051, 14972, 14127, 17874, 18126, 1419	572	108	13588	3.E+00	1.E+00	7.E-02	1.E+01
GOTERM_BP_FAT	GO:0002706~regulation of lymphocyte mediated immunity	9	1.412872841	6.E-03 19370, 14972, 14127, 15170, 15018, 1619	572	65	13588	3.E+00	1.E+00	7.E-02	1.E+01
GOTERM_BP_FAT	GO:0035239~tube morphogenesis	16	2.51177394	6.E-03 22323, 14674, 232906, 16911, 12043, 122	572	171	13588	2.E+00	1.E+00	7.E-02	1.E+01
GOTERM_BP_FAT	GO:0002709~regulation of T cell mediated immunity	5	0.784929356	6.E-03 14972, 15018, 16197, 19056, 12010	572	18	13588	7.E+00	1.E+00	7.E-02	1.E+01
GOTERM_BP_FAT	GO:0043029~T cell homeostasis	5	0.784929356	6.E-03 12442, 12028, 11651, 12043, 19056	572	18	13588	7.E+00	1.E+00	7.E-02	1.E+01
GOTERM_BP_FAT	GO:0051251~positive regulation of lymphocyte activation	11	1.726844584	6.E-03 16408, 19370, 17874, 16818, 12015, 1619	572	94	13588	3.E+00	1.E+00	7.E-02	1.E+01
GOTERM_BP_FAT	GO:0051247~positive regulation of protein metabolic process	12	1.883830455	6.E-03 56717, 17999, 18413, 11651, 12043, 1639	572	109	13588	3.E+00	1.E+00	7.E-02	1.E+01
GOTERM_BP_FAT	GO:0050865~regulation of cell activation	15	2.354788069	6.E-03 19370, 15170, 21898, 22778, 16396, 1640	572	156	13588	2.E+00	1.E+00	7.E-02	1.E+01
GOTERM_BP_FAT	GO:0007507~heart development	19	2.982731554	6.E-03 12831, 19378, 16412, 20416, 20467, 1590	572	223	13588	2.E+00	1.E+00	7.E-02	1.E+01
GOTERM_BP_FAT	GO:0043523~regulation of neuron apoptosis	10	1.569858713	6.E-03 16994, 218397, 12048, 11920, 12028, 154	572	80	13588	3.E+00	1.E+00	7.E-02	1.E+01
GOTERM_BP_FAT	GO:0002252~immune effector process	13	2.040816327	7.E-03 15170, 15018, 108138, 13035, 16803, 120	572	126	13588	2.E+00	1.E+00	8.E-02	1.E+01
GOTERM_BP_FAT	GO:0030099~myeloid cell differentiation	11	1.726844584	7.E-03 18771, 21349, 15415, 20375, 12183, 1645	572	96	13588	3.E+00	1.E+00	8.E-02	1.E+01
GOTERM_BP_FAT	GO:0051640~organelle localization	8	1.25588697	7.E-03 245049, 11657, 77579, 12540, 11891, 171	572	54	13588	4.E+00	1.E+00	8.E-02	1.E+01
GOTERM_BP_FAT	GO:0014706~striated muscle tissue development	13	2.040816327	7.E-03 15430, 18479, 16412, 20467, 11848, 1543	572	127	13588	2.E+00	1.E+00	8.E-02	1.E+01
GOTERM_BP_FAT	GO:0006732~coenzyme metabolic process	14	2.197802198	7.E-03 17448, 19895, 17970, 14782, 103988, 661	572	143	13588	2.E+00	1.E+00	8.E-02	1.E+01
GOTERM_BP_FAT	GO:0002285~lymphocyte activation during immune response	5	0.784929356	7.E-03 12051, 11486, 18826, 234779, 11891	572	19	13588	6.E+00	1.E+00	8.E-02	1.E+01
GOTERM_BP_FAT	GO:0009161~ribonucleoside monophosphate metabolic process	5	0.784929356	7.E-03 11486, 11717, 56749, 11566, 99586	572	19	13588	6.E+00	1.E+00	8.E-02	1.E+01
GOTERM_BP_FAT	GO:0051249~regulation of lymphocyte activation	14	2.197802198	8.E-03 19370, 15170, 21898, 22778, 16396, 1640	572	144	13588	2.E+00	1.E+00	9.E-02	1.E+01
GOTERM_BP_FAT	GO:0043388~positive regulation of DNA binding	7	1.098901099	8.E-03 17874, 16179, 12315, 12314, 12313, 2189	572	42	13588	4.E+00	1.E+00	9.E-02	1.E+01
GOTERM_BP_FAT	GO:0042108~positive regulation of cytokine biosynthetic process	7	1.098901099	8.E-03 12051, 16994, 17874, 11807, 21899, 2189	572	42	13588	4.E+00	1.E+00	9.E-02	1.E+01
GOTERM_BP_FAT	GO:0035295~tube development	21	3.296703297	8.E-03 22323, 14674, 14178, 232906, 16911, 193	572	264	13588	2.E+00	1.E+00	9.E-02	1.E+01
GOTERM_BP_FAT	GO:0009116~nucleoside metabolic process	8	1.25588697	9.E-03 22017, 11486, 72269, 232087, 56749, 708	572	56	13588	3.E+00	1.E+00	1.E-01	1.E+01
GOTERM_BP_FAT	GO:0001816~cytokine production	7	1.098901099	9.E-03 18019, 17874, 21898, 16822, 16803, 5412	572	43	13588	4.E+00	1.E+00	1.E-01	1.E+01
GOTERM_BP_FAT	GO:0045786~negative regulation of cell cycle	7	1.098901099	9.E-03 11852, 11920, 12043, 56150, 12568, 2046	572	43	13588	4.E+00	1.E+00	1.E-01	1.E+01
GOTERM_BP_FAT	GO:0009064~glutamine family amino acid metabolic process	7	1.098901099	9.E-03 227231, 18126, 18416, 217214, 109900, 1	572	43	13588	4.E+00	1.E+00	1.E-01	1.E+01
GOTERM_BP_FAT	GO:0006094~gluconeogenesis	5	0.784929356	9.E-03 14751, 18534, 21991, 230163, 74551	572	20	13588	6.E+00	1.E+00	1.E-01	1.E+01
GOTERM_BP_FAT	GO:0042743~hydrogen peroxide metabolic process	5	0.784929356	9.E-03 672195, 50493, 13063, 17969, 13077, 130	572	20	13588	6.E+00	1.E+00	1.E-01	1.E+01
GOTERM_BP_FAT	GO:0002366~leukocyte activation during immune response	6	0.941915228	9.E-03 12051, 11486, 18826, 234779, 11891, 168	572	31	13588	5.E+00	1.E+00	1.E-01	1.E+01
GOTERM_BP_FAT	GO:0002263~cell activation during immune response	6	0.941915228	9.E-03 12051, 11486, 18826, 234779, 11891, 168	572	31	13588	5.E+00	1.E+00	1.E-01	1.E+01
GOTERM_BP_FAT	GO:0046364~monosaccharide biosynthetic process	6	0.941915228	9.E-03 14751, 18534, 21991, 230163, 14381, 745	572	31	13588	5.E+00	1.E+00	1.E-01	1.E+01
GOTERM_BP_FAT	GO:0044271~nitrogen compound biosynthetic process	23	3.610675039	9.E-03 382985, 18416, 109900, 232087, 11847, 1	572	302	13588	2.E+00	1.E+00	1.E-01	1.E+01
GOTERM_BP_FAT	GO:0001501~skeletal system development	22	3.453689168	9.E-03 78294, 12842, 69121, 17869, 12043, 1543	572	285	13588	2.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0045944~positive regulation of transcription from RNA polymerase II promoter	26	4.081632653	9.E-03 17536, 22130, 17869, 22778, 12912, 1291	572	358	13588	2.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0033135~regulation of peptidyl-serine phosphorylation	4	0.627943485	9.E-03 12028, 12018, 18413, 12043	572	11	13588	9.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0032494~response to peptidoglycan	4	0.627943485	9.E-03 17874, 16179, 26416, 24088	572	11	13588	9.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0005978~glycogen biosynthetic process	4	0.627943485	9.E-03 18682, 11651, 27357, 77559	572	11	13588	9.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0009250~glucan biosynthetic process	4	0.627943485	9.E-03 18682, 11651, 27357, 77559	572	11	13588	9.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0031589~cell-substrate adhesion	8	1.25588697	1.E-02 21687, 50768, 12043, 16414, 11856, 1641	572	57	13588	3.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0044092~negative regulation of molecular function	13	2.040816327	1.E-02 15170, 11806, 11807, 14678, 17869, 1184	572	132	13588	2.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0006974~response to DNA damage stimulus	22	3.453689168	1.E-02 382985, 80905, 53610, 16882, 12952, 108	572	287	13588	2.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0021700~developmental maturation	11	1.726844584	1.E-02 108672, 12229, 19713, 11651, 12531, 201	572	101	13588	3.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0043086~negative regulation of catalytic activity	11	1.726844584	1.E-02 15170, 24064, 11806, 11807, 14678, 1319	572	101	13588	3.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0000089~mitotic metaphase	3	0.470957614	1.E-02 67052, 20112, 67141	572	4	13588	2.E+01	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0030300~regulation of intestinal cholesterol absorption	3	0.470957614	1.E-02 11806, 11807, 11808	572	4	13588	2.E+01	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0070059~apoptosis in response to endoplasmic reticulum stress	3	0.470957614	1.E-02 12028, 12018, 12043	572	4	13588	2.E+01	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0006526~arginine biosynthetic process	3	0.470957614	1.E-02 18416, 217214, 109900	572	4	13588	2.E+01	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0042176~regulation of protein catabolic process	6	0.941915228	1.E-02 11865, 17999, 282663, 11651, 192176, 16	572	32	13588	4.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0010553~negative regulation of specific transcription from RNA polymerase II promoter	5	0.784929356	1.E-02 17869, 22778, 18626, 18627, 18628	572	21	13588	6.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0043506~regulation of JUN kinase activity	5	0.784929356	1.E-02 16179, 16334, 21899, 20963, 224014	572	21	13588	6.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0045619~regulation of lymphocyte differentiation	8	1.25588697	1.E-02 15170, 16818, 12015, 16197, 11486, 2277	572	58	13588	3.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0006979~response to oxidative stress	10	1.569858713	1.E-02 382985, 12842, 19053, 11816, 26395, 264	572	87	13588	3.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0046328~regulation of JNK cascade	7	1.098901099	1.E-02 17874, 16179, 16334, 21899, 21898, 2096	572	45	13588	4.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0051099~positive regulation of binding	7	1.098901099	1.E-02 17874, 16179, 12315, 12314, 12313, 2189	572	45	13588	4.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0009057~macromolecule catabolic process	41	6.436420722	1.E-02 56550, 74287, 218793, 11816, 26965, 116	572	654	13588	1.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0010564~regulation of cell cycle process	9	1.412872841	1.E-02 16994, 11920, 52563, 18413, 56371, 1254	572	73	13588	3.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0006357~regulation of transcription from RNA polymerase II promoter	39	6.12244898	1.E-02 17536, 22130, 19720, 17869, 22778, 1291	572	616	13588	2.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0042493~response to drug	10	1.569858713	1.E-02 18669, 16818, 18671, 18670, 232087, 120	572	88	13588	3.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0045859~regulation of protein kinase activity	16	2.51177394	1.E-02 15170, 14678, 21899, 21898, 20416, 2240	572	186	13588	2.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0045088~regulation of innate immune response	7	1.098901099	1.E-02 19370, 17874, 16179, 21898, 27007, 3790	572	46	13588	4.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0070302~regulation of stress-activated protein kinase signaling	7	1.098901099	1.E-02 17874, 16179, 16334, 21899, 21898, 2096	572	46	13588	4.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0051101~regulation of DNA binding	9	1.412872841	1.E-02 17874, 16179, 12315, 12314, 12313, 2189	572	74	13588	3.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0070227~lymphocyte apoptosis	4	0.627943485	1.E-02 12028, 12018, 11651, 17869	572	12	13588	8.E+00	1.E+00	1.E-01	2.E+01



GOTERM_BP_FAT	GO:0002758~innate immune response-activating signal transductio	4	0.627943485	1E-02 17874, 16179, 27007, 24088	572	12	13588	8.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0001909~leukocyte mediated cytotoxicity	4	0.627943485	1E-02 15170, 11891, 13035, 17969	572	12	13588	8.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0006928~cell motion	26	4.081632653	1E-02 117600, 22323, 13649, 238055, 16803, 20	572	367	13588	2.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0002443~leukocyte mediated immunity	10	1.569858713	1E-02 12051, 14127, 15170, 17874, 11891, 1303	572	89	13588	3.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0032844~regulation of homeostatic process	8	1.25588697	1E-02 14127, 16818, 21349, 11486, 12028, 2641	572	60	13588	3.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0051091~positive regulation of transcription factor activity	6	0.941915228	1E-02 17874, 16179, 21898, 16414, 24088, 1291	572	34	13588	4.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0009968~negative regulation of signal transduction	15	2.354788069	1E-02 15170, 69121, 380714, 66042, 20481, 118	572	171	13588	2.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0032880~regulation of protein localization	10	1.569858713	1E-02 16994, 18826, 14570, 104215, 192662, 11	572	90	13588	3.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0051098~regulation of binding	10	1.569858713	1E-02 17874, 16179, 12315, 12314, 12313, 2189	572	90	13588	3.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0007229~integrin-mediated signaling pathway	9	1.412872841	1E-02 16408, 22324, 16411, 232906, 57257, 164	572	76	13588	3.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0006954~inflammatory response	18	2.825745683	1E-02 12475, 239081, 21899, 21898, 11651, 164	572	225	13588	2.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0031343~positive regulation of cell killing	5	0.784929356	1E-02 19370, 14972, 15018, 27007, 379043, 120	572	23	13588	5.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0019835~cytolysis	5	0.784929356	1E-02 14939, 14941, 14940, 14944, 14943	572	23	13588	5.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0032582~negative regulation of gene-specific transcription	5	0.784929356	1E-02 17869, 22778, 18626, 18627, 18628	572	23	13588	5.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0001912~positive regulation of leukocyte mediated cytotoxicity	5	0.784929356	1E-02 19370, 14972, 15018, 27007, 379043, 120	572	23	13588	5.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0045580~regulation of T cell differentiation	7	1.098901099	1E-02 16818, 12015, 16197, 11486, 22778, 1619	572	48	13588	3.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0050731~positive regulation of peptidyl-tyrosine phosphorylati	6	0.941915228	1E-02 56717, 18413, 20963, 16452, 15163, 1709	572	35	13588	4.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0008629~induction of apoptosis by intracellular signals	6	0.941915228	1E-02 12051, 66593, 11920, 12028, 17869, 1707	572	35	13588	4.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0043632~modification-dependent macromolecule catabolic proc	33	5.180533752	1E-02 56550, 74287, 218793, 26965, 59008, 163	572	508	13588	2.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0019941~modification-dependent protein catabolic process	33	5.180533752	1E-02 56550, 74287, 218793, 26965, 59008, 163	572	508	13588	2.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0005976~polysaccharide metabolic process	10	1.569858713	2.E-02 18682, 110095, 16195, 102093, 110094, 1	572	92	13588	3.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0050863~regulation of T cell activation	11	1.726844584	2.E-02 16408, 15170, 16818, 12015, 16197, 2467	572	108	13588	2.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0045767~regulation of anti-apoptosis	4	0.627943485	2.E-02 18709, 218397, 12048, 12028	572	13	13588	7.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0043547~positive regulation of GTPase activity	4	0.627943485	2.E-02 71709, 11856, 19765, 19417	572	13	13588	7.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0044265~cellular macromolecule catabolic process	38	5.965463108	2.E-02 56550, 74287, 218793, 11816, 26965, 238	572	609	13588	1.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0010557~positive regulation of macromolecule biosynthetic prc	34	5.337519623	2.E-02 17536, 22130, 17869, 22778, 12912, 1039	572	530	13588	2.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0003006~reproductive developmental process	20	3.139717425	2.E-02 11651, 12043, 72508, 13382, 67141, 5671	572	264	13588	2.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0001763~morphogenesis of a branching structure	12	1.883830455	2.E-02 15402, 14674, 20779, 24064, 14178, 1270	572	125	13588	2.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0032374~regulation of cholesterol transport	3	0.470957614	2.E-02 11806, 11807, 11808	572	5	13588	1.E+01	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0032371~regulation of sterol transport	3	0.470957614	2.E-02 11806, 11807, 11808	572	5	13588	1.E+01	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0002312~B cell activation during immune response	3	0.470957614	2.E-02 12051, 11486, 234779	572	5	13588	1.E+01	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0002313~mature B cell differentiation during immune response	3	0.470957614	2.E-02 12051, 11486, 234779	572	5	13588	1.E+01	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0008635~activation of caspase activity by cytochrome c	3	0.470957614	2.E-02 672195, 12028, 12018, 13063	572	5	13588	1.E+01	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0031401~positive regulation of protein modification process	9	1.412872841	2.E-02 56717, 18413, 12043, 216080, 20963, 208	572	78	13588	3.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0007517~muscle organ development	15	2.354788069	2.E-02 12955, 15430, 18479, 16412, 20467, 1184	572	176	13588	2.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0007088~regulation of mitosis	6	0.941915228	2.E-02 16994, 11920, 52563, 12540, 56150, 6899	572	36	13588	4.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0050851~antigen receptor-mediated signaling pathway	6	0.941915228	2.E-02 15170, 18803, 16818, 234779, 20963, 170	572	36	13588	4.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0051783~regulation of nuclear division	6	0.941915228	2.E-02 16994, 11920, 52563, 12540, 56150, 6899	572	36	13588	4.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0034655~nucleobase, nucleoside, nucleotide and nucleic acid c	6	0.941915228	2.E-02 11486, 17970, 72269, 17969, 22271, 9958	572	36	13588	4.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0034656~nucleobase, nucleoside and nucleotide catabolic proc	6	0.941915228	2.E-02 11486, 17970, 72269, 17969, 22271, 9958	572	36	13588	4.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0045834~positive regulation of lipid metabolic process	5	0.784929356	2.E-02 18048, 16367, 11816, 57257, 12540	572	24	13588	5.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0042035~regulation of cytokine biosynthetic process	8	1.25588697	2.E-02 12051, 16994, 17874, 11807, 21899, 2189	572	64	13588	3.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0043524~negative regulation of neuron apoptosis	7	1.098901099	2.E-02 218397, 12048, 12028, 15461, 12043, 108	572	50	13588	3.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0030163~protein catabolic process	35	5.494505495	2.E-02 56550, 74287, 218793, 26965, 11651, 590	572	556	13588	1.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0001101~response to acid	4	0.627943485	2.E-02 56717, 20779, 12028, 12043	572	14	13588	7.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0032319~regulation of Rho GTPase activity	4	0.627943485	2.E-02 56717, 71709, 19765, 19417	572	14	13588	7.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0050853~B cell receptor signaling pathway	4	0.627943485	2.E-02 15170, 16818, 20963, 17096	572	14	13588	7.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0007159~leukocyte adhesion	4	0.627943485	2.E-02 16408, 20345, 16414, 16409	572	14	13588	7.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0019725~cellular homeostasis	24	3.767660911	2.E-02 19317, 18453, 11816, 12043, 14827, 1478	572	343	13588	2.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0019319~hexose biosynthetic process	5	0.784929356	2.E-02 14751, 18534, 21991, 230163, 74551	572	25	13588	5.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0051092~positive regulation of NF-kappaB transcription factor	5	0.784929356	2.E-02 17874, 16179, 21898, 16414, 24088	572	25	13588	5.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0010741~negative regulation of protein kinase cascade	5	0.784929356	2.E-02 15170, 12703, 24064, 16001, 17082	572	25	13588	5.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0007346~regulation of mitotic cell cycle	10	1.569858713	2.E-02 16994, 11920, 52563, 12043, 17869, 1254	572	96	13588	2.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0050870~positive regulation of T cell activation	8	1.25588697	2.E-02 16408, 16818, 12015, 16197, 11486, 2277	572	66	13588	3.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0031400~negative regulation of protein modification process	6	0.941915228	2.E-02 15170, 12703, 12028, 12018, 12568, 6714	572	38	13588	4.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0007005~mitochondrion organization	10	1.569858713	2.E-02 382985, 12048, 13052, 12028, 12122, 120	572	97	13588	2.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0051186~cofactor metabolic process	15	2.354788069	2.E-02 17448, 19895, 17970, 14782, 66171, 1039	572	182	13588	2.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0032583~regulation of gene-specific transcription	8	1.25588697	2.E-02 18771, 21349, 17869, 22778, 18626, 2087	572	67	13588	3.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0042509~regulation of tyrosine phosphorylation of STAT protei	4	0.627943485	2.E-02 12703, 16452, 15163, 17096	572	15	13588	6.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0001782~B cell homeostasis	4	0.627943485	2.E-02 12028, 12018, 12043, 18707	572	15	13588	6.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0009084~glutamine family amino acid biosynthetic process	4	0.627943485	2.E-02 18416, 217214, 109900, 14645	572	15	13588	6.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0046131~pyrimidine ribonucleoside metabolic process	4	0.627943485	2.E-02 72269, 56749, 22271, 99586	572	15	13588	6.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0051047~positive regulation of secretion	7	1.098901099	2.E-02 14127, 14661, 12568, 12912, 83671, 1039	572	53	13588	3.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0051173~positive regulation of nitrogen compound metabolic p	33	5.180533752	2.E-02 17536, 22130, 17869, 22778, 12912, 1291	572	526	13588	1.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0009164~nucleoside catabolic process	3	0.470957614	2.E-02 11486, 72269, 99586	572	6	13588	1.E+01	1.E+00	2.E-01	3.E+01



GOTERM_BP_FAT	GO:0001783~B cell apoptosis	3	0.470957614	2E-02 12028, 12018, 17869	572	6	13588	1E+01	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0042537~benzene and derivative metabolic process	3	0.470957614	2E-02 13077, 94284, 14865, 394436	572	6	13588	1E+01	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0019433~triglyceride catabolic process	3	0.470957614	2E-02 11814, 669888, 238055	572	6	13588	1E+01	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0046503~glycerolipid catabolic process	3	0.470957614	2E-02 11814, 669888, 238055	572	6	13588	1E+01	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0031365~N-terminal protein amino acid modification	3	0.470957614	2E-02 18108, 18107, 12914	572	6	13588	1E+01	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0051883~killing of cells in other organism during symbiotic inte	3	0.470957614	2E-02 11657, 13035, 17969	572	6	13588	1E+01	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0044058~regulation of digestive system process	3	0.470957614	2E-02 11806, 11807, 11808	572	6	13588	1E+01	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0051818~disruption of cells of other organism during symbioti	3	0.470957614	2E-02 11657, 13035, 17969	572	6	13588	1E+01	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0051851~modification by host of symbiont morphology or phy	3	0.470957614	2E-02 11657, 13035, 17969	572	6	13588	1E+01	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0032469~endoplasmic reticulum calcium ion homeostasis	3	0.470957614	2E-02 12028, 12018, 12043	572	6	13588	1E+01	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0060068~vagina development	3	0.470957614	2E-02 12028, 12018, 17979	572	6	13588	1E+01	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0046464~acylglycerol catabolic process	3	0.470957614	2E-02 11814, 669888, 238055	572	6	13588	1E+01	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0032368~regulation of lipid transport	3	0.470957614	2E-02 11806, 11807, 11808	572	6	13588	1E+01	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0045123~cellular extravasation	3	0.470957614	2E-02 20345, 16414, 16409	572	6	13588	1E+01	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0042159~lipoprotein catabolic process	3	0.470957614	2E-02 11816, 11920, 238055	572	6	13588	1E+01	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0044269~glycerol ether catabolic process	3	0.470957614	2E-02 11814, 669888, 238055	572	6	13588	1E+01	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0006886~intracellular protein transport	20	3.139717425	2E-02 11865, 269589, 19894, 19384, 380714, 12	572	276	13588	2E+00	1E+00	2E-01	4E+01
GOTERM_BP_FAT	GO:0022612~gland morphogenesis	9	1.412872841	2E-02 13649, 20779, 14178, 12043, 12505, 1600	572	84	13588	3E+00	1E+00	2E-01	4E+01
GOTERM_BP_FAT	GO:0043405~regulation of MAP kinase activity	9	1.412872841	2E-02 15170, 16179, 24064, 16334, 21899, 2639	572	84	13588	3E+00	1E+00	2E-01	4E+01
GOTERM_BP_FAT	GO:0032270~positive regulation of cellular protein metabolic proce	10	1.569858713	2E-02 56717, 18413, 11651, 12043, 216080, 209	572	100	13588	2E+00	1E+00	2E-01	4E+01
GOTERM_BP_FAT	GO:0001838~embryonic epithelial tube formation	7	1.098901099	3E-02 22323, 16911, 232906, 19713, 50768, 123	572	54	13588	3E+00	1E+00	2E-01	4E+01
GOTERM_BP_FAT	GO:0033500~carbohydrate homeostasis	6	0.941915228	3E-02 12015, 380714, 18609, 231103, 18576, 10	572	40	13588	4E+00	1E+00	2E-01	4E+01
GOTERM_BP_FAT	GO:0042593~glucose homeostasis	6	0.941915228	3E-02 12015, 380714, 18609, 231103, 18576, 10	572	40	13588	4E+00	1E+00	2E-01	4E+01
GOTERM_BP_FAT	GO:0002705~positive regulation of leukocyte mediated immunity	6	0.941915228	3E-02 19370, 14972, 14127, 15018, 27007, 3790	572	40	13588	4E+00	1E+00	2E-01	4E+01
GOTERM_BP_FAT	GO:0002708~positive regulation of lymphocyte mediated immunity	6	0.941915228	3E-02 19370, 14972, 14127, 15018, 27007, 3790	572	40	13588	4E+00	1E+00	2E-01	4E+01
GOTERM_BP_FAT	GO:0048568~embryonic organ development	18	2.825745683	3E-02 13649, 19378, 17869, 15430, 11651, 5684	572	241	13588	2E+00	1E+00	2E-01	4E+01
GOTERM_BP_FAT	GO:0007281~germ cell development	10	1.569858713	3E-02 56717, 12048, 12028, 72508, 11651, 1204	572	101	13588	2E+00	1E+00	2E-01	4E+01
GOTERM_BP_FAT	GO:0042158~lipoprotein biosynthetic process	7	1.098901099	3E-02 18108, 18107, 108672, 17777, 11806, 118	572	55	13588	3E+00	1E+00	2E-01	4E+01
GOTERM_BP_FAT	GO:0030032~lamellipodium assembly	4	0.627943485	3E-02 100044475, 17973, 57257, 224014	572	16	13588	6E+00	1E+00	2E-01	4E+01
GOTERM_BP_FAT	GO:0030101~natural killer cell activation	4	0.627943485	3E-02 27007, 16414, 22778, 11891	572	16	13588	6E+00	1E+00	2E-01	4E+01
GOTERM_BP_FAT	GO:0051402~neuron apoptosis	4	0.627943485	3E-02 11920, 12028, 12043, 12568	572	16	13588	6E+00	1E+00	2E-01	4E+01
GOTERM_BP_FAT	GO:0030071~regulation of mitotic metaphase/anaphase transition	4	0.627943485	3E-02 11920, 52563, 56150, 68999	572	16	13588	6E+00	1E+00	2E-01	4E+01
GOTERM_BP_FAT	GO:0051603~proteolysis involved in cellular protein catabolic proce	33	5.180533752	3E-02 56550, 74287, 218793, 26965, 59008, 163	572	534	13588	1E+00	1E+00	2E-01	4E+01
GOTERM_BP_FAT	GO:0015758~glucose transport	5	0.784929356	3E-02 16333, 20525, 16334, 22612, 11651	572	28	13588	4E+00	1E+00	2E-01	4E+01
GOTERM_BP_FAT	GO:0045893~positive regulation of transcription, DNA-dependent	27	4.238618524	3E-02 17536, 22130, 17869, 22778, 12912, 1291	572	416	13588	2E+00	1E+00	2E-01	4E+01
GOTERM_BP_FAT	GO:0033043~regulation of organelle organization	13	2.040816327	3E-02 227753, 16800, 56150, 11848, 16994, 567	572	154	13588	2E+00	1E+00	2E-01	4E+01
GOTERM_BP_FAT	GO:0007292~female gamete generation	7	1.098901099	3E-02 20779, 11920, 12043, 12531, 16847, 2011	572	56	13588	3E+00	1E+00	2E-01	4E+01
GOTERM_BP_FAT	GO:0001934~positive regulation of protein amino acid phosphoryla	7	1.098901099	3E-02 56717, 18413, 12043, 20963, 16452, 1516	572	56	13588	3E+00	1E+00	2E-01	4E+01
GOTERM_BP_FAT	GO:0044257~cellular protein catabolic process	33	5.180533752	3E-02 56550, 74287, 218793, 26965, 59008, 163	572	537	13588	1E+00	1E+00	2E-01	4E+01
GOTERM_BP_FAT	GO:0044270~nitrogen compound catabolic process	6	0.941915228	3E-02 11486, 17970, 72269, 17969, 22271, 9958	572	42	13588	3E+00	1E+00	2E-01	4E+01
GOTERM_BP_FAT	GO:0051254~positive regulation of RNA metabolic process	27	4.238618524	3E-02 17536, 22130, 17869, 22778, 12912, 1291	572	419	13588	2E+00	1E+00	2E-01	4E+01
GOTERM_BP_FAT	GO:0007519~skeletal muscle tissue development	8	1.25588697	3E-02 15438, 26416, 15430, 18479, 11459, 1256	572	72	13588	3E+00	1E+00	2E-01	4E+01
GOTERM_BP_FAT	GO:0009165~nucleotide biosynthetic process	14	2.197802198	3E-02 382985, 11717, 11564, 11566, 99586, 114	572	174	13588	2E+00	1E+00	2E-01	4E+01
GOTERM_BP_FAT	GO:0046461~neutral lipid catabolic process	3	0.470957614	3E-02 11814, 669888, 238055	572	7	13588	1E+01	1E+00	2E-01	4E+01
GOTERM_BP_FAT	GO:0010812~negative regulation of cell-substrate adhesion	3	0.470957614	3E-02 18708, 12842, 218397	572	7	13588	1E+01	1E+00	2E-01	4E+01
GOTERM_BP_FAT	GO:0002224~toll-like receptor signaling pathway	3	0.470957614	3E-02 17874, 16179, 24088	572	7	13588	1E+01	1E+00	2E-01	4E+01
GOTERM_BP_FAT	GO:0051323~metaphase	3	0.470957614	3E-02 67052, 20112, 67141	572	7	13588	1E+01	1E+00	2E-01	4E+01
GOTERM_BP_FAT	GO:0002335~mature B cell differentiation	3	0.470957614	3E-02 12051, 11486, 234779	572	7	13588	1E+01	1E+00	2E-01	4E+01
GOTERM_BP_FAT	GO:0031640~killing of cells of another organism	3	0.470957614	3E-02 11657, 13035, 17969	572	7	13588	1E+01	1E+00	2E-01	4E+01
GOTERM_BP_FAT	GO:0009620~response to fungus	4	0.627943485	3E-02 17874, 12018, 17969, 24088	572	17	13588	6E+00	1E+00	2E-01	4E+01
GOTERM_BP_FAT	GO:0032729~positive regulation of interferon-gamma production	4	0.627943485	3E-02 12051, 19370, 15018, 27007, 379043	572	17	13588	6E+00	1E+00	2E-01	4E+01
GOTERM_BP_FAT	GO:0010332~response to gamma radiation	4	0.627943485	3E-02 12028, 12018, 12043, 108138	572	17	13588	6E+00	1E+00	2E-01	4E+01
GOTERM_BP_FAT	GO:0030593~neutrophil chemotaxis	4	0.627943485	3E-02 20310, 14127, 16414, 16409	572	17	13588	6E+00	1E+00	2E-01	4E+01
GOTERM_BP_FAT	GO:0048599~oocyte development	4	0.627943485	3E-02 12043, 12531, 20112, 67141	572	17	13588	6E+00	1E+00	2E-01	4E+01
GOTERM_BP_FAT	GO:0006366~transcription from RNA polymerase II promoter	8	1.25588697	4E-02 13872, 69920, 16911, 17420, 17869, 1488	572	74	13588	3E+00	1E+00	3E-01	5E+01
GOTERM_BP_FAT	GO:0060538~skeletal muscle organ development	8	1.25588697	4E-02 15438, 26416, 15430, 18479, 11459, 1256	572	74	13588	3E+00	1E+00	3E-01	5E+01
GOTERM_BP_FAT	GO:0008645~hexose transport	5	0.784929356	4E-02 16333, 20525, 16334, 22612, 11651	572	30	13588	4E+00	1E+00	3E-01	5E+01
GOTERM_BP_FAT	GO:0043279~response to alkaloid	5	0.784929356	4E-02 12043, 17869, 12568, 16847, 13385	572	30	13588	4E+00	1E+00	3E-01	5E+01
GOTERM_BP_FAT	GO:0045860~positive regulation of protein kinase activity	11	1.726844584	4E-02 16179, 16334, 21899, 14678, 26395, 2189	572	124	13588	2E+00	1E+00	3E-01	5E+01
GOTERM_BP_FAT	GO:0035148~tube lumen formation	7	1.098901099	4E-02 22323, 16911, 232906, 19713, 50768, 123	572	59	13588	3E+00	1E+00	3E-01	5E+01
GOTERM_BP_FAT	GO:0043406~positive regulation of MAP kinase activity	7	1.098901099	4E-02 16179, 16334, 21899, 26395, 20416, 2096	572	59	13588	3E+00	1E+00	3E-01	5E+01
GOTERM_BP_FAT	GO:0051090~regulation of transcription factor activity	7	1.098901099	4E-02 17874, 16179, 21898, 16414, 192176, 240	572	59	13588	3E+00	1E+00	3E-01	5E+01
GOTERM_BP_FAT	GO:0008104~protein localization	43	6.750392465	4E-02 269589, 11852, 11816, 19384, 238055, 12	572	753	13588	1E+00	1E+00	3E-01	5E+01
GOTERM_BP_FAT	GO:0009994~oocyte differentiation	4	0.627943485	4E-02 12043, 12531, 20112, 67141	572	18	13588	5E+00	1E+00	3E-01	5E+01
GOTERM_BP_FAT	GO:0032755~positive regulation of interleukin-6 production	4	0.627943485	4E-02 14127, 17874, 21898, 24088	572	18	13588	5E+00	1E+00	3E-01	5E+01



GOTERM_BP_FAT	GO:0060674~placenta blood vessel development	4	0.627943485	4.E-02 12702, 26395, 11651, 16477	572	18	13588	5.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0008544~epidermis development	11	1.726844584	4.E-02 16994, 12831, 13649, 12842, 14178, 2639	572	125	13588	2.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0051046~regulation of secretion	11	1.726844584	4.E-02 14127, 14661, 11486, 380714, 18413, 185	572	125	13588	2.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0080135~regulation of cellular response to stress	8	1.25588697	4.E-02 56717, 17874, 16179, 16334, 21899, 2189	572	75	13588	3.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0034654~nucleobase, nucleoside, nucleotide and nucleic acid b	14	2.197802198	4.E-02 382985, 11717, 11564, 11566, 99586, 114	572	179	13588	2.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0034404~nucleobase, nucleoside and nucleotide biosynthetic p	14	2.197802198	4.E-02 382985, 11717, 11564, 11566, 99586, 114	572	179	13588	2.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0060341~regulation of cellular localization	13	2.040816327	4.E-02 380714, 68092, 12912, 103988, 24069, 14	572	161	13588	2.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0009124~nucleoside monophosphate biosynthetic process	6	0.941915228	4.E-02 11486, 11514, 11717, 56749, 11566, 9958	572	45	13588	3.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0042327~positive regulation of phosphorylation	7	1.098901099	4.E-02 56717, 18413, 12043, 20963, 16452, 1516	572	60	13588	3.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0015749~monosaccharide transport	5	0.784929356	4.E-02 16333, 20525, 16334, 22612, 11651	572	31	13588	4.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0016050~vesicle organization	5	0.784929356	4.E-02 108672, 57257, 12043, 67141, 13385	572	31	13588	4.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0002449~lymphocyte mediated immunity	8	1.25588697	4.E-02 12051, 14127, 15170, 17874, 11891, 1081	572	76	13588	3.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0048754~branching morphogenesis of a tube	9	1.412872841	4.E-02 15402, 14674, 20779, 24064, 12043, 1250	572	93	13588	2.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0009263~deoxyribonucleotide biosynthetic process	3	0.470957614	4.E-02 382985, 20133, 20135	572	8	13588	9.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0031017~exocrine pancreas development	3	0.470957614	4.E-02 18609, 16001, 16000	572	8	13588	9.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0002685~regulation of leukocyte migration	3	0.470957614	4.E-02 11486, 20339, 24088	572	8	13588	9.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0048857~neural nucleus development	3	0.470957614	4.E-02 15407, 12043, 56847	572	8	13588	9.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0043491~protein kinase B signaling cascade	3	0.470957614	4.E-02 16367, 72508, 11651	572	8	13588	9.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0010522~regulation of calcium ion transport into cytosol	3	0.470957614	4.E-02 12028, 12018, 12043	572	8	13588	9.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0032321~positive regulation of Rho GTPase activity	3	0.470957614	4.E-02 71709, 19765, 19417	572	8	13588	9.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0002320~lymphoid progenitor cell differentiation	3	0.470957614	4.E-02 20375, 12043, 108138	572	8	13588	9.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0048041~focal adhesion formation	3	0.470957614	4.E-02 50768, 12043, 11856	572	8	13588	9.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0051646~mitochondrion localization	3	0.470957614	4.E-02 11657, 59040, 214952	572	8	13588	9.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0051702~interaction with symbiont	3	0.470957614	4.E-02 11657, 13035, 17969	572	8	13588	9.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0055001~muscle cell development	7	1.098901099	4.E-02 13052, 77579, 11464, 16412, 18479, 1145	572	61	13588	3.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0009112~nucleobase metabolic process	4	0.627943485	4.E-02 11486, 11717, 56749, 99586	572	19	13588	5.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0030239~myofibril assembly	4	0.627943485	4.E-02 77579, 11464, 16412, 11459	572	19	13588	5.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0043525~positive regulation of neuron apoptosis	4	0.627943485	4.E-02 16994, 11920, 12028, 12568	572	19	13588	5.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0046638~positive regulation of alpha-beta T cell differentiation	4	0.627943485	4.E-02 11486, 22778, 16190, 20963	572	19	13588	5.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0048535~lymph node development	4	0.627943485	4.E-02 16994, 16197, 22778, 15902	572	19	13588	5.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0046425~regulation of JAK-STAT cascade	4	0.627943485	4.E-02 12703, 16452, 15163, 17096	572	19	13588	5.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0043271~negative regulation of ion transport	4	0.627943485	4.E-02 16994, 17999, 14678, 12043	572	19	13588	5.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0034330~cell junction organization	5	0.784929356	4.E-02 13052, 50768, 12043, 11856, 12540	572	32	13588	4.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0032675~regulation of interleukin-6 production	5	0.784929356	4.E-02 14127, 17874, 21899, 21898, 24088	572	32	13588	4.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0051248~negative regulation of protein metabolic process	8	1.25588697	5.E-02 15170, 13685, 12703, 12028, 12018, 1921	572	78	13588	2.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0045937~positive regulation of phosphate metabolic process	7	1.098901099	5.E-02 56717, 18413, 12043, 20963, 16452, 1516	572	62	13588	3.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0010562~positive regulation of phosphorus metabolic process	7	1.098901099	5.E-02 56717, 18413, 12043, 20963, 16452, 1516	572	62	13588	3.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0001649~osteoblast differentiation	6	0.941915228	5.E-02 78294, 12842, 12161, 208727, 16000, 142	572	47	13588	3.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0043010~camera-type eye development	11	1.726844584	5.E-02 18771, 12955, 232906, 77579, 12028, 120	572	130	13588	2.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0006281~DNA repair	16	2.51177394	5.E-02 80905, 382985, 53610, 16882, 12952, 108	572	222	13588	2.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0030030~cell projection organization	21	3.296703297	5.E-02 22323, 100044475, 73750, 17973, 11651	572	319	13588	2.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0030900~forebrain development	13	2.040816327	5.E-02 13649, 232906, 19378, 22778, 56847, 129	572	167	13588	2.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0033692~cellular polysaccharide biosynthetic process	4	0.627943485	5.E-02 18682, 11651, 27357, 77559	572	20	13588	5.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0043270~positive regulation of ion transport	4	0.627943485	5.E-02 234779, 12028, 12018, 11651	572	20	13588	5.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0018904~organic ether metabolic process	6	0.941915228	5.E-02 17777, 11814, 669888, 18534, 238055, 13	572	48	13588	3.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0000165~MAPKKK cascade	10	1.569858713	5.E-02 17874, 19713, 16334, 14784, 14678, 2639	572	114	13588	2.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0050670~regulation of lymphocyte proliferation	8	1.25588697	5.E-02 16408, 15170, 17874, 246779, 11486, 218	572	80	13588	2.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0032944~regulation of mononuclear cell proliferation	8	1.25588697	5.E-02 16408, 15170, 17874, 246779, 11486, 218	572	80	13588	2.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0032318~regulation of Ras GTPase activity	8	1.25588697	5.E-02 56717, 24064, 71709, 228998, 19765, 194	572	80	13588	2.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0046112~nucleobase biosynthetic process	3	0.470957614	5.E-02 11486, 56749, 99586	572	9	13588	8.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0002902~regulation of B cell apoptosis	3	0.470957614	5.E-02 11486, 12028, 17869	572	9	13588	8.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0001916~positive regulation of T cell mediated cytotoxicity	3	0.470957614	5.E-02 14972, 15018, 12010	572	9	13588	8.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0042531~positive regulation of tyrosine phosphorylation of ST	3	0.470957614	5.E-02 16452, 15163, 17096	572	9	13588	8.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0051924~regulation of calcium ion transport	5	0.784929356	5.E-02 234779, 14678, 12028, 12018, 12043	572	34	13588	3.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0046634~regulation of alpha-beta T cell activation	5	0.784929356	5.E-02 11486, 22778, 16396, 16190, 20963	572	34	13588	3.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0051656~establishment of organelle localization	5	0.784929356	5.E-02 77579, 12540, 11891, 59040, 214952	572	34	13588	3.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0002824~positive regulation of adaptive immune response bas	5	0.784929356	5.E-02 14972, 14127, 15018, 11486, 12010	572	34	13588	3.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0002821~positive regulation of adaptive immune response	5	0.784929356	5.E-02 14972, 14127, 15018, 11486, 12010	572	34	13588	3.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0009991~response to extracellular stimulus	11	1.726844584	5.E-02 16828, 21687, 11657, 12842, 109900, 116	572	133	13588	2.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0007398~ectoderm development	11	1.726844584	5.E-02 16994, 12831, 13649, 12842, 14178, 2639	572	133	13588	2.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0001525~angiogenesis	11	1.726844584	5.E-02 18771, 14674, 14751, 11852, 26416, 2041	572	133	13588	2.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0048585~negative regulation of response to stimulus	7	1.098901099	5.E-02 56717, 15170, 12703, 16197, 12702, 1148	572	65	13588	3.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0004571~response to ethanol	4	0.627943485	6.E-02 11816, 12043, 14360, 94284, 394436	572	21	13588	5.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0006461~protein complex assembly	16	2.51177394	6.E-02 22142, 227753, 22130, 18416, 17869, 184	572	227	13588	2.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0070271~protein complex biogenesis	16	2.51177394	6.E-02 22142, 227753, 22130, 18416, 17869, 184	572	227	13588	2.E+00	1.E+00	4.E-01	6.E+01



GOTERM_BP_FAT	GO:0070663~regulation of leukocyte proliferation	8	1.25588697	6.E-02 16408, 15170, 17874, 246779, 11486, 218	572	82	13588	2.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0007610~behavior	25	3.924646782	6.E-02 17159, 12765, 11657, 16803, 14661, 1151	572	405	13588	1.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0060711~labyrinthine layer development	5	0.784929356	6.E-02 12702, 14784, 26395, 11651, 16477	572	35	13588	3.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0031098~stress-activated protein kinase signaling pathway	5	0.784929356	6.E-02 17874, 16334, 74155, 20963, 224014	572	35	13588	3.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0048002~antigen processing and presentation of peptide antig	5	0.784929356	6.E-02 15007, 14972, 14127, 15018, 12010	572	35	13588	3.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0030902~hindbrain development	7	1.098901099	6.E-02 77579, 15407, 50768, 19378, 12043, 1256	572	67	13588	2.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0001841~neural tube formation	6	0.941915228	6.E-02 22323, 16911, 232906, 50768, 12370, 240	572	51	13588	3.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0018105~peptidyl-serine phosphorylation	4	0.627943485	6.E-02 11651, 12043, 12568, 20112	572	22	13588	4.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0046637~regulation of alpha-beta T cell differentiation	4	0.627943485	6.E-02 11486, 22778, 16190, 20963	572	22	13588	4.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0006213~pyrimidine nucleoside metabolic process	4	0.627943485	6.E-02 72269, 56749, 22271, 99586	572	22	13588	4.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0051346~negative regulation of hydrolase activity	4	0.627943485	6.E-02 24064, 11806, 11807, 16847	572	22	13588	4.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0002460~adaptive immune response based on somatic recomb	8	1.25588697	6.E-02 12051, 14127, 17874, 21899, 11891, 1081	572	84	13588	2.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0002250~adaptive immune response	8	1.25588697	6.E-02 12051, 14127, 17874, 21899, 11891, 1081	572	84	13588	2.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0006641~triglyceride metabolic process	5	0.784929356	6.E-02 17777, 11814, 669888, 18534, 238055	572	36	13588	3.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0046883~regulation of hormone secretion	5	0.784929356	6.E-02 14661, 18413, 18576, 12912, 103988	572	36	13588	3.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:000302~response to reactive oxygen species	5	0.784929356	6.E-02 12842, 19053, 26462, 50493, 12043	572	36	13588	3.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0006869~lipid transport	10	1.569858713	6.E-02 11813, 17777, 11814, 11806, 11807, 1181	572	119	13588	2.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0046626~regulation of insulin receptor signaling pathway	3	0.470957614	6.E-02 12703, 20779, 12702	572	10	13588	7.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0001556~oocyte maturation	3	0.470957614	6.E-02 12531, 20112, 67141	572	10	13588	7.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0033143~regulation of steroid hormone receptor signaling pat	3	0.470957614	6.E-02 20779, 16000, 11848	572	10	13588	7.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0050829~defense response to Gram-negative bacterium	3	0.470957614	6.E-02 18126, 21898, 16803	572	10	13588	7.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0002221~pattern recognition receptor signaling pathway	3	0.470957614	6.E-02 17874, 16179, 24088	572	10	13588	7.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0040020~regulation of meiosis	3	0.470957614	6.E-02 18413, 56371, 67141	572	10	13588	7.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0032320~positive regulation of Ras GTPase activity	3	0.470957614	6.E-02 71709, 19765, 19417	572	10	13588	7.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0001893~maternal placenta development	3	0.470957614	6.E-02 13857, 11651, 16477	572	10	13588	7.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0035020~regulation of Rac protein signal transduction	3	0.470957614	6.E-02 56717, 19417, 106952	572	10	13588	7.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0009628~response to abiotic stimulus	17	2.668759812	6.E-02 12842, 12955, 232087, 17869, 12043, 108	572	251	13588	2.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0001654~eye development	12	1.883830455	7.E-02 17536, 18771, 12955, 232906, 77579, 120	572	157	13588	2.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0045941~positive regulation of transcription	28	4.395604396	7.E-02 17536, 22130, 17869, 22778, 12912, 1291	572	475	13588	1.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0031016~pancreas development	5	0.784929356	7.E-02 18609, 19378, 16001, 18576, 16000	572	37	13588	3.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0001933~negative regulation of protein amino acid phosphoryl	4	0.627943485	7.E-02 15170, 12703, 12028, 12018	572	23	13588	4.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0009262~deoxyribonucleotide metabolic process	4	0.627943485	7.E-02 382985, 11486, 20133, 20135	572	23	13588	4.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0009896~positive regulation of catabolic process	4	0.627943485	7.E-02 17999, 14447, 11651, 16396	572	23	13588	4.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0031329~regulation of cellular catabolic process	4	0.627943485	7.E-02 56717, 14447, 11651, 208727	572	23	13588	4.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0010038~response to metal ion	6	0.941915228	7.E-02 18669, 11657, 18671, 17420, 230163, 185	572	53	13588	3.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0006351~transcription, DNA-dependent	10	1.569858713	7.E-02 13872, 69920, 69890, 22130, 16911, 1742	572	122	13588	2.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0007155~cell adhesion	32	5.023547881	7.E-02 12831, 69524, 11852, 11856, 20416, 1281	572	561	13588	1.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0001890~placenta development	8	1.25588697	7.E-02 13649, 12702, 11486, 13857, 14784, 2639	572	87	13588	2.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0022610~biological adhesion	32	5.023547881	7.E-02 12831, 69524, 11852, 11856, 20416, 1281	572	562	13588	1.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0040008~regulation of growth	17	2.668759812	7.E-02 11816, 12043, 22778, 22193, 20416, 1291	572	256	13588	2.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0051445~regulation of meiotic cell cycle	3	0.470957614	8.E-02 18413, 56371, 67141	572	11	13588	6.E+00	1.E+00	4.E-01	8.E+01
GOTERM_BP_FAT	GO:0030035~microspike assembly	3	0.470957614	8.E-02 30938, 12540, 224014	572	11	13588	6.E+00	1.E+00	4.E-01	8.E+01
GOTERM_BP_FAT	GO:0051591~response to cAMP	3	0.470957614	8.E-02 12842, 109900, 232087	572	11	13588	6.E+00	1.E+00	4.E-01	8.E+01
GOTERM_BP_FAT	GO:0046427~positive regulation of JAK-STAT cascade	3	0.470957614	8.E-02 16452, 15163, 17096	572	11	13588	6.E+00	1.E+00	4.E-01	8.E+01
GOTERM_BP_FAT	GO:0050856~regulation of T cell receptor signaling pathway	3	0.470957614	8.E-02 15170, 16818, 11486	572	11	13588	6.E+00	1.E+00	4.E-01	8.E+01
GOTERM_BP_FAT	GO:0048070~regulation of pigmentation during development	3	0.470957614	8.E-02 12028, 12043, 14682	572	11	13588	6.E+00	1.E+00	4.E-01	8.E+01
GOTERM_BP_FAT	GO:0055002~striated muscle cell development	6	0.941915228	8.E-02 13052, 77579, 11464, 16412, 18479, 1145	572	54	13588	3.E+00	1.E+00	4.E-01	8.E+01
GOTERM_BP_FAT	GO:0007423~sensory organ development	17	2.668759812	8.E-02 17536, 73750, 12955, 232906, 19378, 178	572	257	13588	2.E+00	1.E+00	4.E-01	8.E+01
GOTERM_BP_FAT	GO:0001503~ossification	9	1.412872841	8.E-02 78294, 12842, 12161, 69121, 12043, 1922	572	106	13588	2.E+00	1.E+00	4.E-01	8.E+01
GOTERM_BP_FAT	GO:0042542~response to hydrogen peroxide	4	0.627943485	8.E-02 12842, 19053, 50493, 12043	572	24	13588	4.E+00	1.E+00	4.E-01	8.E+01
GOTERM_BP_FAT	GO:0009314~response to radiation	11	1.726844584	8.E-02 13872, 12048, 11920, 12028, 232087, 120	572	143	13588	2.E+00	1.E+00	4.E-01	8.E+01
GOTERM_BP_FAT	GO:0060606~tube closure	5	0.784929356	8.E-02 22323, 16911, 232906, 50768, 24069	572	39	13588	3.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0048477~oogenesis	5	0.784929356	8.E-02 20779, 12043, 12531, 20112, 67141	572	39	13588	3.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0009612~response to mechanical stimulus	5	0.784929356	8.E-02 16994, 12842, 17869, 20598, 14360	572	39	13588	3.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0001843~neural tube closure	5	0.784929356	8.E-02 22323, 16911, 232906, 50768, 24069	572	39	13588	3.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0032269~negative regulation of cellular protein metabolic proc	7	1.098901099	8.E-02 15170, 13685, 12703, 12028, 12018, 1256	572	72	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0002755~MyD88-dependent toll-like receptor signaling pathwa	2	0.313971743	8.E-02 17874, 24088	572	2	13588	2.E+01	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0018377~protein myristoylation	2	0.313971743	8.E-02 18108, 18107	572	2	13588	2.E+01	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0009173~pyrimidine ribonucleoside monophosphate metabolic	2	0.313971743	8.E-02 56749, 99586	572	2	13588	2.E+01	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0009174~pyrimidine ribonucleoside monophosphate biosynthe	2	0.313971743	8.E-02 56749, 99586	572	2	13588	2.E+01	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0006499~N-terminal protein myristoylation	2	0.313971743	8.E-02 18108, 18107	572	2	13588	2.E+01	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0018319~protein amino acid myristoylation	2	0.313971743	8.E-02 18108, 18107	572	2	13588	2.E+01	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0002339~B cell selection	2	0.313971743	8.E-02 12028, 12018	572	2	13588	2.E+01	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0018008~N-terminal peptidyl-glycine N-myristoylation	2	0.313971743	8.E-02 18108, 18107	572	2	13588	2.E+01	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0046049~UMP metabolic process	2	0.313971743	8.E-02 56749, 99586	572	2	13588	2.E+01	1.E+00	5.E-01	8.E+01



GOTERM_BP_FAT	GO:0032497~detection of lipopolysaccharide	2	0.313971743	8.E-02 17087, 21898	572	2	13588	2.E+01	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0018201~peptidyl-glycine modification	2	0.313971743	8.E-02 18108, 18107	572	2	13588	2.E+01	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0032471~reduction of endoplasmic reticulum calcium ion concn	2	0.313971743	8.E-02 12028, 12018	572	2	13588	2.E+01	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0051496~positive regulation of stress fiber formation	2	0.313971743	8.E-02 56717, 11848	572	2	13588	2.E+01	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0002352~B cell negative selection	2	0.313971743	8.E-02 12028, 12018	572	2	13588	2.E+01	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0006222~UMP biosynthetic process	2	0.313971743	8.E-02 56749, 99586	572	2	13588	2.E+01	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0032774~RNA biosynthetic process	10	1.569858713	8.E-02 13872, 69920, 69890, 22130, 16911, 1742	572	126	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0006606~protein import into nucleus	6	0.941915228	9.E-02 11865, 19384, 231103, 12953, 70572, 164	572	56	13588	3.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0044242~cellular lipid catabolic process	6	0.941915228	9.E-02 18803, 11814, 669888, 234779, 238055, 1	572	56	13588	3.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0009954~proximal/distal pattern formation	4	0.627943485	9.E-02 15438, 15405, 19378, 15430	572	25	13588	4.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0051651~maintenance of location in cell	4	0.627943485	9.E-02 11657, 11816, 192176, 24069	572	25	13588	4.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0045639~positive regulation of myeloid cell differentiation	4	0.627943485	9.E-02 21349, 26416, 22778, 15902	572	25	13588	4.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0008624~induction of apoptosis by extracellular signals	4	0.627943485	9.E-02 12015, 14939, 12028, 26885	572	25	13588	4.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0045184~establishment of protein localization	36	5.651491366	9.E-02 269589, 11852, 19384, 238055, 12953, 14	572	656	13588	1.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0042330~taxiis	9	1.412872841	9.E-02 20310, 14127, 12765, 19354, 16414, 2020	572	109	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0006935~chemotaxis	9	1.412872841	9.E-02 20310, 14127, 12765, 19354, 16414, 2020	572	109	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0051928~positive regulation of calcium ion transport	3	0.470957614	9.E-02 234779, 12028, 12018	572	12	13588	6.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0042100~B cell proliferation	3	0.470957614	9.E-02 16197, 12028, 12043	572	12	13588	6.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0033059~cellular pigmentation	3	0.470957614	9.E-02 12043, 11891, 171531	572	12	13588	6.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0002244~hemopoietic progenitor cell differentiation	3	0.470957614	9.E-02 20375, 12043, 108138	572	12	13588	6.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0031532~actin cytoskeleton reorganization	3	0.470957614	9.E-02 20202, 192176, 20416	572	12	13588	6.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0031663~lipopolysaccharide-mediated signaling pathway	3	0.470957614	9.E-02 17874, 16179, 26416	572	12	13588	6.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0010628~positive regulation of gene expression	28	4.395604396	9.E-02 17536, 22130, 17869, 22778, 12912, 1291	572	488	13588	1.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0010876~lipid localization	10	1.569858713	9.E-02 11813, 17777, 11814, 11806, 11807, 1181	572	128	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0048738~cardiac muscle tissue development	6	0.941915228	9.E-02 13052, 77579, 11464, 16412, 20467, 1420	572	57	13588	3.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0006887~exocytosis	9	1.412872841	9.E-02 269589, 19894, 77579, 380714, 27359, 11	572	110	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0035272~exocrine system development	5	0.784929356	9.E-02 13649, 14178, 18609, 16001, 16000	572	41	13588	3.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0055092~sterol homeostasis	4	0.627943485	9.E-02 17777, 11807, 11816, 238055	572	26	13588	4.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0046635~positive regulation of alpha-beta T cell activation	4	0.627943485	9.E-02 11486, 22778, 16190, 20963	572	26	13588	4.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0007006~mitochondrial membrane organization	4	0.627943485	9.E-02 12028, 12122, 12018, 12043	572	26	13588	4.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0042632~cholesterol homeostasis	4	0.627943485	9.E-02 17777, 11807, 11816, 238055	572	26	13588	4.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0048469~cell maturation	7	1.098901099	9.E-02 12229, 19713, 12531, 20112, 13382, 6714	572	75	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0019216~regulation of lipid metabolic process	6	0.941915228	1.E-01 18048, 16367, 11816, 57257, 238055, 125	572	58	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0051170~nuclear import	6	0.941915228	1.E-01 11865, 19384, 231103, 12953, 70572, 164	572	58	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0048608~reproductive structure development	10	1.569858713	1.E-01 20779, 12048, 12028, 12018, 12043, 1250	572	130	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0048705~skeletal system morphogenesis	10	1.569858713	1.E-01 15402, 18596, 15438, 12842, 15415, 1540	572	130	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0014070~response to organic cyclic substance	5	0.784929356	1.E-01 12048, 12043, 12568, 16847, 13385	572	42	13588	3.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0014020~primary neural tube formation	5	0.784929356	1.E-01 22323, 16911, 232906, 50768, 24069	572	42	13588	3.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0032386~regulation of intracellular transport	5	0.784929356	1.E-01 18826, 68092, 192176, 12568, 24069	572	42	13588	3.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0042060~wound healing	9	1.412872841	1.E-01 14060, 14674, 14432, 77579, 74145, 1406	572	112	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_CC_FAT	GO:0005829~cytosol	54	8.477237049	1.E-11 672195, 56150, 18709, 18019, 18126, 187	434	549	12504	3.E+00	3.E-09	3.E-09	1.E-08
GOTERM_CC_FAT	GO:0005819~spindle	18	2.825745683	2.E-07 26934, 20871, 18005, 17869, 20878, 1165	434	109	12504	5.E+00	7.E-05	3.E-05	3.E-04
GOTERM_CC_FAT	GO:0000267~cell fraction	46	7.221350078	7.E-07 672195, 269589, 11852, 12955, 238055, 7	434	596	12504	2.E+00	2.E-04	8.E-05	9.E-04
GOTERM_CC_FAT	GO:0044459~plasma membrane part	93	14.59968603	1.E-06 22323, 228543, 19744, 15018, 69524, 941	434	1633	12504	2.E+00	4.E-04	9.E-05	1.E-03
GOTERM_CC_FAT	GO:0005626~insoluble fraction	42	6.593406593	1.E-06 269589, 11852, 12955, 238055, 72508, 16	434	528	12504	2.E+00	4.E-04	7.E-05	1.E-03
GOTERM_CC_FAT	GO:0030027~lamellipodium	13	2.040816327	1.E-06 22323, 227753, 14163, 54519, 11651, 170	434	63	12504	6.E+00	5.E-04	8.E-05	2.E-03
GOTERM_CC_FAT	GO:0005856~cytoskeleton	70	10.98901099	2.E-06 22323, 94190, 54519, 54354, 16800, 7181	434	1122	12504	2.E+00	5.E-04	8.E-05	2.E-03
GOTERM_CC_FAT	GO:0005624~membrane fraction	40	6.279434851	3.E-06 269589, 11852, 72508, 238055, 16396, 14	434	510	12504	2.E+00	1.E-03	1.E-04	4.E-03
GOTERM_CC_FAT	GO:0031252~cell leading edge	16	2.51177394	7.E-06 22323, 14163, 227753, 54519, 228359, 11	434	112	12504	4.E+00	2.E-03	3.E-04	1.E-02
GOTERM_CC_FAT	GO:0042995~cell projection	42	6.593406593	9.E-06 22323, 18746, 227753, 94190, 16952, 545	434	575	12504	2.E+00	3.E-03	3.E-04	1.E-02
GOTERM_CC_FAT	GO:0005886~plasma membrane	138	21.66405024	3.E-05 22323, 12475, 19744, 15018, 69524, 9419	434	2906	12504	1.E+00	1.E-02	9.E-04	4.E-02
GOTERM_CC_FAT	GO:0048770~pigment granule	13	2.040816327	3.E-05 269589, 14674, 18453, 20525, 19384, 148	434	85	12504	4.E+00	1.E-02	1.E-03	5.E-02
GOTERM_CC_FAT	GO:0042470~melanosome	13	2.040816327	3.E-05 269589, 14674, 18453, 20525, 19384, 148	434	85	12504	4.E+00	1.E-02	1.E-03	5.E-02
GOTERM_CC_FAT	GO:0046581~intercellular canalculus	5	0.784929356	5.E-05 18669, 18671, 18670, 12780, 27413	434	7	12504	2.E+01	2.E-02	1.E-03	6.E-02
GOTERM_CC_FAT	GO:0042627~chylomicron	5	0.784929356	9.E-05 11813, 11814, 669888, 11816, 11808	434	8	12504	2.E+01	3.E-02	2.E-03	1.E-01
GOTERM_CC_FAT	GO:0005675~holo TFIIH complex	5	0.784929356	3.E-04 13872, 17420, 14884, 14885, 66671	434	10	12504	1.E+01	8.E-02	6.E-03	3.E-01
GOTERM_CC_FAT	GO:0034358~plasma lipoprotein particle	7	1.098901099	3.E-04 11813, 11814, 669888, 11806, 11807, 118	434	27	12504	7.E+00	9.E-02	6.E-03	4.E-01
GOTERM_CC_FAT	GO:0032994~protein-lipid complex	7	1.098901099	3.E-04 11813, 11814, 669888, 11806, 11807, 118	434	27	12504	7.E+00	9.E-02	6.E-03	4.E-01
GOTERM_CC_FAT	GO:0015629~actin cytoskeleton	19	2.982731554	3.E-04 215280, 73750, 19894, 232906, 94190, 11	434	205	12504	3.E+00	9.E-02	6.E-03	4.E-01
GOTERM_CC_FAT	GO:0009897~external side of plasma membrane	19	2.982731554	3.E-04 19370, 14972, 15018, 11816, 27007, 1478	434	206	12504	3.E+00	1.E-01	6.E-03	4.E-01
GOTERM_CC_FAT	GO:0044445~cytosolic part	10	1.569858713	3.E-04 18709, 18708, 56421, 12028, 433182, 309	434	63	12504	5.E+00	1.E-01	5.E-03	4.E-01
GOTERM_CC_FAT	GO:0030426~growth cone	9	1.412872841	3.E-04 73750, 77579, 18479, 12568, 170758, 539	434	51	12504	5.E+00	1.E-01	6.E-03	5.E-01
GOTERM_CC_FAT	GO:0030427~site of polarized growth	9	1.412872841	3.E-04 73750, 77579, 18479, 12568, 170758, 539	434	51	12504	5.E+00	1.E-01	6.E-03	5.E-01
GOTERM_CC_FAT	GO:0043232~intracellular non-membrane-bounded organelle	94	14.7566719	3.E-04 22323, 22130, 218294, 94190, 54519, 168	434	1919	12504	1.E+00	1.E-01	6.E-03	5.E-01
GOTERM_CC_FAT	GO:0043228~non-membrane-bounded organelle	94	14.7566719	3.E-04 22323, 22130, 218294, 94190, 54519, 168	434	1919	12504	1.E+00	1.E-01	6.E-03	5.E-01



GOTERM_CC_FAT	GO:0009898~internal side of plasma membrane	23	3.610675039	4.E-04	228543, 19744, 102093, 11853, 243362, 7	434	287	12504	2.E+00	1.E-01	7.E-03	6.E-01
GOTERM_CC_FAT	GO:0019898~extrinsic to membrane	32	5.023547881	5.E-04	269589, 11816, 54519, 15275, 11855, 145	434	472	12504	2.E+00	2.E-01	7.E-03	6.E-01
GOTERM_CC_FAT	GO:0019897~extrinsic to plasma membrane	9	1.412872841	6.E-04	269589, 14674, 14675, 11816, 14673, 836	434	55	12504	5.E+00	2.E-01	8.E-03	8.E-01
GOTERM_CC_FAT	GO:0043235~receptor complex	11	1.726844584	6.E-04	16408, 15170, 12475, 16411, 21898, 1641	434	83	12504	4.E+00	2.E-01	8.E-03	8.E-01
GOTERM_CC_FAT	GO:0031988~membrane-bounded vesicle	29	4.552590267	7.E-04	13649, 215280, 269589, 19384, 171531, 1	434	420	12504	2.E+00	2.E-01	1.E-02	1.E+00
GOTERM_CC_FAT	GO:0009986~cell surface	23	3.610675039	9.E-04	19370, 14972, 15018, 11816, 27007, 1641	434	305	12504	2.E+00	3.E-01	1.E-02	1.E+00
GOTERM_CC_FAT	GO:0000151~ubiquitin ligase complex	9	1.412872841	1.E-03	17999, 26965, 52563, 99152, 16396, 2140	434	60	12504	4.E+00	3.E-01	1.E-02	1.E+00
GOTERM_CC_FAT	GO:0031982~vesicle	33	5.180533752	1.E-03	215280, 13649, 269589, 19384, 16396, 11	434	519	12504	2.E+00	3.E-01	1.E-02	2.E+00
GOTERM_CC_FAT	GO:0005667~transcription factor complex	19	2.982731554	1.E-03	11865, 12753, 16911, 20375, 22778, 1428	434	234	12504	2.E+00	4.E-01	2.E-02	2.E+00
GOTERM_CC_FAT	GO:0015630~microtubule cytoskeleton	29	4.552590267	2.E-03	13430, 17869, 54354, 11651, 71819, 1680	434	450	12504	2.E+00	5.E-01	2.E-02	3.E+00
GOTERM_CC_FAT	GO:0044429~mitochondrial part	32	5.023547881	3.E-03	672195, 68263, 66593, 18416, 15275, 214	434	524	12504	2.E+00	6.E-01	3.E-02	3.E+00
GOTERM_CC_FAT	GO:0005739~mitochondrion	65	10.20408163	4.E-03	18746, 672195, 68263, 18416, 243362, 12	434	1322	12504	1.E+00	7.E-01	4.E-02	5.E+00
GOTERM_CC_FAT	GO:0005581~collagen	5	0.784929356	4.E-03	12843, 12831, 12842, 16948, 12815	434	19	12504	8.E+00	7.E-01	4.E-02	5.E+00
GOTERM_CC_FAT	GO:0034385~triglyceride-rich lipoprotein particle	4	0.627943485	4.E-03	11813, 11814, 669888, 11816	434	10	12504	1.E+01	8.E-01	4.E-02	6.E+00
GOTERM_CC_FAT	GO:0034361~very-low-density lipoprotein particle	4	0.627943485	4.E-03	11813, 11814, 669888, 11816	434	10	12504	1.E+01	8.E-01	4.E-02	6.E+00
GOTERM_CC_FAT	GO:0044430~cytoskeletal part	42	6.593406593	4.E-03	13430, 11651, 54354, 17869, 71819, 1680	434	774	12504	2.E+00	8.E-01	4.E-02	6.E+00
GOTERM_CC_FAT	GO:0000775~chromosome, centromeric region	11	1.726844584	5.E-03	67052, 19053, 20871, 12236, 18005, 2277	434	111	12504	3.E+00	8.E-01	5.E-02	7.E+00
GOTERM_CC_FAT	GO:0030175~filopodium	5	0.784929356	6.E-03	22323, 12568, 19684, 224014, 24001	434	22	12504	7.E+00	9.E-01	6.E-02	8.E+00
GOTERM_CC_FAT	GO:0005741~mitochondrial outer membrane	9	1.412872841	6.E-03	56717, 56615, 12015, 12048, 12028, 1527	434	80	12504	3.E+00	9.E-01	6.E-02	8.E+00
GOTERM_CC_FAT	GO:0000015~phosphopyruvate hydratase complex	3	0.470957614	7.E-03	433182, 13807, 13806, 13808, 100044223	434	4	12504	2.E+01	9.E-01	6.E-02	9.E+00
GOTERM_CC_FAT	GO:0005942~phosphoinositide 3-kinase complex	4	0.627943485	7.E-03	18709, 18708, 30955, 18707	434	12	12504	1.E+01	9.E-01	6.E-02	9.E+00
GOTERM_CC_FAT	GO:0031974~membrane-enclosed lumen	57	8.948194662	8.E-03	672195, 68263, 22130, 218294, 18416, 22	434	1174	12504	1.E+00	9.E-01	7.E-02	1.E+01
GOTERM_CC_FAT	GO:0005792~microsome	14	2.197802198	8.E-03	18453, 76279, 238055, 12043, 98238, 664	434	176	12504	2.E+00	9.E-01	7.E-02	1.E+01
GOTERM_CC_FAT	GO:0045121~membrane raft	9	1.412872841	9.E-03	14127, 12475, 16818, 14678, 104215, 164	434	85	12504	3.E+00	1.E+00	7.E-02	1.E+01
GOTERM_CC_FAT	GO:0016023~cytoplasmic membrane-bounded vesicle	25	3.924646782	1.E-02	13649, 215280, 269589, 19384, 171531, 1	434	414	12504	2.E+00	1.E+00	7.E-02	1.E+01
GOTERM_CC_FAT	GO:0043233~organelle lumen	55	8.63422292	1.E-02	672195, 68263, 22130, 218294, 18416, 22	434	1136	12504	1.E+00	1.E+00	7.E-02	1.E+01
GOTERM_CC_FAT	GO:0031968~organelle outer membrane	9	1.412872841	1.E-02	56717, 56615, 12015, 12048, 12028, 1527	434	87	12504	3.E+00	1.E+00	8.E-02	1.E+01
GOTERM_CC_FAT	GO:0031410~cytoplasmic vesicle	29	4.552590267	1.E-02	13649, 215280, 269589, 19384, 16396, 17	434	508	12504	2.E+00	1.E+00	7.E-02	1.E+01
GOTERM_CC_FAT	GO:0042598~vesicular fraction	14	2.197802198	1.E-02	18453, 76279, 238055, 12043, 98238, 664	434	182	12504	2.E+00	1.E+00	7.E-02	1.E+01
GOTERM_CC_FAT	GO:0005759~mitochondrial matrix	13	2.040816327	1.E-02	672195, 15107, 68263, 17448, 18416, 133	434	163	12504	2.E+00	1.E+00	8.E-02	1.E+01
GOTERM_CC_FAT	GO:0031980~mitochondrial lumen	13	2.040816327	1.E-02	672195, 15107, 68263, 17448, 18416, 133	434	163	12504	2.E+00	1.E+00	8.E-02	1.E+01
GOTERM_CC_FAT	GO:0019867~outer membrane	9	1.412872841	1.E-02	56717, 56615, 12015, 12048, 12028, 1527	434	90	12504	3.E+00	1.E+00	8.E-02	2.E+01
GOTERM_CC_FAT	GO:0031967~organelle envelope	30	4.709576138	1.E-02	66593, 18416, 19720, 15275, 214952, 567	434	540	12504	2.E+00	1.E+00	8.E-02	2.E+01
GOTERM_CC_FAT	GO:0031975~envelope	30	4.709576138	1.E-02	66593, 18416, 19720, 15275, 214952, 567	434	542	12504	2.E+00	1.E+00	9.E-02	2.E+01
GOTERM_CC_FAT	GO:0005925~focal adhesion	7	1.098901099	1.E-02	22323, 12549, 236920, 54519, 18479, 231	434	57	12504	4.E+00	1.E+00	9.E-02	2.E+01
GOTERM_CC_FAT	GO:0070013~intracellular organelle lumen	54	8.477237049	1.E-02	672195, 68263, 22130, 218294, 18416, 22	434	1133	12504	1.E+00	1.E+00	9.E-02	2.E+01
GOTERM_CC_FAT	GO:0044427~chromosomal part	20	3.139717425	1.E-02	19891, 621893, 67052, 20871, 18005, 122	434	318	12504	2.E+00	1.E+00	9.E-02	2.E+01
GOTERM_CC_FAT	GO:0008305~integrin complex	5	0.784929356	2.E-02	16408, 16411, 16414, 16412, 16409	434	28	12504	5.E+00	1.E+00	9.E-02	2.E+01
GOTERM_CC_FAT	GO:0034364~high-density lipoprotein particle	4	0.627943485	2.E-02	11806, 11807, 11816, 11808	434	16	12504	7.E+00	1.E+00	1.E-01	2.E+01
GOTERM_CC_FAT	GO:0005740~mitochondrial envelope	23	3.610675039	2.E-02	15107, 17448, 66593, 18416, 18408, 1212	434	391	12504	2.E+00	1.E+00	1.E-01	2.E+01
GOTERM_CC_FAT	GO:0005924~cell-substrate adherens junction	7	1.098901099	2.E-02	22323, 12549, 236920, 54519, 18479, 231	434	61	12504	3.E+00	1.E+00	1.E-01	2.E+01
GOTERM_CC_FAT	GO:0005884~actin filament	5	0.784929356	2.E-02	73750, 18826, 11459, 170758, 66440, 668	434	30	12504	5.E+00	1.E+00	1.E-01	2.E+01
GOTERM_CC_FAT	GO:0030141~secretory granule	10	1.569858713	2.E-02	26934, 19894, 16334, 17970, 380714, 273	434	117	12504	2.E+00	1.E+00	1.E-01	2.E+01
GOTERM_CC_FAT	GO:0001726~ruffle	6	0.941915228	2.E-02	14163, 218397, 18826, 228359, 19684, 10	434	47	12504	4.E+00	1.E+00	1.E-01	3.E+01
GOTERM_CC_FAT	GO:0016323~basolateral plasma membrane	11	1.726844584	2.E-02	22323, 12549, 13649, 20525, 236920, 169	434	141	12504	2.E+00	1.E+00	1.E-01	3.E+01
GOTERM_CC_FAT	GO:0030055~cell-substrate junction	7	1.098901099	3.E-02	22323, 12549, 236920, 54519, 18479, 231	434	66	12504	3.E+00	1.E+00	1.E-01	3.E+01
GOTERM_CC_FAT	GO:0031225~anchored to membrane	14	2.197802198	3.E-02	19370, 12475, 14674, 11852, 70231, 1707	434	207	12504	2.E+00	1.E+00	1.E-01	3.E+01
GOTERM_CC_FAT	GO:0005912~adherens junction	9	1.412872841	3.E-02	22323, 12549, 69524, 13052, 236920, 545	434	106	12504	2.E+00	1.E+00	2.E-01	3.E+01
GOTERM_CC_FAT	GO:0031966~mitochondrial membrane	21	3.296703297	3.E-02	15107, 17448, 18416, 18408, 12122, 1204	434	368	12504	2.E+00	1.E+00	2.E-01	4.E+01
GOTERM_CC_FAT	GO:0031594~neuromuscular junction	4	0.627943485	4.E-02	77579, 16412, 12568, 208727	434	22	12504	5.E+00	1.E+00	2.E-01	4.E+01
GOTERM_CC_FAT	GO:0031965~nuclear membrane	5	0.784929356	4.E-02	19720, 12043, 23897, 18538, 22218	434	38	12504	4.E+00	1.E+00	2.E-01	4.E+01
GOTERM_CC_FAT	GO:0005654~nucleoplasm	30	4.709576138	4.E-02	19720, 17869, 22778, 12912, 12914, 1387	434	599	12504	1.E+00	1.E+00	2.E-01	5.E+01
GOTERM_CC_FAT	GO:0009922~spindle pole	4	0.627943485	4.E-02	13006, 26416, 18005, 56150	434	23	12504	5.E+00	1.E+00	2.E-01	5.E+01
GOTERM_CC_FAT	GO:0016591~DNA-directed RNA polymerase II, holoenzyme	6	0.941915228	4.E-02	13872, 69920, 17420, 14884, 14885, 6667	434	56	12504	3.E+00	1.E+00	2.E-01	5.E+01
GOTERM_CC_FAT	GO:0043005~neuron projection	15	2.354788069	5.E-02	73750, 94190, 17869, 16800, 18479, 1707	434	245	12504	2.E+00	1.E+00	2.E-01	5.E+01
GOTERM_CC_FAT	GO:0044451~nucleoplasm part	26	4.081632653	5.E-02	17869, 22778, 12912, 12914, 13872, 1540	434	513	12504	1.E+00	1.E+00	2.E-01	5.E+01
GOTERM_CC_FAT	GO:0005680~anaphase-promoting complex	3	0.470957614	5.E-02	52563, 66440, 668450, 68999	434	11	12504	8.E+00	1.E+00	2.E-01	5.E+01
GOTERM_CC_FAT	GO:0005625~soluble fraction	8	1.25588697	6.E-02	110095, 672195, 269589, 12955, 11852, 1	434	99	12504	2.E+00	1.E+00	2.E-01	5.E+01
GOTERM_CC_FAT	GO:0030054~cell junction	24	3.767660911	6.E-02	22323, 19894, 69524, 16456, 94190, 2369	434	470	12504	1.E+00	1.E+00	2.E-01	6.E+01
GOTERM_CC_FAT	GO:0070161~anchoring junction	9	1.412872841	6.E-02	22323, 12549, 69524, 13052, 236920, 545	434	123	12504	2.E+00	1.E+00	3.E-01	6.E+01
GOTERM_CC_FAT	GO:0042641~actomyosin	4	0.627943485	7.E-02	77579, 11459, 208727, 19200	434	27	12504	4.E+00	1.E+00	3.E-01	6.E+01
GOTERM_CC_FAT	GO:0005694~chromosome	20	3.139717425	7.E-02	19891, 621893, 67052, 20871, 18005, 122	434	378	12504	2.E+00	1.E+00	3.E-01	6.E+01
GOTERM_CC_FAT	GO:000806~Y chromosome	2	0.313971743	7.E-02	12566, 20467	434	2	12504	3.E+01	1.E+00	3.E-01	6.E+01
GOTERM_CC_FAT	GO:0005584~collagen type I	2	0.313971743	7.E-02	12843, 12842	434	2	12504	3.E+01	1.E+00	3.E-01	6.E+01
GOTERM_CC_FAT	GO:0001772~immunological synapse	3	0.470957614	7.E-02	16408, 192662, 74734	434	13	12504	7.E+00	1.E+00	3.E-01	6.E+01



GOTERM_CC_FAT	GO:0000152~nuclear ubiquitin ligase complex	3	0.470957614	7.E-02 52563, 66440, 668450, 68999	434	13	12504	7.E+00	1.E+00	3.E-01	6.E+01
GOTERM_CC_FAT	GO:0044420~extracellular matrix part	7	1.098901099	1.E-01 12843, 12831, 11657, 12842, 20692, 1694	434	92	12504	2.E+00	1.E+00	4.E-01	8.E+01
GOTERM_CC_FAT	GO:0045177~apical part of cell	9	1.412872841	1.E-01 18669, 18671, 18670, 12780, 27413, 1707	434	136	12504	2.E+00	1.E+00	4.E-01	8.E+01
GOTERM_MF_FAT	GO:0030695~GTPase regulator activity	81	12.71585557	9.E-37 22324, 228482, 94190, 192662, 243362, 1	550	361	13288	5.E+00	6.E-34	6.E-34	1.E-33
GOTERM_MF_FAT	GO:0060589~nucleoside-triphosphatase regulator activity	81	12.71585557	3.E-36 22324, 228482, 94190, 192662, 243362, 1	550	367	13288	5.E+00	2.E-33	1.E-33	5.E-33
GOTERM_MF_FAT	GO:0005083~small GTPase regulator activity	53	8.320251177	3.E-25 22324, 192662, 16800, 171531, 16801, 22	550	223	13288	6.E+00	2.E-22	8.E-23	5.E-22
GOTERM_MF_FAT	GO:0005096~GTPase activator activity	48	7.535321821	8.E-24 117600, 94190, 232906, 228482, 192662,	550	192	13288	6.E+00	5.E-21	1.E-21	1.E-20
GOTERM_MF_FAT	GO:0008047~enzyme activator activity	51	8.006279435	3.E-21 94190, 228482, 243362, 192662, 225358,	550	249	13288	5.E+00	2.E-18	4.E-19	5.E-18
GOTERM_MF_FAT	GO:0005089~Rho guanyl-nucleotide exchange factor activity	25	3.924646782	3.E-16 22324, 13605, 16800, 442801, 53972, 218	550	71	13288	9.E+00	2.E-13	4.E-14	5.E-13
GOTERM_MF_FAT	GO:0005088~Ras guanyl-nucleotide exchange factor activity	25	3.924646782	2.E-14 22324, 13605, 16800, 442801, 53972, 218	550	83	13288	7.E+00	1.E-11	2.E-12	3.E-11
GOTERM_MF_FAT	GO:0017076~purine nucleotide binding	144	22.60596546	3.E-14 18746, 19744, 71819, 14782, 170758, 745	550	1871	13288	2.E+00	2.E-11	2.E-12	5.E-11
GOTERM_MF_FAT	GO:0032555~purine ribonucleotide binding	139	21.82103611	7.E-14 18746, 19744, 71819, 170758, 74551, 808	550	1796	13288	2.E+00	4.E-11	5.E-12	1.E-10
GOTERM_MF_FAT	GO:0032553~ribonucleotide binding	139	21.82103611	7.E-14 18746, 19744, 71819, 170758, 74551, 808	550	1796	13288	2.E+00	4.E-11	5.E-12	1.E-10
GOTERM_MF_FAT	GO:0000166~nucleotide binding	158	24.80376766	2.E-13 18746, 19744, 71819, 14782, 170758, 745	550	2183	13288	2.E+00	1.E-10	1.E-11	3.E-10
GOTERM_MF_FAT	GO:0017016~Ras GTPase binding	17	2.668759812	7.E-10 117600, 269589, 19894, 17970, 380714, 1	550	57	13288	7.E+00	5.E-07	4.E-08	1.E-06
GOTERM_MF_FAT	GO:0031267~small GTPase binding	17	2.668759812	1.E-09 117600, 269589, 19894, 17970, 380714, 1	550	59	13288	7.E+00	8.E-07	7.E-08	2.E-06
GOTERM_MF_FAT	GO:0005085~guanyl-nucleotide exchange factor activity	26	4.081632653	1.E-09 22324, 13605, 16800, 442801, 53972, 218	550	147	13288	4.E+00	1.E-06	8.E-08	2.E-06
GOTERM_MF_FAT	GO:0051020~GTPase binding	17	2.668759812	3.E-09 117600, 269589, 19894, 17970, 380714, 1	550	62	13288	7.E+00	2.E-06	1.E-07	4.E-06
GOTERM_MF_FAT	GO:0001882~nucleoside binding	111	17.42543171	7.E-09 18746, 71819, 14782, 23920, 20779, 1934	550	1558	13288	2.E+00	5.E-06	3.E-07	1.E-05
GOTERM_MF_FAT	GO:0001883~purine nucleoside binding	110	17.26844584	1.E-08 18746, 71819, 14782, 23920, 20779, 1146	550	1548	13288	2.E+00	7.E-06	4.E-07	1.E-05
GOTERM_MF_FAT	GO:0005100~Rho GTPase activator activity	10	1.569858713	1.E-08 117600, 71709, 17925, 50768, 228359, 76	550	18	13288	1.E+01	8.E-06	4.E-07	2.E-05
GOTERM_MF_FAT	GO:0030554~adenyl nucleotide binding	109	17.11145997	1.E-08 18746, 71819, 14782, 23920, 20779, 1146	550	1535	13288	2.E+00	8.E-06	4.E-07	2.E-05
GOTERM_MF_FAT	GO:0017137~Rab GTPase binding	10	1.569858713	2.E-08 245049, 269589, 19894, 320051, 380714,	550	19	13288	1.E+01	1.E-05	7.E-07	3.E-05
GOTERM_MF_FAT	GO:0032559~adenyl ribonucleotide binding	104	16.32653061	3.E-08 18746, 71819, 23920, 20779, 11464, 2701	550	1460	13288	2.E+00	2.E-05	8.E-07	4.E-05
GOTERM_MF_FAT	GO:0004715~non-membrane spanning protein tyrosine kinase acti	13	2.040816327	4.E-08 11350, 12229, 16818, 14191, 22390, 2077	550	40	13288	8.E+00	3.E-05	1.E-06	6.E-05
GOTERM_MF_FAT	GO:0005524~ATP binding	102	16.01255887	5.E-08 18746, 71819, 23920, 20779, 11464, 2701	550	1443	13288	2.E+00	4.E-05	2.E-06	8.E-05
GOTERM_MF_FAT	GO:0004672~protein kinase activity	51	8.006279435	7.E-07 72508, 16818, 23920, 20779, 14884, 1256	550	583	13288	2.E+00	5.E-04	2.E-05	1.E-03
GOTERM_MF_FAT	GO:0005525~GTP binding	36	5.651491366	2.E-06 228543, 19744, 232906, 11852, 19384, 13	550	354	13288	2.E+00	1.E-03	4.E-05	2.E-03
GOTERM_MF_FAT	GO:0032561~guanyl ribonucleotide binding	36	5.651491366	3.E-06 228543, 19744, 232906, 11852, 19384, 13	550	363	13288	2.E+00	2.E-03	7.E-05	4.E-03
GOTERM_MF_FAT	GO:0019001~guanyl nucleotide binding	36	5.651491366	3.E-06 228543, 19744, 232906, 11852, 19384, 13	550	363	13288	2.E+00	2.E-03	7.E-05	4.E-03
GOTERM_MF_FAT	GO:0019899~enzyme binding	27	4.238618524	3.E-06 117600, 269589, 26965, 13605, 16800, 17	550	229	13288	3.E+00	2.E-03	7.E-05	4.E-03
GOTERM_MF_FAT	GO:0004713~protein tyrosine kinase activity	22	3.453689168	4.E-06 11350, 13649, 21687, 12229, 23920, 1681	550	164	13288	3.E+00	3.E-03	1.E-04	6.E-03
GOTERM_MF_FAT	GO:0003924~GTPase activity	19	2.982731554	5.E-06 22142, 14674, 14675, 19384, 14678, 1362	550	128	13288	4.E+00	3.E-03	1.E-04	8.E-03
GOTERM_MF_FAT	GO:0005092~GDP-dissociation inhibitor activity	5	0.784929356	1.E-05 14570, 192662, 14567, 11857, 14569	550	5	13288	2.E+01	9.E-03	3.E-04	2.E-02
GOTERM_MF_FAT	GO:0019904~protein domain specific binding	22	3.453689168	5.E-05 22323, 11350, 15170, 20401, 19317, 1797	550	192	13288	3.E+00	3.E-02	1.E-03	7.E-02
GOTERM_MF_FAT	GO:0019955~cytokine binding	14	2.197802198	6.E-05 12765, 18414, 21937, 16195, 18824, 1298	550	88	13288	4.E+00	4.E-02	1.E-03	9.E-02
GOTERM_MF_FAT	GO:0004896~cytokine receptor activity	11	1.726844584	7.E-05 12765, 16195, 12983, 16197, 50498, 1385	550	55	13288	5.E+00	5.E-02	1.E-03	1.E-01
GOTERM_MF_FAT	GO:0008353~RNA polymerase II carboxy-terminal domain kinase ac	6	0.941915228	7.E-05 13872, 17420, 14884, 14885, 12534, 6667	550	12	13288	1.E+01	5.E-02	1.E-03	1.E-01
GOTERM_MF_FAT	GO:0042043~neurexin binding	5	0.784929356	9.E-05 269589, 27359, 83671, 13385, 83672	550	7	13288	2.E+01	6.E-02	2.E-03	1.E-01
GOTERM_MF_FAT	GO:0008289~lipid binding	4	4.866562009	1.E-04 22324, 11657, 11814, 18416, 11816, 1695	550	345	13288	2.E+00	6.E-02	2.E-03	1.E-01
GOTERM_MF_FAT	GO:0030675~Rac GTPase activator activity	51	0.784929356	3.E-04 228359, 76117, 19765, 233071, 106952	550	9	13288	1.E+01	2.E-01	6.E-03	5.E-01
GOTERM_MF_FAT	GO:0005099~Ras GTPase activator activity	11	1.726844584	3.E-04 117600, 71709, 17925, 50768, 228359, 76	550	65	13288	4.E+00	2.E-01	5.E-03	5.E-01
GOTERM_MF_FAT	GO:0017124~SH3 domain binding	12	1.883830455	4.E-04 22323, 12549, 15170, 20401, 19317, 8098	550	79	13288	4.E+00	2.E-01	7.E-03	6.E-01
GOTERM_MF_FAT	GO:0019992~diacylglycerol binding	10	1.569858713	7.E-04 22324, 26934, 78816, 17925, 70719, 2701	550	59	13288	4.E+00	3.E-01	1.E-02	1.E+00
GOTERM_MF_FAT	GO:0035004~phosphoinositide 3-kinase activity	5	0.784929356	8.E-04 18709, 18708, 11920, 30955, 18707	550	11	13288	1.E+01	4.E-01	1.E-02	1.E+00
GOTERM_MF_FAT	GO:0016303~1-phosphatidylinositol-3-kinase activity	5	0.784929356	8.E-04 18709, 18708, 11920, 30955, 18707	550	11	13288	1.E+01	4.E-01	1.E-02	1.E+00
GOTERM_MF_FAT	GO:0004396~hexokinase activity	4	0.627943485	1.E-03 15275, 15277, 103988, 212032	550	6	13288	2.E+01	6.E-01	2.E-02	2.E+00
GOTERM_MF_FAT	GO:0016668~oxidoreductase activity, acting on sulfur group of dor	4	0.627943485	1.E-03 26462, 50493, 14782, 13382	550	6	13288	2.E+01	6.E-01	2.E-02	2.E+00
GOTERM_MF_FAT	GO:0000287~magnesium ion binding	31	4.866562009	2.E-03 228543, 80905, 18746, 19744, 232087, 54	550	409	13288	2.E+00	7.E-01	3.E-02	3.E+00
GOTERM_MF_FAT	GO:0005516~calmodulin binding	13	2.040816327	3.E-03 102093, 18679, 18682, 18126, 14432, 775	550	114	13288	3.E+00	8.E-01	4.E-02	4.E+00
GOTERM_MF_FAT	GO:0019205~nucleobase, nucleoside, nucleotide kinase activity	7	1.098901099	3.E-03 80914, 68556, 22245, 14923, 11636, 6658	550	36	13288	5.E+00	9.E-01	5.E-02	5.E+00
GOTERM_MF_FAT	GO:0001530~lipopolysaccharide binding	4	0.627943485	3.E-03 12475, 17087, 21898, 16803	550	8	13288	1.E+01	9.E-01	5.E-02	5.E+00
GOTERM_MF_FAT	GO:0004842~ubiquitin-protein ligase activity	12	1.883830455	4.E-03 56550, 74287, 17999, 218793, 26965, 163	550	104	13288	3.E+00	9.E-01	5.E-02	5.E+00
GOTERM_MF_FAT	GO:0005158~insulin receptor binding	5	0.784929356	4.E-03 18708, 16367, 27261, 13449, 384783	550	17	13288	7.E+00	9.E-01	6.E-02	6.E+00
GOTERM_MF_FAT	GO:0004674~protein serine/threonine kinase activity	30	4.709576138	5.E-03 11651, 72508, 12236, 545156, 13872, 567	550	421	13288	2.E+00	1.E+00	7.E-02	7.E+00
GOTERM_MF_FAT	GO:0008559~xenobiotic-transporting ATPase activity	3	0.470957614	5.E-03 18669, 18671, 18670	550	3	13288	2.E+01	1.E+00	6.E-02	7.E+00
GOTERM_MF_FAT	GO:0042910~xenobiotic transporter activity	3	0.470957614	5.E-03 18669, 18671, 18670	550	3	13288	2.E+01	1.E+00	6.E-02	7.E+00
GOTERM_MF_FAT	GO:0004748~ribonucleoside-diphosphate reductase activity	3	0.470957614	5.E-03 382985, 20133, 20135	550	3	13288	2.E+01	1.E+00	6.E-02	7.E+00
GOTERM_MF_FAT	GO:0004739~pyruvate dehydrogenase (acetyl-transferring) activity	3	0.470957614	5.E-03 68263, 18597, 18598	550	3	13288	2.E+01	1.E+00	6.E-02	7.E+00
GOTERM_MF_FAT	GO:0005094~Rho GDP-dissociation inhibitor activity	3	0.470957614	5.E-03 14570, 192662, 11857	550	3	13288	2.E+01	1.E+00	6.E-02	7.E+00
GOTERM_MF_FAT	GO:0004082~bisphosphoglycerate mutase activity	3	0.470957614	5.E-03 18648, 12183, 56012	550	3	13288	2.E+01	1.E+00	6.E-02	7.E+00
GOTERM_MF_FAT	GO:0016728~oxidoreductase activity, acting on CH or CH2 groups	3	0.470957614	5.E-03 382985, 20133, 20135	550	3	13288	2.E+01	1.E+00	6.E-02	7.E+00
GOTERM_MF_FAT	GO:0004083~2,3-bisphospho-D-glycerate 2-phosphoglydrolase acti	3	0.470957614	5.E-03 18648, 12183, 56012	550	3	13288	2.E+01	1.E+00	6.E-02	7.E+00
GOTERM_MF_FAT	GO:0004619~phosphoglycerate mutase activity	3	0.470957614	5.E-03 18648, 12183, 56012	550	3	13288	2.E+01	1.E+00	6.E-02	7.E+00
GOTERM_MF_FAT	GO:0034416~bisphosphoglycerate phosphatase activity	3	0.470957614	5.E-03 18648, 12183, 56012	550	3	13288	2.E+01	1.E+00	6.E-02	7.E+00



GOTERM_MF_FAT	GO:0004738~pyruvate dehydrogenase activity	3	0.470957614	5.E-03 68263, 18597, 18598	550	3	13288	2.E+01	1.E+00	6.E-02	7.E+00
GOTERM_MF_FAT	GO:0019787~small conjugating protein ligase activity	13	2.040816327	6.E-03 56550, 74287, 218793, 17999, 26965, 163	550	125	13288	3.E+00	1.E+00	7.E-02	8.E+00
GOTERM_MF_FAT	GO:0016868~intramolecular transferase activity, phosphotransferase	4	0.627943485	7.E-03 18648, 72157, 12183, 56012	550	10	13288	1.E+01	1.E+00	8.E-02	1.E+01
GOTERM_MF_FAT	GO:0004714~transmembrane receptor protein tyrosine kinase activ	8	1.25588697	8.E-03 13836, 18596, 21687, 13649, 23920, 1971	550	56	13288	3.E+00	1.E+00	1.E-01	1.E+01
GOTERM_MF_FAT	GO:0019200~carbohydrate kinase activity	5	0.784929356	8.E-03 56421, 15275, 15277, 103988, 212032	550	20	13288	6.E+00	1.E+00	1.E-01	1.E+01
GOTERM_MF_FAT	GO:0004849~uridine kinase activity	3	0.470957614	1.E-02 80914, 68556, 22245	550	4	13288	2.E+01	1.E+00	1.E-01	1.E+01
GOTERM_MF_FAT	GO:0004634~phosphopyruvate hydratase activity	3	0.470957614	1.E-02 433182, 13807, 13806, 13808, 100044223	550	4	13288	2.E+01	1.E+00	1.E-01	1.E+01
GOTERM_MF_FAT	GO:0004459~L-lactate dehydrogenase activity	3	0.470957614	1.E-02 16828, 16833, 16832	550	4	13288	2.E+01	1.E+00	1.E-01	1.E+01
GOTERM_MF_FAT	GO:0016774~phosphotransferase activity, carboxyl group as accept	3	0.470957614	1.E-02 217214, 18663, 18655	550	4	13288	2.E+01	1.E+00	1.E-01	1.E+01
GOTERM_MF_FAT	GO:0015239~multidrug transporter activity	3	0.470957614	1.E-02 18669, 18671, 18670	550	4	13288	2.E+01	1.E+00	1.E-01	1.E+01
GOTERM_MF_FAT	GO:0042623~ATPase activity, coupled	18	2.825745683	1.E-02 18195, 110957, 13872, 18669, 18671, 186	550	223	13288	2.E+00	1.E+00	1.E-01	2.E+01
GOTERM_MF_FAT	GO:0016879~ligase activity, forming carbon-nitrogen bonds	16	2.51177394	1.E-02 56550, 74287, 218793, 17999, 26965, 163	550	193	13288	2.E+00	1.E+00	2.E-01	2.E+01
GOTERM_MF_FAT	GO:0032403~protein complex binding	9	1.412872841	1.E-02 18708, 14127, 16367, 27261, 13449, 1641	550	78	13288	3.E+00	1.E+00	2.E-01	2.E+01
GOTERM_MF_FAT	GO:0004332~fructose-bisphosphate aldolase activity	3	0.470957614	2.E-02 230163, 11676, 11674	550	5	13288	1.E+01	1.E+00	2.E-01	2.E+01
GOTERM_MF_FAT	GO:0016725~oxidoreductase activity, acting on CH or CH2 groups	3	0.470957614	2.E-02 382985, 20133, 20135	550	5	13288	1.E+01	1.E+00	2.E-01	2.E+01
GOTERM_MF_FAT	GO:0043548~phosphoinositide 3-kinase binding	3	0.470957614	2.E-02 16367, 16001, 384783	550	5	13288	1.E+01	1.E+00	2.E-01	2.E+01
GOTERM_MF_FAT	GO:0004457~lactate dehydrogenase activity	3	0.470957614	2.E-02 16828, 16833, 16832	550	5	13288	1.E+01	1.E+00	2.E-01	2.E+01
GOTERM_MF_FAT	GO:0030676~Rac guanyl-nucleotide exchange factor activity	3	0.470957614	2.E-02 22324, 57257, 16800	550	5	13288	1.E+01	1.E+00	2.E-01	2.E+01
GOTERM_MF_FAT	GO:0017048~Rho GTPase binding	5	0.784929356	2.E-02 117600, 17970, 13605, 16800, 192176	550	24	13288	5.E+00	1.E+00	2.E-01	2.E+01
GOTERM_MF_FAT	GO:0019201~nucleotide kinase activity	4	0.627943485	2.E-02 14923, 11636, 66588, 11637	550	14	13288	7.E+00	1.E+00	2.E-01	2.E+01
GOTERM_MF_FAT	GO:0016860~intramolecular oxidoreductase activity	6	0.941915228	2.E-02 18453, 12304, 14751, 19895, 21991, 1482	550	38	13288	4.E+00	1.E+00	2.E-01	3.E+01
GOTERM_MF_FAT	GO:0004435~phosphoinositide phospholipase C activity	4	0.627943485	2.E-02 18803, 234779, 18797, 18795	550	15	13288	6.E+00	1.E+00	2.E-01	3.E+01
GOTERM_MF_FAT	GO:0048365~Rac GTPase binding	3	0.470957614	2.E-02 17970, 16800, 192176	550	6	13288	1.E+01	1.E+00	2.E-01	3.E+01
GOTERM_MF_FAT	GO:0004721~phosphoprotein phosphatase activity	13	2.040816327	2.E-02 15170, 218294, 19253, 14208, 16818, 190	550	152	13288	2.E+00	1.E+00	2.E-01	3.E+01
GOTERM_MF_FAT	GO:001727~lipid kinase activity	5	0.784929356	2.E-02 18709, 18708, 11920, 30955, 18707	550	27	13288	4.E+00	1.E+00	2.E-01	3.E+01
GOTERM_MF_FAT	GO:0008081~phosphoric diester hydrolase activity	8	1.25588697	3.E-02 18803, 234779, 20598, 18576, 18575, 185	550	72	13288	3.E+00	1.E+00	3.E-01	4.E+01
GOTERM_MF_FAT	GO:0005159~insulin-like growth factor receptor binding	3	0.470957614	3.E-02 18708, 16367, 16000	550	7	13288	1.E+01	1.E+00	3.E-01	4.E+01
GOTERM_MF_FAT	GO:0016832~aldehyde-lyase activity	3	0.470957614	3.E-02 230163, 11676, 11674	550	7	13288	1.E+01	1.E+00	3.E-01	4.E+01
GOTERM_MF_FAT	GO:0004693~cyclin-dependent protein kinase activity	5	0.784929356	3.E-02 12445, 12566, 12568, 12534, 66671	550	30	13288	4.E+00	1.E+00	3.E-01	4.E+01
GOTERM_MF_FAT	GO:0016791~phosphatase activity	17	2.668759812	4.E-02 15170, 182894, 19253, 14208, 12183, 560	550	238	13288	2.E+00	1.E+00	3.E-01	4.E+01
GOTERM_MF_FAT	GO:0003756~protein disulfide isomerase activity	3	0.470957614	4.E-02 18453, 12304, 14827	550	8	13288	9.E+00	1.E+00	3.E-01	5.E+01
GOTERM_MF_FAT	GO:0016864~intramolecular oxidoreductase activity, transposing S-	3	0.470957614	4.E-02 18453, 12304, 14827	550	8	13288	9.E+00	1.E+00	3.E-01	5.E+01
GOTERM_MF_FAT	GO:0004629~phospholipase C activity	4	0.627943485	4.E-02 18803, 234779, 18797, 18795	550	19	13288	5.E+00	1.E+00	3.E-01	5.E+01
GOTERM_MF_FAT	GO:0016881~acid-amino acid ligase activity	13	2.040816327	4.E-02 56550, 74287, 218793, 17999, 26965, 163	550	166	13288	2.E+00	1.E+00	3.E-01	5.E+01
GOTERM_MF_FAT	GO:0016667~oxidoreductase activity, acting on sulfur group of dor	5	0.784929356	5.E-02 93692, 26462, 50493, 14782, 13382	550	33	13288	4.E+00	1.E+00	3.E-01	5.E+01
GOTERM_MF_FAT	GO:0016861~intramolecular oxidoreductase activity, interconverting	3	0.470957614	5.E-02 14751, 19895, 21991	550	9	13288	8.E+00	1.E+00	4.E-01	5.E+01
GOTERM_MF_FAT	GO:0019206~nucleoside kinase activity	3	0.470957614	5.E-02 80914, 68556, 22245	550	9	13288	8.E+00	1.E+00	4.E-01	5.E+01
GOTERM_MF_FAT	GO:0016624~oxidoreductase activity, acting on the aldehyde or ox	3	0.470957614	5.E-02 68263, 18597, 18598	550	9	13288	8.E+00	1.E+00	4.E-01	5.E+01
GOTERM_MF_FAT	GO:0048407~platelet-derived growth factor binding	3	0.470957614	5.E-02 12843, 12831, 12842	550	9	13288	8.E+00	1.E+00	4.E-01	5.E+01
GOTERM_MF_FAT	GO:0016862~intramolecular oxidoreductase activity, interconverting	3	0.470957614	5.E-02 18453, 12304, 14827	550	9	13288	8.E+00	1.E+00	4.E-01	5.E+01
GOTERM_MF_FAT	GO:0050661~NADP or NADPH binding	4	0.627943485	5.E-02 18126, 26462, 50493, 14782	550	21	13288	5.E+00	1.E+00	4.E-01	6.E+01
GOTERM_MF_FAT	GO:0008034~lipoprotein binding	4	0.627943485	5.E-02 11806, 11807, 11816, 21899	550	21	13288	5.E+00	1.E+00	4.E-01	6.E+01
GOTERM_MF_FAT	GO:0004428~inositol or phosphatidylinositol kinase activity	5	0.784929356	5.E-02 18709, 18708, 11920, 30955, 18707	550	35	13288	3.E+00	1.E+00	4.E-01	6.E+01
GOTERM_MF_FAT	GO:0016651~oxidoreductase activity, acting on NADH or NADPH	6	0.941915228	6.E-02 17970, 26462, 50493, 14782, 13382, 1796	550	51	13288	3.E+00	1.E+00	4.E-01	6.E+01
GOTERM_MF_FAT	GO:0046982~protein heterodimerization activity	10	1.569858713	6.E-02 18771, 12048, 11807, 12028, 12043, 1641	550	121	13288	2.E+00	1.E+00	4.E-01	6.E+01
GOTERM_MF_FAT	GO:0016765~transferase activity, transferring alkyl or aryl (other tha	6	0.941915228	7.E-02 56615, 232087, 14863, 66447, 14865, 117	550	53	13288	3.E+00	1.E+00	4.E-01	6.E+01
GOTERM_MF_FAT	GO:0008094~DNA-dependent ATPase activity	5	0.784929356	7.E-02 13872, 17420, 14884, 14885, 66671	550	38	13288	3.E+00	1.E+00	5.E-01	7.E+01
GOTERM_MF_FAT	GO:0046983~protein dimerization activity	21	3.296703297	7.E-02 11807, 16414, 12043, 22778, 14281, 1998	550	340	13288	1.E+00	1.E+00	5.E-01	7.E+01
GOTERM_MF_FAT	GO:0045309~protein phosphorylated amino acid binding	3	0.470957614	7.E-02 15170, 17999, 12928	550	11	13288	7.E+00	1.E+00	5.E-01	7.E+01
GOTERM_MF_FAT	GO:0016866~intramolecular transferase activity	4	0.627943485	7.E-02 18648, 72157, 12183, 56012	550	24	13288	4.E+00	1.E+00	5.E-01	7.E+01
GOTERM_MF_FAT	GO:0016887~ATPase activity	18	2.825745683	7.E-02 18195, 110957, 13872, 18669, 18671, 186	550	281	13288	2.E+00	1.E+00	5.E-01	7.E+01
GOTERM_MF_FAT	GO:0004613~phosphoenolpyruvate carboxykinase (GTP) activity	2	0.313971743	8.E-02 18534, 74551	550	2	13288	2.E+01	1.E+00	5.E-01	7.E+01
GOTERM_MF_FAT	GO:0004152~dihydroorotate dehydrogenase activity	2	0.313971743	8.E-02 56749, 99586	550	2	13288	2.E+01	1.E+00	5.E-01	7.E+01
GOTERM_MF_FAT	GO:0005093~Rab GDP-dissociation inhibitor activity	2	0.313971743	8.E-02 14567, 14569	550	2	13288	2.E+01	1.E+00	5.E-01	7.E+01
GOTERM_MF_FAT	GO:0003913~DNA photolyase activity	2	0.313971743	8.E-02 12952, 12953	550	2	13288	2.E+01	1.E+00	5.E-01	7.E+01
GOTERM_MF_FAT	GO:0004379~glycylpeptide N-tetradecanoyltransferase activity	2	0.313971743	8.E-02 18108, 18107	550	2	13288	2.E+01	1.E+00	5.E-01	7.E+01
GOTERM_MF_FAT	GO:0070064~proline-rich region binding	2	0.313971743	8.E-02 17999, 22601	550	2	13288	2.E+01	1.E+00	5.E-01	7.E+01
GOTERM_MF_FAT	GO:0004611~phosphoenolpyruvate carboxykinase activity	2	0.313971743	8.E-02 18534, 74551	550	2	13288	2.E+01	1.E+00	5.E-01	7.E+01
GOTERM_MF_FAT	GO:0019107~myristoyltransferase activity	2	0.313971743	8.E-02 18108, 18107	550	2	13288	2.E+01	1.E+00	5.E-01	7.E+01
GOTERM_MF_FAT	GO:0031489~myosin V binding	2	0.313971743	8.E-02 11891, 171531	550	2	13288	2.E+01	1.E+00	5.E-01	7.E+01
GOTERM_MF_FAT	GO:0004743~pyruvate kinase activity	2	0.313971743	8.E-02 18746, 18770	550	2	13288	2.E+01	1.E+00	5.E-01	7.E+01
GOTERM_MF_FAT	GO:0004478~methionine adenosyltransferase activity	2	0.313971743	8.E-02 232087, 11720	550	2	13288	2.E+01	1.E+00	5.E-01	7.E+01
GOTERM_MF_FAT	GO:0004158~dihydroorotate oxidase activity	2	0.313971743	8.E-02 56749, 99586	550	2	13288	2.E+01	1.E+00	5.E-01	7.E+01
GOTERM_MF_FAT	GO:0045523~interleukin-27 receptor binding	2	0.313971743	8.E-02 246779, 50498	550	2	13288	2.E+01	1.E+00	5.E-01	7.E+01
GOTERM_MF_FAT	GO:0004618~phosphoglycerate kinase activity	2	0.313971743	8.E-02 18663, 18655	550	2	13288	2.E+01	1.E+00	5.E-01	7.E+01



GOTERM_MF_FAT	GO:0016209--antioxidant activity	5	0.784929356	8.E-02 26462, 50493, 54683, 14782, 19225	550	40	13288	3.E+00	1.E+00	5.E-01	7.E+01
GOTERM_MF_FAT	GO:0030546--receptor activator activity	3	0.470957614	9.E-02 12568, 12815, 17978	550	12	13288	6.E+00	1.E+00	5.E-01	7.E+01
GOTERM_MF_FAT	GO:0004364--glutathione transferase activity	4	0.627943485	9.E-02 56615, 14863, 66447, 14865	550	26	13288	4.E+00	1.E+00	5.E-01	8.E+01
GOTERM_MF_FAT	GO:0017022--myosin binding	3	0.470957614	1.E-01 245049, 11891, 171531	550	13	13288	6.E+00	1.E+00	5.E-01	8.E+01
GOTERM_MF_FAT	GO:0016776--phosphotransferase activity, phosphate group as acce	4	0.627943485	1.E-01 14923, 11636, 66588, 11637	550	27	13288	4.E+00	1.E+00	5.E-01	8.E+01
BIOCARTA	m_il2rbPathway:IL-2 Receptor Beta Chain in T cell Activation	17	2.668759812	7.E-06 15170, 17869, 12043, 72508, 11651, 1428	167	36	1171	3.E+00	2.E-03	2.E-03	9.E-03
BIOCARTA	m_fcer1Pathway:Fc Epsilon Receptor I Signaling in Mast Cells	14	2.197802198	2.E-04 22324, 12229, 14281, 20416, 14127, 1870	167	32	1171	3.E+00	4.E-02	2.E-02	2.E-01
BIOCARTA	m_igf1Pathway:IGF-1 Signaling Pathway	11	1.726844584	2.E-04 18708, 218397, 16367, 14784, 20662, 263	167	21	1171	4.E+00	5.E-02	2.E-02	3.E-01
BIOCARTA	m_ghPathway:Growth Hormone Signaling Pathway	12	1.883830455	2.E-04 18708, 15170, 18803, 12703, 16367, 1633	167	25	1171	3.E+00	5.E-02	1.E-02	3.E-01
BIOCARTA	m_bcrPathway:BCR Signaling Pathway	13	2.040816327	3.E-04 22324, 12229, 14281, 20416, 18803, 1478	167	29	1171	3.E+00	6.E-02	1.E-02	3.E-01
BIOCARTA	m_igf1rPathway:Multiple antiapoptotic pathways from IGF-IR signa	10	1.569858713	5.E-04 18708, 12015, 16367, 14784, 20662, 2639	167	19	1171	4.E+00	1.E-01	2.E-02	6.E-01
BIOCARTA	m_tffPathway:Trefoil Factors Initiate Mucosal Healing	11	1.726844584	5.E-04 18708, 13649, 672195, 12015, 14784, 206	167	23	1171	3.E+00	1.E-01	2.E-02	7.E-01
BIOCARTA	m_spryPathway:Sprouty regulation of tyrosine kinase signals	9	1.412872841	6.E-04 13649, 20779, 218397, 24064, 14784, 206	167	16	1171	4.E+00	1.E-01	2.E-02	8.E-01
BIOCARTA	m_il3Pathway:IL 3 signaling pathway	9	1.412872841	6.E-04 15170, 12983, 14784, 20662, 26395, 1546	167	16	1171	4.E+00	1.E-01	2.E-02	8.E-01
BIOCARTA	m_trkaPathway:Trka Receptor Signaling Pathway	8	1.25588697	8.E-04 18048, 18708, 18803, 14784, 20662, 1546	167	13	1171	4.E+00	2.E-01	2.E-02	1.E+00
BIOCARTA	m_epoPathway:EPO Signaling Pathway	10	1.569858713	1.E-03 15170, 18803, 13857, 14784, 20662, 2639	167	21	1171	3.E+00	2.E-01	3.E-02	2.E+00
BIOCARTA	m_gleevecPathway:Inhibition of Cellular Proliferation by Gleevec	10	1.569858713	2.E-03 18708, 12015, 14784, 20662, 26395, 1546	167	22	1171	3.E+00	3.E-01	3.E-02	2.E+00
BIOCARTA	m_insulinPathway:Insulin Signaling Pathway	10	1.569858713	2.E-03 18708, 218397, 16367, 16334, 14784, 206	167	22	1171	3.E+00	3.E-01	3.E-02	2.E+00
BIOCARTA	m_monocytePathway:Monocyte and its Surface Molecules	7	1.098901099	2.E-03 16408, 20343, 16414, 12505, 16412, 2033	167	11	1171	4.E+00	3.E-01	3.E-02	2.E+00
BIOCARTA	m_neutrophilPathway:Neutrophil and Its Surface Molecules	6	0.941915228	2.E-03 16408, 20343, 16414, 12505, 20339, 1640	167	8	1171	5.E+00	4.E-01	3.E-02	3.E+00
BIOCARTA	m_pyk2Pathway:Links between Pyk2 and Map Kinases	11	1.726844584	2.E-03 18479, 20416, 18803, 20779, 14784, 1231	167	27	1171	3.E+00	4.E-01	4.E-02	3.E+00
BIOCARTA	m_tcrPathway:T Cell Receptor Signaling Pathway	13	2.040816327	3.E-03 22324, 14281, 20416, 16818, 18708, 1880	167	36	1171	3.E+00	4.E-01	4.E-02	3.E+00
BIOCARTA	m_TPOPathway:TPO Signaling Pathway	10	1.569858713	3.E-03 18708, 18803, 218397, 14784, 20662, 263	167	23	1171	3.E+00	4.E-01	3.E-02	3.E+00
BIOCARTA	m_ngfPathway:Nerve growth factor pathway (NGF)	9	1.412872841	3.E-03 18048, 18708, 18803, 14784, 20662, 2639	167	19	1171	3.E+00	4.E-01	3.E-02	3.E+00
BIOCARTA	m_ecmPathway:Erk and PI-3 Kinase Are Necessary for Collagen Bina	9	1.412872841	3.E-03 18708, 20779, 26395, 15461, 11855, 1436	167	19	1171	3.E+00	4.E-01	3.E-02	3.E+00
BIOCARTA	m_metPathway:Signaling of Hepatocyte Growth Factor Receptor	12	1.883830455	3.E-03 18708, 20779, 218397, 14784, 20662, 263	167	32	1171	3.E+00	5.E-01	3.E-02	4.E+00
BIOCARTA	m_nkcellPathway:Ras-Independent pathway in NK cell-mediated cy	8	1.25588697	4.E-03 18708, 15170, 22324, 26395, 16412, 1847	167	16	1171	4.E+00	6.E-01	4.E-02	5.E+00
BIOCARTA	m_igf1mtorPathway:Skeletal muscle hypertrophy is regulated via Akt	9	1.412872841	4.E-03 13684, 18708, 56717, 13685, 13665, 7250	167	20	1171	3.E+00	6.E-01	4.E-02	5.E+00
BIOCARTA	m_rasPathway:Ras Signaling Pathway	9	1.412872841	4.E-03 18708, 12015, 12048, 26395, 15461, 1165	167	20	1171	3.E+00	6.E-01	4.E-02	5.E+00
BIOCARTA	m_eif4Pathway:Regulation of eIF4e and p70 S6 Kinase	9	1.412872841	4.E-03 13684, 18708, 56717, 13685, 16367, 2641	167	20	1171	3.E+00	6.E-01	4.E-02	5.E+00
BIOCARTA	m_chemicalPathway:Apoptotic Signaling in Response to DNA Damage	9	1.412872841	4.E-03 672195, 12015, 12048, 11920, 12028, 121	167	20	1171	3.E+00	6.E-01	4.E-02	5.E+00
BIOCARTA	m_lymphocytePathway:Adhesion Molecules on Lymphocyte	6	0.941915228	4.E-03 16408, 20343, 16414, 12505, 16412, 2033	167	9	1171	5.E+00	6.E-01	4.E-02	5.E+00
BIOCARTA	m_HBxPathway:Calcium Signaling by HBx of Hepatitis B virus	6	0.941915228	4.E-03 20779, 14784, 20662, 15461, 20416, 1291	167	9	1171	5.E+00	6.E-01	4.E-02	5.E+00
BIOCARTA	m_integrinPathway:Integrin Signaling Pathway	11	1.726844584	4.E-03 20779, 14784, 20662, 26395, 15461, 1436	167	29	1171	3.E+00	6.E-01	4.E-02	5.E+00
BIOCARTA	m_Par1Pathway:Thrombin signaling and protease-activated recepto	8	1.25588697	6.E-03 18708, 14674, 14065, 14682, 16801, 1406	167	17	1171	3.E+00	7.E-01	5.E-02	7.E+00
BIOCARTA	m_erk1Pathway:Erk1/Erk2 Mapk Signaling pathway	11	1.726844584	8.E-03 18048, 13649, 20779, 14784, 20662, 2639	167	31	1171	2.E+00	8.E-01	7.E-02	9.E+00
BIOCARTA	m_badPathway:Regulation of BAD phosphorylation	8	1.25588697	8.E-03 18708, 12015, 12048, 12028, 11651, 1204	167	18	1171	3.E+00	8.E-01	7.E-02	1.E+01
BIOCARTA	m_erk5Pathway:Role of Erk5 in Neuronal Survival	7	1.098901099	8.E-03 18708, 18803, 14784, 15461, 11651, 2041	167	14	1171	4.E+00	8.E-01	7.E-02	1.E+01
BIOCARTA	m_plcPathway:Phospholipase C Signaling Pathway	5	0.784929356	1.E-02 18708, 22324, 18803, 11651, 18795	167	7	1171	5.E+00	9.E-01	7.E-02	1.E+01
BIOCARTA	m_biopeptidesPathway:Bioactive Peptide Induced Signaling Pathwa	11	1.726844584	1.E-02 20416, 18803, 14784, 12315, 26416, 1231	167	32	1171	2.E+00	9.E-01	7.E-02	1.E+01
BIOCARTA	m_hdacPathway:Control of skeletal myogenesis by HDAC & calcium	8	1.25588697	1.E-02 18019, 18708, 16334, 12315, 12314, 2641	167	19	1171	3.E+00	9.E-01	8.E-02	1.E+01
BIOCARTA	m_A11rPathway:Angiotensin II mediated activation of JNK Pathway	10	1.569858713	1.E-02 13649, 20779, 12315, 14784, 20662, 1231	167	28	1171	3.E+00	9.E-01	8.E-02	1.E+01
BIOCARTA	m_egfPathway:EGF Signaling Pathway	10	1.569858713	1.E-02 18708, 13649, 18803, 218397, 14784, 206	167	28	1171	3.E+00	9.E-01	8.E-02	1.E+01
BIOCARTA	m_longevityPathway:The IGF-1 Receptor and Longevity	6	0.941915228	1.E-02 18708, 15461, 11651, 16001, 20416, 1600	167	11	1171	4.E+00	9.E-01	8.E-02	1.E+01
BIOCARTA	m_il4Pathway:IL 4 signaling pathway	6	0.941915228	2.E-02 16367, 14784, 72508, 11651, 16190, 2041	167	12	1171	4.E+00	1.E+00	1.E-01	2.E+01
BIOCARTA	m_mitochondriaPathway:Role of Mitochondria in Apoptotic Signali	8	1.25588697	2.E-02 672195, 66593, 12048, 12028, 12122, 120	167	21	1171	3.E+00	1.E+00	1.E-01	2.E+01
BIOCARTA	m_her2Pathway:Role of ERBB2 in Signal Transduction and Oncolog	8	1.25588697	3.E-02 18708, 13649, 16195, 14784, 20662, 2639	167	22	1171	3.E+00	1.E+00	2.E-01	3.E+01
BIOCARTA	m_mTORPathway:mTOR Signaling Pathway	8	1.25588697	3.E-02 13684, 18708, 56717, 19744, 13685, 7250	167	22	1171	3.E+00	1.E+00	2.E-01	3.E+01
BIOCARTA	m_pdgfPathway:PDGF Signaling Pathway	9	1.412872841	3.E-02 18708, 18803, 218397, 14784, 20662, 263	167	28	1171	2.E+00	1.E+00	2.E-01	4.E+01
BIOCARTA	m_circadianPathway:Circadian Rhythms	4	0.627943485	4.E-02 11865, 12753, 12952, 18626	167	6	1171	5.E+00	1.E+00	2.E-01	4.E+01
BIOCARTA	m_mrpPathway:Multi-Drug Resistance Factors	4	0.627943485	4.E-02 18669, 18671, 27413, 17250	167	6	1171	5.E+00	1.E+00	2.E-01	4.E+01
BIOCARTA	m_rhoPathway:Rho cell motility signaling pathway	7	1.098901099	4.E-02 20779, 94190, 11856, 11855, 171207, 168	167	19	1171	3.E+00	1.E+00	2.E-01	4.E+01
BIOCARTA	m_il2Pathway:IL 2 signaling pathway	8	1.25588697	4.E-02 16818, 14784, 20662, 26395, 15461, 1428	167	24	1171	2.E+00	1.E+00	2.E-01	4.E+01
BIOCARTA	m_rac1Pathway:Rac 1 cell motility signaling pathway	7	1.098901099	5.E-02 18708, 22324, 17970, 72508, 18479, 1976	167	20	1171	2.E+00	1.E+00	3.E-01	5.E+01
BIOCARTA	m_ptenPathway:PTEN dependent cell cycle arrest and apoptosis	7	1.098901099	5.E-02 18708, 14784, 20662, 11651, 16412, 2041	167	20	1171	2.E+00	1.E+00	3.E-01	5.E+01
BIOCARTA	m_gsk3Pathway:Inactivation of Gsk3 by AKT causes accumulation o	8	1.25588697	5.E-02 18708, 17874, 12475, 16179, 17087, 2189	167	25	1171	2.E+00	1.E+00	3.E-01	5.E+01
BIOCARTA	m_rbPathway:RB Tumor Suppressor/Checkpoint Signaling in respon	5	0.784929356	6.E-02 22390, 11920, 12532, 12566, 12534	167	11	1171	3.E+00	1.E+00	3.E-01	5.E+01
BIOCARTA	m_d4gdiPathway:D4-GDI Signaling Pathway	5	0.784929356	6.E-02 672195, 14939, 11855, 11857, 13063, 123	167	11	1171	3.E+00	1.E+00	3.E-01	5.E+01
BIOCARTA	m_il7Pathway:IL-7 Signal Transduction	6	0.941915228	6.E-02 18708, 16818, 16197, 12043, 14360, 1291	167	16	1171	3.E+00	1.E+00	3.E-01	6.E+01
BIOCARTA	m_p53Pathway:p53 Signaling Pathway	6	0.941915228	6.E-02 11920, 12028, 13197, 12043, 12566, 1853	167	16	1171	3.E+00	1.E+00	3.E-01	6.E+01
BIOCARTA	m_cdc25Pathway:cdc25 and chk1 Regulatory Pathway in response t	4	0.627943485	6.E-02 22390, 11920, 12532, 12534	167	7	1171	4.E+00	1.E+00	3.E-01	6.E+01
BIOCARTA	m_sam68Pathway:Regulation of Splicing through Sam68	4	0.627943485	6.E-02 20779, 218397, 15461, 12534	167	7	1171	4.E+00	1.E+00	3.E-01	6.E+01
BIOCARTA	m_srcRPTPathway:Activation of Src by Protein-tyrosine phosphata:	4	0.627943485	6.E-02 20779, 14784, 12532, 12534	167	7	1171	4.E+00	1.E+00	3.E-01	6.E+01
BIOCARTA	m_il6Pathway:IL 6 signaling pathway	7	1.098901099	6.E-02 16195, 14784, 20662, 26395, 15461, 1428	167	21	1171	2.E+00	1.E+00	3.E-01	6.E+01
BIOCARTA	m_crebPathway:Transcription factor CREB and its extracellular signa	7	1.098901099	6.E-02 18708, 14784, 20662, 26416, 15461, 1165	167	21	1171	2.E+00	1.E+00	3.E-01	6.E+01



BIOCARTA	m_fMLPpathway:fMLP induced chemokine gene expression in HMC	8	1.25588697	8.E-02 12315, 17970, 12314, 26416, 26395, 1231	167	27	1171	2.E+00	1.E+00	3.E-01	6.E+01
BIOCARTA	m_nfatPathway:NFAT and Hypertrophy of the heart (Transcription i	10	1.569858713	8.E-02 18708, 12315, 12314, 26416, 26395, 1231	167	38	1171	2.E+00	1.E+00	3.E-01	6.E+01
BIOCARTA	m_ceramidePathway:Ceramide Signaling Pathway	7	1.098901099	8.E-02 672195, 12015, 12028, 26395, 12043, 130	167	22	1171	2.E+00	1.E+00	3.E-01	6.E+01
BIOCARTA	m_cardiacegfPathway:Role of EGF Receptor Transactivation by GPCl	6	0.941915228	8.E-02 13649, 18803, 15461, 17869, 14281, 1184	167	17	1171	2.E+00	1.E+00	3.E-01	7.E+01
BIOCARTA	m_ptdinsPathway:Phosphoinositides and their downstream targets.	6	0.941915228	1.E-01 18803, 12229, 12015, 72508, 11651, 1709	167	18	1171	2.E+00	1.E+00	4.E-01	7.E+01
KEGG_PATHWAY	mmu04914:Progesterone-mediated oocyte maturation	38	5.965463108	4.E-21 11651, 59008, 56150, 18709, 18708, 1244	409	85	5738	6.E+00	7.E-19	7.E-19	5.E-18
KEGG_PATHWAY	mmu00010:Glycolysis / Gluconeogenesis	34	5.337519623	1.E-20 18746, 68263, 100042746, 15275, 15277,	409	68	5738	7.E+00	2.E-18	8.E-19	1.E-17
KEGG_PATHWAY	mmu04114:Oocyte meiosis	39	6.12244898	1.E-16 26965, 59008, 56150, 103583, 67141, 122	409	115	5738	5.E+00	2.E-14	6.E-15	1.E-13
KEGG_PATHWAY	mmu04910:Insulin signaling pathway	42	6.593406593	5.E-16 13684, 19744, 13685, 11651, 15275, 7250	409	138	5738	4.E+00	7.E-14	2.E-14	5.E-13
KEGG_PATHWAY	mmu04110:Cell cycle	40	6.279434851	9.E-16 218294, 26965, 12236, 17869, 59008, 561	409	128	5738	4.E+00	1.E-13	3.E-14	1.E-12
KEGG_PATHWAY	mmu04650:Natural killer cell mediated cytotoxicity	38	5.965463108	7.E-15 14972, 22324, 14939, 20416, 170758, 187	409	122	5738	4.E+00	1.E-12	2.E-13	8.E-12
KEGG_PATHWAY	mmu04012:ErbB signaling pathway	27	4.238618524	1.E-10 13649, 13685, 72508, 17869, 11651, 2041	409	87	5738	4.E+00	2.E-08	3.E-09	1.E-07
KEGG_PATHWAY	mmu04662:B cell receptor signaling pathway	25	3.924646782	6.E-10 22324, 11651, 170758, 18019, 18709, 187	409	80	5738	4.E+00	9.E-08	1.E-08	7.E-07
KEGG_PATHWAY	mmu04660:T cell receptor signaling pathway	30	4.709576138	2.E-09 22324, 11651, 18019, 18709, 18803, 1870	409	118	5738	4.E+00	3.E-07	3.E-08	2.E-06
KEGG_PATHWAY	mmu04670:Leukocyte transendothelial migration	30	4.709576138	2.E-09 22323, 22324, 69524, 232906, 54354, 118	409	119	5738	4.E+00	3.E-07	3.E-08	3.E-06
KEGG_PATHWAY	mmu04930:Type II diabetes mellitus	19	2.982731554	2.E-09 18746, 320207, 15275, 15277, 384783, 10	409	49	5738	5.E+00	3.E-07	3.E-08	3.E-06
KEGG_PATHWAY	mmu04510:Focal adhesion	40	6.279434851	3.E-09 22323, 12831, 22324, 13649, 232906, 116	409	198	5738	3.E+00	4.E-07	4.E-08	3.E-06
KEGG_PATHWAY	mmu04664:Fc epsilon RI signaling pathway	24	3.767660911	6.E-09 22324, 12229, 320207, 11651, 57257, 170	409	82	5738	4.E+00	9.E-07	7.E-08	7.E-06
KEGG_PATHWAY	mmu05215:Prostate cancer	25	3.924646782	8.E-09 13649, 11651, 12912, 12914, 18709, 1870	409	90	5738	4.E+00	1.E-06	9.E-08	9.E-06
KEGG_PATHWAY	mmu04810:Regulation of actin cytoskeleton	41	6.436420722	1.E-08 12475, 227753, 22324, 13649, 14178, 170	409	217	5738	3.E+00	2.E-06	1.E-07	2.E-05
KEGG_PATHWAY	mmu04722:Neurotrophin signaling pathway	30	4.709576138	2.E-08 192662, 11651, 11857, 20416, 18709, 188	409	130	5738	3.E+00	3.E-06	2.E-07	2.E-05
KEGG_PATHWAY	mmu05214:Glioma	20	3.139717425	4.E-08 13649, 320207, 11651, 20416, 18709, 567	409	64	5738	4.E+00	7.E-06	4.E-07	5.E-05
KEGG_PATHWAY	mmu05200:Pathways in cancer	51	8.006279435	7.E-08 672195, 14178, 54354, 170758, 12914, 18	409	323	5738	2.E+00	1.E-05	6.E-07	9.E-05
KEGG_PATHWAY	mmu04210:Apoptosis	23	3.610675039	1.E-07 672195, 320207, 12122, 19088, 11651, 12	409	87	5738	4.E+00	2.E-05	8.E-07	1.E-04
KEGG_PATHWAY	mmu04062:Chemokine signaling pathway	35	5.494505495	1.E-07 12765, 22324, 11651, 20416, 21844, 1879	409	182	5738	3.E+00	2.E-05	9.E-07	1.E-04
KEGG_PATHWAY	mmu04370:VEGF signaling pathway	21	3.296703297	2.E-07 320207, 11651, 170758, 18709, 18019, 18	409	76	5738	4.E+00	3.E-05	1.E-06	2.E-04
KEGG_PATHWAY	mmu05210:Colorectal cancer	22	3.453689168	4.E-07 13649, 672195, 320207, 11651, 17869, 12	409	86	5738	4.E+00	6.E-05	3.E-06	4.E-04
KEGG_PATHWAY	mmu00030:Pentose phosphate pathway	12	1.883830455	6.E-07 56421, 14751, 19895, 21351, 230163, 721	409	26	5738	6.E+00	9.E-05	4.E-06	7.E-04
KEGG_PATHWAY	mmu04120:Ubiquitin mediated proteolysis	28	4.395604396	7.E-07 56550, 218793, 26965, 246710, 59008, 16	409	136	5738	3.E+00	1.E-04	5.E-06	9.E-04
KEGG_PATHWAY	mmu04666:Fc gamma R-mediated phagocytosis	23	3.610675039	9.E-07 22323, 22324, 227753, 320207, 13430, 11	409	98	5738	3.E+00	1.E-04	6.E-06	1.E-03
KEGG_PATHWAY	mmu05221:Acute myeloid leukemia	17	2.668759812	1.E-06 13685, 320207, 17869, 20375, 72508, 116	409	57	5738	4.E+00	2.E-04	7.E-06	1.E-03
KEGG_PATHWAY	mmu00620:Pyruvate metabolism	14	2.197802198	3.E-06 18746, 68263, 17448, 18534, 13382, 7455	409	41	5738	5.E+00	4.E-04	2.E-05	3.E-03
KEGG_PATHWAY	mmu05223:Non-small cell lung cancer	16	2.51177394	3.E-06 13649, 320207, 54354, 11651, 18709, 187	409	54	5738	4.E+00	5.E-04	2.E-05	4.E-03
KEGG_PATHWAY	mmu04150:mTOR signaling pathway	16	2.51177394	3.E-06 13684, 13685, 19744, 320207, 72508, 116	409	54	5738	4.E+00	5.E-04	2.E-05	4.E-03
KEGG_PATHWAY	mmu05220:Chronic myeloid leukemia	18	2.825745683	2.E-05 11350, 320207, 17869, 11651, 12928, 204	409	76	5738	3.E+00	3.E-03	9.E-05	2.E-02
KEGG_PATHWAY	mmu04115:p53 signaling pathway	17	2.668759812	2.E-05 382985, 672195, 12122, 12445, 12442, 20	409	69	5738	3.E+00	3.E-03	1.E-04	2.E-02
KEGG_PATHWAY	mmu04630:Iak-STA T signaling pathway	27	4.238618524	2.E-05 18414, 17869, 11651, 12914, 18709, 1870	409	152	5738	2.E+00	3.E-03	1.E-04	2.E-02
KEGG_PATHWAY	mmu05211:Renal cell carcinoma	17	2.668759812	2.E-05 20525, 320207, 11651, 12928, 18479, 129	409	70	5738	3.E+00	4.E-03	1.E-04	3.E-02
KEGG_PATHWAY	mmu05213:Endometrial cancer	14	2.197802198	5.E-05 13649, 320207, 17869, 11651, 18709, 187	409	52	5738	4.E+00	8.E-03	2.E-04	6.E-02
KEGG_PATHWAY	mmu04620:Toll-like receptor signaling pathway	20	3.139717425	5.E-05 12475, 320207, 27056, 21899, 21898, 116	409	99	5738	3.E+00	8.E-03	2.E-04	6.E-02
KEGG_PATHWAY	mmu05222:Small cell lung cancer	18	2.825745683	8.E-05 22029, 672195, 320207, 11651, 17869, 12	409	85	5738	3.E+00	1.E-02	3.E-04	9.E-02
KEGG_PATHWAY	mmu04360:Axon guidance	23	3.610675039	1.E-04 117600, 11350, 100044475, 11854, 14678	409	131	5738	2.E+00	2.E-02	5.E-04	1.E-01
KEGG_PATHWAY	mmu04710:Circadian rhythm	7	1.098901099	1.E-04 11865, 12753, 12952, 18626, 12953, 1862	409	13	5738	8.E+00	2.E-02	6.E-04	2.E-01
KEGG_PATHWAY	mmu05212:Pancreatic cancer	15	2.354788069	4.E-04 13649, 320207, 11651, 170758, 73341, 18	409	72	5738	3.E+00	7.E-02	2.E-03	5.E-01
KEGG_PATHWAY	mmu00020:Citrate cycle (TCA cycle)	9	1.412872841	1.E-03 68263, 17448, 235339, 18597, 18598, 185	409	31	5738	4.E+00	2.E-01	5.E-03	1.E+00
KEGG_PATHWAY	mmu05218:Melanoma	14	2.197802198	1.E-03 13649, 14178, 320207, 11651, 18709, 185	409	71	5738	3.E+00	2.E-01	5.E-03	2.E+00
KEGG_PATHWAY	mmu05014:Amyotrophic lateral sclerosis (ALS)	12	1.883830455	2.E-03 672195, 12122, 12043, 21937, 12015, 120	409	57	5738	3.E+00	3.E-01	7.E-03	2.E+00
KEGG_PATHWAY	mmu04010:MAPK signaling pathway	33	5.180533752	2.E-03 12475, 13649, 14178, 11651, 17869, 1707	409	265	5738	2.E+00	3.E-01	7.E-03	2.E+00
KEGG_PATHWAY	mmu04960:Aldosterone-regulated sodium reabsorption	10	1.569858713	2.E-03 18709, 18708, 16367, 16333, 16334, 3202	409	42	5738	3.E+00	3.E-01	8.E-03	3.E+00
KEGG_PATHWAY	mmu05416:Viral myocarditis	16	2.51177394	2.E-03 15007, 14972, 11350, 672195, 15018, 121	409	94	5738	2.E+00	3.E-01	8.E-03	3.E+00
KEGG_PATHWAY	mmu04540:Gap junction	15	2.354788069	3.E-03 22142, 13649, 14678, 18797, 18795, 1859	409	86	5738	2.E+00	3.E-01	9.E-03	3.E+00
KEGG_PATHWAY	mmu00240:Pyrimidine metabolism	16	2.51177394	3.E-03 80914, 382985, 22245, 22271, 103149, 99	409	96	5738	2.E+00	4.E-01	1.E-02	3.E+00
KEGG_PATHWAY	mmu00500:Starch and sucrose metabolism	9	1.412872841	3.E-03 110095, 14751, 15275, 72157, 15277, 103	409	36	5738	4.E+00	4.E-01	1.E-02	4.E+00
KEGG_PATHWAY	mmu04720:Long-term potentiation	13	2.040816327	3.E-03 18797, 12914, 18795, 11514, 12315, 1231	409	70	5738	3.E+00	4.E-01	1.E-02	4.E+00
KEGG_PATHWAY	mmu00983:Drug metabolism	10	1.569858713	6.E-03 80914, 68556, 22017, 72269, 22245, 1308	409	48	5738	3.E+00	6.E-01	2.E-02	7.E+00
KEGG_PATHWAY	mmu03420:Nucleotide excision repair	9	1.412872841	1.E-02 13872, 19891, 19358, 68240, 17420, 1488	409	43	5738	3.E+00	8.E-01	3.E-02	1.E+01
KEGG_PATHWAY	mmu00480:Glutathione metabolism	10	1.569858713	1.E-02 382985, 56615, 20133, 14863, 14782, 664	409	52	5738	3.E+00	8.E-01	3.E-02	1.E+01
KEGG_PATHWAY	mmu04730:Long-term depression	12	1.883830455	1.E-02 14674, 19053, 14678, 26395, 15461, 1600	409	72	5738	2.E+00	9.E-01	4.E-02	1.E+01
KEGG_PATHWAY	mmu00051:Fructose and mannose metabolism	8	1.25588697	1.E-02 56421, 15275, 21991, 230163, 15277, 116	409	37	5738	3.E+00	9.E-01	4.E-02	2.E+01
KEGG_PATHWAY	mmu00250:Alanine, aspartate and glutamate metabolism	7	1.098901099	2.E-02 227231, 14661, 109900, 11564, 11566, 14	409	30	5738	3.E+00	9.E-01	5.E-02	2.E+01
KEGG_PATHWAY	mmu04520:Adherens junction	12	1.883830455	2.E-02 15170, 19354, 13649, 20779, 22612, 1254	409	76	5738	2.E+00	9.E-01	5.E-02	2.E+01
KEGG_PATHWAY	mmu04920:Adipocytokine signaling pathway	11	1.726844584	2.E-02 56717, 12702, 16367, 20525, 18534, 1165	409	67	5738	2.E+00	1.E+00	5.E-02	2.E+01
KEGG_PATHWAY	mmu04912:GnRH signaling pathway	14	2.197802198	2.E-02 13649, 18797, 18795, 20779, 11514, 1478	409	97	5738	2.E+00	1.E+00	5.E-02	2.E+01
KEGG_PATHWAY	mmu00270:Cysteine and methionine metabolism	7	1.098901099	3.E-02 16828, 232087, 13436, 16833, 16832, 229	409	33	5738	3.E+00	1.E+00	7.E-02	3.E+01
KEGG_PATHWAY	mmu00230:Purine metabolism	19	2.982731554	3.E-02 18746, 382985, 14923, 11717, 11564, 115	409	157	5738	2.E+00	1.E+00	8.E-02	3.E+01



KEGG_PATHWAY	mmu00052:Galactose metabolism	6	0.941915228	4.E-02	56421, 15275, 72157, 15277, 103988, 212	409	27	5738	3.E+00	1.E+00	1.E-01	4.E+01
KEGG_PATHWAY	mmu04020:Calcium signaling pathway	21	3.296703297	5.E-02	13649, 14675, 102093, 18679, 11740, 187	409	191	5738	2.E+00	1.E+00	1.E-01	5.E+01
KEGG_PATHWAY	mmu04310:Wnt signaling pathway	17	2.668759812	6.E-02	26965, 17869, 103583, 21402, 170758, 18	409	149	5738	2.E+00	1.E+00	2.E-01	5.E+01
KEGG_PATHWAY	mmu04320:Dorso-ventral axis formation	5	0.784929356	7.E-02	13649, 14784, 20662, 20663, 26395	409	22	5738	3.E+00	1.E+00	2.E-01	6.E+01
KEGG_PATHWAY	mmu04514:Cell adhesion molecules (CAMs)	17	2.668759812	8.E-02	15007, 14972, 15018, 69524, 16456, 1641	409	154	5738	2.E+00	1.E+00	2.E-01	6.E+01
KEGG_PATHWAY	mmu00330:Arginine and proline metabolism	8	1.25588697	8.E-02	227231, 18126, 14661, 18416, 217214, 10	409	53	5738	2.E+00	1.E+00	2.E-01	6.E+01
KEGG_PATHWAY	mmu00982:Drug metabolism	10	1.569858713	8.E-02	56615, 76279, 14863, 13087, 56847, 6644	409	75	5738	2.E+00	1.E+00	2.E-01	6.E+01
KEGG_PATHWAY	mmu04070:Phosphatidylinositol signaling system	10	1.569858713	8.E-02	18709, 18708, 18803, 234779, 12315, 320	409	75	5738	2.E+00	1.E+00	2.E-01	6.E+01
KEGG_PATHWAY	mmu05010:Alzheimer's disease	19	2.982731554	9.E-02	672195, 100042746, 11816, 18797, 21937	409	182	5738	1.E+00	1.E+00	2.E-01	7.E+01
KEGG_PATHWAY	mmu02010:ABC transporters	7	1.098901099	1.E-01	18669, 18671, 18670, 27421, 12780, 2741	409	45	5738	2.E+00	1.E+00	2.E-01	7.E+01

Annotation Cluster 1	Enrichment Score: 35.47406469638261											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR000198:RhoGAP	46	7.221350078	1.E-49	117600, 94190, 232906, 228482, 243362,	630	67	17763	2.E+01	1.E-46	1.E-46	2.E-46
SMART	SM00324:RhoGAP	46	7.221350078	5.E-45	117600, 94190, 232906, 228482, 243362,	418	67	9131	1.E+01	9.E-43	9.E-43	6.E-42
UP_SEQ_FEATURE	domain:Rho-GAP	41	6.436420722	6.E-44	117600, 228482, 232906, 94190, 243362,	618	57	16021	2.E+01	9.E-41	9.E-41	5.E-41
GOTERM_MF_FAT	GO:0030695~GTPase regulator activity	81	12.71585557	9.E-37	22324, 228482, 94190, 192662, 243362, 1	550	361	13288	5.E+00	6.E-34	6.E-34	1.E-33
GOTERM_MF_FAT	GO:0060589~nucleoside-triphosphatase regulator activity	81	12.71585557	3.E-36	22324, 228482, 94190, 192662, 243362, 1	550	367	13288	5.E+00	2.E-33	1.E-33	5.E-33
SP_PIR_KEYWORDS	GTPase activation	47	7.37833595	6.E-33	117600, 94190, 232906, 228482, 192662,	629	136	17854	1.E+01	2.E-30	1.E-30	8.E-30
GOTERM_MF_FAT	GO:0005096~GTPase activator activity	48	7.535321821	8.E-24	117600, 94190, 232906, 228482, 192662,	550	192	13288	6.E+00	5.E-21	1.E-21	1.E-20
GOTERM_MF_FAT	GO:0008047~enzyme activator activity	51	8.006279435	3.E-21	94190, 228482, 243362, 192662, 225358,	550	249	13288	5.E+00	2.E-18	4.E-19	5.E-18

Annotation Cluster 2	Enrichment Score: 27.32358166159791											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0006006~glucose metabolic process	54	8.477237049	5.E-37	18746, 68263, 18679, 11676, 56012, 1167	572	140	13588	9.E+00	1.E-33	1.E-33	9.E-34
GOTERM_BP_FAT	GO:0019318~hexose metabolic process	55	8.63422292	3.E-33	18746, 68263, 18679, 11676, 56012, 1167	572	169	13588	8.E+00	8.E-30	4.E-30	5.E-30
GOTERM_BP_FAT	GO:0019320~hexose catabolic process	34	5.337519623	5.E-33	18746, 68263, 100042746, 15275, 15277,	572	52	13588	2.E+01	1.E-29	5.E-30	1.E-29
GOTERM_BP_FAT	GO:0006007~glucose catabolic process	34	5.337519623	5.E-33	18746, 68263, 100042746, 15275, 15277,	572	52	13588	2.E+01	1.E-29	5.E-30	1.E-29
SP_PIR_KEYWORDS	glycolysis	30	4.709576138	6.E-33	18746, 68263, 100042746, 15275, 15277,	629	42	17854	2.E+01	3.E-30	8.E-31	8.E-30
GOTERM_BP_FAT	GO:0046365~monosaccharide catabolic process	34	5.337519623	3.E-32	18746, 68263, 100042746, 15275, 15277,	572	54	13588	1.E+01	9.E-29	2.E-29	6.E-29
GOTERM_BP_FAT	GO:0005996~monosaccharide metabolic process	56	8.791208791	3.E-31	18746, 68263, 18679, 11676, 56012, 1167	572	191	13588	7.E+00	8.E-28	2.E-28	5.E-28
GOTERM_BP_FAT	GO:0044275~cellular carbohydrate catabolic process	34	5.337519623	4.E-30	18746, 68263, 100042746, 15275, 15277,	572	60	13588	1.E+01	1.E-26	2.E-27	8.E-27
GOTERM_BP_FAT	GO:0046164~alcohol catabolic process	35	5.494505495	6.E-30	18746, 68263, 100042746, 15275, 15277,	572	65	13588	1.E+01	2.E-26	2.E-27	1.E-26
GOTERM_BP_FAT	GO:0006096~glycolysis	30	4.709576138	8.E-30	18746, 68263, 100042746, 15275, 15277,	572	44	13588	2.E+01	2.E-26	3.E-27	1.E-26
GOTERM_BP_FAT	GO:0016052~carbohydrate catabolic process	34	5.337519623	1.E-24	18746, 68263, 100042746, 15275, 15277,	572	81	13588	1.E+01	3.E-21	4.E-22	2.E-21
KEGG_PATHWAY	mmu00010:Glycolysis / Gluconeogenesis	34	5.337519623	1.E-20	18746, 68263, 100042746, 15275, 15277,	409	68	5738	7.E+00	2.E-18	8.E-19	1.E-17
GOTERM_BP_FAT	GO:0006091~generation of precursor metabolites and energy	49	7.692307692	2.E-18	18746, 672195, 68263, 18679, 11676, 560	572	261	13588	4.E+00	6.E-15	5.E-16	4.E-15
UP_SEQ_FEATURE	binding site:Substrate	29	4.552590267	3.E-06	18746, 22245, 11676, 103988, 11674, 186	618	275	16021	3.E+00	5.E-03	3.E-04	5.E-03

Annotation Cluster 3	Enrichment Score: 14.428797441942018											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0005083~small GTPase regulator activity	53	8.320251177	3.E-25	22324, 192662, 16800, 171531, 16801, 22	550	223	13288	6.E+00	2.E-22	8.E-23	5.E-22
INTERPRO	IPR000219:DbI homology (DH) domain	25	3.924646782	9.E-19	22324, 13605, 16800, 442801, 53972, 218	630	65	17763	1.E+01	9.E-16	5.E-16	1.E-15
GOTERM_BP_FAT	GO:0035023~regulation of Rho protein signal transduction	29	4.552590267	5.E-18	22324, 13605, 16800, 442801, 53972, 218	572	86	13588	8.E+00	1.E-14	1.E-15	8.E-15
UP_SEQ_FEATURE	domain:DH	23	3.610675039	3.E-17	14163, 277360, 22324, 13605, 101497, 57	618	56	16021	1.E+01	5.E-14	3.E-14	5.E-14
INTERPRO	IPR001849:Pleckstrin homology	43	6.750392465	1.E-16	22324, 94190, 13430, 54519, 11651, 1680	630	261	17763	5.E+00	1.E-13	3.E-14	2.E-13
INTERPRO	IPR011993:Pleckstrin homology-type	45	7.064364207	2.E-16	22323, 94190, 13430, 54519, 11651, 1680	630	289	17763	4.E+00	2.E-13	4.E-14	4.E-13
SMART	SM00325:RhoGEF	25	3.924646782	2.E-16	22324, 13605, 16800, 442801, 53972, 218	418	65	9131	8.E+00	4.E-14	2.E-14	3.E-13
GOTERM_MF_FAT	GO:0005089~Rho guanyl-nucleotide exchange factor activity	25	3.924646782	3.E-16	22324, 13605, 16800, 442801, 53972, 218	550	71	13288	9.E+00	2.E-13	4.E-14	5.E-13
INTERPRO	IPR001331:Guanine-nucleotide dissociation stimulator, CDC24, cons	21	3.296703297	5.E-16	14163, 277360, 22324, 13605, 101497, 57	630	53	17763	1.E+01	4.E-13	6.E-14	7.E-13
GOTERM_MF_FAT	GO:0005088~Ras guanyl-nucleotide exchange factor activity	25	3.924646782	2.E-14	22324, 13605, 16800, 442801, 53972, 218	550	83	13288	7.E+00	1.E-11	2.E-12	3.E-11
SP_PIR_KEYWORDS	guanine-nucleotide releasing factor	25	3.924646782	9.E-14	22324, 13605, 16800, 442801, 53972, 218	629	102	17854	7.E+00	4.E-11	2.E-12	1.E-10
SMART	SM00233:PH	43	6.750392465	5.E-13	22324, 94190, 13430, 54519, 11651, 1680	418	261	9131	4.E+00	9.E-11	2.E-11	6.E-10
GOTERM_BP_FAT	GO:0046578~regulation of Ras protein signal transduction	32	5.023547881	2.E-11	22324, 13605, 442801, 16800, 53972, 218	572	181	13588	4.E+00	6.E-08	3.E-09	4.E-08
UP_SEQ_FEATURE	domain:PH	30	4.709576138	9.E-10	22324, 94190, 54519, 13430, 13605, 1165	618	202	16021	4.E+00	2.E-06	3.E-07	2.E-06
GOTERM_MF_FAT	GO:0005085~guanyl-nucleotide exchange factor activity	26	4.081632653	1.E-09	22324, 13605, 16800, 442801, 53972, 218	550	147	13288	4.E+00	1.E-06	8.E-08	2.E-06



GOTERM_BP_FAT	GO:0051056~regulation of small GTPase mediated signal transducti	33	5.180533752	2.E-09	22324, 13605, 442801, 16800, 53972, 218	572	228	13588	3.E+00	5.E-06	2.E-07	3.E-06
Annotation Cluster 4	Enrichment Score: 12.700369750426042											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
KEGG_PATHWAY	mmu04914:Progesterone-mediated oocyte maturation	38	5.965463108	4.E-21	11651, 59008, 56150, 18709, 18708, 1244	409	85	5738	6.E+00	7.E-19	7.E-19	5.E-18
KEGG_PATHWAY	mmu04114:Oocyte meiosis	39	6.12244898	1.E-16	26965, 59008, 56150, 103583, 67141, 122	409	115	5738	5.E+00	2.E-14	6.E-15	1.E-13
KEGG_PATHWAY	mmu04110:Cell cycle	40	6.279434851	9.E-16	218294, 26965, 12236, 17869, 59008, 561	409	128	5738	4.E+00	1.E-13	3.E-14	1.E-12
SP_PIR_KEYWORDS	cell division	41	6.436420722	2.E-15	19384, 12454, 12236, 16800, 59008, 5615	629	256	17854	5.E+00	7.E-13	9.E-14	2.E-12
SP_PIR_KEYWORDS	mitosis	33	5.180533752	3.E-14	19384, 12454, 12236, 59008, 16800, 5615	629	179	17854	5.E+00	1.E-11	9.E-13	4.E-11
SP_PIR_KEYWORDS	cell cycle	53	8.320251177	3.E-14	19384, 243362, 16800, 59008, 22778, 561	629	447	17854	3.E+00	1.E-11	9.E-13	4.E-11
GOTERM_BP_FAT	GO:0000278~mitotic cell cycle	41	6.436420722	1.E-13	19384, 12454, 12236, 16800, 59008, 5615	572	244	13588	4.E+00	3.E-10	2.E-11	2.E-10
GOTERM_BP_FAT	GO:0007067~mitosis	35	5.494505495	6.E-13	19384, 12454, 12236, 59008, 16800, 5615	572	190	13588	4.E+00	2.E-09	1.E-10	1.E-09
GOTERM_BP_FAT	GO:0000280~nuclear division	35	5.494505495	6.E-13	19384, 12454, 12236, 59008, 16800, 5615	572	190	13588	4.E+00	2.E-09	1.E-10	1.E-09
GOTERM_BP_FAT	GO:0051301~cell division	43	6.750392465	6.E-13	19384, 12454, 12236, 16800, 59008, 5615	572	281	13588	4.E+00	2.E-09	1.E-10	1.E-09
GOTERM_BP_FAT	GO:0000087~M phase of mitotic cell cycle	35	5.494505495	1.E-12	19384, 12454, 12236, 59008, 16800, 5615	572	194	13588	4.E+00	3.E-09	2.E-10	2.E-09
GOTERM_BP_FAT	GO:0048285~organelle fission	35	5.494505495	2.E-12	19384, 12454, 12236, 59008, 16800, 5615	572	197	13588	4.E+00	5.E-09	3.E-10	3.E-09
GOTERM_BP_FAT	GO:0007049~cell cycle	64	10.04709576	3.E-11	19384, 16952, 243362, 22778, 59008, 168	572	611	13588	2.E+00	8.E-08	4.E-09	5.E-08
GOTERM_BP_FAT	GO:0022402~cell cycle process	46	7.221350078	9.E-10	19384, 12454, 12236, 16800, 59008, 5615	572	393	13588	3.E+00	2.E-06	1.E-07	2.E-06
GOTERM_BP_FAT	GO:0022403~cell cycle phase	41	6.436420722	1.E-09	19384, 12454, 12236, 16800, 59008, 5615	572	328	13588	3.E+00	3.E-06	1.E-07	2.E-06
GOTERM_BP_FAT	GO:0000279~M phase	36	5.651491366	1.E-08	19384, 12454, 12236, 16800, 59008, 5615	572	283	13588	3.E+00	3.E-05	9.E-07	2.E-05
Annotation Cluster 5	Enrichment Score: 12.38232300096245											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR000980:SH2 motif	30	4.709576138	1.E-17	22324, 20416, 20491, 18709, 18708, 1681	630	111	17763	8.E+00	1.E-14	4.E-15	2.E-14
INTERPRO	IPR001452:Src homology-3 domain	38	5.965463108	6.E-16	117600, 22324, 75415, 171207, 53972, 20	630	211	17763	5.E+00	5.E-13	7.E-14	9.E-13
SP_PIR_KEYWORDS	sh3 domain	37	5.808477237	9.E-16	117600, 22324, 75415, 53972, 20491, 545	629	204	17854	5.E+00	4.E-13	5.E-14	1.E-12
SMART	SM00252:SH2	30	4.709576138	7.E-15	22324, 20416, 20491, 18709, 18708, 1681	418	111	9131	6.E+00	1.E-12	4.E-13	9.E-12
SP_PIR_KEYWORDS	SH2 domain	26	4.081632653	1.E-14	22324, 20416, 20491, 18709, 18708, 1681	629	103	17854	7.E+00	5.E-12	5.E-13	2.E-11
SMART	SM00326:SH3	38	5.965463108	9.E-13	117600, 22324, 75415, 171207, 53972, 20	418	211	9131	4.E+00	2.E-10	3.E-11	1.E-09
UP_SEQ_FEATURE	domain:SH2	20	3.139717425	1.E-09	11350, 22324, 12229, 57257, 12928, 2041	618	90	16021	6.E+00	2.E-06	3.E-07	2.E-06
UP_SEQ_FEATURE	domain:SH3	25	3.924646782	2.E-08	117600, 75415, 53972, 20491, 15163, 187	618	163	16021	4.E+00	3.E-05	3.E-06	3.E-05
GOTERM_MF_FAT	GO:0004715~non-membrane spanning protein tyrosine kinase acti	13	2.040816327	4.E-08	11350, 12229, 16818, 14191, 22390, 2077	550	40	13288	8.E+00	3.E-05	1.E-06	6.E-05
Annotation Cluster 6	Enrichment Score: 8.211446573804054											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0030029~actin filament-based process	33	5.180533752	2.E-12	22323, 215280, 227753, 94190, 11856, 16	572	176	13588	4.E+00	5.E-09	3.E-10	3.E-09
GOTERM_BP_FAT	GO:0030036~actin cytoskeleton organization	30	4.709576138	5.E-11	22323, 227753, 94190, 11856, 16800, 204	572	165	13588	4.E+00	1.E-07	6.E-09	8.E-08
GOTERM_BP_FAT	GO:0007010~cytoskeleton organization	35	5.494505495	1.E-06	22323, 227753, 94190, 11856, 16800, 204	572	326	13588	3.E+00	3.E-03	6.E-05	2.E-03
GOTERM_BP_FAT	GO:0007015~actin filament organization	12	1.883830455	2.E-05	227753, 100044475, 18826, 17973, 11464	572	56	13588	5.E+00	5.E-02	7.E-04	3.E-02
Annotation Cluster 7	Enrichment Score: 7.825219234244761											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	nucleotide-binding	137	21.50706436	2.E-22	18746, 19744, 71819, 170758, 74551, 808	629	1631	17854	2.E+00	9.E-20	2.E-20	3.E-19
SP_PIR_KEYWORDS	kinase	74	11.61695447	7.E-17	18746, 72508, 18679, 18709, 23920, 1870	629	707	17854	3.E+00	5.E-14	8.E-15	2.E-13
SP_PIR_KEYWORDS	ATP	31	4.866562009	9.E-15	13649, 15275, 103988, 18663, 18596, 186	629	151	17854	6.E+00	4.E-12	4.E-13	1.E-11
SP_PIR_KEYWORDS	phosphotransferase	28	4.395604396	2.E-14	18746, 15275, 18679, 103988, 18663, 187	629	124	17854	6.E+00	8.E-12	7.E-13	3.E-11
GOTERM_MF_FAT	GO:0017076~purine nucleotide binding	144	22.60596546	3.E-14	18746, 19744, 71819, 14782, 170758, 745	550	1871	13288	2.E+00	2.E-11	2.E-12	5.E-11
GOTERM_MF_FAT	GO:0032555~purine ribonucleotide binding	139	21.82103611	7.E-14	18746, 19744, 71819, 170758, 74551, 808	550	1796	13288	2.E+00	4.E-11	5.E-12	1.E-10
GOTERM_MF_FAT	GO:0032553~ribonucleotide binding	139	21.82103611	7.E-14	18746, 19744, 71819, 170758, 74551, 808	550	1796	13288	2.E+00	4.E-11	5.E-12	1.E-10
SP_PIR_KEYWORDS	atp-binding	100	15.69858713	8.E-14	18746, 71819, 23920, 20779, 11464, 2701	629	1287	17854	2.E+00	3.E-11	2.E-12	1.E-10
GOTERM_MF_FAT	GO:0001066~nucleotide binding	158	24.80376766	2.E-13	18746, 19744, 71819, 14782, 170758, 745	550	2183	13288	2.E+00	1.E-10	1.E-11	3.E-10
UP_SEQ_FEATURE	active site:Proton acceptor	68	10.67503925	3.E-13	72508, 14782, 11676, 11674, 23920, 1681	618	662	16021	3.E+00	6.E-10	1.E-10	6.E-10
SP_PIR_KEYWORDS	transferase	97	15.22762951	8.E-11	18746, 18416, 22271, 12914, 23920, 2077	629	1385	17854	2.E+00	3.E-08	2.E-09	1.E-07
SP_PIR_KEYWORDS	tyrosine-protein kinase	22	3.453689168	6.E-10	11350, 13649, 21687, 12229, 23920, 1681	629	116	17854	5.E+00	3.E-07	1.E-08	8.E-07
INTERPRO	IPR008266:Tyrosine protein kinase, active site	20	3.139717425	2.E-09	11350, 13649, 21687, 12229, 23920, 1681	630	101	17763	6.E+00	2.E-06	2.E-07	4.E-06
GOTERM_MF_FAT	GO:0001882~nucleoside binding	111	17.42543171	7.E-09	18746, 71819, 14782, 23920, 20779, 1934	550	1558	13288	2.E+00	5.E-06	3.E-07	1.E-05
GOTERM_MF_FAT	GO:0001883~purine nucleoside binding	110	17.26844584	1.E-08	18746, 71819, 14782, 23920, 20779, 1146	550	1548	13288	2.E+00	7.E-06	4.E-07	1.E-05
GOTERM_MF_FAT	GO:0030554~adenyl nucleotide binding	109	17.11145997	1.E-08	18746, 71819, 14782, 23920, 20779, 1146	550	1535	13288	2.E+00	8.E-06	4.E-07	2.E-05
GOTERM_MF_FAT	GO:0032559~adenyl ribonucleotide binding	104	16.32653061	3.E-08	18746, 71819, 23920, 20779, 11464, 2701	550	1460	13288	2.E+00	2.E-05	8.E-07	4.E-05
UP_SEQ_FEATURE	binding site:ATP	50	7.849293564	3.E-08	72508, 16818, 23920, 20779, 12566, 1256	618	545	16021	2.E+00	5.E-05	5.E-06	5.E-05
GOTERM_MF_FAT	GO:0004715~non-membrane spanning protein tyrosine kinase acti	13	2.040816327	4.E-08	11350, 12229, 16818, 14191, 22390, 2077	550	40	13288	8.E+00	3.E-05	1.E-06	6.E-05
GOTERM_BP_FAT	GO:0016310~phosphorylation	63	9.89010989	5.E-08	13665, 72508, 12912, 16818, 18708, 2392	572	718	13588	2.E+00	1.E-04	4.E-06	8.E-05
GOTERM_MF_FAT	GO:0005524~ATP binding	102	16.01255887	5.E-08	18746, 71819, 23920, 20779, 11464, 2701	550	1443	13288	2.E+00	4.E-05	2.E-06	8.E-05
INTERPRO	IPR001245:Tyrosine protein kinase	20	3.139717425	7.E-08	11350, 13649, 21687, 12229, 23920, 1681	630	124	17763	5.E+00	7.E-05	6.E-06	1.E-04
GOTERM_BP_FAT	GO:0006796~phosphate metabolic process	71	11.14599686	8.E-08	218294, 13665, 72508, 12912, 23920, 187	572	866	13588	2.E+00	2.E-04	6.E-06	1.E-04



GOTERM_BP_FAT	GO:0006793~phosphorus metabolic process	71	11.14599686	8.E-08	218294, 13665, 72508, 12912, 23920, 187	572	866	13588	2.E+00	2.E-04	6.E-06	1.E-04
INTERPRO	IPR017441:Protein kinase, ATP binding site	42	6.593406593	9.E-08	13649, 11651, 12236, 72508, 545156, 138	630	467	17763	3.E+00	9.E-05	6.E-06	1.E-04
GOTERM_BP_FAT	GO:0006468~protein amino acid phosphorylation	56	8.791208791	3.E-07	13665, 72508, 12912, 16818, 18708, 2392	572	640	13588	2.E+00	9.E-04	2.E-05	6.E-04
UP_SEQ_FEATURE	nucleotide-specific phosphate-binding region:ATP	67	10.51805338	4.E-07	72508, 23920, 16818, 13006, 20779, 7757	618	907	16021	2.E+00	7.E-04	6.E-05	7.E-04
GOTERM_MF_FAT	GO:0004672~protein kinase activity	51	8.006279435	7.E-07	72508, 16818, 23920, 20779, 14884, 1256	550	583	13288	2.E+00	5.E-04	2.E-05	1.E-03
INTERPRO	IPR000719:Protein kinase, core	41	6.436420722	9.E-07	13649, 11651, 12236, 72508, 545156, 138	630	491	17763	2.E+00	9.E-04	6.E-05	1.E-03
SMART	SM00219:TyrKc	20	3.139717425	3.E-06	11350, 13649, 21687, 12229, 23920, 1681	418	124	9131	4.E+00	6.E-04	8.E-05	4.E-03
GOTERM_MF_FAT	GO:0004713~protein tyrosine kinase activity	22	3.453689168	4.E-06	11350, 13649, 21687, 12229, 23920, 1681	550	164	13288	3.E+00	3.E-03	1.E-04	6.E-03
SP_PIR_KEYWORDS	tyrosine-specific protein kinase	10	1.569858713	4.E-06	18596, 21687, 14191, 20779, 19713, 1430	629	37	17854	8.E+00	2.E-03	6.E-05	6.E-03
UP_SEQ_FEATURE	domain:Protein kinase	40	6.279434851	8.E-06	13649, 11651, 12236, 72508, 545156, 138	618	476	16021	2.E+00	1.E-02	7.E-04	1.E-02
GOTERM_BP_FAT	GO:0018212~peptidyl-tyrosine modification	9	1.412872841	1.E-04	11350, 16818, 12229, 20779, 18413, 1436	572	37	13588	6.E+00	3.E-01	4.E-03	2.E-01
GOTERM_BP_FAT	GO:0018108~peptidyl-tyrosine phosphorylation	9	1.412872841	1.E-04	11350, 16818, 12229, 20779, 18413, 1436	572	37	13588	6.E+00	3.E-01	4.E-03	2.E-01
GOTERM_BP_FAT	GO:0046777~protein amino acid autophosphorylation	11	1.726844584	4.E-04	56717, 13649, 16818, 23920, 16179, 2261	572	66	13588	4.E+00	7.E-01	1.E-02	7.E-01
GOTERM_MF_FAT	GO:0004674~protein serine/threonine kinase activity	30	4.709576138	5.E-03	11651, 72508, 12236, 545156, 13872, 567	550	421	13288	2.E+00	1.E+00	7.E-02	7.E+00
INTERPRO	IPR002290:Serine/threonine protein kinase	18	2.825745683	1.E-02	270672, 20871, 18005, 11651, 72508, 208	630	265	17763	2.E+00	1.E+00	2.E-01	2.E+01
INTERPRO	IPR008271:Serine/threonine protein kinase, active site	22	3.453689168	2.E-02	270672, 20871, 18005, 11651, 20878, 725	630	360	17763	2.E+00	1.E+00	3.E-01	2.E+01
SP_PIR_KEYWORDS	serine/threonine-protein kinase	22	3.453689168	3.E-02	270672, 20871, 18005, 11651, 20878, 725	629	384	17854	2.E+00	1.E+00	1.E-01	4.E+01
INTERPRO	IPR017442:Serine/threonine protein kinase-related	21	3.296703297	4.E-02	270672, 20871, 18005, 11651, 72508, 208	630	374	17763	2.E+00	1.E+00	5.E-01	5.E+01
SMART	SM00220:S_TKc	18	2.825745683	1.E-01	270672, 20871, 18005, 11651, 72508, 208	418	265	9131	1.E+00	1.E+00	5.E-01	7.E+01

Annotation Cluster 8	Enrichment Score: 7.670551558352981											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR003578:Ras small GTPase, Rho type	15	2.354788069	4.E-16	228543, 11852, 69288, 246710, 11854, 11	630	21	17763	2.E+01	3.E-13	5.E-14	5.E-13
SMART	SM00174:RHO	15	2.354788069	1.E-14	228543, 11852, 69288, 246710, 11854, 11	418	21	9131	2.E+01	2.E-12	6.E-13	1.E-11
GOTERM_BP_FAT	GO:0007264~small GTPase mediated signal transduction	42	6.593406593	1.E-13	228543, 117600, 19744, 232906, 11852, 1	572	258	13588	4.E+00	4.E-10	3.E-11	3.E-10
SP_PIR_KEYWORDS	methylation	34	5.337519623	2.E-12	19744, 100042746, 27041, 12955, 11852,	629	221	17854	4.E+00	8.E-10	5.E-11	3.E-09
PIR_SUPERFAMILY	PIRSF037169:small GTPase, Rho type	11	1.726844584	4.E-10	80837, 228543, 11852, 11854, 104215, 11	400	16	8136	1.E+01	2.E-07	2.E-07	6.E-07
INTERPRO	IPR001806:Ras GTPase	23	3.610675039	1.E-09	228543, 19744, 69288, 11852, 232906, 24	630	130	17763	5.E+00	1.E-06	1.E-07	2.E-06
INTERPRO	IPR013753:Ras	22	3.453689168	2.E-09	228543, 19744, 69288, 11852, 232906, 19	630	121	17763	5.E+00	1.E-06	1.E-07	2.E-06
SP_PIR_KEYWORDS	gtp-binding	34	5.337519623	2.E-08	228543, 19744, 11852, 19384, 13628, 118	629	313	17854	3.E+00	8.E-06	4.E-07	3.E-05
UP_SEQ_FEATURE	nucleotide phosphate-binding region:GTP	31	4.866562009	3.E-07	228543, 19744, 11852, 19384, 11854, 246	618	274	16021	3.E+00	4.E-04	4.E-05	4.E-04
INTERPRO	IPR005225:Small GTP-binding protein	22	3.453689168	4.E-07	228543, 19744, 69288, 11852, 19384, 246	630	164	17763	4.E+00	4.E-04	2.E-05	6.E-04
GOTERM_MF_FAT	GO:0005525~GTP binding	36	5.651491366	2.E-06	228543, 19744, 232906, 11852, 19384, 13	550	354	13288	2.E+00	1.E-03	4.E-05	2.E-03
GOTERM_MF_FAT	GO:0032561~guanyl ribonucleotide binding	36	5.651491366	3.E-06	228543, 19744, 232906, 11852, 19384, 13	550	363	13288	2.E+00	2.E-03	7.E-05	4.E-03
GOTERM_MF_FAT	GO:0019001~guanyl nucleotide binding	36	5.651491366	3.E-06	228543, 19744, 232906, 11852, 19384, 13	550	363	13288	2.E+00	2.E-03	7.E-05	4.E-03
GOTERM_MF_FAT	GO:0003924~GTPase activity	19	2.982731554	5.E-06	22142, 14674, 14675, 19384, 14678, 1362	550	128	13288	4.E+00	3.E-03	1.E-04	8.E-03
UP_SEQ_FEATURE	short sequence motif:Effector region	15	2.354788069	1.E-05	19744, 11852, 11854, 11853, 74734, 1707	618	92	16021	4.E+00	2.E-02	9.E-04	2.E-02
SP_PIR_KEYWORDS	prenylation	18	2.825745683	1.E-05	19744, 11852, 11854, 102093, 11853, 747	629	145	17854	4.E+00	6.E-03	2.E-04	2.E-02
UP_SEQ_FEATURE	propeptide:Removed in mature form	18	2.825745683	5.E-03	19370, 19744, 12475, 11852, 11854, 1185	618	220	16021	2.E+00	1.E+00	2.E-01	8.E+00
UP_SEQ_FEATURE	lipid moiety-binding region:S-geranylgeranyl cysteine	10	1.569858713	1.E-02	19354, 11854, 11853, 23912, 74734, 1254	618	95	16021	3.E+00	1.E+00	3.E-01	2.E+01

Annotation Cluster 9	Enrichment Score: 6.993657665981487											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
KEGG_PATHWAY	mmu04650:Natural killer cell mediated cytotoxicity	38	5.965463108	7.E-15	14972, 22324, 14939, 20416, 170758, 187	409	122	5738	4.E+00	1.E-12	2.E-13	8.E-12
KEGG_PATHWAY	mmu04012:ErbB signaling pathway	27	4.238618524	1.E-10	13649, 13685, 72508, 17869, 11651, 2041	409	87	5738	4.E+00	2.E-08	3.E-09	1.E-07
KEGG_PATHWAY	mmu04662:B cell receptor signaling pathway	25	3.924646782	6.E-10	22324, 11651, 170758, 18019, 18709, 187	409	80	5738	4.E+00	9.E-08	1.E-08	7.E-07
KEGG_PATHWAY	mmu04660:T cell receptor signaling pathway	30	4.709576138	2.E-09	22324, 11651, 18019, 18709, 18803, 1870	409	118	5738	4.E+00	3.E-07	3.E-08	2.E-06
KEGG_PATHWAY	mmu04510:Focal adhesion	40	6.279434851	3.E-09	22323, 12831, 22324, 13649, 232906, 116	409	198	5738	3.E+00	4.E-07	4.E-08	3.E-06
KEGG_PATHWAY	mmu04664:Fc epsilon RI signaling pathway	24	3.767660911	6.E-09	22324, 12229, 320207, 11651, 57257, 170	409	82	5738	4.E+00	9.E-07	7.E-08	7.E-06
KEGG_PATHWAY	mmu05215:Prostate cancer	25	3.924646782	8.E-09	13649, 11651, 12912, 12914, 18709, 1870	409	90	5738	4.E+00	1.E-06	9.E-08	9.E-06
KEGG_PATHWAY	mmu04722:Neurotrophin signaling pathway	30	4.709576138	2.E-08	192662, 11651, 11857, 20416, 18709, 188	409	130	5738	3.E+00	3.E-06	2.E-07	2.E-05
KEGG_PATHWAY	mmu05214:Glioma	20	3.139717425	4.E-08	13649, 320207, 11651, 20416, 18709, 567	409	64	5738	4.E+00	7.E-06	4.E-07	5.E-05
KEGG_PATHWAY	mmu05200:Pathways in cancer	51	8.006279435	7.E-08	672195, 14178, 54354, 170758, 12914, 18	409	323	5738	2.E+00	1.E-05	6.E-07	9.E-05
KEGG_PATHWAY	mmu04062:Chemokine signaling pathway	35	5.494505495	1.E-07	12765, 22324, 11651, 20416, 21844, 1879	409	182	5738	3.E+00	2.E-05	9.E-07	1.E-04
KEGG_PATHWAY	mmu04370:VEGF signaling pathway	21	3.296703297	2.E-07	320207, 11651, 170758, 18709, 18019, 18	409	76	5738	4.E+00	3.E-05	1.E-06	2.E-04
KEGG_PATHWAY	mmu05210:Colorectal cancer	22	3.453689168	4.E-07	13649, 672195, 320207, 11651, 17869, 12	409	86	5738	4.E+00	6.E-05	3.E-06	4.E-04
KEGG_PATHWAY	mmu04666:Fc gamma R-mediated phagocytosis	23	3.610675039	9.E-07	22323, 22324, 227753, 320207, 13430, 11	409	98	5738	3.E+00	1.E-04	6.E-06	1.E-03
KEGG_PATHWAY	mmu05221:Acute myeloid leukemia	17	2.668759812	1.E-06	13685, 320207, 17869, 20375, 72508, 116	409	57	5738	4.E+00	2.E-04	7.E-06	1.E-03
KEGG_PATHWAY	mmu05223:Non-small cell lung cancer	16	2.51177394	3.E-06	13649, 320207, 54354, 11651, 18709, 187	409	54	5738	4.E+00	5.E-04	2.E-05	4.E-03
KEGG_PATHWAY	mmu05220:Chronic myeloid leukemia	18	2.825745683	2.E-05	11350, 320207, 17869, 11651, 12928, 204	409	76	5738	3.E+00	3.E-03	9.E-05	2.E-02
KEGG_PATHWAY	mmu05211:Renal cell carcinoma	17	2.668759812	2.E-05	20525, 320207, 11651, 12928, 18479, 129	409	70	5738	3.E+00	4.E-03	1.E-04	3.E-02
KEGG_PATHWAY	mmu05213:Endometrial cancer	14	2.197802198	5.E-05	13649, 320207, 17869, 11651, 18709, 187	409	52	5738	4.E+00	8.E-03	2.E-04	6.E-02
KEGG_PATHWAY	mmu05212:Pancratic cancer	15	2.354788069	4.E-04	13649, 320207, 11651, 170758, 73341, 18	409	72	5738	3.E+00	7.E-02	2.E-03	5.E-01
KEGG_PATHWAY	mmu05218:Melanoma	14	2.197802198	1.E-03	13649, 14178, 320207, 11651, 18709, 185	409	71	5738	3.E+00	2.E-01	5.E-03	2.E+00



Annotation Cluster 10		Enrichment Score: 6.213529328937457												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR		
SP_PIR_KEYWORDS	ubli conjugation	51	8.006279435		2.E-10 19384, 22778, 319191, 56012, 12914, 159	629	524	17854	3.E+00	6.E-08	3.E-09	2.E-07		
SP_PIR_KEYWORDS	isopeptide bond	27	4.238618524		6.E-06 13649, 19384, 26965, 16952, 22778, 3191	629	277	17854	3.E+00	2.E-03	8.E-05	8.E-03		
UP_SEQ_FEATURE	cross-link:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter i	18	2.825745683		3.E-04 621893, 15387, 78294, 13649, 19384, 269	618	168	16021	3.E+00	4.E-01	2.E-02	4.E-01		
Annotation Cluster 11		Enrichment Score: 5.9024891267014965												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR		
GOTERM_CC_FAT	GO:0000267~cell fraction	46	7.221350078		7.E-07 672195, 269589, 11852, 12955, 238055, 7	434	596	12504	2.E+00	2.E-04	8.E-05	9.E-04		
GOTERM_CC_FAT	GO:0005626~insoluble fraction	42	6.593406593		1.E-06 269589, 11852, 12955, 238055, 72508, 16	434	528	12504	2.E+00	4.E-04	7.E-05	1.E-03		
GOTERM_CC_FAT	GO:0005624~membrane fraction	40	6.279434851		3.E-06 269589, 11852, 72508, 238055, 16396, 14	434	510	12504	2.E+00	1.E-03	1.E-04	4.E-03		
Annotation Cluster 12		Enrichment Score: 5.445077422932769												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR		
GOTERM_BP_FAT	GO:0051336~regulation of hydrolase activity	27	4.238618524		2.E-07 22324, 672195, 66593, 17869, 11856, 145	572	196	13588	3.E+00	5.E-04	1.E-05	4.E-04		
GOTERM_BP_FAT	GO:0043085~positive regulation of catalytic activity	30	4.709576138		2.E-06 672195, 66593, 11856, 17869, 20416, 168	572	261	13588	3.E+00	5.E-03	1.E-04	3.E-03		
GOTERM_BP_FAT	GO:0051345~positive regulation of hydrolase activity	13	2.040816327		1.E-04 672195, 66593, 17869, 11856, 16818, 717	572	81	13588	4.E+00	3.E-01	4.E-03	2.E-01		
Annotation Cluster 13		Enrichment Score: 5.184189134299275												
Category	Term: Immune cell activation	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR		
GOTERM_BP_FAT	GO:0045321~leukocyte activation	34	5.337519623		2.E-10 22324, 22778, 16803, 22376, 58240, 1205	572	219	13588	4.E+00	4.E-07	2.E-08	3.E-07		
GOTERM_BP_FAT	GO:0001775~cell activation	36	5.651491366		2.E-10 22324, 22778, 16803, 22376, 58240, 1205	572	246	13588	3.E+00	6.E-07	3.E-08	4.E-07		
GOTERM_BP_FAT	GO:0046649~lymphocyte activation	29	4.552590267		7.E-09 22324, 22778, 22376, 58240, 16408, 1205	572	191	13588	4.E+00	2.E-05	7.E-07	1.E-05		
GOTERM_BP_FAT	GO:0042110~T cell activation	22	3.453689168		1.E-08 22324, 16414, 12043, 22778, 74734, 1081	572	116	13588	5.E+00	4.E-05	1.E-06	2.E-05		
GOTERM_BP_FAT	GO:0030097~hemopoiesis	30	4.709576138		8.E-07 22324, 22778, 15163, 15902, 58240, 1205	572	251	13588	3.E+00	2.E-03	5.E-05	1.E-03		
GOTERM_BP_FAT	GO:0048534~hemopoietic or lymphoid organ development	32	5.023547881		9.E-07 22324, 22778, 15163, 15902, 58240, 1205	572	281	13588	3.E+00	2.E-03	5.E-05	2.E-03		
GOTERM_BP_FAT	GO:0002520~immune system development	32	5.023547881		3.E-06 22324, 22778, 15163, 15902, 58240, 1205	572	295	13588	3.E+00	7.E-03	1.E-04	4.E-03		
GOTERM_BP_FAT	GO:0030098~lymphocyte differentiation	18	2.825745683		5.E-06 22324, 12043, 20375, 74734, 22778, 1081	572	114	13588	4.E+00	1.E-02	3.E-04	9.E-03		
GOTERM_BP_FAT	GO:0002521~leukocyte differentiation	19	2.982731554		3.E-05 22324, 12043, 20375, 74734, 22778, 1081	572	142	13588	3.E+00	7.E-02	1.E-03	5.E-02		
GOTERM_BP_FAT	GO:0048872~homeostasis of number of cells	16	2.51177394		8.E-05 12043, 20375, 11651, 12183, 15902, 1516	572	113	13588	3.E+00	2.E-01	2.E-03	1.E-01		
GOTERM_BP_FAT	GO:0030217~T cell differentiation	12	1.883830455		3.E-04 12051, 22324, 16818, 18771, 16197, 1204	572	76	13588	4.E+00	6.E-01	9.E-03	6.E-01		
GOTERM_BP_FAT	GO:0042113~B cell activation	11	1.726844584		2.E-03 12051, 18708, 16197, 11486, 234779, 120	572	78	13588	3.E+00	1.E+00	3.E-02	3.E+00		
GOTERM_BP_FAT	GO:0030183~B cell differentiation	8	1.25588697		3.E-03 12051, 18708, 11486, 234779, 12028, 120	572	46	13588	4.E+00	1.E+00	4.E-02	5.E+00		
GOTERM_BP_FAT	GO:0030218~erythrocyte differentiation	8	1.25588697		4.E-03 18771, 21349, 20375, 12183, 14381, 1590	572	48	13588	4.E+00	1.E+00	5.E-02	6.E+00		
GOTERM_BP_FAT	GO:0034101~erythrocyte homeostasis	8	1.25588697		5.E-03 18771, 21349, 20375, 12183, 14381, 1590	572	51	13588	4.E+00	1.E+00	7.E-02	9.E+00		
GOTERM_BP_FAT	GO:0030099~myeloid cell differentiation	11	1.726844584		7.E-03 18771, 21349, 15415, 20375, 12183, 1645	572	96	13588	3.E+00	1.E+00	8.E-02	1.E+01		
Annotation Cluster 14		Enrichment Score: 4.988198316456065												
Category	Term: Rho/Rac/Ras GTPase activator activity	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR		
GOTERM_MF_FAT	GO:0005100~Rho GTPase activator activity	10	1.569858713		1.E-08 117600, 71709, 17925, 50768, 228359, 76	550	18	13288	1.E+01	8.E-06	4.E-07	2.E-05		
GOTERM_MF_FAT	GO:0030675~Rac GTPase activator activity	5	0.784929356		3.E-04 228359, 76117, 19765, 233071, 106952	550	9	13288	1.E+01	2.E-01	6.E-03	5.E-01		
GOTERM_MF_FAT	GO:0005099~Ras GTPase activator activity	11	1.726844584		3.E-04 117600, 71709, 17925, 50768, 228359, 76	550	65	13288	4.E+00	2.E-01	5.E-03	5.E-01		
Annotation Cluster 15		Enrichment Score: 4.828550876613079												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR		
GOTERM_CC_FAT	GO:0030027~lamellipodium	13	2.040816327		1.E-06 22323, 227753, 14163, 54519, 11651, 170	434	63	12504	6.E+00	5.E-04	8.E-05	2.E-03		
GOTERM_CC_FAT	GO:0031252~cell leading edge	16	2.51177394		7.E-06 22323, 14163, 227753, 54519, 228359, 11	434	112	12504	4.E+00	2.E-03	3.E-04	1.E-02		
GOTERM_CC_FAT	GO:0042995~cell projection	42	6.593406593		9.E-06 22323, 18746, 227753, 94190, 16952, 545	434	575	12504	2.E+00	3.E-03	3.E-04	1.E-02		
SP_PIR_KEYWORDS	cell projection	18	2.825745683		6.E-04 22323, 14163, 73750, 94190, 16952, 5451	629	196	17854	3.E+00	2.E-01	5.E-03	8.E-01		
Annotation Cluster 16		Enrichment Score: 6.477151436753687												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR		
GOTERM_MF_FAT	GO:0004715~non-membrane spanning protein tyrosine kinase acti	13	2.040816327		4.E-08 11350, 12229, 16818, 14191, 22390, 2077	550	40	13288	8.E+00	3.E-05	1.E-06	6.E-05		
SP_PIR_KEYWORDS	domain:RabBD	10	1.569858713		3.E-11 245049, 269589, 19894, 320051, 380714, 1	629	37	17854	8.E+00	2.E-03	6.E-08	6.E-03		
SP_PIR_KEYWORDS	myristylation	7	1.098901099		1.E-04 14191, 20779, 14678, 14302, 19059, 1436	629	23	17854	9.E+00	5.E-02	1.E-03	2.E-01		
SP_PIR_KEYWORDS	autophosphorylation	8	1.25588697		2.E-04 18596, 21687, 14191, 20779, 14360, 1297	629	34	17854	7.E+00	6.E-02	1.E-03	2.E-01		
PIRSUPERFAMILY	PIRSF000601:tyrosine-protein kinase, proto-oncogene SRC type	5	0.784929356		1.E-03 14191, 20779, 22612, 14302, 17096	400	11	8136	9.E+00	4.E-01	1.E-01	2.E+00		
Annotation Cluster 17		Enrichment Score: 4.533019180978523												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR		
INTERSEQ	IPR010911:Rab-binding domain	10	1.569858713		2.E-11 245049, 269589, 19894, 320051, 380714, 1	630	12	17763	2.E+01	2.E-08	2.E-09	3.E-08		
UP_SEQ_FEATURE	domain:RabBD	10	1.569858713		3.E-11 245049, 269589, 19894, 320051, 380714, 1	618	12	16021	2.E+01	6.E-08	1.E-08	6.E-08		
GOTERM_MF_FAT	GO:0017016~Ras GTPase binding	17	2.668759812		7.E-10 117600, 269589, 19894, 17970, 380714, 1	550	57	13288	7.E+00	5.E-07	4.E-08	1.E-06		
GOTERM_MF_FAT	GO:0031267~small GTPase binding	17	2.668759812		1.E-09 117600, 269589, 19894, 17970, 380714, 1	550	59	13288	7.E+00	8.E-07	7.E-08	2.E-06		
GOTERM_MF_FAT	GO:0051020~GTPase binding	17	2.668759812		3.E-09 117600, 269589, 19894, 17970, 380714, 1	550	62	13288	7.E+00	2.E-06	1.E-07	4.E-06		



GOTERM_MF_FAT	GO:0017137~Rab GTPase binding	10	1.569858713	2.E-08	245049, 269589, 19894, 320051, 380714,	550	19	13288	1.E+01	1.E-05	7.E-07	3.E-05
GOTERM_MF_FAT	GO:0019899~enzyme binding	27	4.238618524	3.E-06	117600, 269589, 26965, 13605, 16800, 17	550	229	13288	3.E+00	2.E-03	7.E-05	4.E-03
INTERPRO	IPR003315:Rabphilin-3A effector, zinc-binding	5	0.784929356	2.E-05	19894, 380714, 27359, 236643, 83672	630	6	17763	2.E+01	2.E-02	1.E-03	3.E-02
GOTERM_MF_FAT	GO:0042043~neurexin binding	5	0.784929356	9.E-05	269589, 27359, 83671, 13385, 83672	550	7	13288	2.E+01	6.E-02	2.E-03	1.E-01
GOTERM_BP_FAT	GO:0034613~cellular protein localization	24	3.767660911	4.E-03	11865, 269589, 19894, 19384, 380714, 12	572	299	13588	2.E+00	1.E+00	5.E-02	7.E+00
GOTERM_BP_FAT	GO:0070727~cellular macromolecule localization	24	3.767660911	4.E-03	11865, 269589, 19894, 19384, 380714, 12	572	301	13588	2.E+00	1.E+00	6.E-02	7.E+00
GOTERM_BP_FAT	GO:0006886~intracellular protein transport	20	3.139717425	2.E-02	11865, 269589, 19894, 19384, 380714, 12	572	276	13588	2.E+00	1.E+00	2.E-01	4.E+01
UP_SEQ_FEATURE	domain:C2 1	6	0.941915228	7.E-02	269589, 19894, 27359, 83671, 236643, 83	618	57	16021	3.E+00	1.E+00	8.E-01	7.E+01
UP_SEQ_FEATURE	domain:C2 2	6	0.941915228	7.E-02	269589, 19894, 27359, 83671, 236643, 83	618	57	16021	3.E+00	1.E+00	8.E-01	7.E+01
GOTERM_BP_FAT	GO:0006887~exocytosis	9	1.412872841	9.E-02	269589, 19894, 77579, 380714, 27359, 11	572	110	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0032940~secretion by cell	12	1.883830455	2.E-01	269589, 19894, 16367, 77579, 380714, 27	572	186	13588	2.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0046903~secretion	13	2.040816327	2.E-01	269589, 19894, 16952, 380714, 236643, 1	572	221	13588	1.E+00	1.E+00	8.E-01	1.E+02
SP_PIR_KEYWORDS	exocytosis	4	0.627943485	3.E-01	269589, 380714, 11891, 83671	629	50	17854	2.E+00	1.E+00	6.E-01	1.E+02

Annotation Cluster 18	Enrichment Score: 4.377361651627234											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0010033~response to organic substance	49	7.692307692	1.E-07	12475, 16803, 12912, 14645, 12010, 1590	572	505	13588	2.E+00	3.E-04	8.E-06	2.E-04
GOTERM_BP_FAT	GO:0009725~response to hormone stimulus	23	3.610675039	2.E-06	13685, 12842, 109900, 232087, 11651, 12	572	165	13588	3.E+00	4.E-03	9.E-05	3.E-03
GOTERM_BP_FAT	GO:0009719~response to endogenous stimulus	23	3.610675039	1.E-05	13685, 12842, 109900, 232087, 11651, 12	572	184	13588	3.E+00	3.E-02	5.E-04	2.E-02
GOTERM_BP_FAT	GO:0043434~response to peptide hormone stimulus	15	2.354788069	4.E-05	13685, 12842, 109900, 12043, 11651, 384	572	95	13588	4.E+00	1.E-01	2.E-03	7.E-02
GOTERM_BP_FAT	GO:0032869~cellular response to insulin stimulus	9	1.412872841	4.E-04	18709, 18708, 13685, 16367, 16334, 1042	572	43	13588	5.E+00	6.E-01	9.E-03	6.E-01
GOTERM_BP_FAT	GO:0032870~cellular response to hormone stimulus	10	1.569858713	6.E-04	18709, 18708, 13685, 16367, 16334, 1042	572	58	13588	4.E+00	8.E-01	1.E-02	1.E+00
GOTERM_BP_FAT	GO:0032868~response to insulin stimulus	10	1.569858713	7.E-04	18709, 18708, 56717, 13685, 16367, 1633	572	59	13588	4.E+00	9.E-01	2.E-02	1.E+00
GOTERM_BP_FAT	GO:0008286~insulin receptor signaling pathway	7	1.098901099	9.E-04	18709, 18708, 13685, 16367, 16334, 1165	572	28	13588	6.E+00	9.E-01	2.E-02	2.E+00

Annotation Cluster 19	Enrichment Score: 4.088381787868006											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0005819~spindle	18	2.825745683	2.E-07	26934, 20871, 18005, 17869, 20878, 1165	434	109	12504	5.E+00	7.E-05	3.E-05	3.E-04
GOTERM_CC_FAT	GO:0005856~cytoskeleton	70	10.98901099	2.E-06	22323, 94190, 54519, 54354, 16800, 7181	434	1122	12504	2.E+00	5.E-04	8.E-05	2.E-03
GOTERM_CC_FAT	GO:0043232~intracellular non-membrane-bounded organelle	94	14.7566719	3.E-04	22323, 22130, 218294, 94190, 54519, 168	434	1919	12504	1.E+00	1.E-01	6.E-03	5.E-01
GOTERM_CC_FAT	GO:0043228~non-membrane-bounded organelle	94	14.7566719	3.E-04	22323, 22130, 218294, 94190, 54519, 168	434	1919	12504	1.E+00	1.E-01	6.E-03	5.E-01
GOTERM_CC_FAT	GO:0015630~microtubule cytoskeleton	29	4.552590267	2.E-03	13430, 17869, 54354, 11651, 71819, 1680	434	450	12504	2.E+00	5.E-01	2.E-02	3.E+00
GOTERM_CC_FAT	GO:0044430~cytoskeletal part	42	6.593406593	4.E-03	13430, 11651, 54354, 17869, 71819, 1680	434	774	12504	2.E+00	8.E-01	4.E-02	6.E+00

Annotation Cluster 20	Enrichment Score: 4.045479760902571											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0002684~positive regulation of immune system process	26	4.081632653	2.E-06	14972, 15018, 22778, 16396, 16803, 1201	572	206	13588	3.E+00	5.E-03	1.E-04	3.E-03
UP_SEQ_FEATURE	domain:SH2 2	6	0.941915228	9.E-06	18709, 18708, 15170, 18803, 234779, 209	618	9	16021	2.E+01	1.E-02	8.E-04	2.E-02
UP_SEQ_FEATURE	domain:SH2 1	6	0.941915228	9.E-06	18709, 18708, 15170, 18803, 234779, 209	618	9	16021	2.E+01	1.E-02	8.E-04	2.E-02
GOTERM_BP_FAT	GO:0048584~positive regulation of response to stimulus	23	3.610675039	1.E-05	19370, 14972, 15170, 11657, 15018, 2700	572	186	13588	3.E+00	3.E-02	5.E-04	2.E-02
GOTERM_BP_FAT	GO:0050778~positive regulation of immune response	19	2.982731554	2.E-05	19370, 14972, 15170, 15018, 27007, 2189	572	136	13588	3.E+00	4.E-02	7.E-04	3.E-02
GOTERM_BP_FAT	GO:0002757~immune response-activating signal transduction	11	1.726844584	2.E-05	14127, 15170, 17874, 18803, 16818, 1617	572	48	13588	5.E+00	7.E-02	1.E-03	4.E-02
GOTERM_BP_FAT	GO:0002764~immune response-regulating signal transduction	11	1.726844584	5.E-05	14127, 15170, 17874, 18803, 16818, 1617	572	52	13588	5.E+00	1.E-01	2.E-03	9.E-02
GOTERM_BP_FAT	GO:0002253~activation of immune response	13	2.040816327	2.E-04	15170, 27007, 21898, 16818, 17874, 1880	572	86	13588	4.E+00	5.E-01	7.E-03	4.E-01
GOTERM_BP_FAT	GO:0002429~immune response-activating cell surface receptor sign	9	1.412872841	3.E-04	14127, 15170, 18803, 16818, 234779, 270	572	41	13588	5.E+00	5.E-01	7.E-03	5.E-01
GOTERM_BP_FAT	GO:0002768~immune response-regulating cell surface receptor sign	9	1.412872841	4.E-04	14127, 15170, 18803, 16818, 234779, 270	572	44	13588	5.E+00	7.E-01	1.E-02	8.E-01
GOTERM_BP_FAT	GO:0050851~antigen receptor-mediated signaling pathway	6	0.941915228	2.E-02	15170, 18803, 16818, 234779, 20963, 170	572	36	13588	4.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0050853~B cell receptor signaling pathway	4	0.627943485	2.E-02	15170, 16818, 20963, 17096	572	14	13588	7.E+00	1.E+00	2.E-01	3.E+01

Annotation Cluster 21	Enrichment Score: 3.7436816214089297											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0007169~transmembrane receptor protein tyrosine kinase signa	26	4.081632653	5.E-07	13649, 13685, 14178, 11651, 21844, 1870	572	192	13588	3.E+00	1.E-03	3.E-05	9.E-04
GOTERM_BP_FAT	GO:0007167~enzyme linked receptor protein signaling pathway	29	4.552590267	1.E-05	13649, 13685, 14178, 11651, 21844, 1870	572	273	13588	3.E+00	3.E-02	6.E-04	2.E-02
GOTERM_BP_FAT	GO:0007166~cell surface receptor linked signal transduction	65	10.20408163	1.E+00	12765, 22324, 14178, 18414, 21937, 1640	572	2495	13588	6.E-01	1.E+00	1.E+00	1.E+02

Annotation Cluster 22	Enrichment Score: 3.690568955581573											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0043603~cellular amide metabolic process	13	2.040816327	4.E-08	18416, 19895, 17970, 109900, 11847, 103	572	39	13588	8.E+00	1.E-04	3.E-06	7.E-05
GOTERM_BP_FAT	GO:0006739~NADP metabolic process	8	1.25588697	6.E-07	19895, 17970, 21991, 21351, 17969, 6617	572	14	13588	1.E+01	2.E-03	4.E-05	1.E-03
GOTERM_BP_FAT	GO:0009820~alkaloid metabolic process	8	1.25588697	4.E-05	19895, 17970, 21991, 21351, 17969, 6617	572	24	13588	8.E+00	1.E-01	2.E-03	7.E-02
GOTERM_BP_FAT	GO:0006769~nicotinamide metabolic process	8	1.25588697	4.E-05	19895, 17970, 21991, 21351, 17969, 6617	572	24	13588	8.E+00	1.E-01	2.E-03	7.E-02
GOTERM_BP_FAT	GO:0046496~nicotinamide nucleotide metabolic process	8	1.25588697	4.E-05	19895, 17970, 21991, 21351, 17969, 6617	572	24	13588	8.E+00	1.E-01	2.E-03	7.E-02
GOTERM_BP_FAT	GO:0019362~pyridine nucleotide metabolic process	8	1.25588697	1.E-04	19895, 17970, 21991, 21351, 17969, 6617	572	28	13588	7.E+00	3.E-01	4.E-03	2.E-01
GOTERM_BP_FAT	GO:0019748~secondary metabolic process	12	1.883830455	1.E-04	19895, 17970, 19378, 12043, 21991, 2135	572	69	13588	4.E+00	3.E-01	4.E-03	2.E-01
GOTERM_BP_FAT	GO:0006733~oxidoreduction coenzyme metabolic process	8	1.25588697	9.E-04	19895, 17970, 21991, 21351, 17969, 6617	572	38	13588	5.E+00	9.E-01	2.E-02	2.E+00



GOTERM_BP_FAT	GO:0006098~pentose-phosphate shunt	4	0.627943485	4.E-03	19895, 21991, 21351, 66171	572	8	13588	1.E+01	1.E+00	5.E-02	6.E+00
GOTERM_BP_FAT	GO:0006732~coenzyme metabolic process	14	2.197802198	7.E-03	17448, 19895, 17970, 14782, 103988, 661	572	143	13588	2.E+00	1.E+00	8.E-02	1.E+01
GOTERM_BP_FAT	GO:0051186~cofactor metabolic process	15	2.354788069	2.E-02	17448, 19895, 17970, 14782, 66171, 1039	572	182	13588	2.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0006767~water-soluble vitamin metabolic process	3	0.470957614	4.E-01	17970, 17969, 14381	572	34	13588	2.E+00	1.E+00	9.E-01	1.E+02
Annotation Cluster 23	Enrichment Score: 3.6642020291047275											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	myristylation	7	1.098901099		1.E-04 14191, 20779, 14678, 14302, 19059, 1436	629	23	17854	9.E+00	5.E-02	1.E-03	2.E-01
SP_PIR_KEYWORDS	myristate	14	2.197802198		1.E-04 11350, 14678, 70231, 21844, 20491, 2400	629	109	17854	4.E+00	5.E-02	1.E-03	2.E-01
UP_SEQ_FEATURE	lipid moiety-binding region:N-myristoyl glycine	13	2.040816327		8.E-04 14678, 70231, 21844, 20491, 24001, 1681	618	106	16021	3.E+00	7.E-01	4.E-02	1.E+00
Annotation Cluster 24	Enrichment Score: 3.5216759325523648											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	magnesium	31	4.866562009		1.E-04 228543, 80905, 18746, 19744, 232087, 54	629	403	17854	2.E+00	4.E-02	1.E-03	1.E-01
UP_SEQ_FEATURE	metal ion-binding site:Magnesium	14	2.197802198		2.E-04 18746, 80905, 19744, 232087, 13807, 721	618	103	16021	4.E+00	2.E-01	1.E-02	3.E-01
GOTERM_MF_FAT	GO:0000287~magnesium ion binding	31	4.866562009		2.E-03 228543, 80905, 18746, 19744, 232087, 54	550	409	13288	2.E+00	7.E-01	3.E-02	3.E+00
Annotation Cluster 25	Enrichment Score: 3.518367298549825											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_SEQ_FEATURE	domain:PH 1	11	1.726844584		3.E-07 14163, 18803, 26382, 30938, 19417, 2122	618	33	16021	9.E+00	4.E-04	4.E-05	5.E-04
UP_SEQ_FEATURE	domain:PH 2	10	1.569858713		2.E-06 14163, 26382, 30938, 19417, 212285, 218	618	32	16021	8.E+00	4.E-03	3.E-04	4.E-03
UP_SEQ_FEATURE	zinc finger region:FYVE-type	10	1.569858713		8.E-06 14163, 245049, 19894, 26382, 380714, 30	618	37	16021	7.E+00	1.E-02	7.E-04	1.E-02
PIR_SUPERFAMILY	PIRSF037335:FYVE, RhoGEF and PH domain containing protein(1-4)	4	0.627943485		5.E-04 14163, 26382, 30938, 224014	400	4	8136	2.E+01	2.E-01	5.E-02	6.E-01
INTERPRO	IPR017455:Zinc finger, FYVE-related	6	0.941915228		7.E-03 14163, 19894, 26382, 380714, 30938, 224	630	35	17763	5.E+00	1.E+00	2.E-01	1.E+01
INTERPRO	IPR000306:Zinc finger, FYVE-type	4	0.627943485		9.E-02 14163, 26382, 30938, 224014	630	30	17763	4.E+00	1.E+00	7.E-01	8.E+01
SMART	SM00064:FYVE	4	0.627943485		2.E-01 14163, 26382, 30938, 224014	418	30	9131	3.E+00	1.E+00	6.E-01	9.E+01
Annotation Cluster 26	Enrichment Score: 3.5109005632672137											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0001568~blood vessel development	27	4.238618524		1.E-05 12831, 11852, 11816, 238055, 11651, 204	572	244	13588	3.E+00	3.E-02	6.E-04	2.E-02
GOTERM_BP_FAT	GO:0001944~vasculature development	27	4.238618524		2.E-05 12831, 11852, 11816, 238055, 11651, 204	572	250	13588	3.E+00	5.E-02	8.E-04	3.E-02
GOTERM_BP_FAT	GO:0048514~blood vessel morphogenesis	20	3.139717425		7.E-04 19317, 14674, 11852, 11816, 238055, 204	572	198	13588	2.E+00	9.E-01	1.E-02	1.E+00
GOTERM_BP_FAT	GO:0001525~angiogenesis	11	1.726844584		5.E-02 18771, 14674, 14751, 11852, 26416, 2041	572	133	13588	2.E+00	1.E+00	4.E-01	6.E+01
Annotation Cluster 27	Enrichment Score: 3.427734592074189											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0010627~regulation of protein kinase cascade	22	3.453689168		2.E-06 15170, 21899, 21898, 12234, 224014, 151	572	155	13588	3.E+00	6.E-03	1.E-04	4.E-03
GOTERM_BP_FAT	GO:0043122~regulation of I-kappaB kinase/NF-kappaB cascade	9	1.412872841		2.E-04 16994, 17874, 21899, 21898, 56722, 1921	572	40	13588	5.E+00	5.E-01	6.E-03	4.E-01
GOTERM_BP_FAT	GO:0009967~positive regulation of signal transduction	18	2.825745683		9.E-04 21899, 21898, 56847, 15163, 11848, 1699	572	172	13588	2.E+00	9.E-01	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0010740~positive regulation of protein kinase cascade	12	1.883830455		1.E-03 16994, 17874, 21899, 21898, 18413, 5672	572	88	13588	3.E+00	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0043123~positive regulation of I-kappaB kinase/NF-kappaB cas	7	1.098901099		2.E-03 16994, 17874, 21899, 21898, 56722, 1921	572	33	13588	5.E+00	1.E+00	4.E-02	4.E+00
GOTERM_BP_FAT	GO:0010647~positive regulation of cell communication	18	2.825745683		3.E-03 21899, 21898, 56847, 15163, 11848, 1699	572	189	13588	2.E+00	1.E+00	4.E-02	5.E+00
Annotation Cluster 28	Enrichment Score: 3.3849026335560755											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0044042~glucan metabolic process	10	1.569858713		6.E-06 18682, 110095, 16195, 102093, 110094, 1	572	33	13588	7.E+00	2.E-02	3.E-04	1.E-02
GOTERM_BP_FAT	GO:0005977~glycogen metabolic process	10	1.569858713		6.E-06 18682, 110095, 16195, 102093, 110094, 1	572	33	13588	7.E+00	2.E-02	3.E-04	1.E-02
GOTERM_BP_FAT	GO:0006073~cellular glucan metabolic process	10	1.569858713		6.E-06 18682, 110095, 16195, 102093, 110094, 1	572	33	13588	7.E+00	2.E-02	3.E-04	1.E-02
GOTERM_BP_FAT	GO:0006112~energy reserve metabolic process	10	1.569858713		2.E-05 18682, 110095, 16195, 102093, 110094, 1	572	37	13588	6.E+00	5.E-02	7.E-04	3.E-02
GOTERM_BP_FAT	GO:0015980~energy derivation by oxidation of organic compound:	15	2.354788069		6.E-05 17448, 102093, 18534, 11651, 13382, 186	572	98	13588	4.E+00	1.E-01	2.E-03	1.E-01
GOTERM_BP_FAT	GO:0044264~cellular polysaccharide metabolic process	10	1.569858713		6.E-05 18682, 110095, 16195, 102093, 110094, 1	572	43	13588	6.E+00	2.E-01	2.E-03	1.E-01
SP_PIR_KEYWORDS	carbohydrate metabolism	11	1.726844584		2.E-04 18682, 110095, 16333, 16334, 102093, 11	629	73	17854	4.E+00	9.E-02	2.E-03	3.E-01
SP_PIR_KEYWORDS	glycogen metabolism	6	0.941915228		4.E-04 18682, 110095, 102093, 110094, 11651, 1	629	19	17854	9.E+00	2.E-01	3.E-03	6.E-01
GOTERM_BP_FAT	GO:0009250~glucan biosynthetic process	4	0.627943485		9.E-03 18682, 11651, 27357, 77559	572	11	13588	9.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0005978~glycogen biosynthetic process	4	0.627943485		9.E-03 18682, 11651, 27357, 77559	572	11	13588	9.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0005976~polysaccharide metabolic process	10	1.569858713		2.E-02 18682, 110095, 16195, 102093, 110094, 1	572	92	13588	3.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0033692~cellular polysaccharide biosynthetic process	4	0.627943485		5.E-02 18682, 11651, 27357, 77559	572	20	13588	5.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0000271~polysaccharide biosynthetic process	4	0.627943485		1.E-01 18682, 11651, 27357, 77559	572	30	13588	3.E+00	1.E+00	6.E-01	9.E+01
Annotation Cluster 29	Enrichment Score: 3.330953131519027											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0043009~chordate embryonic development	37	5.808477237		4.E-05 22323, 13649, 18107, 232906, 11651, 238	572	421	13588	2.E+00	1.E-01	2.E-03	7.E-02
GOTERM_BP_FAT	GO:0009792~embryonic development ending in birth or egg hatch	37	5.808477237		5.E-05 22323, 13649, 18107, 232906, 11651, 238	572	425	13588	2.E+00	1.E-01	2.E-03	9.E-02
GOTERM_BP_FAT	GO:0001701~in utero embryonic development	22	3.453689168		4.E-03 13649, 14674, 18107, 11651, 238055, 138	572	267	13588	2.E+00	1.E+00	6.E-02	8.E+00
GOTERM_BP_FAT	GO:0048598~embryonic morphogenesis	27	4.238618524		5.E-03 22323, 232906, 17869, 56847, 15402, 138	572	359	13588	2.E+00	1.E+00	6.E-02	9.E+00



Annotation Cluster 30		Enrichment Score: 3.2797507296130926											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_BP_FAT	GO:0043067~regulation of programmed cell death	45	7.064364207	5.E-05	22029, 672195, 11657, 66593, 11816, 149	572	572	560	13588	2.E+00	1.E-01	2.E-03	8.E-02
GOTERM_BP_FAT	GO:0010941~regulation of cell death	45	7.064364207	5.E-05	22029, 672195, 11657, 66593, 11816, 149	572	572	563	13588	2.E+00	1.E-01	2.E-03	1.E-01
GOTERM_BP_FAT	GO:0042981~regulation of apoptosis	44	6.907378336	7.E-05	22029, 672195, 11657, 66593, 11816, 149	572	572	553	13588	2.E+00	2.E-01	2.E-03	1.E-01
GOTERM_BP_FAT	GO:0043065~positive regulation of apoptosis	24	3.767660911	3.E-04	672195, 66593, 14939, 11816, 17869, 568	572	572	248	13588	2.E+00	6.E-01	9.E-03	6.E-01
GOTERM_BP_FAT	GO:0043068~positive regulation of programmed cell death	24	3.767660911	4.E-04	672195, 66593, 14939, 11816, 17869, 568	572	572	250	13588	2.E+00	6.E-01	9.E-03	6.E-01
GOTERM_BP_FAT	GO:0010942~positive regulation of cell death	24	3.767660911	4.E-04	672195, 66593, 14939, 11816, 17869, 568	572	572	252	13588	2.E+00	7.E-01	1.E-02	7.E-01
GOTERM_BP_FAT	GO:0043069~negative regulation of programmed cell death	23	3.610675039	6.E-04	11657, 13628, 11651, 17869, 12043, 1081	572	572	244	13588	2.E+00	8.E-01	1.E-02	1.E+00
GOTERM_BP_FAT	GO:0060548~negative regulation of cell death	23	3.610675039	7.E-04	11657, 13628, 11651, 17869, 12043, 1081	572	572	245	13588	2.E+00	8.E-01	1.E-02	1.E+00
GOTERM_BP_FAT	GO:0043281~regulation of caspase activity	9	1.412872841	1.E-03	16818, 672195, 12015, 66593, 12028, 120	572	572	50	13588	4.E+00	9.E-01	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0052548~regulation of endopeptidase activity	9	1.412872841	1.E-03	16818, 672195, 12015, 66593, 12028, 120	572	572	50	13588	4.E+00	9.E-01	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0043066~negative regulation of apoptosis	22	3.453689168	1.E-03	11657, 13628, 11651, 17869, 12043, 1081	572	572	239	13588	2.E+00	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0052547~regulation of peptidase activity	9	1.412872841	1.E-03	16818, 672195, 12015, 66593, 12028, 120	572	572	51	13588	4.E+00	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0006917~induction of apoptosis	16	2.51177394	5.E-03	382985, 15170, 66593, 11816, 14939, 178	572	572	167	13588	2.E+00	1.E+00	6.E-02	8.E+00
GOTERM_BP_FAT	GO:0012502~induction of programmed cell death	16	2.51177394	5.E-03	382985, 15170, 66593, 11816, 14939, 178	572	572	167	13588	2.E+00	1.E+00	6.E-02	8.E+00

Annotation Cluster 31	Enrichment Score: 3.266161858299822											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0042325--regulation of phosphorylation	35	5.494505495	6.E-08	13649, 20416, 15163, 18709, 56717, 1859	572	290	13588	3.E+00	2.E-04	5.E-06	1.E-04
GOTERM_BP_FAT	GO:0044093--positive regulation of molecular function	36	5.651491366	7.E-08	672195, 66593, 11856, 17869, 20416, 129	572	306	13588	3.E+00	2.E-04	6.E-06	1.E-04
GOTERM_BP_FAT	GO:0031399--regulation of protein modification process	25	3.924646782	1.E-07	13649, 67141, 15163, 18596, 56717, 1270	572	165	13588	4.E+00	3.E-04	8.E-06	2.E-04
GOTERM_BP_FAT	GO:0001932--regulation of protein amino acid phosphorylation	21	3.296703297	1.E-07	13649, 15170, 11806, 21899, 19088, 1204	572	121	13588	4.E+00	4.E-04	1.E-05	3.E-04
GOTERM_BP_FAT	GO:0019220--regulation of phosphate metabolic process	35	5.494505495	1.E-07	13649, 20416, 15163, 18709, 56717, 1859	572	301	13588	3.E+00	4.E-04	1.E-05	3.E-04
GOTERM_BP_FAT	GO:0051174--regulation of phosphorus metabolic process	35	5.494505495	1.E-07	13649, 20416, 15163, 18709, 56717, 1859	572	301	13588	3.E+00	4.E-04	1.E-05	3.E-04
GOTERM_BP_FAT	GO:0032268--regulation of cellular protein metabolic process	32	5.023547881	8.E-07	13684, 13649, 13685, 13665, 11651, 6714	572	280	13588	3.E+00	2.E-03	5.E-05	1.E-03
GOTERM_BP_FAT	GO:0043085--positive regulation of catalytic activity	30	4.709576138	2.E-06	672195, 66593, 11856, 17869, 20416, 168	572	261	13588	3.E+00	5.E-03	1.E-04	3.E-03
GOTERM_BP_FAT	GO:0051338--regulation of transferase activity	21	3.296703297	3.E-04	15170, 11806, 14678, 21899, 21898, 5725	572	199	13588	3.E+00	5.E-01	8.E-03	5.E-01
GOTERM_BP_FAT	GO:0043549--regulation of kinase activity	20	3.139717425	5.E-04	15170, 14678, 21899, 21898, 57257, 2041	572	192	13588	2.E+00	7.E-01	1.E-02	8.E-01
GOTERM_BP_FAT	GO:0051347--positive regulation of transferase activity	16	2.51177394	5.E-04	11806, 14678, 21899, 21898, 57257, 2041	572	135	13588	3.E+00	8.E-01	1.E-02	1.E+00
GOTERM_BP_FAT	GO:0033674--positive regulation of kinase activity	15	2.354788069	1.E-03	14678, 21899, 21898, 57257, 20416, 2240	572	130	13588	3.E+00	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0043408--regulation of MAPKKK cascade	12	1.883830455	2.E-03	15170, 17874, 16179, 24064, 16334, 1478	572	93	13588	3.E+00	1.E+00	3.E-02	3.E+00
GOTERM_BP_FAT	GO:0043507--positive regulation of JUN kinase activity	5	0.784929356	4.E-03	16179, 16334, 21899, 20963, 224014	572	16	13588	7.E+00	1.E+00	5.E-02	6.E+00
GOTERM_BP_FAT	GO:0042108--positive regulation of cytokine biosynthetic process	7	1.098901099	8.E-03	12051, 16994, 17874, 11807, 21899, 2189	572	42	13588	4.E+00	1.E+00	9.E-02	1.E+01
GOTERM_BP_FAT	GO:0043506--regulation of JUN kinase activity	5	0.784929356	1.E-02	16179, 16334, 21899, 20963, 224014	572	21	13588	6.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0046328--regulation of JNK cascade	7	1.098901099	1.E-02	17874, 16179, 16334, 21899, 21898, 2096	572	45	13588	4.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0045859--regulation of protein kinase activity	16	2.51177394	1.E-02	15170, 14678, 21899, 21898, 20416, 2240	572	186	13588	2.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0070302--regulation of stress-activated protein kinase signaling	7	1.098901099	1.E-02	17874, 16179, 16334, 21899, 21898, 2096	572	46	13588	4.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0042035--regulation of cytokine biosynthetic process	8	1.25588697	2.E-02	12051, 16994, 17874, 11807, 21899, 2189	572	64	13588	3.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0043405--regulation of MAP kinase activity	9	1.412872841	2.E-02	15170, 16179, 24064, 16334, 21899, 2639	572	84	13588	3.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0045860--positive regulation of protein kinase activity	11	1.726844584	4.E-02	16179, 16334, 21899, 14678, 26395, 2189	572	124	13588	2.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0043406--positive regulation of MAP kinase activity	7	1.098901099	4.E-02	16179, 16334, 21899, 26395, 20416, 2096	572	59	13588	3.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0080135--regulation of cellular response to stress	8	1.25588697	4.E-02	56717, 17874, 16179, 16334, 21899, 2189	572	75	13588	3.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0000165--MAPKKK cascade	10	1.569858713	5.E-02	17874, 19713, 16334, 14784, 14678, 2639	572	114	13588	2.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0031098--stress-activated protein kinase signaling pathway	5	0.784929356	6.E-02	17874, 16334, 74155, 20963, 224014	572	35	13588	3.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0007257--activation of JUN kinase activity	3	0.470957614	1.E-01	16334, 20963, 224014	572	13	13588	5.E+00	1.E+00	5.E-01	9.E+01
GOTERM_BP_FAT	GO:0007254--JNK cascade	4	0.627943485	1.E-01	17874, 16334, 20963, 224014	572	32	13588	3.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0000187--activation of MAPK activity	5	0.784929356	2.E-01	16334, 26395, 20416, 20963, 224014	572	50	13588	2.E+00	1.E+00	7.E-01	1.E+02

Annotation Cluster 32		Enrichment Score: 3.085657389219293										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	gluconeogenesis	9	1.412872841	4.E-08	100042746, 18534, 11676, 11674, 100041	629	17	17854	2.E+01	2.E-05	7.E-07	6.E-05
GOTERM_BP_FAT	GO:0034637~cellular carbohydrate biosynthetic process	11	1.726844584	1.E-04	18682, 14751, 234779, 18534, 11651, 219	572	56	13588	5.E+00	2.E-01	3.E-03	2.E-01
GOTERM_BP_FAT	GO:0016051~carbohydrate biosynthetic process	11	1.726844584	2.E-03	18682, 14751, 234779, 18534, 11651, 219	572	83	13588	3.E+00	1.E+00	4.E-02	4.E+00
GOTERM_BP_FAT	GO:0006090~pyruvate metabolic process	6	0.941915228	3.E-03	14751, 235339, 18534, 21991, 230163, 74	572	25	13588	6.E+00	1.E+00	5.E-02	6.E+00
GOTERM_BP_FAT	GO:0046165~alcohol biosynthetic process	7	1.098901099	4.E-03	14751, 234779, 18534, 21991, 230163, 14	572	37	13588	4.E+00	1.E+00	6.E-02	7.E+00
GOTERM_BP_FAT	GO:0006094~gluconeogenesis	5	0.784929356	9.E-03	14751, 18534, 21991, 230163, 74551	572	20	13588	6.E+00	1.E+00	1.E-01	1.E+01
GOTERM_BP_FAT	GO:0046364~monosaccharide biosynthetic process	6	0.941915228	9.E-03	14751, 18534, 21991, 230163, 14381, 745	572	31	13588	5.E+00	1.E+00	1.E-01	1.E+01
GOTERM_BP_FAT	GO:0019319~hexose biosynthetic process	5	0.784929356	2.E-02	14751, 18534, 21991, 230163, 74551	572	25	13588	5.E+00	1.E+00	2.E-01	3.E+01

Annotation Cluster 33		Enrichment Score: 2.998562611580506										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_SEQ_FEATURE	domain:SH3 1	8	1.25588697	2.E-04	22324, 17970, 14784, 57257, 12928, 1796	618	33	16021	6.E+00	3.E-01	1.E-02	4.E-01
UP_SEQ_FEATURE	domain:SH3 2	8	1.25588697	3.E-04	22324, 17970, 14784, 57257, 12928, 1796	618	34	16021	6.E+00	3.E-01	2.E-02	4.E-01



INTERPRO	IPR011511:Variant SH3	7	1.098901099	2.E-02	23880, 22324, 57257, 12928, 233071, 545	630	59	17763	3.E+00	1.E+00	3.E-01	2.E+01
Annotation Cluster 34	Enrichment Score: 2.98072198568244											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
KEGG_PATHWAY	mmu04150:mTOR signaling pathway	16	2.51177394	3.E-06	13684, 13685, 19744, 320207, 72508, 116	409	54	5738	4.E+00	5.E-04	2.E-05	4.E-03
BIOCARTA	m_igf1mtorpathway:Skeletal muscle hypertrophy is regulated via Akt	9	1.412872841	4.E-03	13684, 18708, 56717, 13685, 13665, 7250	167	20	1171	3.E+00	6.E-01	4.E-02	5.E+00
BIOCARTA	m_eif4PPathway:Regulation of eIF4e and p70 S6 Kinase	9	1.412872841	4.E-03	13684, 18708, 56717, 13685, 16367, 2641	167	20	1171	3.E+00	6.E-01	4.E-02	5.E+00
BIOCARTA	m_mTORPathway:mTOR Signaling Pathway	8	1.25588697	3.E-02	13684, 18708, 56717, 19744, 13685, 7250	167	22	1171	3.E+00	1.E+00	2.E-01	3.E+01
Annotation Cluster 35	Enrichment Score: 2.9597658527734043											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0048770~pigment granule	13	2.040816327	3.E-05	269589, 14674, 18453, 20525, 19384, 148	434	85	12504	4.E+00	1.E-02	1.E-03	5.E-02
GOTERM_CC_FAT	GO:0042470~melanosome	13	2.040816327	3.E-05	269589, 14674, 18453, 20525, 19384, 148	434	85	12504	4.E+00	1.E-02	1.E-03	5.E-02
GOTERM_CC_FAT	GO:0031988~membrane-bounded vesicle	29	4.552590267	7.E-04	13649, 215280, 269589, 19384, 171531, 1	434	420	12504	2.E+00	2.E-01	1.E-02	1.E+00
GOTERM_CC_FAT	GO:0031982~vesicle	33	5.180533752	1.E-03	215280, 13649, 269589, 19384, 16396, 11	434	519	12504	2.E+00	3.E-01	1.E-02	2.E+00
GOTERM_CC_FAT	GO:0016023~cytoplasmic membrane-bounded vesicle	29	3.924646782	1.E-02	13649, 215280, 269589, 19384, 171531, 1	434	414	12504	2.E+00	1.E+00	7.E-02	1.E+01
GOTERM_CC_FAT	GO:0031410~cytoplasmic vesicle	25	4.552590267	1.E-02	13649, 215280, 269589, 19384, 16396, 17	434	508	12504	2.E+00	1.E+00	7.E-02	1.E+01
GOTERM_CC_FAT	GO:0030141~secretory granule	10	1.569858713	2.E-02	26934, 19894, 16334, 17970, 380714, 273	434	117	12504	2.E+00	1.E+00	1.E-01	2.E+01
Annotation Cluster 36	Enrichment Score: 2.95152477192451											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0009617~response to bacterium	19	2.982731554	1.E-04	14972, 12475, 239081, 21898, 13035, 168	572	157	13588	3.E+00	3.E-01	3.E-03	2.E-01
GOTERM_BP_FAT	GO:0009611~response to wounding	30	4.709576138	3.E-04	12475, 11651, 16803, 21937, 18126, 1406	572	347	13588	2.E+00	6.E-01	9.E-03	6.E-01
GOTERM_BP_FAT	GO:0032680~regulation of tumor necrosis factor production	7	1.098901099	7.E-04	12051, 14127, 17874, 12475, 21898, 2408	572	27	13588	6.E+00	9.E-01	2.E-02	1.E+00
GOTERM_BP_FAT	GO:0006952~defense response	32	5.023547881	5.E-03	14972, 12475, 15018, 11651, 16803, 1201	572	448	13588	2.E+00	1.E+00	6.E-02	8.E+00
GOTERM_BP_FAT	GO:0006954~inflammatory response	18	2.825745683	1.E-02	12475, 239081, 21899, 21898, 11651, 164	572	225	13588	2.E+00	1.E+00	1.E-01	2.E+01
Annotation Cluster 37	Enrichment Score: 2.9267049202997004											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_SEQ_FEATURE	zinc finger region:Phorbol-ester/DAG-type	9	1.412872841	8.E-05	22324, 26934, 78816, 17925, 70719, 5435	618	38	16021	6.E+00	1.E-01	6.E-03	1.E-01
INTERPRO	IPR002219:Protein kinase C-like phorbol ester/diacylglycerol bindin	10	1.569858713	5.E-04	22324, 26934, 78816, 17925, 70719, 2701	630	66	17763	4.E+00	4.E-01	2.E-02	8.E-01
GOTERM_MF_FAT	GO:0019992~diacylglycerol binding	10	1.569858713	7.E-04	22324, 26934, 78816, 17925, 70719, 2701	550	59	13288	4.E+00	3.E-01	1.E-02	1.E+00
INTERPRO	IPR002219:Protein kinase C, phorbol ester/diacylglycerol binding	8	1.25588697	2.E-03	22324, 78816, 17925, 70719, 270163, 543	630	52	17763	4.E+00	9.E-01	7.E-02	4.E+00
SMART	SM00109:C1	10	1.569858713	3.E-03	22324, 26934, 78816, 17925, 70719, 2701	418	66	9131	3.E+00	4.E-01	5.E-02	4.E+00
GOTERM_MF_FAT	GO:0030676~Rac guanyl-nucleotide exchange factor activity	3	0.470957614	2.E-02	22324, 57257, 16800	550	5	13288	1.E+01	1.E+00	2.E-01	2.E+01
Annotation Cluster 38	Enrichment Score: 2.9046143190759404											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0048009~insulin-like growth factor receptor signaling pathway	5	0.784929356	3.E-04	18708, 16367, 11651, 16001, 16000	572	9	13588	1.E+01	6.E-01	9.E-03	6.E-01
BIOCARTA	m_igf1rPathway:Multiple antiapoptotic pathways from IGF-1R signa	10	1.569858713	5.E-04	18708, 12015, 16367, 14784, 20662, 2639	167	19	1171	4.E+00	1.E-01	2.E-02	6.E-01
BIOCARTA	m_longevityPathway:The IGF-1 Receptor and Longevity	6	0.941915228	1.E-02	18708, 15461, 11651, 16001, 20416, 1600	167	11	1171	4.E+00	9.E-01	8.E-02	1.E+01
Annotation Cluster 39	Enrichment Score: 2.87993968629212											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0001836~release of cytochrome c from mitochondria	7	1.098901099	3.E-05	12048, 12028, 12122, 12018, 12043, 1786	572	16	13588	1.E+01	8.E-02	1.E-03	5.E-02
GOTERM_BP_FAT	GO:0008637~apoptotic mitochondrial changes	8	1.25588697	6.E-05	12048, 12028, 12122, 12018, 11651, 1204	572	25	13588	8.E+00	1.E-01	2.E-03	1.E-01
GOTERM_BP_FAT	GO:0051345~positive regulation of hydrolase activity	13	2.040816327	1.E-04	672195, 66593, 17869, 11856, 16818, 717	572	81	13588	4.E+00	3.E-01	4.E-03	2.E-01
GOTERM_BP_FAT	GO:0006919~activation of caspase activity	8	1.25588697	4.E-04	16818, 672195, 66593, 12028, 12018, 178	572	33	13588	6.E+00	6.E-01	9.E-03	7.E-01
GOTERM_BP_FAT	GO:0043280~positive regulation of caspase activity	8	1.25588697	6.E-04	16818, 672195, 66593, 12028, 12018, 178	572	36	13588	5.E+00	8.E-01	1.E-02	1.E+00
GOTERM_BP_FAT	GO:0010952~positive regulation of peptidase activity	8	1.25588697	6.E-04	16818, 672195, 66593, 12028, 12018, 178	572	36	13588	5.E+00	8.E-01	1.E-02	1.E+00
GOTERM_BP_FAT	GO:0043281~regulation of caspase activity	9	1.412872841	1.E-03	16818, 672195, 12015, 66593, 12028, 120	572	50	13588	4.E+00	9.E-01	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0052548~regulation of endopeptidase activity	9	1.412872841	1.E-03	16818, 672195, 12015, 66593, 12028, 120	572	50	13588	4.E+00	9.E-01	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0052547~regulation of peptidase activity	9	1.412872841	1.E-03	16818, 672195, 12015, 66593, 12028, 120	572	51	13588	4.E+00	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0006917~induction of apoptosis	16	2.51177394	5.E-03	382985, 15170, 66593, 11816, 14939, 178	572	167	13588	2.E+00	1.E+00	6.E-02	8.E+00
GOTERM_BP_FAT	GO:0012502~induction of programmed cell death	16	2.51177394	5.E-03	382985, 15170, 66593, 11816, 14939, 178	572	167	13588	2.E+00	1.E+00	6.E-02	8.E+00
GOTERM_BP_FAT	GO:0070227~lymphocyte apoptosis	4	0.627943485	1.E-02	12028, 12018, 11651, 17869	572	12	13588	8.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0008629~induction of apoptosis by intracellular signals	6	0.941915228	1.E-02	12051, 66593, 11920, 12028, 17869, 1707	572	35	13588	4.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0008635~activation of caspase activity by cytochrome c	3	0.470957614	2.E-02	672195, 12028, 12018, 13063	572	5	13588	1.E+01	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0001783~B cell apoptosis	3	0.470957614	2.E-02	12028, 12018, 17869	572	6	13588	1.E+01	1.E+00	2.E-01	3.E+01
Annotation Cluster 40	Enrichment Score: 2.7818133937047387											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0005092~GDP-dissociation inhibitor activity	5	0.784929356	1.E-05	14570, 192662, 14567, 11857, 14569	550	5	13288	2.E+01	9.E-03	3.E-04	2.E-02
INTERPRO	IPR000406:RHO protein GDP dissociation inhibitor	3	0.470957614	4.E-03	14570, 192662, 11857	630	3	17763	3.E+01	1.E+00	1.E-01	6.E+00
GOTERM_MF_FAT	GO:0005094~Rho GDP-dissociation inhibitor activity	3	0.470957614	5.E-03	14570, 192662, 11857	550	3	13288	2.E+01	1.E+00	6.E-02	7.E+00



PIR_SUPERFAMILY	PIRSF015597:rho GDP dissociation inhibitor	3	0.470957614	7.E-03	14570, 192662, 11857	400	3	8136	2.E+01	9.E-01	3.E-01	9.E+00
PIR_SUPERFAMILY	PIRSF500829:animal rho GDP dissociation inhibitor	3	0.470957614	7.E-03	14570, 192662, 11857	400	3	8136	2.E+01	9.E-01	3.E-01	9.E+00
Annotation Cluster 41	Enrichment Score: 2.7666067017514533											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0008219~cell death	39	6.12244898	4.E-04	22029, 12765, 672195, 66593, 11852, 149	572	507	13588	2.E+00	7.E-01	1.E-02	7.E-01
GOTERM_BP_FAT	GO:0016265~death	39	6.12244898	6.E-04	22029, 12765, 672195, 66593, 11852, 149	572	519	13588	2.E+00	8.E-01	1.E-02	1.E+00
GOTERM_BP_FAT	GO:0006915~apoptosis	35	5.494505495	1.E-03	22029, 12765, 672195, 66593, 11852, 149	572	465	13588	2.E+00	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0012501~programmed cell death	35	5.494505495	2.E-03	22029, 12765, 672195, 66593, 11852, 149	572	473	13588	2.E+00	1.E+00	3.E-02	3.E+00
SP_PIR_KEYWORDS	Apoptosis	20	3.139717425	3.E-02	22029, 66593, 11852, 14939, 12122, 5435	629	337	17854	2.E+00	1.E+00	1.E-01	3.E+01
Annotation Cluster 42	Enrichment Score: 2.526449038868631											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	nucleotide binding	12	1.883830455	1.E-05	110957, 19354, 18669, 18671, 14674, 186	629	64	17854	5.E+00	5.E-03	2.E-04	2.E-02
SP_PIR_KEYWORDS	P-loop	12	1.883830455	1.E-05	110957, 19354, 18669, 18671, 14674, 186	629	65	17854	5.E+00	6.E-03	2.E-04	2.E-02
SP_PIR_KEYWORDS	GTP binding	8	1.25588697	2.E-04	19354, 14674, 14675, 14678, 11854, 1254	629	35	17854	6.E+00	7.E-02	2.E-03	3.E-01
GOTERM_CC_FAT	GO:0019897~extrinsic to plasma membrane	9	1.412872841	6.E-04	269589, 14674, 14675, 11816, 14673, 836	434	55	12504	5.E+00	2.E-01	8.E-03	8.E-01
INTERPRO	IPR001019:Guanine nucleotide binding protein (G-protein), alpha st	5	0.784929356	2.E-03	14674, 14675, 14678, 14673, 14682	630	16	17763	9.E+00	9.E-01	7.E-02	3.E+00
PIR_SUPERFAMILY	PIRSF002400:GTP-binding regulatory protein Gs alpha chain	5	0.784929356	4.E-03	14674, 14675, 14678, 14673, 14682	400	14	8136	7.E+00	8.E-01	2.E-01	5.E+00
GOTERM_CC_FAT	GO:0005834~heterotrimeric G-protein complex	4	0.627943485	1.E-01	14674, 14675, 14673, 14682	434	35	12504	3.E+00	1.E+00	4.E-01	8.E+01
SP_PIR_KEYWORDS	transducer	14	2.197802198	1.E+00	12765, 14674, 14675, 14678, 384783, 187	629	1467	17854	3.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0007186~G-protein coupled receptor protein signaling pathway	11	1.726844584	1.E+00	12765, 18126, 14674, 14675, 14678, 1406	572	1877	13588	1.E-01	1.E+00	1.E+00	1.E+02
Annotation Cluster 43	Enrichment Score: 2.4592446443336407											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0051674~localization of cell	24	3.767660911	2.E-03	117600, 13649, 100044475, 11806, 17973	572	284	13588	2.E+00	1.E+00	3.E-02	4.E+00
GOTERM_BP_FAT	GO:0048870~cell motility	24	3.767660911	2.E-03	117600, 13649, 100044475, 11806, 17973	572	284	13588	2.E+00	1.E+00	3.E-02	4.E+00
GOTERM_BP_FAT	GO:0016477~cell migration	21	3.296703297	3.E-03	117600, 13649, 100044475, 11806, 17973	572	240	13588	2.E+00	1.E+00	4.E-02	5.E+00
GOTERM_BP_FAT	GO:0006928~cell motion	26	4.081632653	1.E-02	117600, 22323, 13649, 238055, 16803, 20	572	367	13588	2.E+00	1.E+00	1.E-01	2.E+01
Annotation Cluster 44	Enrichment Score: 2.4419099768212233											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
BIOCARTA	m_il2rbPathway:IL-2 Receptor Beta Chain in T cell Activation	17	2.668759812	7.E-06	15170, 17869, 12043, 72508, 11651, 1428	167	36	1171	3.E+00	2.E-03	2.E-03	9.E-03
KEGG_PATHWAY	mmu05220:Chronic myeloid leukemia	18	2.825745683	2.E-05	11350, 320207, 17869, 11651, 12928, 204	409	76	5738	3.E+00	3.E-03	9.E-05	2.E-02
BIOCARTA	m_fcer1pPathway:Fc Epsilon Receptor I Signaling in Mast Cells	14	2.197802198	2.E-04	22324, 12229, 14281, 20416, 14127, 1870	167	32	1171	3.E+00	4.E-02	2.E-02	2.E-01
BIOCARTA	m_igf1Pathway:IGF-1 Signaling Pathway	11	1.726844584	2.E-04	18708, 218397, 16367, 14784, 20662, 263	167	21	1171	4.E+00	5.E-02	2.E-02	3.E-01
BIOCARTA	m_ghPathway:Growth Hormone Signaling Pathway	12	1.883830455	2.E-04	18708, 15170, 18803, 12703, 16367, 1633	167	25	1171	3.E+00	5.E-02	1.E-02	3.E-01
BIOCARTA	m_bcrPathway:BCR Signaling Pathway	13	2.040816327	3.E-04	22324, 12229, 14281, 20416, 18803, 1478	167	29	1171	3.E+00	6.E-02	1.E-02	3.E-01
BIOCARTA	m_igf1rPathway:Multiple antiapoptotic pathways from IGF-1R signa	10	1.569858713	5.E-04	18708, 12015, 16367, 14784, 20662, 2639	167	19	1171	4.E+00	1.E-01	2.E-02	6.E-01
BIOCARTA	m_tffPathway:Trefoil Factors Initiate Mucosal Healing	11	1.726844584	5.E-04	18708, 13649, 672195, 12015, 14784, 206	167	23	1171	3.E+00	1.E-01	2.E-02	7.E-01
BIOCARTA	m_il3Pathway:IL 3 signaling pathway	9	1.412872841	6.E-04	15170, 12983, 14784, 20662, 26395, 1546	167	16	1171	4.E+00	1.E-01	2.E-02	8.E-01
BIOCARTA	m_spryPathway:Sprouty regulation of tyrosine kinase signals	9	1.412872841	6.E-04	13649, 20779, 218397, 24064, 14784, 206	167	16	1171	4.E+00	1.E-01	2.E-02	8.E-01
BIOCARTA	m_trkaPathway:Trka Receptor Signaling Pathway	8	1.25588697	8.E-04	18048, 18708, 18803, 14784, 20662, 1546	167	13	1171	4.E+00	2.E-01	2.E-02	1.E+00
BIOCARTA	m_epoPathway:EPO Signaling Pathway	10	1.569858713	1.E-03	15170, 18803, 13857, 14784, 20662, 2639	167	21	1171	3.E+00	2.E-01	3.E-02	2.E+00
BIOCARTA	m_insulinPathway:Insulin Signaling Pathway	10	1.569858713	2.E-03	18708, 218397, 16367, 16334, 14784, 206	167	22	1171	3.E+00	3.E-01	3.E-02	2.E+00
BIOCARTA	m_gleevecPathway:Inhibition of Cellular Proliferation by Gleevec	10	1.569858713	2.E-03	18708, 12015, 14784, 20662, 26395, 1546	167	22	1171	3.E+00	3.E-01	3.E-02	2.E+00
BIOCARTA	m_pyk2Pathway:Links between Pyk2 and Map Kinases	11	1.726844584	2.E-03	18479, 20416, 18803, 20779, 14784, 1231	167	27	1171	3.E+00	4.E-01	4.E-02	3.E+00
BIOCARTA	m_tcrPathway:T Cell Receptor Signaling Pathway	13	2.040816327	3.E-03	22324, 14281, 20416, 16818, 18708, 1880	167	36	1171	3.E+00	4.E-01	4.E-02	3.E+00
BIOCARTA	m_TPOPathway:TPO Signaling Pathway	10	1.569858713	3.E-03	18708, 18803, 218397, 14784, 20662, 263	167	23	1171	3.E+00	4.E-01	3.E-02	3.E+00
BIOCARTA	m_ngfPathway:Nerve growth factor pathway (NGF)	9	1.412872841	3.E-03	18048, 18708, 18803, 14784, 20662, 2639	167	19	1171	3.E+00	4.E-01	3.E-02	3.E+00
BIOCARTA	m_metPathway:Signaling of Hepatocyte Growth Factor Receptor	12	1.883830455	3.E-03	18708, 20779, 218397, 14784, 20662, 263	167	32	1171	3.E+00	5.E-01	3.E-02	4.E+00
BIOCARTA	m_HbXPathway:Calcium Signaling by HBx of Hepatitis B virus	6	0.941915228	4.E-03	20779, 14784, 20662, 15461, 20416, 1291	167	9	1171	5.E+00	6.E-01	4.E-02	5.E+00
BIOCARTA	m_integrinPathway:Integrin Signaling Pathway	11	1.726844584	4.E-03	20779, 14784, 20662, 26395, 15461, 1436	167	29	1171	3.E+00	6.E-01	4.E-02	5.E+00
BIOCARTA	m_erkPathway:Erk1/Erk2 Mapk Signaling pathway	11	1.726844584	8.E-03	18048, 13649, 20779, 14784, 20662, 2639	167	31	1171	2.E+00	8.E-01	7.E-02	9.E+00
BIOCARTA	m_erk5Pathway:Role of Erk5 in Neuronal Survival	7	1.098901099	8.E-03	18708, 18803, 14784, 15461, 11651, 2041	167	14	1171	4.E+00	8.E-01	7.E-02	1.E+01
BIOCARTA	m_biopeptidesPathway:Bioactive Peptide Induced Signaling Pathwa	11	1.726844584	1.E-02	20416, 18803, 14784, 12315, 26416, 1231	167	32	1171	2.E+00	9.E-01	7.E-02	1.E+01
BIOCARTA	m_A1rPathway:Angiotensin II mediated activation of JNK Pathway	10	1.569858713	1.E-02	13649, 20779, 12315, 14784, 20662, 1231	167	28	1171	3.E+00	9.E-01	8.E-02	1.E+01
BIOCARTA	m_egfPathway:EGF Signaling Pathway	10	1.569858713	1.E-02	18708, 13649, 18803, 218397, 14784, 206	167	28	1171	3.E+00	9.E-01	8.E-02	1.E+01
BIOCARTA	m_her2Pathway:Role of ERBB2 in Signal Transduction and Oncolog	8	1.25588697	3.E-02	18708, 13649, 16195, 14784, 20662, 2639	167	22	1171	3.E+00	1.E+00	2.E-01	3.E+01
BIOCARTA	m_pdgfPathway:PDGF Signaling Pathway	9	1.412872841	3.E-02	18708, 18803, 218397, 14784, 20662, 263	167	28	1171	2.E+00	1.E+00	2.E-01	4.E+01
BIOCARTA	m_il2Pathway:IL 2 signaling pathway	8	1.25588697	4.E-02	16818, 14784, 20662, 26395, 15461, 1428	167	24	1171	2.E+00	1.E+00	2.E-01	4.E+01
BIOCARTA	m_ptenPathway:PTEN dependent cell cycle arrest and apoptosis	7	1.098901099	5.E-02	18708, 14784, 20662, 11651, 16412, 2041	167	20	1171	2.E+00	1.E+00	3.E-01	5.E+01
BIOCARTA	m_il6Pathway:IL 6 signaling pathway	7	1.098901099	6.E-02	16195, 14784, 20662, 26395, 15461, 1428	167	21	1171	2.E+00	1.E+00	3.E-01	6.E+01
BIOCARTA	m_crebPathway:Transcription factor CREB and its extracellular signa	7	1.098901099	6.E-02	18708, 14784, 20662, 26416, 15461, 1165	167	21	1171	2.E+00	1.E+00	3.E-01	6.E+01
KEGG_PATHWAY	mmu04320:Dorso-ventral axis formation	5	0.784929356	7.E-02	13649, 14784, 20662, 20663, 26395	409	22	5738	3.E+00	1.E+00	2.E-01	6.E+01



BIOCARTA	m_hcmvPathway:Human Cytomegalovirus and Map Kinase Pathway	5	0.784929356	1.E-01	18708, 26416, 26395, 11651, 12912	167	14	1171	3.E+00	1.E+00	4.E-01	8.E+01
BIOCARTA	m_p38mapkPathway:p38 MAPK Signaling Pathway	8	1.25588697	2.E-01	14784, 26416, 15461, 17869, 12540, 2041	167	32	1171	2.E+00	1.E+00	5.E-01	9.E+01
BIOCARTA	m_mapkPathway:MAPKinase Signaling Pathway	12	1.883830455	6.E-01	14784, 26416, 26395, 15461, 72508, 1786	167	80	1171	1.E+00	1.E+00	9.E-01	1.E+02
Annotation Cluster 45	Enrichment Score: 2.40926527086554											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	glycogen metabolism	6	0.941915228	4.E-04	18682, 110095, 102093, 110094, 11651, 1	629	19	17854	9.E+00	2.E-01	3.E-03	6.E-01
INTERPRO	IPR008734:Phosphorylase kinase alpha	3	0.470957614	4.E-03	102093, 110094, 18679	630	3	17763	3.E+01	1.E+00	1.E-01	6.E+00
UP_SEQ_FEATURE	region of interest:Calmodulin-binding	6	0.941915228	4.E-02	18126, 102093, 110094, 18679, 19056, 18	618	49	16021	3.E+00	1.E+00	7.E-01	5.E+01
Annotation Cluster 46	Enrichment Score: 2.3880221958388224											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0030334~regulation of cell migration	13	2.040816327	5.E-04	21687, 14674, 73167, 12043, 11855, 3847	572	92	13588	3.E+00	7.E-01	1.E-02	8.E-01
GOTERM_BP_FAT	GO:0051270~regulation of cell motion	14	2.197802198	5.E-04	21687, 14674, 73167, 12043, 11855, 3847	572	107	13588	3.E+00	8.E-01	1.E-02	1.E+00
GOTERM_BP_FAT	GO:0030335~positive regulation of cell migration	8	1.25588697	8.E-04	18708, 16367, 73167, 12043, 11855, 2033	572	37	13588	5.E+00	9.E-01	2.E-02	1.E+00
GOTERM_BP_FAT	GO:0051272~positive regulation of cell motion	8	1.25588697	1.E-03	18708, 16367, 73167, 12043, 11855, 2033	572	41	13588	5.E+00	1.E+00	3.E-02	3.E+00
GOTERM_BP_FAT	GO:0040017~positive regulation of locomotion	8	1.25588697	2.E-03	18708, 16367, 73167, 12043, 11855, 2033	572	44	13588	4.E+00	1.E+00	4.E-02	4.E+00
GOTERM_BP_FAT	GO:0040012~regulation of locomotion	13	2.040816327	2.E-03	21687, 14674, 73167, 12043, 11855, 3847	572	110	13588	3.E+00	1.E+00	4.E-02	4.E+00
GOTERM_BP_FAT	GO:002053~positive regulation of mesenchymal cell proliferation	3	0.470957614	2.E-01	16367, 11855, 384783	572	22	13588	3.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0010464~regulation of mesenchymal cell proliferation	3	0.470957614	3.E-01	16367, 11855, 384783	572	23	13588	3.E+00	1.E+00	8.E-01	1.E+02
Annotation Cluster 47	Enrichment Score: 2.365110771493373											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_SEQ_FEATURE	short sequence motif:Box 1 motif	8	1.25588697	3.E-05	16195, 12983, 16197, 13857, 18414, 1616	618	25	16021	8.E+00	5.E-02	2.E-03	5.E-02
GOTERM_MF_FAT	GO:0019955~cytokine binding	14	2.197802198	6.E-05	12765, 18414, 21937, 16195, 18824, 1298	550	88	13288	4.E+00	4.E-02	1.E-03	9.E-02
GOTERM_MF_FAT	GO:0004896~cytokine receptor activity	11	1.726844584	7.E-05	12765, 16195, 12983, 16197, 50498, 1385	550	55	13288	5.E+00	5.E-02	1.E-03	1.E-01
UP_SEQ_FEATURE	short sequence motif:WSXWS motif	8	1.25588697	1.E-04	16195, 12983, 16197, 13857, 18414, 1616	618	31	16021	7.E+00	2.E-01	1.E-02	2.E-01
INTERPRO	IPR003531:Short hematopoietin receptor, family 1, conserved site	4	0.627943485	4.E-03	12983, 16197, 16190, 16847	630	10	17763	1.E+01	1.E+00	1.E-01	7.E+00
INTERPRO	IPR008957:Fibronectin, type III-like fold	15	2.354788069	7.E-03	21687, 18414, 545156, 23920, 16195, 138	630	187	17763	2.E+00	1.E+00	1.E-01	1.E+01
INTERPRO	IPR003961:Fibronectin, type III	14	2.197802198	2.E-02	21687, 18414, 545156, 23920, 16195, 138	630	191	17763	2.E+00	1.E+00	3.E-01	3.E+01
SP_PIR_KEYWORDS	cytokine receptor	4	0.627943485	4.E-02	12983, 16197, 16190, 21937	629	21	17854	5.E+00	1.E+00	2.E-01	4.E+01
SMART	SM00060:FN3	14	2.197802198	1.E-01	21687, 18414, 545156, 23920, 16195, 138	418	191	9131	2.E+00	1.E+00	5.E-01	7.E+01
UP_SEQ_FEATURE	domain:Fibronectin type-III	4	0.627943485	3.E-01	16197, 13857, 16190, 545156	618	51	16021	2.E+00	1.E+00	1.E+00	1.E+02
KEGG_PATHWAY	mmu04060:Cytokine-cytokine receptor interaction	16	2.51177394	8.E-01	13649, 12765, 18414, 21937, 16994, 2031	409	244	5738	9.E-01	1.E+00	9.E-01	1.E+02
Annotation Cluster 48	Enrichment Score: 2.3586196047224255											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
COG_ONTOLOGY	Nucleotide transport and metabolism	5	0.784929356	9.E-05	80914, 68556, 22245, 56749, 99586	50	11	2040	2.E+01	2.E-03	2.E-03	6.E-02
GOTERM_MF_FAT	GO:0019205~nucleobase, nucleoside, nucleotide kinase activity	7	1.098901099	3.E-03	80914, 68556, 22245, 14923, 11636, 6658	550	36	13288	5.E+00	9.E-01	5.E-02	5.E+00
INTERPRO	IPR000764:Uridine kinase	3	0.470957614	7.E-03	80914, 68556, 22245	630	4	17763	2.E+01	1.E+00	2.E-01	1.E+01
INTERPRO	IPR006083:Phosphoribulokinase/uridine kinase	3	0.470957614	7.E-03	80914, 68556, 22245	630	4	17763	2.E+01	1.E+00	2.E-01	1.E+01
GOTERM_MF_FAT	GO:0004849~uridine kinase activity	3	0.470957614	1.E-02	80914, 68556, 22245	550	4	13288	2.E+01	1.E+00	1.E-01	1.E+01
GOTERM_MF_FAT	GO:0019206~nucleoside kinase activity	3	0.470957614	5.E-02	80914, 68556, 22245	550	9	13288	8.E+00	1.E+00	4.E-01	5.E+01
Annotation Cluster 49	Enrichment Score: 2.3335556260154755											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0007623~circadian rhythm	9	1.412872841	1.E-04	11865, 12753, 11657, 232087, 12952, 186	572	37	13588	6.E+00	3.E-01	4.E-03	2.E-01
KEGG_PATHWAY	mmu04710:Circadian rhythm	7	1.098901099	1.E-04	11865, 12753, 12952, 18626, 12953, 1862	409	13	5738	8.E+00	2.E-02	6.E-04	2.E-01
SP_PIR_KEYWORDS	biological rhythms	6	0.941915228	7.E-04	12753, 12952, 18626, 12953, 18627, 1862	629	21	17854	8.E+00	2.E-01	5.E-03	9.E-01
INTERPRO	IPR000014:PAS	7	1.098901099	8.E-04	11865, 12753, 18626, 17978, 17979, 1862	630	32	17763	6.E+00	5.E-01	3.E-02	1.E+00
GOTERM_BP_FAT	GO:0048511~rhythmic process	13	2.040816327	8.E-04	11865, 12753, 11657, 232087, 12043, 129	572	98	13588	3.E+00	9.E-01	2.E-02	1.E+00
INTERPRO	IPR001610:PAC motif	6	0.941915228	2.E-03	11865, 12753, 18626, 17978, 18627, 1862	630	26	17763	7.E+00	9.E-01	7.E-02	3.E+00
SMART	SM00091:PAS	7	1.098901099	3.E-03	11865, 12753, 18626, 17978, 17979, 1862	418	32	9131	5.E+00	4.E-01	5.E-02	4.E+00
INTERPRO	IPR013655:PAS fold-3	5	0.784929356	3.E-03	11865, 12753, 18626, 18627, 18628	630	18	17763	8.E+00	1.E+00	9.E-02	5.E+00
UP_SEQ_FEATURE	region of interest:CRY binding domain	3	0.470957614	4.E-03	18626, 18627, 18628	618	3	16021	3.E+01	1.E+00	2.E-01	7.E+00
UP_SEQ_FEATURE	region of interest:CSNK1E binding domain	3	0.470957614	4.E-03	18626, 18627, 18628	618	3	16021	3.E+01	1.E+00	2.E-01	7.E+00
GOTERM_BP_FAT	GO:0010551~regulation of specific transcription from RNA polymer	8	1.25588697	5.E-03	18711, 21349, 17869, 22778, 18626, 2087	572	51	13588	4.E+00	1.E+00	7.E-02	9.E+00
UP_SEQ_FEATURE	domain:PAS 1	5	0.784929356	5.E-03	11865, 12753, 18626, 18627, 18628	618	19	16021	7.E+00	1.E+00	2.E-01	9.E+00
UP_SEQ_FEATURE	domain:PAS 2	5	0.784929356	5.E-03	11865, 12753, 18626, 18627, 18628	618	19	16021	7.E+00	1.E+00	2.E-01	9.E+00
SMART	SM00086:PAC	6	0.941915228	6.E-03	11865, 12753, 18626, 17978, 18627, 1862	418	26	9131	5.E+00	7.E-01	8.E-02	7.E+00
GOTERM_BP_FAT	GO:0010553~negative regulation of specific transcription from RNA	5	0.784929356	1.E-02	17869, 22778, 18626, 18627, 18628	572	21	13588	6.E+00	1.E+00	1.E-01	2.E+01
UP_SEQ_FEATURE	domain:PAC	5	0.784929356	1.E-02	11865, 12753, 18626, 18627, 18628	618	24	16021	5.E+00	1.E+00	3.E-01	2.E+01
GOTERM_BP_FAT	GO:0032582~negative regulation of gene-specific transcription	5	0.784929356	1.E-02	17869, 22778, 18626, 18627, 18628	572	23	13588	5.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0032583~regulation of gene-specific transcription	8	1.25588697	2.E-02	18711, 21349, 17869, 22778, 18626, 2087	572	67	13588	3.E+00	1.E+00	2.E-01	3.E+01
BIOCARTA	m_circadianPathway:Circadian Rhythms	4	0.627943485	4.E-02	11865, 12753, 12952, 18626	167	6	1171	5.E+00	1.E+00	2.E-01	4.E+01



UP_SEQ_FEATURE	short sequence motif:Nuclear export signal	4	0.627943485	2.E-01 18626, 208727, 18627, 18628	618	36	16021	3.E+00	1.E+00	1.E+00	9.E+01	
GOTERM_BP_FAT	GO:0000122~negative regulation of transcription from RNA polyme	14	2.197802198	2.E-01 19720, 17869, 22778, 20481, 20466, 2406	572	231	13588	1.E+00	1.E+00	7.E-01	1.E+02	
Annotation Cluster 50	Enrichment Score: 2.3326606173907405											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR018029:C2 membrane targeting protein	14	2.197802198		9.E-05 269589, 19894, 17999, 16396, 18797, 109	630	106	17763	4.E+00	9.E-02	5.E-03	1.E-01
INTERPRO	IPR000008:C2 calcium-dependent membrane targeting	15	2.354788069		2.E-04 269589, 19894, 17999, 16396, 18797, 109	630	130	17763	3.E+00	2.E-01	1.E-02	3.E-01
SMART	SM00239:C2	15	2.354788069		2.E-03 269589, 19894, 17999, 16396, 18797, 109	418	130	9131	3.E+00	4.E-01	5.E-02	3.E+00
UP_SEQ_FEATURE	domain:C2	7	1.098901099		5.E-02 18803, 17999, 234779, 16396, 18797, 109	618	68	16021	3.E+00	1.E+00	7.E-01	6.E+01
UP_SEQ_FEATURE	domain:C2 1	6	0.941915228		7.E-02 269589, 19894, 27359, 83671, 236643, 83	618	57	16021	3.E+00	1.E+00	8.E-01	7.E+01
UP_SEQ_FEATURE	domain:C2 2	6	0.941915228		7.E-02 269589, 19894, 27359, 83671, 236643, 83	618	57	16021	3.E+00	1.E+00	8.E-01	7.E+01
Annotation Cluster 51	Enrichment Score: 2.3269410419094343											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_SEQ_FEATURE	domain:Ras-associating	7	1.098901099		2.E-03 17925, 270163, 54519, 54354, 212285, 24	618	34	16021	5.E+00	9.E-01	8.E-02	3.E+00
INTERPRO	IPR000159:Ras-association	7	1.098901099		4.E-03 17925, 270163, 54519, 54354, 212285, 24	630	44	17763	4.E+00	1.E+00	1.E-01	7.E+00
SMART	SM00314:RA	7	1.098901099		1.E-02 17925, 270163, 54519, 54354, 212285, 24	418	44	9131	3.E+00	9.E-01	2.E-01	2.E+01
Annotation Cluster 52	Enrichment Score: 2.2644132866238293											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	pentose phosphate pathway	4	0.627943485		2.E-04 21991, 11676, 11674, 14381	629	4	17854	3.E+01	7.E-02	2.E-03	2.E-01
INTERPRO	IPR013785:Aldolase-type TIM barrel	7	1.098901099		4.E-03 21991, 21351, 56749, 230163, 11676, 116	630	43	17763	5.E+00	1.E+00	1.E-01	6.E+00
SP_PIR_KEYWORDS	Schiff base	4	0.627943485		4.E-03 80905, 230163, 11676, 11674	629	10	17854	1.E+01	8.E-01	3.E-02	6.E+00
UP_SEQ_FEATURE	active site:Schiff-base intermediate with dihydroxyacetone-P	3	0.470957614		4.E-03 230163, 11676, 11674	618	3	16021	3.E+01	1.E+00	2.E-01	7.E+00
UP_SEQ_FEATURE	site:Necessary for preference for fructose 1,6-bisphosphate over fr	3	0.470957614		4.E-03 230163, 11676, 11674	618	3	16021	3.E+01	1.E+00	2.E-01	7.E+00
INTERPRO	IPR000741:Fructose-bisphosphate aldolase, class-I	3	0.470957614		1.E-02 230163, 11676, 11674	630	5	17763	2.E+01	1.E+00	2.E-01	2.E+01
KEGG_PATHWAY	mmu00051:Fructose and mannose metabolism	8	1.25588697		1.E-02 56421, 15275, 21991, 230163, 15277, 116	409	37	5738	3.E+00	9.E-01	4.E-02	2.E+01
GOTERM_MF_FAT	GO:0004332~fructose-bisphosphate aldolase activity	3	0.470957614		2.E-02 230163, 11676, 11674	550	5	13288	1.E+01	1.E+00	2.E-01	2.E+01
GOTERM_MF_FAT	GO:0016832~aldehyde-lyase activity	3	0.470957614		3.E-02 230163, 11676, 11674	550	7	13288	1.E+01	1.E+00	3.E-01	4.E+01
Annotation Cluster 53	Enrichment Score: 2.251143882800853											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0051726~regulation of cell cycle	26	4.081632653		4.E-06 11852, 17869, 56150, 67141, 12234, 1699	572	214	13588	3.E+00	1.E-02	2.E-04	7.E-03
GOTERM_BP_FAT	GO:0010564~regulation of cell cycle process	9	1.412872841		1.E-02 16994, 11920, 52563, 18413, 56371, 1254	572	73	13588	3.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0007088~regulation of mitosis	6	0.941915228		2.E-02 16994, 11920, 52563, 12540, 56150, 6899	572	36	13588	4.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0051783~regulation of nuclear division	6	0.941915228		2.E-02 16994, 11920, 52563, 12540, 56150, 6899	572	36	13588	4.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0007346~regulation of mitotic cell cycle	10	1.569858713		2.E-02 16994, 11920, 52563, 12043, 17869, 1254	572	96	13588	2.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0030071~regulation of mitotic metaphase/anaphase transition	4	0.627943485		3.E-02 11920, 52563, 56150, 68999	572	16	13588	6.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0033043~regulation of organelle organization	13	2.040816327		3.E-02 227753, 16800, 56150, 11848, 16994, 567	572	154	13588	2.E+00	1.E+00	2.E-01	4.E+01
Annotation Cluster 54	Enrichment Score: 2.240748793044755											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0017124~SH3 domain binding	12	1.883830455		4.E-04 22323, 12549, 15170, 20401, 19317, 8098	550	79	13288	4.E+00	2.E-01	7.E-03	6.E-01
SP_PIR_KEYWORDS	sh3-binding	7	1.098901099		1.E-02 22323, 20401, 19317, 80987, 30939, 2283	629	57	17854	3.E+00	1.E+00	7.E-02	2.E+01
UP_SEQ_FEATURE	short sequence motif:SH3-binding	6	0.941915228		3.E-02 14163, 20401, 19317, 30939, 228359, 118	618	47	16021	3.E+00	1.E+00	6.E-01	4.E+01
Annotation Cluster 55	Enrichment Score: 2.2138934099517837											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	calmodulin-binding	13	2.040816327		3.E-04 102093, 18679, 18682, 18126, 14432, 775	629	103	17854	4.E+00	1.E-01	2.E-03	4.E-01
GOTERM_MF_FAT	GO:0005516~calmodulin binding	13	2.040816327		3.E-03 102093, 18679, 18682, 18126, 14432, 775	550	114	13288	3.E+00	8.E-01	4.E-02	4.E+00
UP_SEQ_FEATURE	region of interest:Calmodulin-binding	6	0.941915228		4.E-02 18126, 102093, 110094, 18679, 19056, 18	618	49	16021	3.E+00	1.E+00	7.E-01	5.E+01
KEGG_PATHWAY	mmu04020:Calcium signaling pathway	21	3.296703297		5.E-02 13649, 14675, 102093, 18679, 11740, 187	409	191	5738	2.E+00	1.E+00	1.E-01	5.E+01
Annotation Cluster 56	Enrichment Score: 2.198048850665754											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0043551~regulation of phosphoinositide 3-kinase activity	4	0.627943485		1.E-03 18048, 16367, 57257, 12540	572	6	13588	2.E+01	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0043552~positive regulation of phosphoinositide 3-kinase activ	4	0.627943485		1.E-03 18048, 16367, 57257, 12540	572	6	13588	2.E+01	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0043550~regulation of lipid kinase activity	4	0.627943485		4.E-03 18048, 16367, 57257, 12540	572	8	13588	1.E+01	1.E+00	5.E-02	6.E+00
GOTERM_BP_FAT	GO:0045834~positive regulation of lipid metabolic process	5	0.784929356		2.E-02 18048, 16367, 11816, 57257, 12540	572	24	13588	5.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0019216~regulation of lipid metabolic process	6	0.941915228		1.E-01 18048, 16367, 11816, 57257, 238055, 125	572	58	13588	2.E+00	1.E+00	5.E-01	8.E+01
Annotation Cluster 57	Enrichment Score: 2.1858878615659454											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR019807:Hexokinase, conserved site	4	0.627943485		4.E-04 15275, 15277, 103988, 212032	630	5	17763	2.E+01	3.E-01	2.E-02	7.E-01
INTERPRO	IPR001312:Hexokinase	4	0.627943485		8.E-04 15275, 15277, 103988, 212032	630	6	17763	2.E+01	6.E-01	3.E-02	1.E+00



GOTERM_MF_FAT	GO:0004396~hexokinase activity	4	0.627943485	1.E-03	15275, 15277, 103988, 212032	550	6	13288	2.E+01	6.E-01	2.E-02	2.E+00
KEGG_PATHWAY	mmu00500:Starch and sucrose metabolism	9	1.412872841	3.E-03	110095, 14751, 15275, 72157, 15277, 103	409	36	5738	4.E+00	4.E-01	1.E-02	4.E+00
COG_ONTOLOGY	Carbohydrate transport and metabolism	5	0.784929356	6.E-03	15275, 15277, 103988, 23971, 212032	50	32	2040	6.E+00	1.E-01	6.E-02	5.E+00
GOTERM_MF_FAT	GO:0019200~carbohydrate kinase activity	5	0.784929356	8.E-03	56421, 15275, 15277, 103988, 212032	550	20	13288	6.E+00	1.E+00	1.E-01	1.E+01
UP_SEQ_FEATURE	region of interest:Regulatory	3	0.470957614	8.E-03	15275, 15277, 212032	618	4	16021	2.E+01	1.E+00	3.E-01	1.E+01
PIR_SUPERFAMILY	PIRSF000527:hexokinase I	3	0.470957614	1.E-02	15275, 15277, 212032	400	4	8136	2.E+01	1.E+00	5.E-01	2.E+01
KEGG_PATHWAY	mmu00051:Fructose and mannose metabolism	8	1.25588697	1.E-02	56421, 15275, 21991, 230163, 15277, 116	409	37	5738	3.E+00	9.E-01	4.E-02	2.E+01
KEGG_PATHWAY	mmu00052:Galactose metabolism	6	0.941915228	4.E-02	56421, 15275, 72157, 15277, 103988, 212	409	27	5738	3.E+00	1.E+00	1.E-01	4.E+01
KEGG_PATHWAY	mmu00520:Amino sugar and nucleotide sugar metabolism	6	0.941915228	2.E-01	14751, 15275, 72157, 15277, 103988, 212	409	44	5738	2.E+00	1.E+00	4.E-01	9.E+01
Annotation Cluster 58	Enrichment Score: 2.1510411068165265											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_SEQ_FEATURE	binding site:NAD	9	1.412872841	3.E-04	15107, 100042746, 17448, 13382, 100041	618	46	16021	5.E+00	4.E-01	2.E-02	6.E-01
UP_SEQ_FEATURE	nucleotide phosphate-binding region:NAD	11	1.726844584	5.E-04	15107, 100042746, 17448, 19378, 56847,	618	73	16021	4.E+00	5.E-01	2.E-02	8.E-01
INTERPRO	IPR001557:L-lactate/malate dehydrogenase	4	0.627943485	1.E-03	16828, 17448, 16833, 16832	630	7	17763	2.E+01	7.E-01	5.E-02	2.E+00
INTERPRO	IPR015955:Lactate dehydrogenase/glycoside hydrolase, family 4, C-	4	0.627943485	2.E-03	16828, 17448, 16833, 16832	630	8	17763	1.E+01	9.E-01	7.E-02	3.E+00
INTERPRO	IPR001236:Lactate/malate dehydrogenase	4	0.627943485	2.E-03	16828, 17448, 16833, 16832	630	8	17763	1.E+01	9.E-01	7.E-02	3.E+00
PIR_SUPERFAMILY	PIRSF000102:Lac_mal_DH	4	0.627943485	4.E-03	16828, 17448, 16833, 16832	400	7	8136	1.E+01	7.E-01	2.E-01	5.E+00
UP_SEQ_FEATURE	binding site:NAD or substrate	3	0.470957614	4.E-03	16828, 16833, 16832	618	3	16021	3.E+01	1.E+00	2.E-01	7.E+00
INTERPRO	IPR011304:L-lactate dehydrogenase	3	0.470957614	7.E-03	16828, 16833, 16832	630	4	17763	2.E+01	1.E+00	2.E-01	1.E+01
INTERPRO	IPR018177:L-lactate dehydrogenase active site	3	0.470957614	7.E-03	16828, 16833, 16832	630	4	17763	2.E+01	1.E+00	2.E-01	1.E+01
GOTERM_MF_FAT	GO:0004459~L-lactate dehydrogenase activity	3	0.470957614	1.E-02	16828, 16833, 16832	550	4	13288	2.E+01	1.E+00	1.E-01	1.E+01
GOTERM_MF_FAT	GO:0004457~lactate dehydrogenase activity	3	0.470957614	2.E-02	16828, 16833, 16832	550	5	13288	1.E+01	1.E+00	2.E-01	2.E+01
KEGG_PATHWAY	mmu00270:Cysteine and methionine metabolism	7	1.098901099	3.E-02	16828, 232087, 13436, 16833, 16832, 229	409	33	5738	3.E+00	1.E+00	7.E-02	3.E+01
SP_PIR_KEYWORDS	1.883830455	12	1.883830455	4.E-02	15107, 100042746, 17448, 19378, 56847,	629	169	17854	2.E+00	1.E+00	2.E-01	4.E+01
KEGG_PATHWAY	mmu00640:Propanoate metabolism	5	0.784929356	2.E-01	16828, 68738, 16833, 16832, 20916	409	30	5738	2.E+00	1.E+00	3.E-01	9.E+01
INTERPRO	IPR016040:NA(DP)-binding domain	8	1.25588697	3.E-01	15107, 100042746, 100041325, 99586, 10	630	151	17763	1.E+00	1.E+00	1.E+00	1.E+02
Annotation Cluster 59	Enrichment Score: 2.134751282425181											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0030427~site of polarized growth	9	1.412872841	3.E-04	73750, 77579, 18479, 12568, 170758, 539	434	51	12504	5.E+00	1.E-01	6.E-03	5.E-01
GOTERM_CC_FAT	GO:0030426~growth cone	9	1.412872841	3.E-04	73750, 77579, 18479, 12568, 170758, 539	434	51	12504	5.E+00	1.E-01	6.E-03	5.E-01
GOTERM_CC_FAT	GO:0043005~neuron projection	15	2.354788069	5.E-02	73750, 94190, 17869, 16800, 18479, 1707	434	245	12504	2.E+00	1.E+00	2.E-01	5.E+01
GOTERM_BP_FAT	GO:0031175~neuron projection development	10	1.569858713	6.E-01	22323, 14432, 77579, 12043, 18479, 1256	572	218	13588	1.E+00	1.E+00	1.E+00	1.E+02
Annotation Cluster 60	Enrichment Score: 2.1073428371613243											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0031960~response to corticosteroid stimulus	8	1.25588697	3.E-05	20779, 12842, 18670, 109900, 26395, 120	572	23	13588	8.E+00	8.E-02	1.E-03	5.E-02
GOTERM_BP_FAT	GO:0051384~response to glucocorticoid stimulus	6	0.941915228	9.E-04	18670, 109900, 26395, 12043, 230163, 94	572	19	13588	8.E+00	9.E-01	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0048545~response to steroid hormone stimulus	9	1.412872841	3.E-03	20779, 12842, 18670, 109900, 26395, 120	572	60	13588	4.E+00	1.E+00	5.E-02	6.E+00
GOTERM_BP_FAT	GO:0009991~response to extracellular stimulus	11	1.726844584	5.E-02	16828, 21687, 11657, 12842, 109900, 116	572	133	13588	2.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0031667~response to nutrient levels	9	1.412872841	1.E-01	21687, 11657, 12842, 109900, 11651, 120	572	115	13588	2.E+00	1.E+00	5.E-01	9.E+01
GOTERM_BP_FAT	GO:0007584~response to nutrient	5	0.784929356	4.E-01	21687, 12842, 109900, 12043, 94284, 394	572	76	13588	2.E+00	1.E+00	9.E-01	1.E+02
Annotation Cluster 61	Enrichment Score: 2.0947781383442723											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	pyruvate	7	1.098901099	2.E-05	18746, 18770, 68263, 27402, 18597, 1859	629	18	17854	1.E+01	1.E-02	3.E-04	3.E-02
KEGG_PATHWAY	mmu00020:Citrate cycle (TCA cycle)	9	1.412872841	1.E-03	68263, 17448, 235339, 18597, 18598, 185	409	31	5738	4.E+00	2.E-01	5.E-03	1.E+00
GOTERM_MF_FAT	GO:0004739~pyruvate dehydrogenase (acetyl-transferring) activity	3	0.470957614	5.E-03	68263, 18597, 18598	550	3	13288	2.E+01	1.E+00	6.E-02	7.E+00
GOTERM_MF_FAT	GO:0004738~pyruvate dehydrogenase activity	3	0.470957614	5.E-03	68263, 18597, 18598	550	3	13288	2.E+01	1.E+00	6.E-02	7.E+00
SP_PIR_KEYWORDS	thiamine pyrophosphate	4	0.627943485	6.E-03	68263, 18597, 18598, 21881	629	11	17854	1.E+01	9.E-01	3.E-02	8.E+00
GOTERM_MF_FAT	GO:0016624~oxidoreductase activity, acting on the aldehyde or ox	3	0.470957614	5.E-02	68263, 18597, 18598	550	9	13288	8.E+00	1.E+00	4.E-01	5.E+01
KEGG_PATHWAY	mmu00290:Valine, leucine and isoleucine biosynthesis	3	0.470957614	2.E-01	68263, 18597, 18598	409	11	5738	4.E+00	1.E+00	4.E-01	9.E+01
KEGG_PATHWAY	mmu00650:Butanoate metabolism	4	0.627943485	5.E-01	68263, 15107, 18597, 18598	409	37	5738	2.E+00	1.E+00	7.E-01	1.E+02
Annotation Cluster 62	Enrichment Score: 2.082841531780251											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0001906~cell killing	5	0.784929356	4.E-03	15170, 11657, 11891, 13035, 17969	572	16	13588	7.E+00	1.E+00	5.E-02	6.E+00
GOTERM_BP_FAT	GO:0001909~leukocyte mediated cytotoxicity	4	0.627943485	1.E-02	15170, 11891, 13035, 17969	572	12	13588	8.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0002443~leukocyte mediated immunity	10	1.569858713	1.E-02	12051, 14127, 15170, 17874, 11891, 1303	572	89	13588	3.E+00	1.E+00	1.E-01	2.E+01
Annotation Cluster 63	Enrichment Score: 2.0239629719809726											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0030705~cytoskeleton-dependent intracellular transport	7	1.098901099	2.E-03	245049, 215280, 17925, 77579, 59040, 22	572	33	13588	5.E+00	1.E+00	4.E-02	4.E+00
GOTERM_BP_FAT	GO:0051640~organelle localization	8	1.25588697	7.E-03	245049, 11657, 77579, 12540, 11891, 171	572	54	13588	4.E+00	1.E+00	8.E-02	1.E+01



GOTERM_BP_FAT	GO:0051656~establishment of organelle localization	5	0.784929356	5.E-02	77579, 12540, 11891, 59040, 214952	572	34	13588	3.E+00	1.E+00	3.E-01	6.E+01
Annotation Cluster 64	Enrichment Score: 2.0211034579470324											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0050900~leukocyte migration	8	1.25588697	2.E-03	20310, 14127, 20345, 12490, 16414, 2020	572	43	13588	4.E+00	1.E+00	3.E-02	3.E+00
GOTERM_BP_FAT	GO:0007159~leukocyte adhesion	4	0.627943485	2.E-02	16408, 20345, 16414, 16409	572	14	13588	7.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0045123~cellular extravasation	3	0.470957614	2.E-02	20345, 16414, 16409	572	6	13588	1.E+01	1.E+00	2.E-01	3.E+01
Annotation Cluster 65	Enrichment Score: 1.9909256928481351											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0008353~RNA polymerase II carboxy-terminal domain kinase ac	6	0.941915228	7.E-05	13872, 17420, 14884, 14885, 12534, 6667	550	12	13288	1.E+01	5.E-02	1.E-03	1.E-01
GOTERM_CC_FAT	GO:0005675~holo TFIIH complex	5	0.784929356	3.E-04	13872, 17420, 14884, 14885, 66671	434	10	12504	1.E+01	8.E-02	6.E-03	3.E-01
KEGG_PATHWAY	mmu03420Nucleotide excision repair	9	1.412872841	1.E-02	13872, 19891, 19358, 68240, 17420, 1488	409	43	5738	3.E+00	8.E-01	3.E-02	1.E+01
GOTERM_BP_FAT	GO:0006366~transcription from RNA polymerase II promoter	8	1.25588697	4.E-02	13872, 69920, 16911, 17420, 17869, 1488	572	74	13588	3.E+00	1.E+00	3.E-01	5.E+01
GOTERM_CC_FAT	GO:0016591~DNA-directed RNA polymerase II, holoenzyme	6	0.941915228	4.E-02	13872, 69920, 17420, 14884, 14885, 6667	434	56	12504	3.E+00	1.E+00	2.E-01	5.E+01
GOTERM_MF_FAT	GO:0008094~DNA-dependent ATPase activity	5	0.784929356	7.E-02	13872, 17420, 14884, 14885, 66671	550	38	13288	3.E+00	1.E+00	5.E-01	7.E+01
GOTERM_BP_FAT	GO:0006351~transcription, DNA-dependent	10	1.569858713	7.E-02	13872, 69920, 69890, 22130, 16911, 1742	572	122	13588	2.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0032774~RNA biosynthetic process	10	1.569858713	8.E-02	13872, 69920, 69890, 22130, 16911, 1742	572	126	13588	2.E+00	1.E+00	5.E-01	8.E+01
Annotation Cluster 66	Enrichment Score: 1.9842427781339937											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0005158~insulin receptor binding	5	0.784929356	4.E-03	18708, 16367, 27261, 13449, 384783	550	17	13288	7.E+00	9.E-01	6.E-02	6.E+00
UP_SEQ_FEATURE	domain:IRS-type PTB	4	0.627943485	1.E-02	16367, 27261, 13449, 384783	618	12	16021	9.E+00	1.E+00	3.E-01	1.E+01
INTERPRO	IPR002404Insulin receptor substrate-1, PTB	4	0.627943485	1.E-02	16367, 27261, 13449, 384783	630	13	17763	9.E+00	1.E+00	2.E-01	1.E+01
GOTERM_MF_FAT	GO:0032403~protein complex binding	9	1.412872841	1.E-02	18708, 14127, 16367, 27261, 13449, 1641	550	78	13288	3.E+00	1.E+00	2.E-01	2.E+01
SMART	SM00310.PTBI	4	0.627943485	2.E-02	16367, 27261, 13449, 384783	418	13	9131	7.E+00	1.E+00	2.E-01	2.E+01
Annotation Cluster 67	Enrichment Score: 1.9841873754311707											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0048732~gland development	19	2.982731554	2.E-03	13649, 14178, 11806, 12043, 22778, 1185	572	197	13588	2.E+00	1.E+00	3.E-02	3.E+00
GOTERM_BP_FAT	GO:0035239~tube morphogenesis	16	2.51177394	6.E-03	22323, 14674, 232906, 16911, 12043, 122	572	171	13588	2.E+00	1.E+00	7.E-02	1.E+01
GOTERM_BP_FAT	GO:0035295~tube development	21	3.296703297	8.E-03	22323, 14674, 14178, 232906, 16911, 193	572	264	13588	2.E+00	1.E+00	9.E-02	1.E+01
GOTERM_BP_FAT	GO:0001763~morphogenesis of a branching structure	12	1.883830455	2.E-02	15402, 14674, 20779, 24064, 14178, 1270	572	125	13588	2.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0022612~gland morphogenesis	9	1.412872841	2.E-02	13649, 20779, 14178, 12043, 12505, 1600	572	84	13588	3.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0048754~branching morphogenesis of a tube	9	1.412872841	4.E-02	15402, 14674, 20779, 24064, 12043, 1250	572	93	13588	2.E+00	1.E+00	3.E-01	5.E+01
Annotation Cluster 68	Enrichment Score: 1.965355602143961											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
KEGG_PATHWAY	mmu04120Ubiquitin mediated proteolysis	28	4.395604396	7.E-07	56550, 218793, 26965, 246710, 59008, 16	409	136	5738	3.E+00	1.E-04	5.E-06	9.E-04
SP_PIR_KEYWORDS	ubi conjugation pathway	31	4.866562009	2.E-03	56550, 74287, 218793, 26965, 59008, 163	629	484	17854	2.E+00	6.E-01	1.E-02	3.E+00
GOTERM_MF_FAT	GO:0004842~ubiquitin-protein ligase activity	12	1.883830455	4.E-03	56550, 74287, 17999, 218793, 26965, 163	550	104	13288	3.E+00	9.E-01	5.E-02	5.E+00
GOTERM_MF_FAT	GO:0019787~small conjugating protein ligase activity	13	2.040816327	6.E-03	56550, 74287, 218793, 17999, 26965, 163	550	125	13288	3.E+00	1.E+00	7.E-02	8.E+00
UP_SEQ_FEATURE	active site:Glycyl thioester intermediate	8	1.25588697	9.E-03	100041766, 56550, 218793, 17999, 10004	618	61	16021	3.E+00	1.E+00	3.E-01	1.E+01
GOTERM_BP_FAT	GO:0009057~macromolecule catabolic process	41	6.436420722	1.E-02	56550, 74287, 218793, 11816, 26965, 116	572	654	13588	1.E+00	1.E+00	1.E-01	2.E+01
GOTERM_MF_FAT	GO:0016879~ligase activity, forming carbon-nitrogen bonds	16	2.51177394	1.E-02	56550, 74287, 218793, 17999, 26965, 163	550	193	13288	2.E+00	1.E+00	2.E-01	2.E+01
GOTERM_BP_FAT	GO:0043632~modification-dependent macromolecule catabolic pro	33	5.180533752	1.E-02	56550, 74287, 218793, 26965, 59008, 163	572	508	13588	2.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0019941~modification-dependent protein catabolic process	33	5.180533752	1.E-02	56550, 74287, 218793, 26965, 59008, 163	572	508	13588	2.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0044265~cellular macromolecule catabolic process	38	5.965463108	2.E-02	56550, 74287, 218793, 11816, 26965, 238	572	609	13588	1.E+00	1.E+00	1.E-01	2.E+01
INTERPRO	IPR000608Ubiquitin-conjugating enzyme, E2	6	0.941915228	2.E-02	100041766, 56550, 218793, 100047012, 6	630	42	17763	4.E+00	1.E+00	3.E-01	2.E+01
GOTERM_BP_FAT	GO:0030163~protein catabolic process	35	5.494505495	2.E-02	56550, 74287, 218793, 26965, 11651, 590	572	556	13588	1.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0051603~proteolysis involved in cellular protein catabolic proce	33	5.180533752	3.E-02	56550, 74287, 218793, 26965, 59008, 163	572	534	13588	1.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0044257~cellular protein catabolic process	33	5.180533752	3.E-02	56550, 74287, 218793, 26965, 59008, 163	572	537	13588	1.E+00	1.E+00	2.E-01	4.E+01
INTERPRO	IPR016135Ubiquitin-conjugating enzyme/RWD-like	6	0.941915228	3.E-02	100041766, 56550, 218793, 100047012, 6	630	50	17763	3.E+00	1.E+00	4.E-01	4.E+01
SMART	SM00212.UBCc	6	0.941915228	4.E-02	100041766, 56550, 218793, 100047012, 6	418	42	9131	3.E+00	1.E+00	3.E-01	4.E+01
GOTERM_MF_FAT	GO:0016881~acid-amino acid ligase activity	13	2.040816327	4.E-02	56550, 74287, 218793, 17999, 26965, 163	550	166	13288	2.E+00	1.E+00	3.E-01	5.E+01
SP_PIR_KEYWORDS	ligase	17	2.668759812	5.E-02	56550, 74287, 218793, 17999, 16882, 163	629	290	17854	2.E+00	1.E+00	2.E-01	5.E+01
GOTERM_BP_FAT	GO:0006508~proteolysis	45	7.064364207	5.E-01	56550, 74287, 218793, 14939, 26965, 590	572	1034	13588	1.E+00	1.E+00	1.E+00	1.E+02
Annotation Cluster 69	Enrichment Score: 1.9431158750768345											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR005952Phosphoglycerate mutase 1	3	0.470957614	4.E-03	18648, 12183, 56012	630	3	17763	3.E+01	1.E+00	1.E-01	6.E+00
UP_SEQ_FEATURE	site:Interaction with carboxyl group of phosphoglycerates	3	0.470957614	4.E-03	18648, 12183, 56012	618	3	16021	3.E+01	1.E+00	2.E-01	7.E+00
GOTERM_MF_FAT	GO:0004082~bisphosphoglycerate mutase activity	3	0.470957614	5.E-03	18648, 12183, 56012	550	3	13288	2.E+01	1.E+00	6.E-02	7.E+00
GOTERM_MF_FAT	GO:0004083~2,3-bisphospho-D-glycerate 2-phosphohydrolase acti	3	0.470957614	5.E-03	18648, 12183, 56012	550	3	13288	2.E+01	1.E+00	6.E-02	7.E+00
GOTERM_MF_FAT	GO:0034416~bisphosphoglycerate phosphatase activity	3	0.470957614	5.E-03	18648, 12183, 56012	550	3	13288	2.E+01	1.E+00	6.E-02	7.E+00



GOTERM_MF_FAT	GO:0004619~phosphoglycerate mutase activity	3	0.470957614	5.E-03	18648	12183	56012	550	3	13288	2.E+01	1.E+00	6.E-02	7.E+00	
GOTERM_MF_FAT	GO:0016868~intramolecular transferase activity, phosphotransferase	4	0.627943485	7.E-03	18648	72157	12183	56012	550	10	13288	1.E+01	1.E+00	8.E-02	1.E+01
SP_PIR_KEYWORDS	Isomerase	11	1.726844584	9.E-03	18453	12304	14751	18648	19895	118	17854	3.E+00	1.E+00	5.E-02	1.E+01
PIR_SUPERFAMILY	PIRSF001490:cofactor-dependent phosphoglycerate mutase	3	0.470957614	1.E-02	18648	12183	56012	400	4	8136	2.E+01	1.E+00	5.E-01	2.E+01	
INTERPRO	IPR001345:Phosphoglycerate/bisphosphoglycerate mutase	3	0.470957614	4.E-02	18648	12183	56012	630	9	17763	9.E+00	1.E+00	4.E-01	5.E+01	
UP_SEQ_FEATURE	active site:Tele-phosphohistidine intermediate	3	0.470957614	4.E-02	18648	12183	56012	618	9	16021	9.E+00	1.E+00	7.E-01	5.E+01	
INTERPRO	IPR013078:Phosphoglycerate mutase	3	0.470957614	6.E-02	18648	12183	56012	630	11	17763	8.E+00	1.E+00	6.E-01	6.E+01	
GOTERM_MF_FAT	GO:0016866~intramolecular transferase activity	4	0.627943485	7.E-02	18648	72157	12183	56012	550	24	13288	4.E+00	1.E+00	5.E-01	7.E+01

Annotation Cluster 70	Enrichment Score: 1.9241384034369255														
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR			
GOTERM_BP_FAT	GO:0002009~morphogenesis of an epithelium	19	2.982731554	4.E-04	22323	13649	232906	16911	19378	120	572	173	13588	3.E+00	6.E-01
GOTERM_BP_FAT	GO:0048729~tissue morphogenesis	23	3.610675039	5.E-04	22323	13649	14178	232906	16911	193	572	238	13588	2.E+00	8.E-01
GOTERM_BP_FAT	GO:0060562~epithelial tube morphogenesis	13	2.040816327	2.E-03	22323	232906	16911	12043	12234	240	572	111	13588	3.E+00	4.E+00
GOTERM_BP_FAT	GO:0060429~epithelium development	23	3.610675039	3.E-03	22323	13649	16456	232906	16911	193	572	271	13588	2.E+00	4.E+00
GOTERM_BP_FAT	GO:0016331~morphogenesis of embryonic epithelium	10	1.569858713	5.E-03	22323	16911	232906	19713	50768	186	572	78	13588	3.E+00	9.E+00
GOTERM_BP_FAT	GO:0035239~tube morphogenesis	16	2.51177394	6.E-03	22323	14674	232906	16911	12043	122	572	171	13588	2.E+00	1.E+01
GOTERM_BP_FAT	GO:0035295~tube development	21	3.296703297	8.E-03	22323	14674	14178	232906	16911	193	572	264	13588	2.E+00	1.E+01
GOTERM_BP_FAT	GO:0001838~embryonic epithelial tube formation	7	1.098901099	3.E-02	22323	16911	232906	19713	50768	123	572	54	13588	3.E+00	4.E+01
GOTERM_BP_FAT	GO:0035148~tube lumen formation	7	1.098901099	4.E-02	22323	16911	232906	19713	50768	123	572	59	13588	3.E+00	5.E-01
GOTERM_BP_FAT	GO:0001841~neural tube formation	6	0.941915228	6.E-02	22323	16911	232906	50768	12370	240	572	51	13588	3.E+00	7.E+01
GOTERM_BP_FAT	GO:0060606~tube closure	5	0.784929356	8.E-02	22323	16911	232906	50768	24069		572	39	13588	3.E+00	8.E+01
GOTERM_BP_FAT	GO:0001843~neural tube closure	5	0.784929356	8.E-02	22323	16911	232906	50768	24069		572	39	13588	3.E+00	8.E+01
GOTERM_BP_FAT	GO:0014020~primary neural tube formation	5	0.784929356	1.E-01	22323	16911	232906	50768	24069		572	42	13588	3.E+00	8.E+01
GOTERM_BP_FAT	GO:0021915~neural tube development	7	1.098901099	1.E-01	22323	13836	16911	232906	50768	123	572	83	13588	2.E+00	9.E+01

Annotation Cluster 71	Enrichment Score: 1.9198109508114443														
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR			
UP_SEQ_FEATURE	domain:ABC transmembrane type-1 1	7	1.098901099	4.E-06	18669	18671	18670	27421	12780	2741	618	13	16021	1.E+01	7.E-03
UP_SEQ_FEATURE	domain:ABC transmembrane type-1 2	7	1.098901099	4.E-06	18669	18671	18670	27421	12780	2741	618	13	16021	1.E+01	7.E-03
UP_SEQ_FEATURE	nucleotide phosphate-binding region:ATP 2	9	1.412872841	2.E-05	18669	18671	18670	27421	12780	2741	618	31	16021	8.E+00	3.E-02
UP_SEQ_FEATURE	nucleotide phosphate-binding region:ATP 1	9	1.412872841	2.E-05	18669	18671	18670	27421	12780	2741	618	31	16021	8.E+00	3.E-02
GOTERM_CC_FAT	GO:0046581~intercellular canalculus	5	0.784929356	5.E-05	18669	18671	18670	12780	27413		434	7	12504	2.E+01	6.E-02
INTERPRO	IPR001140:ABC transporter, transmembrane region	7	1.098901099	1.E-04	18669	18671	18670	27421	12780	2741	630	23	17763	9.E+00	2.E-01
INTERPRO	IPR017940:ABC transporter integral membrane type 1	7	1.098901099	3.E-04	18669	18671	18670	27421	12780	2741	630	27	17763	7.E+00	5.E-01
PIR_SUPERFAMILY	PIRSF002773:multidrug resistance protein	4	0.627943485	5.E-04	18669	18671	18670	27413			400	4	8136	2.E+01	6.E-01
UP_SEQ_FEATURE	domain:ABC transporter 2	7	1.098901099	6.E-04	18669	18671	18670	27421	12780	2741	618	28	16021	6.E+00	1.E+00
UP_SEQ_FEATURE	domain:ABC transporter 1	7	1.098901099	6.E-04	18669	18671	18670	27421	12780	2741	618	28	16021	6.E+00	1.E+00
GOTERM_MF_FAT	GO:0042910~xenobiotic transporter activity	3	0.470957614	5.E-03	18669	18671	18670				550	3	13288	2.E+01	7.E+00
GOTERM_MF_FAT	GO:0008559~xenobiotic-transporting ATPase activity	3	0.470957614	5.E-03	18669	18671	18670				550	3	13288	2.E+01	7.E+00
INTERPRO	IPR005292:Multi drug resistance-associated protein (MRP)	3	0.470957614	7.E-03	27421	12780	17250				630	4	17763	2.E+01	1.E+01
INTERPRO	IPR017871:ABC transporter, conserved site	8	1.25588697	7.E-03	18669	18671	13006	18670	27421	1278	630	64	17763	4.E+00	1.E+01
GOTERM_MF_FAT	GO:0015239~multidrug transporter activity	3	0.470957614	1.E-02	18669	18671	18670				550	4	13288	2.E+01	1.E+01
INTERPRO	IPR003439:ABC transporter-like	7	1.098901099	1.E-02	18669	18671	18670	27421	12780	2741	630	53	17763	4.E+00	2.E+01
GOTERM_MF_FAT	GO:0042623~ATPase activity, coupled	18	2.825745683	1.E-02	18195	110957	13872	18669	18671	186	550	223	13288	2.E+00	2.E+01
PIR_SUPERFAMILY	PIRSF002775:human multidrug resistance protein cMOAT2	3	0.470957614	3.E-02	27421	12780	17250				400	6	8136	1.E+01	4.E+01
BIOCARTA	m_mrpPathway:Multi-Drug Resistance Factors	4	0.627943485	4.E-02	18669	18671	27413	17250			167	6	1171	5.E+00	4.E+01
GOTERM_MF_FAT	GO:0016887~ATPase activity	18	2.825745683	7.E-02	18195	110957	13872	18669	18671	186	550	281	13288	2.E+00	7.E+01
KEGG_PATHWAY	mmu02010:ABC transporters	7	1.098901099	1.E-01	18669	18671	18670	27421	12780	2741	409	45	5738	2.E+00	7.E+01
GOTERM_CC_FAT	GO:0045177~apical part of cell	9	1.412872841	1.E-01	18669	18671	18670	12780	27413	1707	434	136	12504	2.E+00	8.E+01
GOTERM_MF_FAT	GO:0015238~drug transporter activity	3	0.470957614	1.E-01	18669	18671	18670				550	14	13288	5.E+00	8.E+01
GOTERM_MF_FAT	GO:0043492~ATPase activity, coupled to movement of substances	7	1.098901099	2.E-01	18669	18671	18670	27421	12780	2741	550	97	13288	2.E+00	1.E+02
GOTERM_MF_FAT	GO:0042626~ATPase activity, coupled to transmembrane movemen	7	1.098901099	2.E-01	18669	18671	18670	27421	12780	2741	550	97	13288	2.E+00	1.E+02
GOTERM_MF_FAT	GO:0016820~hydrolase activity, acting on acid anhydrides, catalyzi	7	1.098901099	2.E-01	18669	18671	18670	27421	12780	2741	550	97	13288	2.E+00	1.E+02
INTERPRO	IPR003593:ATPase, AAA + type, core	8	1.25588697	2.E-01	18669	18671	18670	27421	12780	2741	630	138	17763	2.E+00	1.E+02
GOTERM_CC_FAT	GO:0005911~cell-cell junction	9	1.412872841	3.E-01	18669	18671	16456	18670	69524	1305	434	173	12504	1.E+00	1.E+02
GOTERM_MF_FAT	GO:0015405~P-P-bond-hydrolysis-driven transmembrane transport	7	1.098901099	3.E-01	18669	18671	18670	27421	12780	2741	550	107	13288	2.E+00	1.E+02
GOTERM_MF_FAT	GO:0015399~primary active transmembrane transporter activity	7	1.098901099	3.E-01	18669	18671	18670	27421	12780	2741	550	108	13288	2.E+00	1.E+02
SMART	SM00382:AAA	8	1.25588697	4.E-01	18669	18671	18670	27421	12780	2741	418	138	9131	1.E+00	1.E+02
GOTERM_CC_FAT	GO:0016324~apical plasma membrane	5	0.784929356	4.E-01	18669	18671	18670	12780	14064		434	99	12504	1.E+00	1.E+02
BIOCARTA	m_nuclearRsPathway:Nuclear Receptors in Lipid Metabolism and Tc	6	0.941915228	5.E-01	18669	18671	12780	27413	13077	1310	167	33	1171	1.E+00	1.E+02
GOTERM_CC_FAT	GO:0000139~Golgi membrane	3	0.470957614	1.E+00	18669	18671	18670				434	137	12504	6.E-01	1.E+02
GOTERM_CC_FAT	GO:0044431~Golgi apparatus part	5	0.784929356	1.E+00	18669	18671	18670	70231	192176		434	227	12504	6.E-01	1.E+02
GOTERM_BP_FAT	GO:0055085~transmembrane transport	12	1.883830455	1.E+00	18669	18671	18670	27421	231042	205	572	460	13588	6.E-01	1.E+02



Annotation Cluster 72	Enrichment Score: 1.9104304733531643											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	<b>cyclin</b>		8	1.25588697	1.E-03 12445, 12442, 209091, 12454, 12566, 125	629	48	17854	5.E+00	4.E-01	1.E-02	2.E+00
INTERPRO	IPR006671:Cyclin, N-terminal	6	0.941915228		2.E-03 12445, 12442, 209091, 12454, 268697, 66	630	27	17763	6.E+00	9.E-01	7.E-02	4.E+00
INTERPRO	IPR013763:Cyclin-related	6	0.941915228		6.E-03 12445, 12442, 209091, 12454, 268697, 66	630	33	17763	5.E+00	1.E+00	1.E-01	9.E+00
INTERPRO	IPR006670:Cyclin	6	0.941915228		6.E-03 12445, 12442, 209091, 12454, 268697, 66	630	33	17763	5.E+00	1.E+00	1.E-01	9.E+00
INTERPRO	IPR004367:Cyclin, C-terminal	4	0.627943485		1.E-02 12445, 12442, 209091, 268697	630	15	17763	8.E+00	1.E+00	2.E-01	2.E+01
SMART	SM00385:CYCLIN	6	0.941915228		2.E-02 12445, 12442, 209091, 12454, 268697, 66	418	33	9131	4.E+00	9.E-01	2.E-01	2.E+01
INTERPRO	IPR014400:Cyclin, A/B/D/E	3	0.470957614		5.E-02 12445, 12442, 268697	630	10	17763	8.E+00	1.E+00	5.E-01	5.E+01
PIR_SUPERFAMILY	PIRSF001771:cyclin, A/B/D/E types	3	0.470957614		7.E-02 12445, 12442, 268697	400	9	8136	7.E+00	1.E+00	9.E-01	6.E+01
PIR_SUPERFAMILY	PIRSF001771:Cyclin_A_B_D_E	3	0.470957614		8.E-02 12445, 12442, 268697	400	10	8136	6.E+00	1.E+00	9.E-01	7.E+01
Annotation Cluster 73	Enrichment Score: 1.9082650076516168											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	<b>urea cycle</b>		5	0.784929356	5.E-05 227231, 18416, 217214, 109900, 11847	629	7	17854	2.E+01	2.E-02	5.E-04	7.E-02
GOTERM_BP_FAT	GO:0006525~arginine metabolic process	5	0.784929356		3.E-04 18126, 18416, 217214, 109900, 11847	572	9	13588	1.E+01	6.E-01	9.E-03	6.E-01
GOTERM_BP_FAT	GO:0000050~urea cycle	5	0.784929356		3.E-04 227231, 18416, 217214, 109900, 11847	572	9	13588	1.E+01	6.E-01	9.E-03	6.E-01
GOTERM_BP_FAT	GO:0019627~urea metabolic process	5	0.784929356		3.E-04 227231, 18416, 217214, 109900, 11847	572	9	13588	1.E+01	6.E-01	9.E-03	6.E-01
GOTERM_BP_FAT	GO:0043604~amide biosynthetic process	5	0.784929356		5.E-04 227231, 18416, 217214, 109900, 11847	572	10	13588	1.E+01	8.E-01	1.E-02	9.E-01
GOTERM_BP_FAT	GO:0009064~glutamine family amino acid metabolic process	7	1.098901099		9.E-03 227231, 18126, 18416, 217214, 109900, 1	572	43	13588	4.E+00	1.E+00	1.E-01	1.E+01
GOTERM_BP_FAT	GO:0006526~arginine biosynthetic process	3	0.470957614		1.E-02 18416, 217214, 109900	572	4	13588	2.E+01	1.E+00	1.E-01	2.E+01
KEGG_PATHWAY	mmu00250:Alanine, aspartate and glutamate metabolism	7	1.098901099		2.E-02 227231, 14661, 109900, 11564, 11566, 14	409	30	5738	3.E+00	9.E-01	5.E-02	2.E+01
GOTERM_BP_FAT	GO:0009084~glutamine family amino acid biosynthetic process	4	0.627943485		2.E-02 18416, 217214, 109900, 14645	572	15	13588	6.E+00	1.E+00	2.E-01	3.E+01
KEGG_PATHWAY	mmu00330:Arginine and proline metabolism	8	1.25588697		8.E-02 227231, 18126, 14661, 18416, 217214, 10	409	53	5738	2.E+00	1.E+00	2.E-01	6.E+01
GOTERM_BP_FAT	GO:0008652~cellular amino acid biosynthetic process	5	0.784929356		1.E-01 18416, 217214, 109900, 232087, 14645	572	44	13588	3.E+00	1.E+00	5.E-01	9.E+01
GOTERM_BP_FAT	GO:0006541~glutamine metabolic process	3	0.470957614		2.E-01 227231, 109900, 14645	572	19	13588	4.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0009309~amine biosynthetic process	6	0.941915228		2.E-01 18416, 217214, 109900, 232087, 14462, 1	572	73	13588	2.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0046394~carboxylic acid biosynthetic process	9	1.412872841		2.E-01 19317, 18416, 217214, 109900, 232087, 2	572	141	13588	2.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0016053~organic acid biosynthetic process	9	1.412872841		2.E-01 19317, 18416, 217214, 109900, 232087, 2	572	141	13588	2.E+00	1.E+00	8.E-01	1.E+02
KEGG_PATHWAY	mmu00910:Nitrogen metabolism	3	0.470957614		5.E-01 227231, 14661, 14645	409	23	5738	2.E+00	1.E+00	7.E-01	1.E+02
Annotation Cluster 74	Enrichment Score: 1.8812029987965495											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0005886~plasma membrane	138	21.66405024		3.E-05 22323, 12475, 19744, 15018, 69524, 9419	434	2906	12504	1.E+00	1.E-02	9.E-04	4.E-02
SP_PIR_KEYWORDS	<b>cell membrane</b>		72	11.30298273	8.E-02 22323, 228543, 12765, 12475, 19744, 695	629	1713	17854	1.E+00	1.E+00	3.E-01	7.E+01
SP_PIR_KEYWORDS	membrane	176	27.62951334		1.E+00 22323, 19744, 12475, 15018, 69524, 1695	629	5507	17854	9.E-01	1.E+00	1.E+00	1.E+02
Annotation Cluster 75	Enrichment Score: 1.833132355633516											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
BIOCARTA	<b>m_spryPathway:Sprouty regulation of tyrosine kinase signals</b>		9	1.412872841	6.E-04 13649, 20779, 218397, 24064, 14784, 206	167	16	1171	4.E+00	1.E-01	2.E-02	8.E-01
KEGG_PATHWAY	mmu04540:Gap junction	15	2.354788069		3.E-03 22142, 13649, 14678, 18797, 18795, 1859	409	86	5738	2.E+00	3.E-01	9.E-03	3.E+00
KEGG_PATHWAY	mmu04720:Long-term potentiation	13	2.040816327		3.E-03 18797, 12914, 18795, 11514, 12315, 1231	409	70	5738	3.E+00	4.E-01	1.E-02	4.E+00
BIOCARTA	m_At1rPathway:Angiotensin II mediated activation of JNK Pathway	10	1.569858713		1.E-02 13649, 20779, 12315, 14784, 20662, 1231	167	28	1171	3.E+00	9.E-01	8.E-02	1.E+01
KEGG_PATHWAY	mmu04730:Long-term depression	12	1.883830455		1.E-02 14674, 19053, 14678, 26395, 15461, 1600	409	72	5738	2.E+00	9.E-01	4.E-02	1.E+01
KEGG_PATHWAY	mmu04912:GnRH signaling pathway	14	2.197802198		2.E-02 13649, 18797, 18795, 20779, 11514, 1478	409	97	5738	2.E+00	1.E+00	5.E-02	2.E+01
KEGG_PATHWAY	mmu04916:Melanogenesis	10	1.569858713		3.E-01 11514, 12315, 12314, 14678, 26395, 1231	409	100	5738	1.E+00	1.E+00	5.E-01	1.E+02
KEGG_PATHWAY	mmu04270:Vascular smooth muscle contraction	10	1.569858713		5.E-01 14674, 11514, 12315, 12314, 26395, 1231	409	120	5738	1.E+00	1.E+00	7.E-01	1.E+02
Annotation Cluster 76	Enrichment Score: 1.819615398712539											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	chylomicron	6	0.941915228		1.E-05 11813, 11814, 669888, 11816, 238055, 11	629	10	17854	2.E+01	5.E-03	2.E-04	2.E-02
GOTERM_CC_FAT	GO:0042627~chylomicron	5	0.784929356		9.E-05 11813, 11814, 669888, 11816, 11808	434	8	12504	2.E+01	3.E-02	2.E-03	1.E-01
SP_PIR_KEYWORDS	hdl	5	0.784929356		4.E-04 11813, 11814, 669888, 11816, 238055	629	11	17854	1.E+01	2.E-01	3.E-03	6.E-01
GOTERM_BP_FAT	GO:0019433~triglyceride catabolic process	3	0.470957614		2.E-02 11814, 669888, 238055	572	6	13588	1.E+01	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0044269~glycerol ether catabolic process	3	0.470957614		2.E-02 11814, 669888, 238055	572	6	13588	1.E+01	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0046464~acylglycerol catabolic process	3	0.470957614		2.E-02 11814, 669888, 238055	572	6	13588	1.E+01	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0046503~glycerolipid catabolic process	3	0.470957614		2.E-02 11814, 669888, 238055	572	6	13588	1.E+01	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	<b>GO:0046461~neutral lipid catabolic process</b>		3	0.470957614	3.E-02 11814, 669888, 238055	572	7	13588	1.E+01	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0018904~organic ether metabolic process	6	0.941915228		5.E-02 17777, 11814, 669888, 18534, 238055, 13	572	48	13588	3.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0006641~triglyceride metabolic process	5	0.784929356		6.E-02 17777, 11814, 669888, 18534, 238055	572	36	13588	3.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0044242~cellular lipid catabolic process	6	0.941915228		9.E-02 18803, 11814, 669888, 234779, 238055, 1	572	56	13588	3.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0006639~acylglycerol metabolic process	5	0.784929356		1.E-01 17777, 11814, 669888, 18534, 238055	572	43	13588	3.E+00	1.E+00	5.E-01	9.E+01
GOTERM_BP_FAT	GO:0006662~glycerol ether metabolic process	5	0.784929356		1.E-01 17777, 11814, 669888, 18534, 238055	572	45	13588	3.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0006638~neutral lipid metabolic process	5	0.784929356		1.E-01 17777, 11814, 669888, 18534, 238055	572	45	13588	3.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0046486~glycerolipid metabolic process	8	1.25588697		3.E-01 18708, 17777, 11814, 669888, 30955, 185	572	129	13588	1.E+00	1.E+00	9.E-01	1.E+02



Annotation Cluster 77		Enrichment Score: 1.8176040372687676										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Benferroni	Benjamini	FDR
SP_PIR_KEYWORDS	Redox-active center	10	1.569858713	6.E-06	18453, 12304, 93692, 26462, 50493, 1482	629	39	17854	7.E+00	3.E-03	9.E-05	9.E-03
INTERPRO	IPR012999:Pyridine nucleotide-disulphide oxidoreductase, class I ac	4	0.627943485	4.E-04	26462, 50493, 14782, 13382	630	5	17763	2.E+01	3.E-01	2.E-02	7.E-01
GOTERM_BP_FAT	GO:0045454~cell redox homeostasis	10	1.569858713	1.E-03	18453, 12304, 93692, 26462, 50493, 1482	572	62	13588	4.E+00	9.E-01	2.E-02	2.E+00
GOTERM_MF_FAT	GO:0016668~oxidoreductase activity, acting on sulfur group of dor	4	0.627943485	1.E-03	26462, 50493, 14782, 13382	550	6	13288	2.E+01	6.E-01	2.E-02	2.E+00
INTERPRO	IPR004099:Pyridine nucleotide-disulphide oxidoreductase, dimerisat	4	0.627943485	1.E-03	26462, 50493, 14782, 13382	630	7	17763	2.E+01	7.E-01	5.E-02	2.E+00
INTERPRO	IPR001327:Pyridine nucleotide-disulphide oxidoreductase, NAD-bin-	4	0.627943485	2.E-03	26462, 50493, 14782, 13382	630	8	17763	1.E+01	9.E-01	7.E-02	3.E+00
INTERPRO	IPR013027:FAD-dependent pyridine nucleotide-disulphide oxidored	5	0.784929356	4.E-03	26462, 50493, 14782, 13382, 99586	630	19	17763	7.E+00	1.E+00	1.E-01	6.E+00
INTERPRO	IPR000815:Mercuric reductase	3	0.470957614	7.E-03	50493, 14782, 13382	630	4	17763	2.E+01	1.E+00	2.E-01	1.E+01
GOTERM_MF_FAT	GO:0016667~oxidoreductase activity, acting on sulfur group of dor	5	0.784929356	5.E-02	93692, 26462, 50493, 14782, 13382	550	33	13288	4.E+00	1.E+00	3.E-01	5.E+01
GOTERM_MF_FAT	GO:0050661~NADP or NADPH binding	4	0.627943485	5.E-02	18126, 26462, 50493, 14782	550	21	13288	5.E+00	1.E+00	4.E-01	6.E+01
GOTERM_MF_FAT	GO:0016651~oxidoreductase activity, acting on NADH or NADPH	6	0.941915228	6.E-02	17970, 26462, 50493, 14782, 13382, 1796	550	51	13288	3.E+00	1.E+00	4.E-01	6.E+01
SP_PIR_KEYWORDS	Flavoprotein	8	1.25588697	7.E-02	26462, 50493, 12952, 56749, 12953, 1478	629	103	17854	2.E+00	1.E+00	3.E-01	6.E+01
GOTERM_MF_FAT	GO:0016209~antioxidant activity	5	0.784929356	8.E-02	26462, 50493, 54683, 14782, 19225	550	40	13288	3.E+00	1.E+00	5.E-01	7.E+01
SP_PIR_KEYWORDS	FAD	8	1.25588697	9.E-02	18126, 26462, 50493, 12952, 12953, 1478	629	109	17854	2.E+00	1.E+00	3.E-01	7.E+01
GOTERM_MF_FAT	GO:0050662~coenzyme binding	11	1.726844584	1.E-01	15107, 100042746, 14782, 56847, 13382	550	160	13288	2.E+00	1.E+00	6.E-01	9.E+01
SP_PIR_KEYWORDS	nadp	9	1.412872841	1.E-01	18126, 14661, 26462, 50493, 14782, 1438	629	142	17854	2.E+00	1.E+00	4.E-01	9.E+01
GOTERM_MF_FAT	GO:0009055~electron carrier activity	13	2.040816327	1.E-01	672195, 76279, 14782, 13382, 99586, 181	550	202	13288	2.E+00	1.E+00	6.E-01	9.E+01
GOTERM_MF_FAT	GO:0048037~cofactor binding	14	2.197802198	1.E-01	11657, 15107, 100042746, 14782, 56847,	550	226	13288	1.E+00	1.E+00	6.E-01	9.E+01
UP_SEQ_FEATURE	nucleotide phosphate-binding region:FAD	5	0.784929356	2.E-01	18126, 26462, 50493, 14782, 13382	618	58	16021	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_MF_FAT	GO:0050660~FAD binding	5	0.784929356	3.E-01	18126, 26462, 50493, 14782, 13382	550	71	13288	2.E+00	1.E+00	9.E-01	1.E+02
Annotation Cluster 78		Enrichment Score: 1.8014880410790324										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Benferroni	Benjamini	FDR
SP_PIR_KEYWORDS	glucose metabolism	6	0.941915228	2.E-04	16333, 16334, 11651, 72157, 14381, 1438	629	17	17854	1.E+01	9.E-02	2.E-03	3.E-01
GOTERM_BP_FAT	GO:0015758~glucose transport	5	0.784929356	3.E-02	16333, 20525, 16334, 22612, 11651	572	28	13588	4.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0008645~hexose transport	5	0.784929356	4.E-02	16333, 20525, 16334, 22612, 11651	572	30	13588	4.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0015749~monosaccharide transport	5	0.784929356	4.E-02	16333, 20525, 16334, 22612, 11651	572	31	13588	4.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0008643~carbohydrate transport	6	0.941915228	1.E-01	16333, 20525, 11807, 16334, 22612, 1165	572	60	13588	2.E+00	1.E+00	5.E-01	9.E+01
Annotation Cluster 79		Enrichment Score: 1.8005415989353288										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Benferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0000151~ubiquitin ligase complex	9	1.412872841	1.E-03	17999, 26965, 52563, 99152, 16396, 2140	434	60	12504	4.E+00	3.E-01	1.E-02	1.E+00
GOTERM_CC_FAT	GO:0005680~anaphase-promoting complex	3	0.470957614	5.E-02	52563, 66440, 668450, 68999	434	11	12504	8.E+00	1.E+00	2.E-01	5.E+01
GOTERM_CC_FAT	GO:0000152~nuclear ubiquitin ligase complex	3	0.470957614	7.E-02	52563, 66440, 668450, 68999	434	13	12504	7.E+00	1.E+00	3.E-01	6.E+01
Annotation Cluster 80		Enrichment Score: 1.7992054104449975										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Benferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0046907~intracellular transport	33	5.180533752	1.E-03	215280, 269589, 11852, 19384, 12953, 17	572	431	13588	2.E+00	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0034613~cellular protein localization	24	3.767660911	4.E-03	11865, 269589, 19894, 19384, 380714, 12	572	299	13588	2.E+00	1.E+00	5.E-02	7.E+00
GOTERM_BP_FAT	GO:0070727~cellular macromolecule localization	24	3.767660911	4.E-03	11865, 269589, 19894, 19384, 380714, 12	572	301	13588	2.E+00	1.E+00	6.E-02	7.E+00
GOTERM_BP_FAT	GO:0006886~intracellular protein transport	20	3.139717425	2.E-02	11865, 269589, 19894, 19384, 380714, 12	572	276	13588	2.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0008104~protein localization	43	6.750392465	4.E-02	269589, 11852, 11816, 19384, 238055, 12	572	753	13588	1.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0045184~establishment of protein localization	36	5.651491366	9.E-02	269589, 11852, 19384, 238055, 12953, 14	572	656	13588	1.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0015031~protein transport	34	5.337519623	1.E-01	269589, 11852, 19384, 238055, 12953, 14	572	651	13588	1.E+00	1.E+00	6.E-01	9.E+01
Annotation Cluster 81		Enrichment Score: 1.7891603627953565										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Benferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0016728~oxidoreductase activity, acting on CH or CH2 groups	3	0.470957614	5.E-03	382985, 20133, 20135	550	3	13288	2.E+01	1.E+00	6.E-02	7.E+00
GOTERM_MF_FAT	GO:0004748~ribonucleoside-diphosphate reductase activity	3	0.470957614	5.E-03	382985, 20133, 20135	550	3	13288	2.E+01	1.E+00	6.E-02	7.E+00
GOTERM_MF_FAT	GO:0016725~oxidoreductase activity, acting on CH or CH2 groups	3	0.470957614	2.E-02	382985, 20133, 20135	550	5	13288	1.E+01	1.E+00	2.E-01	2.E+01
GOTERM_BP_FAT	GO:0009263~deoxyribonucleotide biosynthetic process	3	0.470957614	4.E-02	382985, 20133, 20135	572	8	13588	9.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0009262~deoxyribonucleotide metabolic process	4	0.627943485	7.E-02	382985, 11486, 20133, 20135	572	23	13588	4.E+00	1.E+00	4.E-01	7.E+01
Annotation Cluster 82		Enrichment Score: 1.7597937139734612										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Benferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0005667~transcription factor complex	19	2.982731554	1.E-03	11865, 12753, 16911, 20375, 22778, 1428	434	234	12504	2.E+00	4.E-01	2.E-02	2.E+00
GOTERM_CC_FAT	GO:0031974~membrane-enclosed lumen	57	8.948194662	8.E-03	672195, 68263, 22130, 218294, 18416, 22	434	1174	12504	1.E+00	9.E-01	7.E-02	1.E+01
GOTERM_CC_FAT	GO:0043233~organelle lumen	55	8.63422292	1.E-02	672195, 68263, 22130, 218294, 18416, 22	434	1136	12504	1.E+00	1.E+00	7.E-02	1.E+01
GOTERM_CC_FAT	GO:0070013~intracellular organelle lumen	54	8.477237049	1.E-02	672195, 68263, 22130, 218294, 18416, 22	434	1133	12504	1.E+00	1.E+00	9.E-02	2.E+01
GOTERM_CC_FAT	GO:0005654~nucleoplasm	30	4.709576138	4.E-02	19720, 17869, 22778, 12912, 12914, 1387	434	599	12504	1.E+00	1.E+00	2.E-01	5.E+01
GOTERM_CC_FAT	GO:0044451~nucleoplasm part	26	4.081632653	5.E-02	17869, 22778, 12912, 12914, 13872, 1540	434	513	12504	1.E+00	1.E+00	2.E-01	5.E+01
GOTERM_CC_FAT	GO:0031981~nuclear lumen	38	5.965463108	1.E-01	22130, 218294, 19720, 17869, 22778, 129	434	883	12504	1.E+00	1.E+00	4.E-01	9.E+01



Annotation Cluster 83	Enrichment Score: 1.7515908518641379												
Category	Term:immune cell activation during immune response	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_BP_FAT	GO:0002285~lymphocyte activation during immune response	5	0.784929356	7.E-03	12051, 11486, 18826, 234779, 11891	572	19	13588	6.E+00	1.E+00	8.E-02	1.E+01	
GOTERM_BP_FAT	GO:0002366~leukocyte activation during immune response	6	0.941915228	9.E-03	12051, 11486, 18826, 234779, 11891, 168	572	31	13588	5.E+00	1.E+00	1.E-01	1.E+01	
GOTERM_BP_FAT	GO:0002263~cell activation during immune response	6	0.941915228	9.E-03	12051, 11486, 18826, 234779, 11891, 168	572	31	13588	5.E+00	1.E+00	1.E-01	1.E+01	
GOTERM_BP_FAT	GO:0002313~mature B cell differentiation during immune response	3	0.470957614	2.E-02	12051, 11486, 234779	572	5	13588	1.E+01	1.E+00	2.E-01	3.E+01	
GOTERM_BP_FAT	GO:0002312~B cell activation during immune response	3	0.470957614	2.E-02	12051, 11486, 234779	572	5	13588	1.E+01	1.E+00	2.E-01	3.E+01	
GOTERM_BP_FAT	GO:0002335~mature B cell differentiation	3	0.470957614	3.E-02	12051, 11486, 234779	572	7	13588	1.E+01	1.E+00	2.E-01	4.E+01	
GOTERM_BP_FAT	GO:0002286~T cell activation during immune response	3	0.470957614	1.E-01	12051, 18826, 11891	572	14	13588	5.E+00	1.E+00	6.E-01	9.E+01	

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0033554-cellular response to stress	31	4.866562009	2.E-03	80905, 11657, 13665, 12952, 12953, 1205	572	404	13588	2.E+00	1.E+00	3.E-02	3.E+00
GOTERM_BP_FAT	GO:0006974-response to DNA damage stimulus	22	3.453689168	1.E-02	382985, 80905, 53610, 16882, 12952, 108	572	287	13588	2.E+00	1.E+00	1.E-01	2.E+01
SP_PIR_KEYWORDS	dna repair	13	2.040816327	2.E-02	80905, 382985, 53610, 16882, 108138, 13	629	173	17854	2.E+00	1.E+00	9.E-02	2.E+01
SP_PIR_KEYWORDS	DNA damage	14	2.197802198	2.E-02	80905, 382985, 53610, 16882, 108138, 13	629	194	17854	2.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0006281-dna repair	16	2.51177394	5.E-02	80905, 382985, 53610, 16882, 12952, 108	572	222	13588	2.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0006259-dna metabolic process	24	3.767660911	1.E-01	382985, 19891, 80905, 53610, 68240, 168	572	421	13588	1.E+00	1.E+00	6.E-01	9.E+01

Annotation Cluster 85		Enrichment Score: 1.6963546885952674										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0001906--cell killing	5	0.784929356	4.E-03	15170, 11657, 11891, 13035, 17969	572	16	13588	7.E+00	1.E+00	5.E-02	6.E+00
GOTERM_BP_FAT	GO:0051883--killing of cells in other organism during symbiotic inte	3	0.470957614	2.E-02	11657, 13035, 17969	572	6	13588	1.E+01	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0051851--modification by host of symbiont morphology or phy	3	0.470957614	2.E-02	11657, 13035, 17969	572	6	13588	1.E+01	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0051818--disruption of cells of other organism during symbioti	3	0.470957614	2.E-02	11657, 13035, 17969	572	6	13588	1.E+01	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0031640--killing of cells of another organism	3	0.470957614	3.E-02	11657, 13035, 17969	572	7	13588	1.E+01	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0051702--interaction with symbiont	3	0.470957614	4.E-02	11657, 13035, 17969	572	8	13588	9.E+00	1.E+00	3.E-01	5.E+01

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0050730~regulation of peptidyl-tyrosine phosphorylation	10	1.569858713		3.E-04 18596, 56717, 15170, 13649, 12703, 1841	572	53	13588	4.E+00	6.E-01	9.E-03	6.E-01
GOTERM_BP_FAT	GO:0051247~positive regulation of protein metabolic process	12	1.883830455		6.E-03 56717, 17999, 18413, 11651, 12043, 1639	572	109	13588	3.E+00	1.E+00	7.E-02	1.E+01
GOTERM_BP_FAT	GO:0050731~positive regulation of peptidyl-tyrosine phosphorylation	6	0.941915228		1.E-02 56717, 18413, 20963, 16452, 15163, 1709	572	35	13588	4.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0031401~positive regulation of protein modification process	9	1.412872841		2.E-02 56717, 18413, 12043, 216080, 20963, 208	572	78	13588	3.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0042509~regulation of tyrosine phosphorylation of STAT protein	4	0.627943485		2.E-02 12703, 16452, 15163, 17096	572	15	13588	6.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0032270~positive regulation of cellular protein metabolic process	10	1.569858713		2.E-02 56717, 18413, 11651, 12043, 216080, 209	572	100	13588	2.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0001934~positive regulation of protein amino acid phosphorylation	7	1.098901099		3.E-02 56717, 18413, 12043, 20963, 16452, 1516	572	56	13588	3.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0042327~positive regulation of phosphorylation	7	1.098901099		4.E-02 56717, 18413, 12043, 20963, 16452, 1516	572	60	13588	3.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0046425~regulation of JAK-STAT cascade	4	0.627943485		4.E-02 12703, 16452, 15163, 17096	572	19	13588	5.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0045937~positive regulation of phosphate metabolic process	7	1.098901099		5.E-02 56717, 18413, 12043, 20963, 16452, 1516	572	62	13588	3.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0010562~positive regulation of phosphorus metabolic process	7	1.098901099		5.E-02 56717, 18413, 12043, 20963, 16452, 1516	572	62	13588	3.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0042531~positive regulation of tyrosine phosphorylation of STAT protein	3	0.470957614		5.E-02 16452, 15163, 17096	572	9	13588	8.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0046427~positive regulation of JAK-STAT cascade	3	0.470957614		8.E-02 16452, 15163, 17096	572	11	13588	6.E+00	1.E+00	4.E-01	8.E+01

Annotation Cluster 87		Enrichment Score: 1.6870909815232538											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_MF_FAT	GO:0019205~nucleobase, nucleoside, nucleotide kinase activity	7	1.098901099		3.E-03 80914, 68556, 22245, 14923, 11636, 6658	550	36	13288	5.E+00	9.E-01	5.E-02	5.E+00	
GOTERM_MF_FAT	GO:0019201~nucleotide kinase activity	4	0.627943485		2.E-02 14923, 11636, 66588, 11637	550	14	13288	7.E+00	1.E+00	2.E-01	2.E+01	
INTERPRO	IPR000850Aadenylate kinase	3	0.470957614		3.E-02 11636, 66588, 11637	630	8	17763	1.E+01	1.E+00	4.E-01	4.E+01	
GOTERM_MF_FAT	GO:0016776~phosphotransferase activity, phosphate group as acceptor	4	0.627943485		1.E-01 14923, 11636, 66588, 11637	550	27	13288	4.E+00	1.E+00	5.E-01	8.E+01	

Annotation Cluster 88		Enrichment Score: 1.6419445750713724										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0010035~response to inorganic substance	11	1.726844584	5.E-03	18669, 11657, 18671, 12842, 19053, 2646	572	92	13588	3.E+00	1.E+00	7.E-02	9.E+00
GOTERM_BP_FAT	GO:0006979~response to oxidative stress	10	1.569858713	1.E-02	382985, 12842, 19053, 11816, 26395, 264	572	87	13588	3.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0000302~response to reactive oxygen species	5	0.784929356	6.E-02	12842, 19053, 26462, 50493, 12043	572	36	13588	3.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0042542~response to hydrogen peroxide	4	0.627943485	8.E-02	12842, 19053, 50493, 12043	572	24	13588	4.E+00	1.E+00	4.E-01	8.E+01

Annotation Cluster 89	Enrichment Score: 1.6270724061277073											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR001060:Fps/Fes/Fer/CIP4 homology	5	0.784929356	6.E-03	117600, 70719, 14159, 171207, 19200	630	21	17763	7.E+00	1.E+00	1.E-01	9.E+00
SMART	SM00055:FCH	5	0.784929356	1.E-02	117600, 70719, 14159, 171207, 19200	418	21	9131	5.E+00	9.E-01	2.E-01	2.E+01
UP_SEQ_FEATURE	domain:FCH	3	0.470957614	2.E-01	117600, 14159, 19200	618	19	16021	4.E+00	1.E+00	1.E+00	1.E+02



Annotation Cluster 90	Enrichment Score: 1.5856886257867813											
Category	Term: Immune cell proliferation	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0050798~activated T cell proliferation	5	0.784929356		1E-04 16408 16411, 16414, 14360, 16409	572	7	13588	2.E+01	2.E-01	3.E-03	2.E-01
GOTERM_BP_FAT	GO:0046651~lymphocyte proliferation	9	1.412872841		3.E-04 16408 12445, 16197, 16411, 12028, 1204	572	42	13588	5.E+00	6.E-01	8.E-03	5.E-01
GOTERM_BP_FAT	GO:0070661~leukocyte proliferation	9	1.412872841		4.E-04 16408 12445, 16197, 16411, 12028, 1204	572	43	13588	5.E+00	6.E-01	9.E-03	6.E-01
GOTERM_BP_FAT	GO:0032943~mononuclear cell proliferation	9	1.412872841		4.E-04 16408 12445, 16197, 16411, 12028, 1204	572	43	13588	5.E+00	6.E-01	9.E-03	6.E-01
GOTERM_CC_FAT	GO:0043235~receptor complex	11	1.726844584		6.E-04 16408 15170, 12475, 16411, 21898, 1641	434	83	12504	4.E+00	2.E-01	8.E-03	8.E-01
GOTERM_BP_FAT	GO:0042098~T cell proliferation	7	1.098901099		9.E-04 16408 12445, 16411, 12028, 16414, 1436	572	28	13588	6.E+00	9.E-01	2.E-02	2.E+00
BIOCARTA	m_monocytePathway:Monocyte and its Surface Molecules	7	1.098901099		2.E-03 16408 20343, 16414, 12505, 16412, 2033	167	11	1171	4.E+00	3.E-01	3.E-02	2.E+00
BIOCARTA	m_neutrophilPathway:Neutrophil and Its Surface Molecules	6	0.941915228		2.E-03 16408 20343, 16414, 12505, 20339, 1640	167	8	1171	5.E+00	4.E-01	3.E-02	3.E+00
BIOCARTA	m_lymphocytePathway:Adhesion Molecules on Lymphocyte	6	0.941915228		4.E-03 16408 20343, 16414, 12505, 16412, 2033	167	9	1171	5.E+00	6.E-01	4.E-02	5.E+00
GOTERM_BP_FAT	GO:0007229~integrin-mediated signaling pathway	9	1.412872841		1.E-02 16408 22324, 16411, 232906, 57257, 164	572	76	13588	3.E+00	1.E+00	1.E-01	2.E+01
GOTERM_CC_FAT	GO:0008305~integrin complex	5	0.784929356		2.E-02 16408 16411, 16414, 16412, 16409	434	28	12504	5.E+00	1.E+00	9.E-02	2.E+01
GOTERM_BP_FAT	GO:0007159~leukocyte adhesion	4	0.627943485		2.E-02 16408 20345, 16414, 16409	572	14	13588	7.E+00	1.E+00	2.E-01	3.E+01
PIR_SUPERFAMILY	PIRSF002497:integrin alpha with I domain	3	0.470957614		6.E-02 16408 16411, 16409	400	8	8136	8.E+00	1.E+00	8.E-01	5.E+01
UP_SEQ_FEATURE	domain:VWFA	6	0.941915228		6.E-02 16408 16411, 16414, 16412, 12263, 1640	618	54	16021	3.E+00	1.E+00	8.E-01	6.E+01
INTERPRO	IPR013513:Integrin alpha chain, C-terminal cytoplasmic region	3	0.470957614		9.E-02 16408 16411, 16409	630	14	17763	6.E+00	1.E+00	7.E-01	8.E+01
UP_SEQ_FEATURE	short sequence motif:GFFKR motif	3	0.470957614		9.E-02 16408 16411, 16409	618	13	16021	6.E+00	1.E+00	9.E-01	8.E+01
GOTERM_BP_FAT	GO:0042100~B cell proliferation	3	0.470957614		9.E-02 16197, 12028, 12043	572	12	13588	6.E+00	1.E+00	5.E-01	8.E+01
INTERPRO	IPR013649:Integrin alpha-2	3	0.470957614		1.E-01 16408 16411, 16409	630	18	17763	5.E+00	1.E+00	8.E-01	9.E+01
INTERPRO	IPR018184:Integrin alpha chain, C-terminal cytoplasmic region, con:	3	0.470957614		1.E-01 16408 16411, 16409	630	18	17763	5.E+00	1.E+00	8.E-01	9.E+01
INTERPRO	IPR000413:Integrin alpha chain	3	0.470957614		1.E-01 16408 16411, 16409	630	18	17763	5.E+00	1.E+00	8.E-01	9.E+01
UP_SEQ_FEATURE	repeat:FG-GAP 6	3	0.470957614		1.E-01 16408 16411, 16409	618	17	16021	5.E+00	1.E+00	9.E-01	9.E+01
UP_SEQ_FEATURE	repeat:FG-GAP 5	3	0.470957614		1.E-01 16408 16411, 16409	618	17	16021	5.E+00	1.E+00	9.E-01	9.E+01
UP_SEQ_FEATURE	repeat:FG-GAP 7	3	0.470957614		1.E-01 16408 16411, 16409	618	17	16021	5.E+00	1.E+00	9.E-01	9.E+01
UP_SEQ_FEATURE	repeat:FG-GAP 2	3	0.470957614		1.E-01 16408 16411, 16409	618	17	16021	5.E+00	1.E+00	9.E-01	9.E+01
UP_SEQ_FEATURE	repeat:FG-GAP 1	3	0.470957614		1.E-01 16408 16411, 16409	618	17	16021	5.E+00	1.E+00	9.E-01	9.E+01
UP_SEQ_FEATURE	repeat:FG-GAP 4	3	0.470957614		1.E-01 16408 16411, 16409	618	17	16021	5.E+00	1.E+00	9.E-01	9.E+01
UP_SEQ_FEATURE	repeat:FG-GAP 3	3	0.470957614		1.E-01 16408 16411, 16409	618	17	16021	5.E+00	1.E+00	9.E-01	9.E+01
INTERPRO	IPR013519:Integrin alpha beta-propellor	3	0.470957614		1.E-01 16408 16411, 16409	630	19	17763	4.E+00	1.E+00	8.E-01	9.E+01
SP_PIR_KEYWORDS	integrin	5	0.784929356		2.E-01 16408 16411, 16414, 16412, 16409	629	61	17854	2.E+00	1.E+00	4.E-01	9.E+01
INTERPRO	IPR013517:FG-GAP	3	0.470957614		2.E-01 16408 16411, 16409	630	23	17763	4.E+00	1.E+00	9.E-01	1.E+02
INTERPRO	IPR002035:von Willebrand factor, type A	6	0.941915228		2.E-01 16408 16411, 16414, 16412, 12263, 1640	630	88	17763	2.E+00	1.E+00	9.E-01	1.E+02
SMART	SM00191:Int_alpha	3	0.470957614		2.E-01 16408 16411, 16409	418	19	9131	3.E+00	1.E+00	7.E-01	9.E+01
SMART	SM00327:VWA	6	0.941915228		4.E-01 16408 16411, 16414, 16412, 12263, 1640	418	88	9131	1.E+00	1.E+00	9.E-01	1.E+02

Annotation Cluster 91	Enrichment Score: 1.5773685292903001											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0050778~positive regulation of immune response	19	2.982731554		2.E-05 19370 14972, 15170, 15018, 27007, 2189	572	136	13588	3.E+00	4.E-02	7.E-04	3.E-02
KEGG_PATHWAY	mmu04620:Toll-like receptor signaling pathway	20	3.139717425		5.E-05 12475, 320207, 27056, 21899, 21898, 116	409	99	5738	3.E+00	8.E-03	2.E-04	6.E-02
GOTERM_BP_FAT	GO:0051240~positive regulation of multicellular organismal process	19	2.982731554		2.E-04 19370 12475, 11657, 15018, 27007, 2189	572	163	13588	3.E+00	4.E-01	5.E-03	3.E-01
GOTERM_BP_FAT	GO:0002237~response to molecule of bacterial origin	10	1.569858713		2.E-04 17874, 12475, 16179, 17087, 234779, 264	572	49	13588	5.E+00	4.E-01	5.E-03	3.E-01
GOTERM_BP_FAT	GO:0001819~positive regulation of cytokine production	11	1.726844584		2.E-04 12051, 19370, 14127, 17874, 12475, 1501	572	62	13588	4.E+00	5.E-01	7.E-03	4.E-01
GOTERM_BP_FAT	GO:0032760~positive regulation of tumor necrosis factor productio	6	0.941915228		3.E-04 14127, 17874, 12475, 21898, 24088, 1680	572	15	13588	1.E+01	5.E-01	8.E-03	5.E-01
GOTERM_BP_FAT	GO:0070391~response to lipoteichoic acid	4	0.627943485		7.E-04 12475, 21898, 24088, 16803	572	5	13588	2.E+01	9.E-01	1.E-02	1.E+00
GOTERM_BP_FAT	GO:0032680~regulation of tumor necrosis factor production	7	1.098901099		7.E-04 12051, 14127, 17874, 12475, 21898, 2408	572	27	13588	6.E+00	9.E-01	2.E-02	1.E+00
GOTERM_BP_FAT	GO:0032496~response to lipopolysaccharide	8	1.25588697		9.E-04 17874, 12475, 16179, 17087, 234779, 264	572	38	13588	5.E+00	9.E-01	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0045428~regulation of nitric oxide biosynthetic process	6	0.941915228		9.E-04 19370, 21898, 27007, 11847, 16414, 3790	572	19	13588	8.E+00	9.E-01	2.E-02	2.E+00
INTERPRO	IPR000157:Toll-Interleukin receptor	6	0.941915228		1.E-03 17874, 239081, 21899, 21898, 24088, 170	630	24	17763	7.E+00	7.E-01	5.E-02	2.E+00
GOTERM_BP_FAT	GO:0045087~innate immune response	13	2.040816327		2.E-03 15170, 239081, 21899, 21898, 16803, 178	572	107	13588	3.E+00	1.E+00	3.E-02	3.E+00
GOTERM_BP_FAT	GO:0001817~regulation of cytokine production	15	2.354788069		2.E-03 19370, 12475, 15018, 11807, 21899, 2700	572	139	13588	3.E+00	1.E+00	4.E-02	4.E+00
GOTERM_BP_FAT	GO:0002218~activation of innate immune response	5	0.784929356		2.E-03 17874, 16179, 21898, 27007, 24088	572	14	13588	8.E+00	1.E+00	4.E-02	4.E+00
GOTERM_BP_FAT	GO:0050830~defense response to Gram-positive bacterium	6	0.941915228		2.E-03 17874, 14191, 13035, 17969, 24088, 1680	572	23	13588	6.E+00	1.E+00	4.E-02	4.E+00
UP_SEQ_FEATURE	domain:TIR	6	0.941915228		2.E-03 17874, 239081, 21899, 21898, 24088, 170	618	25	16021	6.E+00	1.E+00	9.E-02	4.E+00
GOTERM_BP_FAT	GO:0031349~positive regulation of defense response	9	1.412872841		2.E-03 19370, 14127, 17874, 16179, 21898, 2700	572	57	13588	4.E+00	1.E+00	4.E-02	4.E+00
GOTERM_BP_FAT	GO:0045429~positive regulation of nitric oxide biosynthetic proces	5	0.784929356		3.E-03 19370, 21898, 27007, 16414, 379043, 240	572	15	13588	8.E+00	1.E+00	4.E-02	5.E+00
GOTERM_MF_FAT	GO:0001530~lipopolysaccharide binding	4	0.627943485		3.E-03 12475, 17087, 21898, 16803	550	8	13288	1.E+01	9.E-01	5.E-02	5.E+00
GOTERM_BP_FAT	GO:0045089~positive regulation of innate immune response	7	1.098901099		4.E-03 19370, 17874, 16179, 21898, 27007, 3790	572	36	13588	5.E+00	1.E+00	5.E-02	6.E+00
SMART	SM00255:TIR	6	0.941915228		4.E-03 17874, 239081, 21899, 21898, 24088, 170	418	24	9131	5.E+00	5.E-01	6.E-02	5.E+00
GOTERM_BP_FAT	GO:0042742~defense response to bacterium	12	1.883830455		6.E-03 12051, 14972, 14127, 17874, 18126, 1419	572	108	13588	3.E+00	1.E+00	7.E-02	1.E+01
SP_PIR_KEYWORDS	inflammatory response	9	1.412872841		6.E-03 20310, 17874, 12475, 239081, 246779, 17	629	78	17854	3.E+00	9.E-01	4.E-02	8.E+00
INTERPRO	IPR017241:Toll-like receptor	3	0.470957614		7.E-03 21899, 21898, 24088	630	4	17763	2.E+01	1.E+00	2.E-01	1.E+01
GOTERM_BP_FAT	GO:0043388~positive regulation of DNA binding	7	1.098901099		8.E-03 17874, 16179, 12315, 12314, 12313, 2189	572	42	13588	4.E+00	1.E+00	9.E-02	1.E+01
GOTERM_BP_FAT	GO:0032494~response to peptidoglycan	4	0.627943485		9.E-03 17874, 16179, 26416, 24088	572	11	13588	9.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0051099~positive regulation of binding	7	1.098901099		1.E-02 17874, 16179, 12315, 12314, 12313, 2189	572	45	13588	4.E+00	1.E+00	1.E-01	2.E+01



GOTERM_BP_FAT	GO:0045088~regulation of innate immune response	7	1.098901099	1E-02 19370, 17874, 16179, 21898, 27007, 3790	572	46	13588	4.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0051101~regulation of DNA binding	9	1.412872841	1E-02 17874, 16179, 12315, 12314, 12313, 2189	572	74	13588	3.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0002758~innate immune response-activating signal transductio	4	0.627943485	1E-02 17874, 16179, 27007, 24088	572	12	13588	8.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0051091~positive regulation of transcription factor activity	6	0.941915228	1E-02 17874, 16179, 21898, 16414, 24088, 1291	572	34	13588	4.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0051098~regulation of binding	10	1.569858713	1E-02 17874, 16179, 12315, 12314, 12313, 2189	572	90	13588	3.E+00	1.E+00	1.E-01	2.E+01
PIR_SUPERFAMILY	PIRSF037595:Toll-like_receptor	3	0.470957614	1E-02 21899, 21898, 24088	400	4	8136	2.E+01	1.E+00	5.E-01	2.E+01
GOTERM_BP_FAT	GO:0051092~positive regulation of NF-kappaB transcription factor	5	0.784929356	2.E-02 17874, 16179, 21898, 16414, 24088	572	25	13588	5.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0002224~toll-like receptor signaling pathway	3	0.470957614	3.E-02 17874, 16179, 24088	572	7	13588	1.E+01	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0051090~regulation of transcription factor activity	7	1.098901099	4.E-02 17874, 16179, 21898, 16414, 192176, 240	572	59	13588	3.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0032755~positive regulation of interleukin-6 production	4	0.627943485	4.E-02 14127, 17874, 21898, 24088	572	18	13588	5.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0032675~regulation of interleukin-6 production	5	0.784929356	4.E-02 14127, 17874, 21899, 21898, 24088	572	32	13588	4.E+00	1.E+00	3.E-01	5.E+01
BIOCARTA	m_gsk3Pathway:Inactivation of Gsk3 by AKT causes accumulation o	8	1.25588697	5.E-02 18708, 17874, 12475, 16179, 17087, 2189	167	25	1171	2.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0002221~pattern recognition receptor signaling pathway	3	0.470957614	6.E-02 17874, 16179, 24088	572	10	13588	7.E+00	1.E+00	4.E-01	7.E+01
INTERPRO	IPR004075:Interleukin-1 receptor, type I/Toll precursor	3	0.470957614	7.E-02 21899, 24088, 17082	630	12	17763	7.E+00	1.E+00	6.E-01	7.E+01
GOTERM_BP_FAT	GO:0031663~lipopolysaccharide-mediated signaling pathway	3	0.470957614	9.E-02 17874, 16179, 26416	572	12	13588	6.E+00	1.E+00	5.E-01	8.E+01
SP_PIR_KEYWORDS	innate immunity	6	0.941915228	1.E-01 239081, 246779, 21899, 21898, 12263, 24	629	75	17854	2.E+00	1.E+00	4.E-01	8.E+01
UP_SEQ_FEATURE	repeat:LRR 11	5	0.784929356	4.E-01 12475, 239081, 21899, 21898, 24088	618	88	16021	1.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:LRR 10	5	0.784929356	6.E-01 12475, 239081, 21899, 21898, 24088	618	103	16021	1.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:LRR 14	3	0.470957614	6.E-01 21899, 21898, 24088	618	55	16021	1.E+00	1.E+00	1.E+00	1.E+02
BIOCARTA	m_nthiPathway:NfKb activation by Nontypeable Hemophilus influer	4	0.627943485	7.E-01 17874, 26416, 24088, 12914	167	23	1171	1.E+00	1.E+00	9.E-01	1.E+02
UP_SEQ_FEATURE	repeat:LRR 9	5	0.784929356	7.E-01 12475, 239081, 21899, 21898, 24088	618	122	16021	1.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:LRR 13	3	0.470957614	7.E-01 21899, 21898, 24088	618	65	16021	1.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:LRR 8	5	0.784929356	8.E-01 12475, 239081, 21899, 21898, 24088	618	133	16021	1.E+00	1.E+00	1.E+00	1.E+02
INTERPRO	IPR000483:Cysteine-rich flanking region, C-terminal	3	0.470957614	8.E-01 21899, 21898, 24088	630	83	17763	1.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:LRR 12	3	0.470957614	8.E-01 21899, 21898, 24088	618	79	16021	1.E+00	1.E+00	1.E+00	1.E+02
BIOCARTA	m_nfkbPathway:NF-kB Signaling Pathway	3	0.470957614	8.E-01 17874, 16179, 21898	167	21	1171	1.E+00	1.E+00	1.E+00	1.E+02
INTERPRO	IPR001611:Leucine-rich repeat	6	0.941915228	8.E-01 12475, 239081, 21899, 21898, 98238, 240	630	202	17763	8.E-01	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:LRR 7	5	0.784929356	9.E-01 12475, 239081, 21899, 21898, 24088	618	157	16021	8.E-01	1.E+00	1.E+00	1.E+02
BIOCARTA	m_il1rPathway:Signal transduction through IL1R	3	0.470957614	9.E-01 17874, 16179, 26416	167	25	1171	8.E-01	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:LRR 5	6	0.941915228	9.E-01 12475, 239081, 21899, 21898, 98238, 240	618	203	16021	8.E-01	1.E+00	1.E+00	1.E+02
SMART	SM00802:LRRCT	3	0.470957614	9.E-01 21899, 21898, 24088	418	83	9131	8.E-01	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:LRR 6	5	0.784929356	9.E-01 12475, 239081, 21899, 21898, 24088	618	185	16021	7.E-01	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:LRR 4	6	0.941915228	9.E-01 12475, 239081, 21899, 21898, 98238, 240	618	221	16021	7.E-01	1.E+00	1.E+00	1.E+02
INTERPRO	IPR003591:Leucine-rich repeat, typical subtype	3	0.470957614	9.E-01 239081, 21899, 24088	630	129	17763	7.E-01	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:LRR 3	6	0.941915228	1.E+00 12475, 239081, 21899, 21898, 98238, 240	618	245	16021	6.E-01	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	leucine-rich repeat	6	0.941915228	1.E+00 12475, 239081, 21899, 21898, 98238, 240	629	275	17854	6.E-01	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:LRR 1	6	0.941915228	1.E+00 12475, 239081, 21899, 21898, 98238, 240	618	266	16021	6.E-01	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:LRR 2	6	0.941915228	1.E+00 12475, 239081, 21899, 21898, 98238, 240	618	266	16021	6.E-01	1.E+00	1.E+00	1.E+02
SMART	SM00369:LRR_TYP	3	0.470957614	1.E+00 239081, 21899, 24088	418	129	9131	5.E-01	1.E+00	1.E+00	1.E+02

Annotation Cluster 92		Enrichment Score: 1.5629656844240596										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0044429~mitochondrial part	32	5.023547881	3.E-03	672195, 68263, 66593, 18416, 15275, 214	434	524	12504	2E+00	6.E-01	3.E-02	3.E+00
SP_PIR_KEYWORDS	mitochondrion	44	6.907378336	3.E-03	672195, 68263, 66593, 18416, 243362, 15	629	790	17854	2E+00	7.E-01	2.E-02	4.E+00
GOTERM_CC_FAT	GO:0005739~mitochondrion	65	10.20408163	4.E-03	18746, 672195, 68263, 18416, 243362, 12	434	1322	12504	1E+00	7.E-01	4.E-02	5.E+00
GOTERM_CC_FAT	GO:0005759~mitochondrial matrix	13	2.040816327	1.E-02	672195, 15107, 68263, 17448, 18416, 133	434	163	12504	2E+00	1.E+00	8.E-02	1.E+01
GOTERM_CC_FAT	GO:0031980~mitochondrial lumen	13	2.040816327	1.E-02	672195, 15107, 68263, 17448, 18416, 133	434	163	12504	2E+00	1.E+00	8.E-02	1.E+01
GOTERM_CC_FAT	GO:0031967~organelle envelope	30	4.709576138	1.E-02	66593, 18416, 19720, 15275, 214952, 567	434	540	12504	2E+00	1.E+00	8.E-02	2.E+01
GOTERM_CC_FAT	GO:0031975~envelope	30	4.709576138	1.E-02	66593, 18416, 19720, 15275, 214952, 567	434	542	12504	2E+00	1.E+00	9.E-02	2.E+01
GOTERM_CC_FAT	GO:0005740~mitochondrial envelope	23	3.610675039	2.E-02	15107, 17448, 66593, 18416, 18408, 1212	434	391	12504	2E+00	1.E+00	1.E-01	2.E+01
GOTERM_CC_FAT	GO:0031966~mitochondrial membrane	21	3.296703297	3.E-02	15107, 17448, 18416, 18408, 12122, 1204	434	368	12504	2E+00	1.E+00	2.E-01	4.E+01
SP_PIR_KEYWORDS	transit peptide	23	3.610675039	8.E-02	68263, 15107, 17448, 66593, 18416, 1184	629	457	17854	1E+00	1.E+00	3.E-01	7.E+01
UP_SEQ_FEATURE	transit peptide:Mitochondrion	23	3.610675039	1.E-01	68263, 15107, 17448, 66593, 18416, 1184	618	449	16021	1E+00	1.E+00	9.E-01	9.E+01
GOTERM_CC_FAT	GO:0031090~organelle membrane	34	5.337519623	2.E-01	18416, 11852, 19720, 15275, 214952, 223	434	809	12504	1E+00	1.E+00	5.E-01	9.E+01
GOTERM_CC_FAT	GO:0019866~organelle inner membrane	13	2.040816327	4.E-01	15107, 17448, 18416, 18408, 11740, 2149	434	312	12504	1E+00	1.E+00	8.E-01	1.E+02
GOTERM_CC_FAT	GO:0005743~mitochondrial inner membrane	12	1.883830455	4.E-01	15107, 17448, 18416, 18408, 11740, 2149	434	296	12504	1E+00	1.E+00	9.E-01	1.E+02

Annotation Cluster 93	Enrichment Score: 1.5353092952792866											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR000270:Octicosapeptide/Phox/Bem1p	4	0.627943485	1.E-02	17970, 21787, 17972, 17966	630	14	17763	8.E+00	1.E+00	2.E-01	2.E+01
SMART	SM00666:PB1	4	0.627943485	2.E-02	17970, 21787, 17972, 17966	418	14	9131	6.E+00	1.E+00	2.E-01	3.E+01
UP_SEQ_FEATURE	domain:OPR	3	0.470957614	9.E-02	17970, 17972, 17966	618	13	16021	6.E+00	1.E+00	9.E-01	8.E+01

Annotation Cluster 94	Enrichment Score: 1.5230101593465137											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR



GOTERM_BP_FAT	GO:0019221~cytokine-mediated signaling pathway	9	1.412872841	2.E-03	15170, 17874, 16195, 12703, 12983, 1201	572	56	13588	4.E+00	1.E+00	4.E-02	4.E+00
GOTERM_BP_FAT	GO:0031349~positive regulation of defense response	9	1.412872841	2.E-03	19370, 14127, 17874, 16179, 21898, 2700	572	57	13588	4.E+00	1.E+00	4.E-02	4.E+00
INTERPRO	IPR000488:Death	3	0.470957614	3.E-01	17874, 16179, 21937	630	33	17763	3.E+00	1.E+00	1.E+00	1.E+02
SMART	SM00005:DEA TH	3	0.470957614	4.E-01	17874, 16179, 21937	418	33	9131	2.E+00	1.E+00	9.E-01	1.E+02

Annotation Cluster 95	Enrichment Score: 1.51152876146298											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0044445~cytosolic part	10	1.569858713	3.E-04	18709, 18708, 56421, 12028, 433182, 309	434	63	12504	5.E+00	1.E-01	5.E-03	4.E-01
GOTERM_MF_FAT	GO:0016303~1-phosphatidylinositol-3-kinase activity	5	0.784929356	8.E-04	18709, 18708, 11920, 30955, 18707	550	11	13288	1.E+01	4.E-01	1.E-02	1.E+00
GOTERM_MF_FAT	GO:0035004~phosphoinositide 3-kinase activity	5	0.784929356	8.E-04	18709, 18708, 11920, 30955, 18707	550	11	13288	1.E+01	4.E-01	1.E-02	1.E+00
KEGG_PATHWAY	mmu04960:Aldosterone-regulated sodium reabsorption	10	1.569858713	2.E-03	18709, 18708, 16367, 16333, 16334, 3202	409	42	5738	3.E+00	3.E-01	8.E-03	3.E+00
GOTERM_CC_FAT	GO:0005942~phosphoinositide 3-kinase complex	4	0.627943485	7.E-03	18709, 18708, 30955, 18707	434	12	12504	1.E+01	9.E-01	6.E-02	9.E+00
INTERPRO	IPR018936:Phosphatidylinositol 3- and 4-kinase, conserved site	4	0.627943485	2.E-02	56717, 11920, 30955, 18707	630	17	17763	7.E+00	1.E+00	3.E-01	3.E+01
INTERPRO	IPR000403:Phosphatidylinositol 3- and 4-kinase, catalytic	4	0.627943485	2.E-02	56717, 11920, 30955, 18707	630	17	17763	7.E+00	1.E+00	3.E-01	3.E+01
UP_SEQ_FEATURE	domain:PI3K/PI4K	4	0.627943485	2.E-02	56717, 11920, 30955, 18707	618	16	16021	6.E+00	1.E+00	5.E-01	3.E+01
GOTERM_MF_FAT	GO:0017727~lipid kinase activity	5	0.784929356	2.E-02	18709, 18708, 11920, 30955, 18707	550	27	13288	4.E+00	1.E+00	2.E-01	3.E+01
SMART	SM00146:PI3Kc	4	0.627943485	4.E-02	56717, 11920, 30955, 18707	418	17	9131	5.E+00	1.E+00	3.E-01	4.E+01
GOTERM_MF_FAT	GO:0004428~inositol or phosphatidylinositol kinase activity	5	0.784929356	5.E-02	18709, 18708, 11920, 30955, 18707	550	35	13288	3.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0046854~phosphoinositide phosphorylation	3	0.470957614	1.E-01	18708, 30955, 18707	572	13	13588	5.E+00	1.E+00	5.E-01	9.E+01
GOTERM_BP_FAT	GO:0046834~lipid phosphorylation	3	0.470957614	1.E-01	18708, 30955, 18707	572	14	13588	5.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0046486~glycerolipid metabolic process	8	1.25588697	3.E-01	18708, 17777, 11814, 669888, 30955, 185	572	129	13588	1.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0030258~lipid modification	4	0.627943485	3.E-01	18708, 26416, 30955, 18707	572	47	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0006644~phospholipid metabolic process	8	1.25588697	5.E-01	18708, 18803, 14178, 11806, 234779, 309	572	163	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0030384~phosphoinositide metabolic process	3	0.470957614	7.E-01	18708, 30955, 18707	572	63	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0006650~glycerophospholipid metabolic process	3	0.470957614	9.E-01	18708, 30955, 18707	572	88	13588	8.E-01	1.E+00	1.E+00	1.E+02

Annotation Cluster 96	Enrichment Score: 1.508294938983785											
Category	Term: positive regulation of immune cell differentiation and activation	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0045597~positive regulation of cell differentiation	18	2.825745683	1.E-03	12043, 22778, 108138, 21844, 15902, 118	572	175	13588	2.E+00	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0045582~positive regulation of T cell differentiation	7	1.098901099	2.E-03	16818, 12015, 16197, 11486, 22778, 1619	572	32	13588	5.E+00	1.E+00	3.E-02	3.E+00
GOTERM_BP_FAT	GO:0045621~positive regulation of lymphocyte differentiation	7	1.098901099	3.E-03	16818, 12015, 16197, 11486, 22778, 1619	572	34	13588	5.E+00	1.E+00	4.E-02	5.E+00
GOTERM_BP_FAT	GO:0002696~positive regulation of leukocyte activation	12	1.883830455	3.E-03	19370, 21898, 22778, 16408, 16818, 1787	572	99	13588	3.E+00	1.E+00	4.E-02	5.E+00
GOTERM_BP_FAT	GO:0050867~positive regulation of cell activation	12	1.883830455	3.E-03	19370, 21898, 22778, 16408, 16818, 1787	572	101	13588	3.E+00	1.E+00	5.E-02	6.E+00
GOTERM_BP_FAT	GO:0002694~regulation of leukocyte activation	15	2.354788069	5.E-03	19370, 15170, 21898, 22778, 16396, 1640	572	154	13588	2.E+00	1.E+00	7.E-02	9.E+00
GOTERM_BP_FAT	GO:0051251~positive regulation of lymphocyte activation	11	1.726844584	6.E-03	16408, 19370, 17874, 16818, 12015, 1619	572	94	13588	3.E+00	1.E+00	7.E-02	1.E+01
GOTERM_BP_FAT	GO:0050865~regulation of cell activation	15	2.354788069	6.E-03	19370, 15170, 21898, 22778, 16396, 1640	572	156	13588	2.E+00	1.E+00	7.E-02	1.E+01
GOTERM_BP_FAT	GO:0051249~regulation of lymphocyte activation	14	2.197802198	8.E-03	19370, 15170, 21898, 22778, 16396, 1640	572	144	13588	2.E+00	1.E+00	9.E-02	1.E+01
GOTERM_BP_FAT	GO:0045619~regulation of lymphocyte differentiation	8	1.25588697	1.E-02	15170, 16818, 12015, 16197, 11486, 2277	572	58	13588	3.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0045580~regulation of T cell differentiation	7	1.098901099	1.E-02	16818, 12015, 16197, 11486, 22778, 1619	572	48	13588	3.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0050863~regulation of T cell activation	11	1.726844584	2.E-02	16408, 15170, 16818, 12015, 16197, 2467	572	108	13588	2.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0050870~positive regulation of T cell activation	8	1.25588697	2.E-02	16408, 16818, 12015, 16197, 11486, 2277	572	66	13588	3.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0046638~positive regulation of alpha-beta T cell differentiation	4	0.627943485	4.E-02	11486, 22778, 16190, 20963	572	19	13588	5.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0050670~regulation of lymphocyte proliferation	8	1.25588697	5.E-02	16408, 15170, 17874, 246779, 11486, 218	572	80	13588	2.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0032944~regulation of mononuclear cell proliferation	8	1.25588697	5.E-02	16408, 15170, 17874, 246779, 11486, 218	572	80	13588	2.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0046634~regulation of alpha-beta T cell activation	5	0.784929356	5.E-02	11486, 22778, 16396, 16190, 20963	572	34	13588	3.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0070663~regulation of leukocyte proliferation	8	1.25588697	6.E-02	16408, 15170, 17874, 246779, 11486, 218	572	82	13588	2.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0046637~regulation of alpha-beta T cell differentiation	4	0.627943485	6.E-02	11486, 22778, 16190, 20963	572	22	13588	4.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0046635~positive regulation of alpha-beta T cell activation	4	0.627943485	9.E-02	11486, 22778, 16190, 20963	572	26	13588	4.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0050850~positive regulation of calcium-mediated signaling	3	0.470957614	1.E-01	16408, 11486, 20963	572	16	13588	4.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0045577~regulation of B cell differentiation	3	0.470957614	1.E-01	15170, 12015, 20963	572	16	13588	4.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0032946~positive regulation of mononuclear cell proliferation	5	0.784929356	2.E-01	16408, 17874, 11486, 21898, 20963	572	50	13588	2.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0050671~positive regulation of lymphocyte proliferation	5	0.784929356	2.E-01	16408, 17874, 11486, 21898, 20963	572	50	13588	2.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0050848~regulation of calcium-mediated signaling	3	0.470957614	2.E-01	16408, 11486, 20963	572	18	13588	4.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0070665~positive regulation of leukocyte proliferation	5	0.784929356	2.E-01	16408, 17874, 11486, 21898, 20963	572	52	13588	2.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0050864~regulation of B cell activation	5	0.784929356	2.E-01	15170, 12015, 11486, 21898, 20963	572	55	13588	2.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0050871~positive regulation of B cell activation	4	0.627943485	2.E-01	12015, 11486, 21898, 20963	572	37	13588	3.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0042129~regulation of T cell proliferation	5	0.784929356	2.E-01	16408, 15170, 246779, 16396, 20963	572	59	13588	2.E+00	1.E+00	8.E-01	1.E+02
KEGG_PATHWAY	mmu05340:Primary immunodeficiency	4	0.627943485	5.E-01	16818, 12229, 16197, 11486	409	36	5738	2.E+00	1.E+00	7.E-01	1.E+02

Annotation Cluster 97	Enrichment Score: 1.500799959195038											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
PIR_SUPERFAMILY	PIRSF002367:apolipoprotein A-I	6	0.941915228	5.E-06	11813, 11814, 11806, 11807, 11816, 1180	400	7	8136	2.E+01	2.E-03	1.E-03	7.E-03
SP_PIR_KEYWORDS	chylomicron	6	0.941915228	1.E-05	11813, 11814, 669888, 11816, 238055, 11	629	10	17854	2.E+01	5.E-03	2.E-04	2.E-02
GOTERM_CC_FAT	GO:0042627~chylomicron	5	0.784929356	9.E-05	11813, 11814, 669888, 11816, 11808	434	8	12504	2.E+01	3.E-02	2.E-03	1.E-01
GOTERM_CC_FAT	GO:0032994~protein-lipid complex	7	1.098901099	3.E-04	11813, 11814, 669888, 11806, 11807, 118	434	27	12504	7.E+00	9.E-02	6.E-03	4.E-01



GOTERM_CC_FAT	GO:0034358~plasma lipoprotein particle	7	1.098901099	3.E-04	11813, 11814, 669888, 11806, 11807, 118	434	27	12504	7.E+00	9.E-02	6.E-03	4.E-01
SP_PIR_KEYWORDS	vdli	5	0.784929356	4.E-04	11813, 11814, 669888, 11816, 238055	629	11	17854	1.E+01	2.E-01	3.E-03	6.E-01
GOTERM_BP_FAT	GO:0042157~lipoprotein metabolic process	11	1.726844584	1.E-03	18108, 18107, 108672, 17777, 11814, 118	572	76	13588	3.E+00	1.E+00	2.E-02	2.E+00
SP_PIR_KEYWORDS	lipid transport	8	1.25588697	2.E-03	11813, 11814, 11806, 11807, 11816, 2380	629	51	17854	4.E+00	6.E-01	1.E-02	3.E+00
SP_PIR_KEYWORDS	lipid binding	4	0.627943485	2.E-03	11807, 11816, 238055, 11808	629	8	17854	1.E+01	6.E-01	1.E-02	3.E+00
GOTERM_CC_FAT	GO:0034385~triglyceride-rich lipoprotein particle	4	0.627943485	4.E-03	11813, 11814, 669888, 11816	434	10	12504	1.E+01	8.E-01	4.E-02	6.E+00
GOTERM_CC_FAT	GO:0034361~very-low-density lipoprotein particle	4	0.627943485	4.E-03	11813, 11814, 669888, 11816	434	10	12504	1.E+01	8.E-01	4.E-02	6.E+00
INTERPRO	IPR013326:Apolipoprotein/apolipophorin	3	0.470957614	7.E-03	11806, 11816, 11808	630	4	17763	2.E+01	1.E+00	2.E-01	1.E+01
INTERPRO	IPR000074:Apolipoprotein A1/A4/E	3	0.470957614	7.E-03	11806, 11816, 11808	630	4	17763	2.E+01	1.E+00	2.E-01	1.E+01
GOTERM_BP_FAT	GO:0030300~regulation of intestinal cholesterol absorption	3	0.470957614	1.E-02	11806, 11807, 11808	572	4	13588	2.E+01	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0032374~regulation of cholesterol transport	3	0.470957614	2.E-02	11806, 11807, 11808	572	5	13588	1.E+01	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0032371~regulation of sterol transport	3	0.470957614	2.E-02	11806, 11807, 11808	572	5	13588	1.E+01	1.E+00	2.E-01	3.E+01
GOTERM_CC_FAT	GO:0034364~high-density lipoprotein particle	4	0.627943485	2.E-02	11806, 11807, 11816, 11808	434	16	12504	7.E+00	1.E+00	1.E-01	2.E+01
SP_PIR_KEYWORDS	hdl	4	0.627943485	2.E-02	11806, 11807, 11816, 11808	629	17	17854	7.E+00	1.E+00	1.E-01	3.E+01
GOTERM_BP_FAT	GO:0032368~regulation of lipid transport	3	0.470957614	2.E-02	11806, 11807, 11808	572	6	13588	1.E+01	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0044058~regulation of digestive system process	3	0.470957614	2.E-02	11806, 11807, 11808	572	6	13588	1.E+01	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0042158~lipoprotein biosynthetic process	7	1.098901099	3.E-02	18108, 18107, 108672, 17777, 11806, 118	572	55	13588	3.E+00	1.E+00	2.E-01	4.E+01
GOTERM_MF_FAT	GO:0008034~lipoprotein binding	4	0.627943485	5.E-02	11806, 11807, 11816, 21899	550	21	13288	5.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0051346~negative regulation of hydrolase activity	4	0.627943485	6.E-02	24064, 11806, 11807, 16847	572	22	13588	4.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0006869~lipid transport	10	1.569858713	6.E-02	11813, 17777, 11814, 11806, 11807, 1181	572	119	13588	2.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0010876~lipid localization	10	1.569858713	9.E-02	11813, 17777, 11814, 11806, 11807, 1181	572	128	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0055092~sterol homeostasis	4	0.627943485	9.E-02	17777, 11807, 11816, 238055	572	26	13588	4.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0042632~cholesterol homeostasis	4	0.627943485	9.E-02	17777, 11807, 11816, 238055	572	26	13588	4.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0016042~lipid catabolic process	10	1.569858713	1.E-01	18803, 11813, 11814, 669888, 234779, 16	572	134	13588	2.E+00	1.E+00	5.E-01	9.E+01
GOTERM_BP_FAT	GO:0055088~lipid homeostasis	4	0.627943485	2.E-01	17777, 11807, 11816, 238055	572	34	13588	3.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0030301~cholesterol transport	3	0.470957614	3.E-01	11806, 11816, 238055	572	23	13588	3.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0015918~sterol transport	3	0.470957614	3.E-01	11806, 11816, 238055	572	23	13588	3.E+00	1.E+00	8.E-01	1.E+02
GOTERM_MF_FAT	GO:0005319~lipid transporter activity	4	0.627943485	3.E-01	17777, 11806, 11816, 238055	550	44	13288	2.E+00	1.E+00	8.E-01	1.E+02
SP_PIR_KEYWORDS	cholesterol metabolism	3	0.470957614	3.E-01	17777, 11806, 238055	629	30	17854	3.E+00	1.E+00	6.E-01	1.E+02
UP_SEQ_FEATURE	repeat:6	5	0.784929356	3.E-01	20345, 11806, 11816, 11808, 19989	618	71	16021	2.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0043543~protein amino acid acylation	4	0.627943485	3.E-01	18108, 18107, 108672, 12914	572	48	13588	2.E+00	1.E+00	9.E-01	1.E+02
KEGG_PATHWAY	mmu03320:PPAR signaling pathway	8	1.25588697	3.E-01	78294, 11814, 669888, 11806, 11807, 185	409	79	5738	1.E+00	1.E+00	5.E-01	1.E+02
GOTERM_BP_FAT	GO:0008203~cholesterol metabolic process	5	0.784929356	3.E-01	11814, 11806, 11807, 11816, 16847	572	70	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0006497~protein amino acid lipidation	4	0.627943485	4.E-01	18108, 18107, 108672, 17777	572	50	13588	2.E+00	1.E+00	9.E-01	1.E+02
UP_SEQ_FEATURE	repeat:8	4	0.627943485	4.E-01	20345, 11806, 11816, 11808	618	58	16021	2.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:5	5	0.784929356	4.E-01	20345, 11806, 11816, 11808, 19989	618	84	16021	2.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0016125~sterol metabolic process	5	0.784929356	4.E-01	11814, 11806, 11807, 11816, 16847	572	77	13588	2.E+00	1.E+00	9.E-01	1.E+02
UP_SEQ_FEATURE	repeat:1	7	1.098901099	5.E-01	22323, 18019, 20345, 11806, 11816, 1180	618	148	16021	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:008202~steroid metabolic process	8	1.25588697	5.E-01	11814, 11806, 11807, 11816, 20887, 5420	572	161	13588	1.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:2	7	1.098901099	5.E-01	22323, 18019, 20345, 11806, 11816, 1180	618	151	16021	1.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:10	3	0.470957614	5.E-01	20345, 11806, 11808	618	46	16021	2.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:4	5	0.784929356	5.E-01	20345, 11806, 11816, 11808, 19989	618	101	16021	1.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:7	3	0.470957614	7.E-01	20345, 11816, 11808	618	67	16021	1.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:3	4	0.627943485	8.E-01	20345, 11816, 11808, 19989	618	119	16021	9.E-01	1.E+00	1.E+00	1.E+02
Annotation Cluster 98	Enrichment Score: 1.4811830263613908											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0043547~positive regulation of GTPase activity	4	0.627943485		2.E-02 71709, 11856, 19765, 19417	572	13	13588	7.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0032319~regulation of Rho GTPase activity	4	0.627943485		2.E-02 56717, 71709, 19765, 19417	572	14	13588	7.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0032321~positive regulation of Rho GTPase activity	3	0.470957614		4.E-02 71709, 19765, 19417	572	8	13588	9.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0032318~regulation of Ras GTPase activity	8	1.25588697		5.E-02 56717, 24064, 71709, 228998, 19765, 194	572	80	13588	2.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0032320~positive regulation of Ras GTPase activity	3	0.470957614		6.E-02 71709, 19765, 19417	572	10	13588	7.E+00	1.E+00	4.E-01	7.E+01
Annotation Cluster 99	Enrichment Score: 1.4722375529944358											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	dna replication	10	1.569858713		3.E-03 382985, 19891, 80905, 19714, 68240, 201	629	85	17854	3.E+00	7.E-01	2.E-02	4.E+00
GOTERM_BP_FAT	GO:0006260~DNA replication	11	1.726844584		1.E-01 382985, 19891, 80905, 19714, 68240, 201	572	152	13588	2.E+00	1.E+00	5.E-01	9.E+01
GOTERM_BP_FAT	GO:0006259~DNA metabolic process	24	3.767660911		1.E-01 382985, 19891, 80905, 53610, 68240, 168	572	421	13588	1.E+00	1.E+00	6.E-01	9.E+01
Annotation Cluster 100	Enrichment Score: 1.4423679893871715											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0005925~focal adhesion	7	1.098901099		1.E-02 22323, 12549, 236920, 54519, 18479, 231	434	57	12504	4.E+00	1.E+00	9.E-02	2.E+01
GOTERM_CC_FAT	GO:0005924~cell-substrate adherens junction	7	1.098901099		2.E-02 22323, 12549, 236920, 54519, 18479, 231	434	61	12504	3.E+00	1.E+00	1.E-01	2.E+01
GOTERM_CC_FAT	GO:0016323~basolateral plasma membrane	11	1.726844584		2.E-02 22323, 12549, 13649, 20525, 236920, 169	434	141	12504	2.E+00	1.E+00	1.E-01	3.E+01
GOTERM_CC_FAT	GO:0030055~cell-substrate junction	7	1.098901099		3.E-02 22323, 12549, 236920, 54519, 18479, 231	434	66	12504	3.E+00	1.E+00	1.E-01	3.E+01



GOTERM_CC_FAT	GO:0005912~adherens junction	9	1.412872841	3.E-02	22323, 12549, 69524, 13052, 236920, 545	434	106	12504	2.E+00	1.E+00	2.E-01	3.E+01
GOTERM_CC_FAT	GO:0030054~cell junction	24	3.767660911	6.E-02	22323, 19894, 69524, 16456, 94190, 2369	434	470	12504	1.E+00	1.E+00	2.E-01	6.E+01
GOTERM_CC_FAT	GO:0070161~anchoring junction	9	1.412872841	6.E-02	22323, 12549, 69524, 13052, 236920, 545	434	123	12504	2.E+00	1.E+00	3.E-01	6.E+01
SP_PIR_KEYWORDS	cell junction	19	2.982731554	1.E-01	22323, 69524, 16456, 19894, 94190, 2369	629	392	17854	1.E+00	1.E+00	4.E-01	9.E+01
Annotation Cluster 101	Enrichment Score: 1.4225255182672212											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0010564~regulation of cell cycle process	9	1.412872841	1.E-02	16994, 11920, 52563, 18413, 56371, 1254	572	73	13588	3.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0040020~regulation of meiosis	3	0.470957614	6.E-02	18413, 56371, 67141	572	10	13588	7.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0051445~regulation of meiotic cell cycle	3	0.470957614	8.E-02	18413, 56371, 67141	572	11	13588	6.E+00	1.E+00	4.E-01	8.E+01
Annotation Cluster 102	Enrichment Score: 1.4175543266980588											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0000015~phosphopyruvate hydratase complex	3	0.470957614	7.E-03	433182, 13807, 13806, 13808, 100044223	434	4	12504	2.E+01	9.E-01	6.E-02	9.E+00
INTERPRO	IPR000941:Enolase	3	0.470957614	7.E-03	433182, 13807, 13806, 13808, 100044223	630	4	17763	2.E+01	1.E+00	2.E-01	1.E+01
GOTERM_MF_FAT	GO:0004634~phosphopyruvate hydratase activity	3	0.470957614	1.E-02	433182, 13807, 13806, 13808, 100044223	550	4	13288	2.E+01	1.E+00	1.E-01	1.E+01
PIR_SUPERFAMILY	PIRSF001400:Enolase	3	0.470957614	1.E-02	433182, 13807, 13806, 13808, 100044223	400	4	8136	2.E+01	1.E+00	5.E-01	2.E+01
GOTERM_MF_FAT	GO:0016836~hydro-lyase activity	3	0.470957614	5.E-01	433182, 13807, 13806, 13808, 100044223	550	42	13288	2.E+00	1.E+00	1.E+00	1.E+02
KEGG_PATHWAY	mmu03018:RNA degradation	3	0.470957614	9.E-01	433182, 13807, 13806, 13808, 100044223	409	60	5738	7.E-01	1.E+00	1.E+00	1.E+02
Annotation Cluster 103	Enrichment Score: 1.4055009934724858											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0004714~transmembrane receptor protein tyrosine kinase activ	8	1.25588697	8.E-03	13836, 18596, 21687, 13649, 23920, 1971	550	56	13288	3.E+00	1.E+00	1.E-01	1.E+01
INTERPRO	IPR006211:Furin-like cysteine rich region	3	0.470957614	2.E-02	13649, 23920, 16001	630	7	17763	1.E+01	1.E+00	3.E-01	3.E+01
INTERPRO	IPR000494:EGF receptor, L domain	3	0.470957614	2.E-02	13649, 23920, 16001	630	7	17763	1.E+01	1.E+00	3.E-01	3.E+01
INTERPRO	IPR006212:Furin-like repeat	3	0.470957614	1.E-01	13649, 23920, 16001	630	17	17763	5.E+00	1.E+00	8.E-01	9.E+01
SMART	SM00261:FU	3	0.470957614	2.E-01	13649, 23920, 16001	418	17	9131	4.E+00	1.E+00	7.E-01	9.E+01
Annotation Cluster 104	Enrichment Score: 1.3782396610929972											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0002252~immune effector process	13	2.040816327	7.E-03	15170, 15018, 108138, 13035, 16803, 120	572	126	13588	2.E+00	1.E+00	8.E-02	1.E+01
GOTERM_BP_FAT	GO:0002443~leukocyte mediated immunity	10	1.569858713	1.E-02	12051, 14127, 15170, 17874, 11891, 1303	572	89	13588	3.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0002449~lymphocyte mediated immunity	8	1.25588697	4.E-02	12051, 14127, 15170, 17874, 11891, 1081	572	76	13588	3.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0002250~adaptive immune response	8	1.25588697	6.E-02	12051, 14127, 17874, 21899, 11891, 1081	572	84	13588	2.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0002460~adaptive immune response based on somatic recomb	8	1.25588697	6.E-02	12051, 14127, 17874, 21899, 11891, 1081	572	84	13588	2.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0016064~immunoglobulin mediated immune response	6	0.941915228	1.E-01	12051, 14127, 17874, 108138, 12263, 541	572	63	13588	2.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0019724~B cell mediated immunity	6	0.941915228	1.E-01	12051, 14127, 17874, 108138, 12263, 541	572	65	13588	2.E+00	1.E+00	6.E-01	9.E+01
Annotation Cluster 105	Enrichment Score: 1.3729117638179458											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_SEQ_FEATURE	short sequence motif:BH3	7	1.098901099	7.E-06	12015, 12048, 12028, 12122, 12018, 1204	618	14	16021	1.E+01	1.E-02	7.E-04	1.E-02
GOTERM_BP_FAT	GO:0001836~release of cytochrome c from mitochondria	7	1.098901099	3.E-05	12048, 12028, 12122, 12018, 12043, 1786	572	16	13588	1.E+01	8.E-02	1.E-03	5.E-02
GOTERM_BP_FAT	GO:0008637~apoptotic mitochondrial changes	8	1.25588697	6.E-05	12048, 12028, 12122, 12018, 11651, 1204	572	25	13588	8.E+00	1.E-01	2.E-03	1.E-01
INTERPRO	IPR000712:Apoptosis regulator Bcl-2, BH	7	1.098901099	1.E-04	12015, 12048, 12028, 12122, 12018, 1204	630	23	17763	9.E+00	1.E-01	6.E-03	2.E-01
SMART	SM00337:BCL	7	1.098901099	5.E-04	12015, 12048, 12028, 12122, 12018, 1204	418	23	9131	7.E+00	8.E-02	1.E-02	6.E-01
GOTERM_BP_FAT	GO:0002260~lymphocyte homeostasis	7	1.098901099	1.E-03	12442, 12028, 12018, 11651, 12043, 1905	572	30	13588	6.E+00	1.E+00	2.E-02	2.E+00
KEGG_PATHWAY	mmu05014:Amyotrophic lateral sclerosis (ALS)	12	1.883830455	2.E-03	672195, 12122, 12043, 21937, 12015, 120	409	57	5738	3.E+00	3.E-01	7.E-03	2.E+00
GOTERM_BP_FAT	GO:0030183~B cell differentiation	8	1.25588697	3.E-03	12051, 18708, 11486, 234779, 12028, 120	572	46	13588	4.E+00	1.E+00	4.E-02	5.E+00
GOTERM_BP_FAT	GO:0046902~regulation of mitochondrial membrane permeability	4	0.627943485	4.E-03	12028, 12122, 12018, 12043	572	8	13588	1.E+01	1.E+00	5.E-02	6.E+00
GOTERM_BP_FAT	GO:0010959~regulation of metal ion transport	8	1.25588697	4.E-03	17999, 234779, 14678, 12028, 12018, 116	572	48	13588	4.E+00	1.E+00	5.E-02	6.E+00
BIOCARTA	m_chemicalPathway:Apoptotic Signaling in Response to DNA Dam	9	1.412872841	4.E-03	672195, 12015, 12048, 11920, 12028, 121	167	20	1171	3.E+00	6.E-01	4.E-02	5.E+00
GOTERM_BP_FAT	GO:0043269~regulation of ion transport	9	1.412872841	4.E-03	16994, 17999, 234779, 14678, 12028, 120	572	62	13588	3.E+00	1.E+00	6.E-02	7.E+00
GOTERM_BP_FAT	GO:0001776~leukocyte homeostasis	7	1.098901099	5.E-03	12442, 12028, 12018, 11651, 12043, 1905	572	39	13588	4.E+00	1.E+00	7.E-02	9.E+00
UP_SEQ_FEATURE	short sequence motif:BH1	4	0.627943485	6.E-03	12048, 12028, 12018, 12043	618	10	16021	1.E+01	1.E+00	2.E-01	9.E+00
GOTERM_BP_FAT	GO:0043029~T cell homeostasis	5	0.784929356	6.E-03	12442, 12028, 11651, 12043, 19056	572	18	13588	7.E+00	1.E+00	7.E-02	1.E+01
UP_SEQ_FEATURE	short sequence motif:BH2	4	0.627943485	7.E-03	12048, 12028, 12018, 12043	618	11	16021	9.E+00	1.E+00	2.E-01	1.E+01
BIOCARTA	m_badPathway:Regulation of BAD phosphorylation	8	1.25588697	8.E-03	18708, 12015, 12048, 12028, 11651, 1204	167	18	1171	3.E+00	8.E-01	7.E-02	1.E+01
GOTERM_BP_FAT	GO:0033135~regulation of peptidyl-serine phosphorylation	4	0.627943485	9.E-03	12028, 12018, 18413, 12043	572	11	13588	9.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0070059~apoptosis in response to endoplasmic reticulum stres	3	0.470957614	1.E-02	12028, 12018, 12043	572	4	13588	2.E+01	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0070227~lymphocyte apoptosis	4	0.627943485	1.E-02	12028, 12018, 11651, 17869	572	12	13588	8.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0032844~regulation of homeostatic process	8	1.25588697	1.E-02	14127, 16818, 21349, 11486, 12028, 2641	572	60	13588	3.E+00	1.E+00	1.E-01	2.E+01
INTERPRO	IPR002475:BCL2-like apoptosis inhibitor	4	0.627943485	1.E-02	12048, 12028, 12018, 12043	630	15	17763	8.E+00	1.E+00	2.E-01	2.E+01
GOTERM_BP_FAT	GO:0043524~negative regulation of neuron apoptosis	7	1.098901099	2.E-02	218397, 12048, 12028, 15461, 12043, 108	572	50	13588	3.E+00	1.E+00	2.E-01	3.E+01
BIOCARTA	m_mitochondriaPathway:Role of Mitochondria in Apoptotic Signali	8	1.25588697	2.E-02	672195, 66593, 12048, 12028, 12122, 120	167	21	1171	3.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0007005~mitochondrion organization	10	1.569858713	2.E-02	382985, 12048, 13052, 12028, 12122, 120	572	97	13588	2.E+00	1.E+00	2.E-01	3.E+01



GOTERM_BP_FAT	GO:0001782~B cell homeostasis	4	0.627943485	2.E-02	12028, 12018, 12043, 18707	572	15	13588	6.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0032469~endoplasmic reticulum calcium ion homeostasis	3	0.470957614	2.E-02	12028, 12018, 12043	572	6	13588	1.E+01	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0010332~response to gamma radiation	4	0.627943485	3.E-02	12028, 12018, 12043, 108138	572	17	13588	6.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0010522~regulation of calcium ion transport into cytosol	3	0.470957614	4.E-02	12028, 12018, 12043	572	8	13588	9.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0043271~negative regulation of ion transport	4	0.627943485	4.E-02	16994, 17999, 14678, 12043	572	19	13588	5.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0043270~positive regulation of ion transport	4	0.627943485	5.E-02	234779, 12028, 12018, 11651	572	20	13588	5.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0051924~regulation of calcium ion transport	5	0.784929356	5.E-02	234779, 14678, 12028, 12018, 12043	572	34	13588	3.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0009314~response to radiation	11	1.726844584	8.E-02	13872, 12048, 11920, 12028, 232087, 120	572	143	13588	2.E+00	1.E+00	4.E-01	8.E+01
GOTERM_BP_FAT	GO:0051928~positive regulation of calcium ion transport	3	0.470957614	9.E-02	234779, 12028, 12018	572	12	13588	6.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0007006~mitochondrial membrane organization	4	0.627943485	9.E-02	12028, 12122, 12018, 12043	572	26	13588	4.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0048608~reproductive structure development	10	1.569858713	1.E-01	20779, 12048, 12028, 12018, 12043, 1250	572	130	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0014070~response to organic cyclic substance	5	0.784929356	1.E-01	12048, 12043, 12568, 16847, 13385	572	42	13588	3.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0010212~response to ionizing radiation	5	0.784929356	1.E-01	11920, 12028, 12018, 12043, 108138	572	48	13588	2.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0009791~post-embryonic development	7	1.098901099	2.E-01	12028, 109900, 12018, 238055, 12043, 13	572	87	13588	2.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0006839~mitochondrial transport	4	0.627943485	3.E-01	12028, 12122, 12018, 12043	572	42	13588	2.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0046660~female sex differentiation	5	0.784929356	3.E-01	12048, 12028, 12043, 16847, 17979	572	64	13588	2.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0022602~ovulation cycle process	4	0.627943485	3.E-01	12048, 12028, 12043, 16847	572	47	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0042698~ovulation cycle	4	0.627943485	3.E-01	12048, 12028, 12043, 16847	572	48	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0006874~cellular calcium ion homeostasis	6	0.941915228	3.E-01	16818, 13857, 11816, 12028, 12018, 1204	572	91	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0009636~response to toxin	3	0.470957614	3.E-01	12028, 12018, 12043	572	29	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0050574~calcium ion homeostasis	6	0.941915228	4.E-01	16818, 13857, 11816, 12028, 12018, 1204	572	95	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0008585~female gonad development	4	0.627943485	4.E-01	12048, 12028, 12043, 16847	572	53	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0001541~ovarian follicle development	3	0.470957614	4.E-01	12048, 12028, 12043	572	33	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0006875~cellular metal ion homeostasis	6	0.941915228	4.E-01	16818, 13857, 11816, 12028, 12018, 1204	572	100	13588	1.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0046545~development of primary female sexual characteristics	4	0.627943485	4.E-01	12048, 12028, 12043, 16847	572	57	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0050582~cellular chemical homeostasis	13	2.040816327	5.E-01	19317, 11816, 12043, 13382, 103988, 168	572	268	13588	1.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0050505~metal ion homeostasis	6	0.941915228	5.E-01	16818, 13857, 11816, 12028, 12018, 1204	572	106	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0008584~male gonad development	3	0.470957614	5.E-01	12048, 12028, 12043	572	39	13588	2.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0046546~development of primary male sexual characteristics	3	0.470957614	7.E-01	12048, 12028, 12043	572	53	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0006873~cellular ion homeostasis	11	1.726844584	7.E-01	16818, 19317, 13857, 11816, 12028, 1201	572	261	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0030005~cellular di- tri-valent inorganic cation homeostasis	6	0.941915228	7.E-01	16818, 13857, 11816, 12028, 12018, 1204	572	134	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0046661~male sex differentiation	3	0.470957614	7.E-01	12048, 12028, 12043	572	57	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0008406~gonad development	4	0.627943485	7.E-01	12048, 12028, 12043, 16847	572	88	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0050506~di- tri-valent inorganic cation homeostasis	6	0.941915228	7.E-01	16818, 13857, 11816, 12028, 12018, 1204	572	146	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0030003~cellular cation homeostasis	6	0.941915228	8.E-01	16818, 13857, 11816, 12028, 12018, 1204	572	152	13588	9.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0050801~ion homeostasis	11	1.726844584	8.E-01	16818, 19317, 13857, 11816, 12028, 1201	572	293	13588	9.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0032990~cell part morphogenesis	8	1.25588697	8.E-01	22323, 14432, 77579, 12028, 12018, 1204	572	212	13588	9.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0007548~sex differentiation	5	0.784929356	8.E-01	12048, 12028, 12043, 16847, 17979	572	130	13588	9.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0045137~development of primary sexual characteristics	4	0.627943485	8.E-01	12048, 12028, 12043, 16847	572	104	13588	9.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0050580~cation homeostasis	6	0.941915228	9.E-01	16818, 13857, 11816, 12028, 12018, 1204	572	184	13588	8.E-01	1.E+00	1.E+00	1.E+02

Annotation Cluster 106	Enrichment Score: 1.3656887633270076											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0045619~regulation of lymphocyte differentiation	8	1.25588697	1.E-02	15170, 16818, 12015, 16197, 11486, 2277	572	58	13588	3.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0050856~regulation of T cell receptor signaling pathway	3	0.470957614	8.E-02	15170, 16818, 11486	572	11	13588	6.E+00	1.E+00	4.E-01	8.E+01
GOTERM_BP_FAT	GO:0050854~regulation of antigen receptor-mediated signaling pa	3	0.470957614	1.E-01	15170, 16818, 11486	572	13	13588	5.E+00	1.E+00	5.E-01	9.E+01

Annotation Cluster 107	Enrichment Score: 1.3652774130119059											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0050900~leukocyte migration	8	1.25588697	2.E-03	20310, 14127, 20345, 12490, 16414, 2020	572	43	13588	4.E+00	1.E+00	3.E-02	3.E+00
GOTERM_BP_FAT	GO:0030595~leukocyte chemotaxis	6	0.941915228	5.E-03	20310, 14127, 16414, 20202, 16803, 1640	572	27	13588	5.E+00	1.E+00	6.E-02	8.E+00
GOTERM_BP_FAT	GO:0060326~cell chemotaxis	6	0.941915228	5.E-03	20310, 14127, 16414, 20202, 16803, 1640	572	27	13588	5.E+00	1.E+00	6.E-02	8.E+00
GOTERM_BP_FAT	GO:0030593~neutrophil chemotaxis	4	0.627943485	3.E-02	20310, 14127, 16414, 16409	572	17	13588	6.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0007610~behavior	25	3.924646782	6.E-02	17159, 12765, 11657, 16803, 14661, 1151	572	405	13588	1.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0006935~chemotaxis	9	1.412872841	9.E-02	20310, 14127, 12765, 19354, 16414, 2020	572	109	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0042330~taxis	9	1.412872841	9.E-02	20310, 14127, 12765, 19354, 16414, 2020	572	109	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0007626~locomotory behavior	15	2.354788069	1.E-01	12765, 109900, 16414, 15430, 16803, 133	572	239	13588	1.E+00	1.E+00	6.E-01	9.E+01
SP_PIR_KEYWORDS	chemotaxis	4	0.627943485	4.E-01	20310, 12765, 20202, 20201	629	62	17854	2.E+00	1.E+00	7.E-01	1.E+02
SP_PIR_KEYWORDS	Antimicrobial	3	0.470957614	7.E-01	20202, 20201, 16803	629	68	17854	1.E+00	1.E+00	9.E-01	1.E+02

Annotation Cluster 108	Enrichment Score: 1.3480365808061512											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0001501~skeletal system development	22	3.453689168	9.E-03	78294, 12842, 69121, 17869, 12043, 1543	572	285	13588	2.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0001649~osteoblast differentiation	6	0.941915228	5.E-02	78294, 12842, 12161, 208727, 16000, 142	572	47	13588	3.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0001503~ossification	9	1.412872841	8.E-02	78294, 12842, 12161, 69121, 12043, 1922	572	106	13588	2.E+00	1.E+00	4.E-01	8.E+01



GOTERM_BP_FAT	GO:0060348~bone development	9	1.412872841	1.E-01	78294, 12842, 12161, 69121, 12043, 1922	572	118	13588	2.E+00	1.E+00	6.E-01	9.E+01
Annotation Cluster 109	Enrichment Score: 1.3478891645859494											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0051640~organelle localization	8	1.25588697	7.E-03	245049, 11657, 77579, 12540, 11891, 171	572	54	13588	4.E+00	1.E+00	8.E-02	1.E+01
GOTERM_MF_FAT	GO:0017022~myosin binding	3	0.470957614	1.E-01	245049, 11891, 171531	550	13	13288	6.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0051648~vesicle localization	3	0.470957614	1.E-01	245049, 11891, 171531	572	15	13588	5.E+00	1.E+00	6.E-01	9.E+01
Annotation Cluster 110	Enrichment Score: 1.3353470020211051											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0007281~germ cell development	10	1.569858713	3.E-02	56717, 12048, 12028, 72508, 11651, 1204	572	101	13588	2.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0007292~female gamete generation	7	1.098901099	3.E-02	20779, 11920, 12043, 12531, 16847, 2011	572	56	13588	3.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0048599~oocyte development	4	0.627943485	3.E-02	12043, 12531, 20112, 67141	572	17	13588	6.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0009994~oocyte differentiation	4	0.627943485	4.E-02	12043, 12531, 20112, 67141	572	18	13588	5.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0001556~oocyte maturation	3	0.470957614	6.E-02	12531, 20112, 67141	572	10	13588	7.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0048477~oogenesis	5	0.784929356	8.E-02	20779, 12043, 12531, 20112, 67141	572	39	13588	3.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0048469~cell maturation	7	1.098901099	9.E-02	12229, 19713, 12531, 20112, 13382, 6714	572	75	13588	2.E+00	1.E+00	5.E-01	8.E+01
Annotation Cluster 111	Enrichment Score: 1.3241443909256583											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0002822~regulation of adaptive immune response based on so	9	1.412872841	2.E-03	14972, 14127, 15170, 15018, 16197, 1148	572	56	13588	4.E+00	1.E+00	4.E-02	4.E+00
GOTERM_BP_FAT	GO:0002819~regulation of adaptive immune response	9	1.412872841	2.E-03	14972, 14127, 15170, 15018, 16197, 1148	572	56	13588	4.E+00	1.E+00	4.E-02	4.E+00
GOTERM_BP_FAT	GO:0002706~regulation of lymphocyte mediated immunity	9	1.412872841	6.E-03	19370, 14972, 14127, 15170, 15018, 1619	572	65	13588	3.E+00	1.E+00	7.E-02	1.E+01
GOTERM_BP_FAT	GO:0048585~negative regulation of response to stimulus	7	1.098901099	5.E-02	56717, 15170, 12703, 16197, 12702, 1148	572	65	13588	3.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0002823~negative regulation of adaptive immune response ba	3	0.470957614	1.E-01	15170, 16197, 19056	572	13	13588	5.E+00	1.E+00	5.E-01	9.E+01
GOTERM_BP_FAT	GO:0002820~negative regulation of adaptive immune response	3	0.470957614	1.E-01	15170, 16197, 19056	572	13	13588	5.E+00	1.E+00	5.E-01	9.E+01
GOTERM_BP_FAT	GO:0002704~negative regulation of leukocyte mediated immunity	3	0.470957614	1.E-01	15170, 16197, 19056	572	14	13588	5.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0002707~negative regulation of lymphocyte mediated immunit	3	0.470957614	1.E-01	15170, 16197, 19056	572	14	13588	5.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0002698~negative regulation of immune effector process	3	0.470957614	2.E-01	15170, 16197, 19056	572	20	13588	4.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0002683~negative regulation of immune system process	6	0.941915228	2.E-01	15170, 16197, 11486, 16396, 16190, 1905	572	76	13588	2.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0050777~negative regulation of immune response	3	0.470957614	3.E-01	15170, 16197, 19056	572	26	13588	3.E+00	1.E+00	9.E-01	1.E+02
Annotation Cluster 112	Enrichment Score: 1.3156787572300654											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0009119~ribonucleoside metabolic process	7	1.098901099	5.E-03	22017, 11486, 72269, 232087, 56749, 222	572	39	13588	4.E+00	1.E+00	7.E-02	9.E+00
GOTERM_BP_FAT	GO:0009116~nucleoside metabolic process	8	1.25588697	9.E-03	22017, 11486, 72269, 232087, 56749, 708	572	56	13588	3.E+00	1.E+00	1.E-01	1.E+01
GOTERM_BP_FAT	GO:0034655~nucleobase, nucleoside, nucleotide and nucleic acid c	6	0.941915228	2.E-02	11486, 17970, 72269, 17969, 22271, 9958	572	36	13588	4.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0034656~nucleobase, nucleoside and nucleotide catabolic proc	6	0.941915228	2.E-02	11486, 17970, 72269, 17969, 22271, 9958	572	36	13588	4.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0046131~pyrimidine ribonucleoside metabolic process	4	0.627943485	2.E-02	72269, 56749, 22271, 99586	572	15	13588	6.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0009164~nucleoside catabolic process	3	0.470957614	2.E-02	11486, 72269, 99586	572	6	13588	1.E+01	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0044270~nitrogen compound catabolic process	6	0.941915228	3.E-02	11486, 17970, 72269, 17969, 22271, 9958	572	42	13588	3.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0006213~pyrimidine nucleoside metabolic process	4	0.627943485	6.E-02	72269, 56749, 22271, 99586	572	22	13588	4.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0006220~pyrimidine nucleotide metabolic process	4	0.627943485	1.E-01	56749, 22271, 66588, 99586	572	27	13588	4.E+00	1.E+00	5.E-01	9.E+01
GOTERM_BP_FAT	GO:0009166~nucleotide catabolic process	4	0.627943485	1.E-01	11486, 17970, 17969, 22271	572	31	13588	3.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0046128~purine ribonucleoside metabolic process	3	0.470957614	3.E-01	22017, 11486, 232087	572	24	13588	3.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0042278~purine nucleoside metabolic process	3	0.470957614	3.E-01	22017, 11486, 232087	572	24	13588	3.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0046700~heterocycle catabolic process	3	0.470957614	6.E-01	11486, 72269, 99586	572	46	13588	2.E+00	1.E+00	1.E+00	1.E+02
Annotation Cluster 113	Enrichment Score: 1.3155625587043756											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_SEQ_FEATURE	DNA-binding region:Basic motif	14	2.197802198	7.E-03	11865, 12753, 17869, 14281, 18022, 1428	618	154	16021	2.E+00	1.E+00	2.E-01	1.E+01
INTERPRO	IPR001092:Basic helix-loop-helix dimerisation region bHLH	9	1.412872841	4.E-02	11865, 12753, 21349, 17119, 17869, 1797	630	111	17763	2.E+00	1.E+00	5.E-01	5.E+01
UP_SEQ_FEATURE	domain:Helix-loop-helix motif	9	1.412872841	6.E-02	11865, 12753, 21349, 17119, 17869, 1797	618	109	16021	2.E+00	1.E+00	8.E-01	6.E+01
INTERPRO	IPR013767:PAS fold	4	0.627943485	7.E-02	11865, 12753, 17978, 17979	630	27	17763	4.E+00	1.E+00	6.E-01	7.E+01
INTERPRO	IPR011598:Helix-loop-helix DNA-binding	7	1.098901099	8.E-02	11865, 12753, 21349, 17119, 17869, 1797	630	85	17763	2.E+00	1.E+00	7.E-01	7.E+01
SMART	SM00353:HLH	9	1.412872841	1.E-01	11865, 12753, 21349, 17119, 17869, 1797	418	111	9131	2.E+00	1.E+00	6.E-01	8.E+01
Annotation Cluster 114	Enrichment Score: 1.3062999416357697											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	vidl	5	0.784929356	4.E-04	11813, 11814, 669888, 11816, 238055	629	11	17854	1.E+01	2.E-01	3.E-03	6.E-01
INTERPRO	IPR001711:Phospholipase C, phosphatidylinositol-specific, Y domain	4	0.627943485	1.E-02	18803, 234779, 18797, 18795	630	15	17763	8.E+00	1.E+00	2.E-01	2.E+01
INTERPRO	IPR001192:Phospholipase C, phosphoinositol-specific, C-terminal (P	4	0.627943485	1.E-02	18803, 234779, 18797, 18795	630	15	17763	8.E+00	1.E+00	2.E-01	2.E+01
UP_SEQ_FEATURE	domain:PI-PLC Y-box	4	0.627943485	2.E-02	18803, 234779, 18797, 18795	618	14	16021	7.E+00	1.E+00	4.E-01	2.E+01
UP_SEQ_FEATURE	domain:PI-PLC X-box	4	0.627943485	2.E-02	18803, 234779, 18797, 18795	618	16	16021	6.E+00	1.E+00	5.E-01	3.E+01
GOTERM_MF_FAT	GO:0004435~phosphoinositide phospholipase C activity	4	0.627943485	2.E-02	18803, 234779, 18797, 18795	550	15	13288	6.E+00	1.E+00	2.E-01	3.E+01



INTERPRO	IPR000909:Phospholipase C, phosphatidylinositol-specific, X region	4	0.627943485	3.E-02 18803, 234779, 18797, 18795	630	19	17763	6.E+00	1.E+00	4.E-01	4.E+01
SMART	SM00149:PLCYc	4	0.627943485	3.E-02 18803, 234779, 18797, 18795	418	15	9131	6.E+00	1.E+00	2.E-01	3.E+01
GOTERM_MF_FAT	GO:0008081~phosphoric diester hydrolase activity	8	1.25588697	3.E-02 18803, 234779, 20598, 18576, 18575, 185	550	72	13288	3.E+00	1.E+00	3.E-01	4.E+01
GOTERM_MF_FAT	GO:0004629~phospholipase C activity	4	0.627943485	4.E-02 18803, 234779, 18797, 18795	550	19	13288	5.E+00	1.E+00	3.E-01	5.E+01
UP_SEQ_FEATURE	domain:C2	7	1.098901099	5.E-02 18803, 17999, 234779, 16396, 18797, 109	618	68	16021	3.E+00	1.E+00	7.E-01	6.E+01
SMART	SM00148:PLCXc	4	0.627943485	5.E-02 18803, 234779, 18797, 18795	418	19	9131	5.E+00	1.E+00	4.E-01	5.E+01
INTERPRO	IPR017946:PLC~like phosphodiesterase, TIM beta/alpha-barrel dom	4	0.627943485	6.E-02 18803, 234779, 18797, 18795	630	25	17763	5.E+00	1.E+00	6.E-01	6.E+01
SP_PIR_KEYWORDS	lipid degradation	7	1.098901099	6.E-02 18803, 11813, 11814, 669888, 234779, 18	629	79	17854	3.E+00	1.E+00	2.E-01	6.E+01
KEGG_PATHWAY	mmu04070:Phosphatidylinositol signaling system	10	1.569858713	8.E-02 18709, 18708, 18803, 234779, 12315, 320	409	75	5738	2.E+00	1.E+00	2.E-01	6.E+01
GOTERM_BP_FAT	GO:0044242~cellular lipid catabolic process	6	0.941915228	9.E-02 18803, 11814, 669888, 234779, 238055, 1	572	56	13588	3.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0016042~lipid catabolic process	10	1.569858713	1.E-01 18803, 11813, 11814, 669888, 234779, 16	572	134	13588	2.E+00	1.E+00	5.E-01	9.E+01
GOTERM_BP_FAT	GO:0009395~phospholipid catabolic process	3	0.470957614	2.E-01 18803, 234779, 18797	572	17	13588	4.E+00	1.E+00	7.E-01	1.E+02
KEGG_PATHWAY	mmu00562:inositol phosphate metabolism	7	1.098901099	2.E-01 18803, 234779, 30955, 21991, 18797, 187	409	54	5738	2.E+00	1.E+00	4.E-01	9.E+01
GOTERM_BP_FAT	GO:0019637~organophosphate metabolic process	11	1.726844584	2.E-01 18708, 18803, 14178, 11806, 234779, 179	572	176	13588	1.E+00	1.E+00	7.E-01	1.E+02
GOTERM_MF_FAT	GO:0004620~phospholipase activity	5	0.784929356	3.E-01 18803, 234779, 20598, 18797, 18795	550	63	13288	2.E+00	1.E+00	8.E-01	1.E+02
GOTERM_MF_FAT	GO:0016298~lipase activity	6	0.941915228	3.E-01 18803, 669888, 234779, 20598, 18797, 18	550	84	13288	2.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0006644~phospholipid metabolic process	8	1.25588697	5.E-01 18708, 18803, 14178, 11806, 234779, 309	572	163	13588	1.E+00	1.E+00	1.E+00	1.E+02

Annotation Cluster 115	Enrichment Score: 1.2961479639772813											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0001914~regulation of T cell mediated cytotoxicity	5	0.784929356	8.E-04	14972, 15018, 16197, 19056, 12010	572	11	13588	1.E+01	9.E-01	2.E-02	1.E+00
GOTERM_BP_FAT	GO:0031341~regulation of cell killing	7	1.098901099	1.E-03	19370, 14972, 15018, 16197, 27007, 3790	572	30	13588	6.E+00	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0001910~regulation of leukocyte mediated cytotoxicity	7	1.098901099	1.E-03	19370, 14972, 15018, 16197, 27007, 3790	572	30	13588	6.E+00	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0002822~regulation of adaptive immune response based on so	9	1.412872841	2.E-03	14972, 14127, 15170, 15018, 16197, 1148	572	56	13588	4.E+00	1.E+00	4.E-02	4.E+00
GOTERM_BP_FAT	GO:0002819~regulation of adaptive immune response	9	1.412872841	2.E-03	14972, 14127, 15170, 15018, 16197, 1148	572	56	13588	4.E+00	1.E+00	4.E-02	4.E+00
GOTERM_BP_FAT	GO:0002703~regulation of leukocyte mediated immunity	10	1.569858713	3.E-03	19370, 14972, 14127, 15170, 15018, 1619	572	70	13588	3.E+00	1.E+00	4.E-02	4.E+00
GOTERM_BP_FAT	GO:0002699~positive regulation of immune effector process	8	1.25588697	3.E-03	19370, 14972, 14127, 15018, 27007, 3790	572	46	13588	4.E+00	1.E+00	4.E-02	5.E+00
GOTERM_BP_FAT	GO:0002697~regulation of immune effector process	11	1.726844584	4.E-03	19370, 14972, 14127, 15170, 15018, 1619	572	88	13588	3.E+00	1.E+00	5.E-02	7.E+00
GOTERM_BP_FAT	GO:0002474~antigen processing and presentation of peptide antig	5	0.784929356	5.E-03	15007, 14972, 14127, 15018, 12010	572	17	13588	7.E+00	1.E+00	6.E-02	8.E+00
GOTERM_BP_FAT	GO:0002706~regulation of lymphocyte mediated immunity	9	1.412872841	6.E-03	19370, 14972, 14127, 15170, 15018, 1619	572	65	13588	3.E+00	1.E+00	7.E-02	1.E+01
SP_PIR_KEYWORDS	mhc i	4	0.627943485	6.E-03	15007, 14972, 15018, 12010	629	11	17854	1.E+01	9.E-01	3.E-02	8.E+00
GOTERM_BP_FAT	GO:0002709~regulation of T cell mediated immunity	5	0.784929356	6.E-03	14972, 15018, 16197, 19056, 12010	572	18	13588	7.E+00	1.E+00	7.E-02	1.E+01
GOTERM_BP_FAT	GO:0031343~positive regulation of cell killing	5	0.784929356	1.E-02	19370, 14972, 15018, 27007, 379043, 120	572	23	13588	5.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0001912~positive regulation of leukocyte mediated cytotoxicity	5	0.784929356	1.E-02	19370, 14972, 15018, 27007, 379043, 120	572	23	13588	5.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0002708~positive regulation of lymphocyte mediated immunity	6	0.941915228	3.E-02	19370, 14972, 14127, 15018, 27007, 3790	572	40	13588	4.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0002705~positive regulation of leukocyte mediated immunity	6	0.941915228	3.E-02	19370, 14972, 14127, 15018, 27007, 3790	572	40	13588	4.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0032729~positive regulation of interferon-gamma production	4	0.627943485	3.E-02	12051, 19370, 15018, 27007, 379043	572	17	13588	6.E+00	1.E+00	2.E-01	4.E+01
UP_SEQ_FEATURE	region of interest:Alpha-3	3	0.470957614	4.E-02	15007, 14972, 15018	618	9	16021	9.E+00	1.E+00	7.E-01	5.E+01
GOTERM_BP_FAT	GO:0001916~positive regulation of T cell mediated cytotoxicity	3	0.470957614	5.E-02	14972, 15018, 12010	572	9	13588	8.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0002824~positive regulation of adaptive immune response bas	5	0.784929356	5.E-02	14972, 14127, 15018, 11486, 12010	572	34	13588	3.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0002821~positive regulation of adaptive immune response	5	0.784929356	5.E-02	14972, 14127, 15018, 11486, 12010	572	34	13588	3.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0048002~antigen processing and presentation of peptide antig	5	0.784929356	6.E-02	15007, 14972, 14127, 15018, 12010	572	35	13588	3.E+00	1.E+00	4.E-01	7.E+01
UP_SEQ_FEATURE	region of interest:Alpha-1	3	0.470957614	6.E-02	15007, 14972, 15018	618	11	16021	7.E+00	1.E+00	8.E-01	7.E+01
UP_SEQ_FEATURE	region of interest:Alpha-2	3	0.470957614	6.E-02	15007, 14972, 15018	618	11	16021	7.E+00	1.E+00	8.E-01	7.E+01
UP_SEQ_FEATURE	domain:Ig-like C1-type	4	0.627943485	7.E-02	15007, 14972, 15018, 12010	618	25	16021	4.E+00	1.E+00	8.E-01	7.E+01
GOTERM_BP_FAT	GO:0002711~positive regulation of T cell mediated immunity	3	0.470957614	1.E-01	14972, 15018, 12010	572	13	13588	5.E+00	1.E+00	5.E-01	9.E+01
GOTERM_BP_FAT	GO:0032649~regulation of interferon-gamma production	4	0.627943485	1.E-01	12051, 19370, 15018, 27007, 379043	572	32	13588	3.E+00	1.E+00	6.E-01	9.E+01
GOTERM_CC_FAT	GO:0042612~MHC class I protein complex	4	0.627943485	2.E-01	15007, 14972, 15018, 12010	434	42	12504	3.E+00	1.E+00	5.E-01	9.E+01
INTERPRO	IPR011161:MHC class I-like antigen recognition	4	0.627943485	3.E-01	15007, 19370, 14972, 15018, 379043	630	49	17763	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0002478~antigen processing and presentation of exogenous pi	3	0.470957614	3.E-01	14972, 14127, 12010	572	23	13588	3.E+00	1.E+00	8.E-01	1.E+02
GOTERM_CC_FAT	GO:0042611~MHC protein complex	4	0.627943485	3.E-01	15007, 14972, 15018, 12010	434	52	12504	2.E+00	1.E+00	7.E-01	1.E+02
UP_SEQ_FEATURE	region of interest:Connecting peptide	3	0.470957614	3.E-01	15007, 14972, 15018	618	28	16021	3.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0019882~antigen processing and presentation	6	0.941915228	3.E-01	15007, 19370, 14972, 14127, 15018, 3790	572	87	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0019884~antigen processing and presentation of exogenous ar	3	0.470957614	3.E-01	14972, 14127, 12010	572	28	13588	3.E+00	1.E+00	9.E-01	1.E+02
PIR_SUPERFAMILY	PIRSF001990:class I histocompatibility antigen	3	0.470957614	3.E-01	15007, 14972, 15018	400	24	8136	3.E+00	1.E+00	1.E+00	1.E+02
INTERPRO	IPR001039:MHC class I, alpha chain, alpha1 and alpha2	3	0.470957614	4.E-01	15007, 14972, 15018	630	41	17763	2.E+00	1.E+00	1.E+00	1.E+02
KEGG_PATHWAY	mmu04940:Type I diabetes mellitus	6	0.941915228	5.E-01	15007, 14972, 15018, 16333, 16334, 1493	409	63	5738	1.E+00	1.E+00	7.E-01	1.E+02
INTERPRO	IPR003597:Immunoglobulin C1-set	4	0.627943485	6.E-01	15007, 14972, 15018, 12010	630	83	17763	1.E+00	1.E+00	1.E+00	1.E+02
INTERPRO	IPR003006:Immunoglobulin/major histocompatibility complex, cons	4	0.627943485	7.E-01	15007, 14972, 15018, 12010	630	98	17763	1.E+00	1.E+00	1.E+00	1.E+02
SMART	SM004071:Gc1	4	0.627943485	7.E-01	15007, 14972, 15018, 12010	418	83	9131	1.E+00	1.E+00	1.E+00	1.E+02
KEGG_PATHWAY	mmu04612:Antigen processing and presentation	6	0.941915228	8.E-01	15007, 14972, 15018, 14827, 12912, 1201	409	91	5738	9.E-01	1.E+00	9.E-01	1.E+02
KEGG_PATHWAY	mmu05330:Allograft rejection	4	0.627943485	8.E-01	15007, 14972, 15018, 14939	409	58	5738	1.E+00	1.E+00	9.E-01	1.E+02
KEGG_PATHWAY	mmu05332:Graft-versus-host disease	4	0.627943485	8.E-01	15007, 14972, 15018, 14939	409	58	5738	1.E+00	1.E+00	9.E-01	1.E+02
KEGG_PATHWAY	mmu05320:Autoimmune thyroid disease	4	0.627943485	9.E-01	15007, 14972, 15018, 14939	409	72	5738	8.E-01	1.E+00	1.E+00	1.E+02



[illegible][illegible]

Annotation Cluster 118		Enrichment Score: 1.2616810656414148													
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR			
GOTERM_BP_FAT	GO:0007160~cell-matrix adhesion	8	1.25588697	5.E-03	21687, 50768, 12043, 16414, 11856, 1641	572	572	50	13588	4.E+00	1.E+00	6.E-02	8.E+00		
GOTERM_BP_FAT	GO:0031589~cell-substrate adhesion	8	1.25588697	1.E-02	21687, 50768, 12043, 16414, 11856, 1641	572	572	57	13588	3.E+00	1.E+00	1.E-01	2.E+01		
GOTERM_BP_FAT	GO:0048041~focal adhesion formation	3	0.470957614	4.E-02	50768, 12043, 11856	572	572	8	13588	9.E+00	1.E+00	3.E-01	5.E+01		
GOTERM_BP_FAT	GO:0034330~cell junction organization	5	0.784929356	4.E-02	13052, 50768, 12043, 11856, 12540	572	572	32	13588	4.E+00	1.E+00	3.E-01	5.E+01		
GOTERM_BP_FAT	GO:0007044~cell-substrate junction assembly	3	0.470957614	1.E-01	50768, 12043, 11856	572	572	14	13588	5.E+00	1.E+00	6.E-01	9.E+01		
GOTERM_BP_FAT	GO:0034329~cell junction assembly	3	0.470957614	2.E-01	50768, 12043, 11856	572	572	21	13588	3.E+00	1.E+00	8.E-01	1.E+02		
INTERPRO	IPR013111:EGF, extracellular	3	0.470957614	7.E-01	21687, 16414, 16412	630	630	71	17763	1.E+00	1.E+00	1.E+00	1.E+02		

Annotation Cluster	Enrichment Score: 1.251765784365012																	
Category	Term	Count	%	PValue	Genes	List	Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR					
UP_SEQ_FEATURE	domain:WW 1	5	0.784929356	2.E-02	17999, 223666, 75415, 16396, 22601	618		28	16021	5.E+00	1.E+00	5.E-01	3.E+01					
UP_SEQ_FEATURE	domain:WW 2	5	0.784929356	2.E-02	17999, 223666, 75415, 16396, 22601	618		28	16021	5.E+00	1.E+00	5.E-01	3.E+01					
INTERPRO	IPR001202:WW/Rsp5/WWP	5	0.784929356	1.E-01	17999, 223666, 75415, 16396, 22601	630		51	17763	3.E+00	1.E+00	7.E-01	8.E+01					
SMART	SM00456:WW	5	0.784929356	2.E-01	17999, 223666, 75415, 16396, 22601	418		51	9131	2.E+00	1.E+00	7.E-01	9.E+01					

Annotation Cluster 120	Enrichment Score: 1.2431789239095996														
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR			
UP_SEQ_FEATURE	DNA-binding region:Basic motif	14	2.197802198		7.E-03 11865, 12753, 17869, 14281, 18022, 1428	618	154	16021	2.E+00	1.E+00	2.E-01	1.E+01			
INTERPRO	IPR011616:bZIP transcription factor, bZIP-1	5	0.784929356		2.E-02 16477, 14281, 14282, 18022, 12912	630	30	17763	5.E+00	1.E+00	3.E-01	3.E+01			
INTERPRO	IPR004827:basic-leucine zipper (bZIP) transcription factor	6	0.941915228		4.E-02 16477, 14281, 14282, 18022, 12912, 1713	630	54	17763	3.E+00	1.E+00	5.E-01	5.E+01			
SMART	SM00338:BRLZ	6	0.941915228		1.E-01 16477, 14281, 14282, 18022, 12912, 1713	418	54	9131	2.E+00	1.E+00	5.E-01	7.E+01			
SP_PIR_KEYWORDS	leucine zipper	3	0.470957614		1.E-01 14281, 14282, 17135	629	16	17854	5.E+00	1.E+00	3.E-01	8.E+01			
UP_SEQ_FEATURE	domain:Leucine-zipper	8	1.25588697		1.E-01 17869, 16477, 14281, 14282, 18022, 1291	618	107	16021	2.E+00	1.E+00	9.E-01	9.E+01			
BIOCARTA	m_arenf2P2athway:Oxidative Stress Induced Gene Expression Via Nr	5	0.784929356		3.E-01 26416, 14281, 12912, 94284, 394436, 171	167	19	1171	2.E+00	1.E+00	7.E-01	1.E+02			

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GOTERM_BP_FAT	GO:0001541~ovarian follicle development	3	0.470957614	4.E-01	12048, 12028, 12043	572	33	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0008584~male gonad development	3	0.470957614	5.E-01	12048, 12028, 12043	572	39	13588	2.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0046546~development of primary male sexual characteristics	3	0.470957614	7.E-01	12048, 12028, 12043	572	53	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0046661~male sex differentiation	3	0.470957614	7.E-01	12048, 12028, 12043	572	57	13588	1.E+00	1.E+00	1.E+00	1.E+02
Annotation Cluster 122	Enrichment Score: 1.2336570937991438											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0043523~regulation of neuron apoptosis	10	1.569858713	6.E-03	16994, 218397, 12048, 11920, 12028, 154	572	80	13588	3.E+00	1.E+00	7.E-02	1.E+01
GOTERM_BP_FAT	GO:0051402~neuron apoptosis	4	0.627943485	3.E-02	11920, 12028, 12043, 12568	572	16	13588	6.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0043525~positive regulation of neuron apoptosis	4	0.627943485	4.E-02	16994, 11920, 12028, 12568	572	19	13588	5.E+00	1.E+00	3.E-01	5.E+01
BIOCARTA	m_p53Pathway:p53 Signaling Pathway	6	0.941915228	6.E-02	11920, 12028, 13197, 12043, 12566, 1853	167	16	1171	3.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0009628~response to abiotic stimulus	17	2.668759812	6.E-02	12842, 12955, 232087, 17869, 12043, 108	572	251	13588	2.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0009314~response to radiation	11	1.726844584	8.E-02	13872, 12048, 11920, 12028, 232087, 120	572	143	13588	2.E+00	1.E+00	4.E-01	8.E+01
GOTERM_BP_FAT	GO:0010212~response to ionizing radiation	5	0.784929356	1.E-01	11920, 12028, 12018, 12043, 108138	572	48	13588	2.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0009416~response to light stimulus	6	0.941915228	4.E-01	13872, 12028, 232087, 12043, 12568, 185	572	98	13588	1.E+00	1.E+00	9.E-01	1.E+02
Annotation Cluster 123	Enrichment Score: 1.225208402878029											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0051050~positive regulation of transport	14	2.197802198	4.E-03	68092, 11651, 12912, 103988, 16994, 141	572	132	13588	3.E+00	1.E+00	5.E-02	6.E+00
GOTERM_BP_FAT	GO:0051047~positive regulation of secretion	7	1.098901099	2.E-02	14127, 14661, 12568, 12912, 83671, 1039	572	53	13588	3.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0051046~regulation of secretion	11	1.726844584	4.E-02	14127, 14661, 11486, 380714, 18413, 185	572	125	13588	2.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0060341~regulation of cellular localization	13	2.040816327	4.E-02	380714, 68092, 12912, 103988, 24069, 14	572	161	13588	2.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0046883~regulation of hormone secretion	5	0.784929356	6.E-02	14661, 18413, 18576, 12912, 103988	572	36	13588	3.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0045921~positive regulation of exocytosis	3	0.470957614	1.E-01	14127, 12568, 20963	572	13	13588	5.E+00	1.E+00	5.E-01	9.E+01
GOTERM_BP_FAT	GO:0046887~positive regulation of hormone secretion	3	0.470957614	1.E-01	14661, 12912, 103988	572	14	13588	5.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0017157~regulation of exocytosis	4	0.627943485	1.E-01	14127, 380714, 12568, 20963	572	32	13588	3.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0060627~regulation of vesicle-mediated transport	4	0.627943485	7.E-01	14127, 380714, 12568, 20963	572	83	13588	1.E+00	1.E+00	1.E+00	1.E+02
Annotation Cluster 124	Enrichment Score: 1.2050564543885613											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	phosphoric monoester hydrolase	6	0.941915228	1.E-02	15170, 12532, 12531, 12183, 19056, 1905	629	38	17854	4.E+00	1.E+00	6.E-02	1.E+01
GOTERM_MF_FAT	GO:0004721~phosphoprotein phosphatase activity	13	2.040816327	2.E-02	15170, 218294, 19253, 14208, 16818, 190	550	152	13288	2.E+00	1.E+00	2.E-01	3.E+01
SP_PIR_KEYWORDS	protein phosphatase	10	1.569858713	3.E-02	15170, 218294, 19053, 19253, 14208, 125	629	120	17854	2.E+00	1.E+00	1.E-01	3.E+01
GOTERM_MF_FAT	GO:0016791~phosphatase activity	17	2.668759812	4.E-02	15170, 218294, 19253, 14208, 12183, 560	550	238	13288	2.E+00	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0006470~protein amino acid dephosphorylation	9	1.412872841	1.E-01	15170, 218294, 19253, 14208, 12043, 125	572	114	13588	2.E+00	1.E+00	5.E-01	9.E+01
SP_PIR_KEYWORDS	tyrosine-specific phosphatase	3	0.470957614	2.E-01	15170, 12532, 12531	629	20	17854	4.E+00	1.E+00	4.E-01	9.E+01
GOTERM_MF_FAT	GO:0004725~protein tyrosine phosphatase activity	7	1.098901099	2.E-01	15170, 218294, 19253, 26395, 12532, 125	550	101	13288	2.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0016311~dephosphorylation	9	1.412872841	2.E-01	15170, 218294, 19253, 14208, 12043, 125	572	141	13588	2.E+00	1.E+00	8.E-01	1.E+02
Annotation Cluster 125	Enrichment Score: 1.2036867681421528											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR003096:SM22/calponin	4	0.627943485	4.E-03	73341, 22324, 71994, 57257	630	10	17763	1.E+01	1.E+00	1.E-01	7.E+00
INTERPRO	IPR001715:Calponin-like actin-binding	6	0.941915228	9.E-02	73341, 22324, 18826, 71994, 57257, 1921	630	68	17763	2.E+00	1.E+00	7.E-01	8.E+01
UP_SEQ_FEATURE	domain:CH	4	0.627943485	2.E-01	73341, 22324, 71994, 57257	618	39	16021	3.E+00	1.E+00	1.E+00	1.E+02
SMART	SM00033:CH	6	0.941915228	2.E-01	73341, 22324, 18826, 71994, 57257, 1921	418	68	9131	2.E+00	1.E+00	7.E-01	9.E+01
Annotation Cluster 126	Enrichment Score: 1.198993078259313											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR008957:Fibronectin, type III-like fold	15	2.354788069	7.E-03	21687, 18414, 545156, 23920, 16195, 138	630	187	17763	2.E+00	1.E+00	1.E-01	1.E+01
INTERPRO	IPR003961:Fibronectin, type III	14	2.197802198	2.E-02	21687, 18414, 545156, 23920, 16195, 138	630	191	17763	2.E+00	1.E+00	3.E-01	3.E+01
INTERPRO	IPR003529:Long hematopoietin receptor, gp130 family 2, conserved	3	0.470957614	2.E-02	16195, 18414, 16847	630	7	17763	1.E+01	1.E+00	3.E-01	3.E+01
UP_SEQ_FEATURE	domain:Fibronectin type-III 2	9	1.412872841	9.E-02	13836, 21687, 16195, 23920, 12983, 5049	618	120	16021	2.E+00	1.E+00	9.E-01	8.E+01
UP_SEQ_FEATURE	domain:Fibronectin type-III 1	9	1.412872841	1.E-01	13836, 21687, 16195, 23920, 12983, 5049	618	121	16021	2.E+00	1.E+00	9.E-01	8.E+01
SMART	SM00060:FN3	14	2.197802198	1.E-01	21687, 18414, 545156, 23920, 16195, 138	418	191	9131	2.E+00	1.E+00	5.E-01	7.E+01
UP_SEQ_FEATURE	domain:Fibronectin type-III 3	6	0.941915228	2.E-01	21687, 16195, 23920, 18414, 16001, 1684	618	74	16021	2.E+00	1.E+00	1.E+00	9.E+01
UP_SEQ_FEATURE	domain:Fibronectin type-III 4	3	0.470957614	6.E-01	16195, 18414, 16847	618	56	16021	1.E+00	1.E+00	1.E+00	1.E+02
Annotation Cluster 127	Enrichment Score: 1.1969566320504594											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0031032~actomyosin structure organization	6	0.941915228	3.E-03	26934, 77579, 11464, 71994, 16412, 1145	572	25	13588	6.E+00	1.E+00	5.E-02	6.E+00
GOTERM_BP_FAT	GO:0060537~muscle tissue development	14	2.197802198	5.E-03	15430, 18479, 16412, 20467, 11848, 1543	572	136	13588	2.E+00	1.E+00	6.E-02	8.E+00
GOTERM_BP_FAT	GO:0014706~striated muscle tissue development	13	2.040816327	7.E-03	15430, 18479, 16412, 20467, 11848, 1543	572	127	13588	2.E+00	1.E+00	8.E-02	1.E+01
GOTERM_BP_FAT	GO:0007517~muscle organ development	15	2.354788069	2.E-02	12955, 15430, 18479, 16412, 20467, 1184	572	176	13588	2.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0007519~skeletal muscle tissue development	8	1.25588697	3.E-02	15438, 26416, 15430, 18479, 11459, 1256	572	72	13588	3.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0060538~skeletal muscle organ development	8	1.25588697	4.E-02	15438, 26416, 15430, 18479, 11459, 1256	572	74	13588	3.E+00	1.E+00	3.E-01	5.E+01



GOTERM_BP_FAT	GO:0055001~muscle cell development	7	1.098901099	4.E-02	13052, 77579, 11464, 16412, 18479, 1145	572	61	13588	3.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0030239~myofibril assembly	4	0.627943485	4.E-02	77579, 11464, 16412, 11459	572	19	13588	5.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0055002~striated muscle cell development	6	0.941915228	8.E-02	13052, 77579, 11464, 16412, 18479, 1145	572	54	13588	3.E+00	1.E+00	4.E-01	8.E+01
GOTERM_BP_FAT	GO:0048738~cardiac muscle tissue development	6	0.941915228	9.E-02	13052, 77579, 11464, 16412, 20467, 1420	572	57	13588	3.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0055007~cardiac muscle cell differentiation	4	0.627943485	1.E-01	77579, 11464, 16412, 14200	572	28	13588	3.E+00	1.E+00	5.E-01	9.E+01
GOTERM_BP_FAT	GO:0055006~cardiac cell development	3	0.470957614	1.E-01	77579, 11464, 14200	572	14	13588	5.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0055013~cardiac muscle cell development	3	0.470957614	1.E-01	77579, 11464, 14200	572	14	13588	5.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0042692~muscle cell differentiation	9	1.412872841	1.E-01	19317, 13052, 77579, 11464, 20969, 1641	572	117	13588	2.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0007422~peripheral nervous system development	4	0.627943485	1.E-01	15438, 18413, 15430, 12568	572	30	13588	3.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0035051~cardiac cell differentiation	4	0.627943485	2.E-01	77579, 11464, 16412, 14200	572	33	13588	3.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0051146~striated muscle cell differentiation	7	1.098901099	2.E-01	13052, 77579, 11464, 16412, 18479, 1145	572	89	13588	2.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0010927~cellular component assembly involved in morphogen	4	0.627943485	2.E-01	77579, 11464, 16412, 11459	572	36	13588	3.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0048747~muscle fiber development	3	0.470957614	5.E-01	13052, 18479, 11459	572	38	13588	2.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0030534~adult behavior	4	0.627943485	8.E-01	15438, 15416, 15430, 12568	572	93	13588	1.E+00	1.E+00	1.E+00	1.E+02

Annotation Cluster 128	Enrichment Score: 1.1936284543053282											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0031017~exocrine pancreas development	3	0.470957614		4.E-02 18609, 16001, 16000	572		8	13588	9.E+00	1.E+00	3.E-01
GOTERM_BP_FAT	GO:0031016~pancreas development	5	0.784929356		7.E-02 18609, 19378, 16001, 18576, 16000	572		37	13588	3.E+00	1.E+00	4.E-01
GOTERM_BP_FAT	GO:0035272~exocrine system development	5	0.784929356		9.E-02 13649, 14178, 18609, 16001, 16000	572		41	13588	3.E+00	1.E+00	5.E-01

Annotation Cluster 129	Enrichment Score: 1.1868712390050835											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0060674~placenta blood vessel development	4	0.627943485		4.E-02 12702, 26395, 11651, 16477	572		18	13588	5.E+00	1.E+00	3.E-01
GOTERM_BP_FAT	GO:0060711~labyrinthine layer development	5	0.784929356		6.E-02 12702, 14784, 26395, 11651, 16477	572		35	13588	3.E+00	1.E+00	4.E-01
GOTERM_BP_FAT	GO:0001890~placenta development	8	1.25588697		7.E-02 13649, 12702, 11486, 13857, 14784, 2639	572		87	13588	2.E+00	1.E+00	4.E-01
GOTERM_BP_FAT	GO:0001892~embryonic placenta development	6	0.941915228		1.E-01 13649, 12702, 14784, 26395, 11651, 1647	572		61	13588	2.E+00	1.E+00	5.E-01

Annotation Cluster 130	Enrichment Score: 1.1636886505295119											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0042592~homeostatic process	47	7.37833595		3.E-05 11816, 11651, 238055, 14782, 12815, 103	572		584	13588	2.E+00	8.E-02	1.E-03
GOTERM_BP_FAT	GO:0019725~cellular homeostasis	24	3.767660911		2.E-02 19317, 18453, 11816, 12043, 14827, 1478	572		343	13588	2.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0048878~chemical homeostasis	21	3.296703297		1.E-01 19317, 11807, 11816, 380714, 238055, 12	572		365	13588	1.E+00	1.E+00	6.E-01
GOTERM_BP_FAT	GO:0042391~regulation of membrane potential	7	1.098901099		4.E-01 19317, 12018, 12043, 14360, 12568, 1338	572		119	13588	1.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0055082~cellular chemical homeostasis	13	2.040816327		5.E-01 19317, 11816, 12043, 13382, 103988, 168	572		268	13588	1.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0006873~cellular ion homeostasis	11	1.726844584		7.E-01 16818, 19317, 13857, 11816, 12028, 1201	572		261	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0050801~ion homeostasis	11	1.726844584		8.E-01 16818, 19317, 13857, 11816, 12028, 1201	572		293	13588	9.E-01	1.E+00	1.E+00

Annotation Cluster 131	Enrichment Score: 1.1572054439956243											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0031400~negative regulation of protein modification process	6	0.941915228		2.E-02 15170, 12703, 12028, 12018, 12568, 6714	572		38	13588	4.E+00	1.E+00	2.E-01
GOTERM_BP_FAT	GO:0051248~negative regulation of protein metabolic process	8	1.25588697		5.E-02 15170, 13685, 12703, 12028, 12018, 1921	572		78	13588	2.E+00	1.E+00	3.E-01
GOTERM_BP_FAT	GO:0001933~negative regulation of protein amino acid phosphoryl	4	0.627943485		7.E-02 15170, 12703, 12028, 12018	572		23	13588	4.E+00	1.E+00	4.E-01
GOTERM_BP_FAT	GO:0032269~negative regulation of cellular protein metabolic proc	7	1.098901099		8.E-02 15170, 13685, 12703, 12028, 12018, 1256	572		72	13588	2.E+00	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0042326~negative regulation of phosphorylation	4	0.627943485		1.E-01 15170, 12703, 12028, 12018	572		27	13588	4.E+00	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0045936~negative regulation of phosphate metabolic process	4	0.627943485		1.E-01 15170, 12703, 12028, 12018	572		29	13588	3.E+00	1.E+00	6.E-01
GOTERM_BP_FAT	GO:0010563~negative regulation of phosphorus metabolic process	4	0.627943485		1.E-01 15170, 12703, 12028, 12018	572		29	13588	3.E+00	1.E+00	6.E-01

Annotation Cluster 132	Enrichment Score: 1.1486023817910165											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0005792~microsome	14	2.197802198		8.E-03 18453, 76279, 238055, 12043, 98238, 664	434		176	12504	2.E+00	9.E-01	7.E-02
GOTERM_CC_FAT	GO:0042598~vesicular fraction	14	2.197802198		1.E-02 18453, 76279, 238055, 12043, 98238, 664	434		182	12504	2.E+00	1.E+00	7.E-02
SP_PIR_KEYWORDS	microsome	9	1.412872841		2.E-02 56615, 76279, 13087, 98238, 66447, 1307	629		100	17854	3.E+00	1.E+00	1.E-01
GOTERM_CC_FAT	GO:0005783~endoplasmic reticulum	24	3.767660911		9.E-01 238055, 56615, 56717, 12304, 12018, 238	434		838	12504	8.E-01	1.E+00	1.E+00
SP_PIR_KEYWORDS	endoplasmic reticulum	19	2.982731554		9.E-01 18453, 76279, 12043, 14827, 98238, 6644	629		678	17854	8.E-01	1.E+00	1.E+00

Annotation Cluster 133	Enrichment Score: 1.129399972427128											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0051051~negative regulation of transport	10	1.569858713		3.E-03 16994, 11486, 17999, 14678, 104215, 184	572		72	13588	3.E+00	1.E+00	5.E-02
GOTERM_BP_FAT	GO:0032880~regulation of protein localization	10	1.569858713		1.E-02 16994, 18826, 14570, 104215, 192662, 11	572		90	13588	3.E+00	1.E+00	1.E-01
GOTERM_BP_FAT	GO:0032386~regulation of intracellular transport	5	0.784929356		1.E-01 18826, 68092, 192176, 12568, 24069	572		42	13588	3.E+00	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0033157~regulation of intracellular protein transport	4	0.627943485		1.E-01 18826, 192176, 12568, 24069	572		30	13588	3.E+00	1.E+00	6.E-01
GOTERM_BP_FAT	GO:0070201~regulation of establishment of protein localization	6	0.941915228		2.E-01 16994, 18826, 104215, 192176, 12568, 24	572		71	13588	2.E+00	1.E+00	7.E-01
GOTERM_BP_FAT	GO:0046822~regulation of nucleocytoplasmic transport	4	0.627943485		2.E-01 68092, 192176, 12568, 24069	572		35	13588	3.E+00	1.E+00	7.E-01
GOTERM_BP_FAT	GO:0051224~negative regulation of protein transport	3	0.470957614		2.E-01 192176, 12568, 24069	572		19	13588	4.E+00	1.E+00	7.E-01



GOTERM_BP_FAT	GO:0051223~regulation of protein transport	5	0.784929356	3.E-01	16994, 18826, 192176, 12568, 24069	572	65	13588	2.E+00	1.E+00	8.E-01	1.E+02
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Annotation Cluster 134	Enrichment Score: 1.0678512618009557											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0009156~ribonucleoside monophosphate biosynthetic process	5	0.784929356	5.E-03	11486, 11717, 56749, 11566, 99586	572	17	13588	7.E+00	1.E+00	6.E-02	8.E+00
GOTERM_BP_FAT	GO:0009119~ribonucleoside metabolic process	7	1.098901099	5.E-03	22017, 11486, 72269, 232087, 56749, 222	572	39	13588	4.E+00	1.E+00	7.E-02	9.E+00
GOTERM_BP_FAT	GO:0009161~ribonucleoside monophosphate metabolic process	5	0.784929356	7.E-03	11486, 11717, 56749, 11566, 99586	572	19	13588	6.E+00	1.E+00	8.E-02	1.E+01
GOTERM_BP_FAT	GO:0044271~nitrogen compound biosynthetic process	23	3.610675039	9.E-03	382985, 18416, 109900, 232087, 11847, 1	572	302	13588	2.E+00	1.E+00	1.E-01	1.E+01
KEGG_PATHWAY	mmu00230:Purine metabolism	19	2.982731554	3.E-02	18746, 382985, 14923, 11717, 11564, 115	409	157	5738	2.E+00	1.E+00	8.E-02	3.E+01
GOTERM_BP_FAT	GO:0009165~nucleotide biosynthetic process	14	2.197802198	3.E-02	382985, 11717, 11564, 11566, 99586, 114	572	174	13588	2.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0034404~nucleobase, nucleoside and nucleotide biosynthetic p	14	2.197802198	4.E-02	382985, 11717, 11564, 11566, 99586, 114	572	179	13588	2.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0034654~nucleobase, nucleoside, nucleotide and nucleic acid b	14	2.197802198	4.E-02	382985, 11717, 11564, 11566, 99586, 114	572	179	13588	2.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0009124~nucleoside monophosphate biosynthetic process	6	0.941915228	4.E-02	11486, 11514, 11717, 56749, 11566, 9958	572	45	13588	3.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0009112~nucleobase metabolic process	4	0.627943485	4.E-02	11486, 11717, 56749, 99586	572	19	13588	5.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0046112~nucleobase biosynthetic process	3	0.470957614	5.E-02	11486, 56749, 99586	572	9	13588	8.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0009127~purine nucleoside monophosphate biosynthetic proce	3	0.470957614	1.E-01	11486, 11717, 11566	572	13	13588	5.E+00	1.E+00	5.E-01	9.E+01
GOTERM_BP_FAT	GO:0009168~purine ribonucleoside monophosphate biosynthetic p	3	0.470957614	1.E-01	11486, 11717, 11566	572	13	13588	5.E+00	1.E+00	5.E-01	9.E+01
GOTERM_BP_FAT	GO:0009123~nucleoside monophosphate metabolic process	6	0.941915228	1.E-01	11486, 11514, 11717, 56749, 11566, 9958	572	59	13588	2.E+00	1.E+00	5.E-01	9.E+01
GOTERM_BP_FAT	GO:0009126~purine nucleoside monophosphate metabolic process	3	0.470957614	1.E-01	11486, 11717, 11566	572	15	13588	5.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0009167~purine ribonucleoside monophosphate metabolic pro	3	0.470957614	1.E-01	11486, 11717, 11566	572	15	13588	5.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0009259~ribonucleotide metabolic process	8	1.25588697	3.E-01	11486, 11717, 56749, 11564, 67942, 1156	572	125	13588	2.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0009260~ribonucleotide biosynthetic process	7	1.098901099	3.E-01	11486, 11717, 56749, 11564, 67942, 1156	572	111	13588	1.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0006163~purine nucleotide metabolic process	9	1.412872841	4.E-01	11486, 11514, 14923, 11717, 11564, 6794	572	160	13588	1.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0009150~purine ribonucleotide metabolic process	6	0.941915228	6.E-01	11486, 11717, 11564, 67942, 11566, 1163	572	119	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0009152~purine ribonucleotide biosynthetic process	5	0.784929356	7.E-01	11486, 11717, 11564, 67942, 11566	572	107	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0006164~purine nucleotide biosynthetic process	6	0.941915228	7.E-01	11486, 11514, 11717, 11564, 67942, 1156	572	137	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0009141~nucleoside triphosphate metabolic process	4	0.627943485	9.E-01	382985, 11486, 67942, 11636	572	115	13588	8.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0009144~purine nucleoside triphosphate metabolic process	3	0.470957614	9.E-01	11486, 67942, 11636	572	106	13588	7.E-01	1.E+00	1.E+00	1.E+02

Annotation Cluster 135	Enrichment Score: 1.048202288698312											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0042537~benzene and derivative metabolic process	3	0.470957614	2.E-02	13077, 94284, 14865, 394436	572	6	13588	1.E+01	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0006805~xenobiotic metabolic process	3	0.470957614	1.E-01	13077, 94284, 14865, 394436	572	13	13588	5.E+00	1.E+00	5.E-01	9.E+01
GOTERM_BP_FAT	GO:0009410~response to xenobiotic stimulus	3	0.470957614	1.E-01	13077, 94284, 14865, 394436	572	16	13588	4.E+00	1.E+00	6.E-01	9.E+01
KEGG_PATHWAY	mmu00980:Metabolism of xenobiotics by cytochrome P450	8	1.25588697	2.E-01	56615, 14863, 56847, 66447, 13077, 9428	409	66	5738	2.E+00	1.E+00	4.E-01	9.E+01

Annotation Cluster 136	Enrichment Score: 1.0338717672162303											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
BIOCARTA	m_rbpPathway:RB Tumor Suppressor/Checkpoint Signaling in respon	5	0.784929356	6.E-02	22390, 11920, 12532, 12566, 12534	167	11	1171	3.E+00	1.E+00	3.E-01	5.E+01
BIOCARTA	m_cdc25Pathway:cdc25 and chk1 Regulatory Pathway in response t	4	0.627943485	6.E-02	22390, 11920, 12532, 12534	167	7	1171	4.E+00	1.E+00	3.E-01	6.E+01
BIOCARTA	m_g2Pathway:Cell Cycle: G2/M Checkpoint	6	0.941915228	2.E-01	22390, 18817, 11920, 13197, 12532, 1253	167	23	1171	2.E+00	1.E+00	6.E-01	1.E+02

Annotation Cluster 137	Enrichment Score: 1.0337755982055505											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_SEQ_FEATURE	region of interest:Bait region	3	0.470957614	8.E-03	17836, 17837, 11287	618	4	16021	2.E+01	1.E+00	3.E-01	1.E+01
SP_PIR_KEYWORDS	bait region	3	0.470957614	2.E-02	17836, 17837, 11287	629	6	17854	1.E+01	1.E+00	8.E-02	2.E+01
SP_PIR_KEYWORDS	thioester bond	3	0.470957614	2.E-02	17836, 17837, 11287	629	7	17854	1.E+01	1.E+00	1.E-01	3.E+01
UP_SEQ_FEATURE	cross-link:isoglutamyl cysteine thioester (Cys-Gln)	3	0.470957614	3.E-02	17836, 17837, 11287	618	7	16021	1.E+01	1.E+00	5.E-01	4.E+01
INTERPRO	IPR019565:Alpha-2-macroglobulin thiol-ester bond-forming	3	0.470957614	3.E-02	17836, 17837, 11287	630	8	17763	1.E+01	1.E+00	4.E-01	4.E+01
INTERPRO	IPR011626:A-macroglobulin complement component	3	0.470957614	4.E-02	17836, 17837, 11287	630	9	17763	9.E+00	1.E+00	4.E-01	5.E+01
INTERPRO	IPR011625:Alpha-2-macroglobulin N-terminal 2	3	0.470957614	4.E-02	17836, 17837, 11287	630	9	17763	9.E+00	1.E+00	4.E-01	5.E+01
INTERPRO	IPR001599:Alpha-2-macroglobulin	3	0.470957614	4.E-02	17836, 17837, 11287	630	9	17763	9.E+00	1.E+00	4.E-01	5.E+01
INTERPRO	IPR009048:Alpha-macroglobulin receptor-binding	3	0.470957614	4.E-02	17836, 17837, 11287	630	9	17763	9.E+00	1.E+00	4.E-01	5.E+01
INTERPRO	IPR002890:Alpha-2-macroglobulin N-terminal	3	0.470957614	5.E-02	17836, 17837, 11287	630	10	17763	8.E+00	1.E+00	5.E-01	5.E+01
INTERPRO	IPR019742:Alpha-2-macroglobulin conserved site	3	0.470957614	6.E-02	17836, 17837, 11287	630	11	17763	8.E+00	1.E+00	6.E-01	6.E+01
PIR_SUPERFAMILY	PIRSF001635:alpha-2-macroglobulin	3	0.470957614	7.E-02	17836, 17837, 11287	400	9	8136	7.E+00	1.E+00	9.E-01	6.E+01
SP_PIR_KEYWORDS	Serine protease inhibitor	4	0.627943485	6.E-01	17836, 17837, 282663, 11287	629	82	17854	1.E+00	1.E+00	9.E-01	1.E+02
SP_PIR_KEYWORDS	protease inhibitor	4	0.627943485	7.E-01	17836, 17837, 282663, 11287	629	109	17854	1.E+00	1.E+00	9.E-01	1.E+02
GOTERM_MF_FAT	GO:0004857~enzyme inhibitor activity	9	1.412872841	8.E-01	17836, 12703, 17837, 30939, 16952, 2826	550	243	13288	9.E-01	1.E+00	1.E+00	1.E+02
GOTERM_MF_FAT	GO:0004867~serine-type endopeptidase inhibitor activity	4	0.627943485	9.E-01	17836, 17837, 282663, 11287	550	115	13288	8.E-01	1.E+00	1.E+00	1.E+02
GOTERM_MF_FAT	GO:0004866~endopeptidase inhibitor activity	5	0.784929356	9.E-01	17836, 17837, 30939, 282663, 11287	550	161	13288	8.E-01	1.E+00	1.E+00	1.E+02
GOTERM_MF_FAT	GO:0030414~peptidase inhibitor activity	5	0.784929356	9.E-01	17836, 17837, 30939, 282663, 11287	550	176	13288	7.E-01	1.E+00	1.E+00	1.E+02

Annotation Cluster 138	Enrichment Score: 1.0332782614238611											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR



INTERPRO	IPR000591:Pleckstrin/G-protein, interacting region	4	0.627943485	4.E-02	277360, 218581, 211896, 76131	630	22	17763	5.E+00	1.E+00	5.E-01	5.E+01
SMART	SM00049:DEP	4	0.627943485	8.E-02	277360, 218581, 211896, 76131	418	22	9131	4.E+00	1.E+00	5.E-01	6.E+01
UP_SEQ_FEATURE	domain:DEP	3	0.470957614	1.E-01	218581, 211896, 76131	618	17	16021	5.E+00	1.E+00	9.E-01	9.E+01
INTERPRO	IPR011991:Winged helix repressor DNA-binding	10	1.569858713	2.E-01	19891, 277360, 27056, 26965, 20375, 991	630	175	17763	2.E+00	1.E+00	9.E-01	9.E+01
Annotation Cluster 139	Enrichment Score: 1.0314459990118672											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0008629~induction of apoptosis by intracellular signals	6	0.941915228	1.E-02	12051, 66593, 11920, 12028, 17869, 1707	572	35	13588	4.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0042770~DNA damage response, signal transduction	5	0.784929356	2.E-01	12051, 11920, 26416, 12534, 170770	572	57	13588	2.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0008630~DNA damage response, signal transduction resulting	3	0.470957614	3.E-01	12051, 11920, 170770	572	23	13588	3.E+00	1.E+00	8.E-01	1.E+02
Annotation Cluster 140	Enrichment Score: 0.9994696478265026											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0010604~positive regulation of macromolecule metabolic process	44	6.907378336	1.E-03	17536, 22130, 11651, 17869, 22778, 1639	572	633	13588	2.E+00	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0031328~positive regulation of cellular biosynthetic process	38	5.965463108	3.E-03	17536, 22130, 17869, 22778, 12912, 1039	572	552	13588	2.E+00	1.E+00	5.E-02	6.E+00
GOTERM_BP_FAT	GO:0009891~positive regulation of biosynthetic process	38	5.965463108	4.E-03	17536, 22130, 17869, 22778, 12912, 1039	572	557	13588	2.E+00	1.E+00	5.E-02	7.E+00
GOTERM_BP_FAT	GO:0045944~positive regulation of transcription from RNA polymerase II promoter	26	4.081632653	9.E-03	17536, 22130, 17869, 22778, 12912, 1291	572	358	13588	2.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0006357~regulation of transcription from RNA polymerase II promoter	39	6.12244898	1.E-02	17536, 22130, 19720, 17869, 22778, 1291	572	616	13588	2.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0010557~positive regulation of macromolecule biosynthetic process	34	5.337519623	2.E-02	17536, 22130, 17869, 22778, 12912, 1039	572	530	13588	2.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0051173~positive regulation of nitrogen compound metabolic process	33	5.180533752	2.E-02	17536, 22130, 17869, 22778, 12912, 1291	572	526	13588	1.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0045893~positive regulation of transcription, DNA-dependent	27	4.238618524	3.E-02	17536, 22130, 17869, 22778, 12912, 1291	572	416	13588	2.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0051254~positive regulation of RNA metabolic process	27	4.238618524	3.E-02	17536, 22130, 17869, 22778, 12912, 1291	572	419	13588	2.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0045941~positive regulation of transcription	28	4.395604396	7.E-02	17536, 22130, 17869, 22778, 12912, 1291	572	475	13588	1.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0010628~positive regulation of gene expression	28	4.395604396	9.E-02	17536, 22130, 17869, 22778, 12912, 1291	572	488	13588	1.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0045935~positive regulation of nucleobase, nucleoside, nucleotide	28	4.395604396	1.E-01	17536, 22130, 17869, 22778, 12912, 1291	572	510	13588	1.E+00	1.E+00	6.E-01	9.E+01
SP_PIR_KEYWORDS	nucleus	143	22.44897959	2.E-01	18746, 22130, 218294, 16952, 22778, 129	629	3808	17854	1.E+00	1.E+00	5.E-01	1.E+02
SP_PIR_KEYWORDS	activator	21	3.296703297	3.E-01	11865, 12753, 53610, 17869, 20375, 1446	629	484	17854	1.E+00	1.E+00	6.E-01	1.E+02
SP_PIR_KEYWORDS	dna-binding	54	8.477237049	3.E-01	22130, 22778, 319191, 12912, 17135, 180	629	1404	17854	1.E+00	1.E+00	7.E-01	1.E+02
SP_PIR_KEYWORDS	transcription regulation	58	9.105180534	4.E-01	22130, 12952, 22778, 12953, 12912, 1291	629	1546	17854	1.E+00	1.E+00	7.E-01	1.E+02
GOTERM_MF_FAT	GO:0043565~sequence-specific DNA binding	25	3.924646782	4.E-01	17536, 17869, 22778, 12912, 17135, 1801	550	556	13288	1.E+00	1.E+00	9.E-01	1.E+02
GOTERM_MF_FAT	GO:0030528~transcription regulator activity	52	8.163265306	5.E-01	22130, 22778, 12815, 12912, 12914, 1713	550	1206	13288	1.E+00	1.E+00	9.E-01	1.E+02
GOTERM_MF_FAT	GO:0003700~transcription factor activity	32	5.023547881	6.E-01	17536, 69890, 17869, 22778, 12912, 1713	550	776	13288	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0006355~regulation of transcription, DNA-dependent	59	9.262166405	7.E-01	22130, 22778, 12912, 12914, 21937, 1713	572	1465	13588	1.E+00	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	Transcription	59	9.262166405	7.E-01	22130, 12952, 22778, 12953, 12912, 1291	629	1769	17854	9.E-01	1.E+00	9.E-01	1.E+02
GOTERM_MF_FAT	GO:0003677~DNA binding	70	10.98901099	7.E-01	22130, 22778, 12912, 319191, 12914, 171	550	1781	13288	9.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0051252~regulation of RNA metabolic process	59	9.262166405	8.E-01	22130, 22778, 12912, 12914, 21937, 1713	572	1488	13588	9.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0045449~regulation of transcription	85	13.34379906	9.E-01	22130, 22778, 12952, 12953, 12912, 1291	572	2227	13588	9.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0006350~transcription	60	9.419152276	1.E+00	22130, 12952, 22778, 12953, 12912, 1291	572	1772	13588	8.E-01	1.E+00	1.E+00	1.E+02
Annotation Cluster 141	Enrichment Score: 0.9872920104315488											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR000751:M-phase inducer phosphatase	3	0.470957614	4.E-03	12532, 12531, 12530	630	3	17763	3.E+01	1.E+00	1.E-01	6.E+00
GOTERM_BP_FAT	GO:0006470~protein amino acid dephosphorylation	9	1.412872841	1.E-01	15170, 218294, 19253, 14208, 12043, 125	572	114	13588	2.E+00	1.E+00	5.E-01	9.E+01
UP_SEQ_FEATURE	domain:Rhodanese	3	0.470957614	1.E-01	12532, 12531, 12530	618	15	16021	5.E+00	1.E+00	9.E-01	9.E+01
INTERPRO	IPR001763:Rhodanese-like	3	0.470957614	2.E-01	12532, 12531, 12530	630	22	17763	4.E+00	1.E+00	9.E-01	1.E+02
GOTERM_MF_FAT	GO:0004725~protein tyrosine phosphatase activity	7	1.098901099	2.E-01	15170, 218294, 19253, 26395, 12532, 125	550	101	13288	2.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0016311~dephosphorylation	9	1.412872841	2.E-01	15170, 218294, 19253, 14208, 12043, 125	572	141	13588	2.E+00	1.E+00	8.E-01	1.E+02
SMART	SM00450:RHOD	3	0.470957614	3.E-01	12532, 12531, 12530	418	22	9131	3.E+00	1.E+00	8.E-01	1.E+02
Annotation Cluster 142	Enrichment Score: 0.9852857372190005											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0031365~N-terminal protein amino acid modification	3	0.470957614	2.E-02	18108, 18107, 12914	572	6	13588	1.E+01	1.E+00	2.E-01	3.E+01
GOTERM_MF_FAT	GO:0016410~N-acyltransferase activity	6	0.941915228	1.E-01	18108, 18107, 12753, 217214, 17979, 129	550	67	13288	2.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0043543~protein amino acid acylation	4	0.627943485	3.E-01	18108, 18107, 108672, 12914	572	48	13588	2.E+00	1.E+00	9.E-01	1.E+02
Annotation Cluster 143	Enrichment Score: 0.9826093878867532											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0016765~transferase activity, transferring alkyl or aryl (other than	6	0.941915228	7.E-02	56615, 232087, 14863, 66447, 14865, 117	550	53	13288	3.E+00	1.E+00	4.E-01	6.E+01
GOTERM_MF_FAT	GO:0004364~glutathione transferase activity	4	0.627943485	9.E-02	56615, 14863, 66447, 14865	550	26	13288	4.E+00	1.E+00	5.E-01	8.E+01
KEGG_PATHWAY	mmu00980:Metabolism of xenobiotics by cytochrome P450	8	1.25588697	2.E-01	56615, 14863, 56847, 66447, 13077, 9428	409	66	5738	2.E+00	1.E+00	4.E-01	9.E+01
Annotation Cluster 144	Enrichment Score: 0.9515068744671078											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_SEQ_FEATURE	region of interest:Catalytic	8	1.25588697	2.E-03	235339, 15275, 15277, 18576, 18575, 190	618	47	16021	4.E+00	1.E+00	8.E-02	3.E+00
GOTERM_MF_FAT	GO:0008081~phosphoric diester hydrolase activity	8	1.25588697	3.E-02	18803, 234779, 20598, 18576, 18575, 185	550	72	13288	3.E+00	1.E+00	3.E-01	4.E+01



SP_PIR_KEYWORDS	camp	4	0.627943485	7.E-02	19088, 18576, 18575, 18574	629	28	17854	4.E+00	1.E+00	3.E-01	7.E+01
SP_PIR_KEYWORDS	cGMP	3	0.470957614	2.E-01	18576, 18575, 18574	629	21	17854	4.E+00	1.E+00	4.E-01	9.E+01
INTERPRO	IPR002073:3'5'-cyclic nucleotide phosphodiesterase	3	0.470957614	2.E-01	18576, 18575, 18574	630	21	17763	4.E+00	1.E+00	9.E-01	9.E+01
INTERPRO	IPR003607:Metal-dependent phosphohydrolase, HD region	3	0.470957614	2.E-01	18576, 18575, 18574	630	24	17763	4.E+00	1.E+00	9.E-01	1.E+02
UP_SEQ_FEATURE	metal ion-binding site:Divalent metal cation 1	3	0.470957614	3.E-01	18576, 18575, 18574	618	25	16021	3.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	metal ion-binding site:Divalent metal cation 2	3	0.470957614	3.E-01	18576, 18575, 18574	618	25	16021	3.E+00	1.E+00	1.E+00	1.E+02
GOTERM_MF_FAT	GO:004114~3',5'-cyclic-nucleotide phosphodiesterase activity	3	0.470957614	3.E-01	18576, 18575, 18574	550	24	13288	3.E+00	1.E+00	8.E-01	1.E+02
GOTERM_MF_FAT	GO:004112~cyclic-nucleotide phosphodiesterase activity	3	0.470957614	3.E-01	18576, 18575, 18574	550	25	13288	3.E+00	1.E+00	8.E-01	1.E+02
SMART	SM00471:HDC	3	0.470957614	3.E-01	18576, 18575, 18574	418	24	9131	3.E+00	1.E+00	8.E-01	1.E+02
Annotation Cluster 145	Enrichment Score: 0.9488236254434876											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR002913:Lipid-binding START	3	0.470957614	1.E-01	236920, 50768, 243362	630	15	17763	6.E+00	1.E+00	7.E-01	8.E+01
UP_SEQ_FEATURE	domain:START	3	0.470957614	1.E-01	236920, 50768, 243362	618	14	16021	6.E+00	1.E+00	9.E-01	8.E+01
SMART	SM00234:START	3	0.470957614	1.E-01	236920, 50768, 243362	418	15	9131	4.E+00	1.E+00	6.E-01	9.E+01
Annotation Cluster 146	Enrichment Score: 0.9437304365817875											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR001251:Cellular retinaldehyde-binding/triple function, C-terminal	4	0.627943485	6.E-02	73167, 228359, 109904, 545156	630	26	17763	4.E+00	1.E+00	6.E-01	6.E+01
SMART	SM00516:SEC14	4	0.627943485	1.E-01	73167, 228359, 109904, 545156	418	26	9131	3.E+00	1.E+00	5.E-01	8.E+01
UP_SEQ_FEATURE	domain:CRAL-TRIO	3	0.470957614	2.E-01	73167, 228359, 545156	618	22	16021	4.E+00	1.E+00	1.E+00	1.E+02
Annotation Cluster 147	Enrichment Score: 0.9331239652691354											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0007155~cell adhesion	32	5.023547881	7.E-02	12831, 69524, 11852, 11856, 20416, 1281	572	561	13588	1.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0022610~biological adhesion	32	5.023547881	7.E-02	12831, 69524, 11852, 11856, 20416, 1281	572	562	13588	1.E+00	1.E+00	4.E-01	7.E+01
KEGG_PATHWAY	mmu04514:Cell adhesion molecules (CAMs)	17	2.668759812	8.E-02	15007, 14972, 15018, 69524, 16456, 1641	409	154	5738	2.E+00	1.E+00	2.E-01	6.E+01
SP_PIR_KEYWORDS	cell adhesion	19	2.982731554	1.E-01	11350, 69524, 11852, 16414, 16412, 1712	629	380	17854	1.E+00	1.E+00	4.E-01	8.E+01
GOTERM_BP_FAT	GO:0016337~cell-cell adhesion	12	1.883830455	4.E-01	16408, 15896, 21687, 20779, 69524, 2034	572	236	13588	1.E+00	1.E+00	9.E-01	1.E+02
Annotation Cluster 148	Enrichment Score: 0.927931200395971											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0043467~regulation of generation of precursor metabolites and	3	0.470957614	1.E-01	14447, 103988, 208727	572	13	13588	5.E+00	1.E+00	5.E-01	9.E+01
GOTERM_BP_FAT	GO:0010906~regulation of glucose metabolic process	3	0.470957614	1.E-01	14447, 103988, 208727	572	14	13588	5.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0006109~regulation of carbohydrate metabolic process	3	0.470957614	1.E-01	14447, 103988, 208727	572	15	13588	5.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0010675~regulation of cellular carbohydrate metabolic process	3	0.470957614	1.E-01	14447, 103988, 208727	572	15	13588	5.E+00	1.E+00	6.E-01	9.E+01
Annotation Cluster 149	Enrichment Score: 0.9256831701317876											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0022612~gland morphogenesis	9	1.412872841	2.E-02	13649, 20779, 14178, 12043, 12505, 1600	572	84	13588	3.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0048754~branching morphogenesis of a tube	9	1.412872841	4.E-02	15402, 14674, 20779, 24064, 12043, 1250	572	93	13588	2.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0060444~branching involved in mammary gland duct morphog	3	0.470957614	2.E-01	20779, 17979, 12234	572	19	13588	4.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0060603~mammary gland duct morphogenesis	3	0.470957614	3.E-01	20779, 17979, 12234	572	26	13588	3.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0060443~mammary gland morphogenesis	3	0.470957614	4.E-01	20779, 17979, 12234	572	33	13588	2.E+00	1.E+00	9.E-01	1.E+02
Annotation Cluster 150	Enrichment Score: 0.9212182367328683											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0010812~negative regulation of cell-substrate adhesion	3	0.470957614	3.E-02	18708, 12842, 218397	572	7	13588	1.E+01	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0030155~regulation of cell adhesion	8	1.25588697	1.E-01	16408, 18708, 22324, 20779, 12842, 2183	572	94	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0001952~regulation of cell-matrix adhesion	3	0.470957614	1.E-01	18708, 218397, 12043	572	14	13588	5.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0010810~regulation of cell-substrate adhesion	4	0.627943485	2.E-01	18708, 12842, 218397, 12043	572	40	13588	2.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0007162~negative regulation of cell adhesion	3	0.470957614	3.E-01	18708, 12842, 218397	572	25	13588	3.E+00	1.E+00	8.E-01	1.E+02
Annotation Cluster 151	Enrichment Score: 0.9034828702470189											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
BIOCARTA	m_badPathway:Regulation of BAD phosphorylation	8	1.25588697	8.E-03	18708, 12015, 12048, 12028, 11651, 1204	167	18	1171	3.E+00	8.E-01	7.E-02	1.E+01
BIOCARTA	m_achPathway:Role of nicotinic acetylcholine receptors in the regul	4	0.627943485	3.E-01	18708, 12015, 20779, 11651	167	14	1171	2.E+00	1.E+00	7.E-01	1.E+02
BIOCARTA	m_aktPathway:AKT Signaling Pathway	3	0.470957614	7.E-01	18708, 12015, 11651	167	18	1171	1.E+00	1.E+00	1.E+00	1.E+02
Annotation Cluster 152	Enrichment Score: 0.8889564878441245											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_SEQ_FEATURE	zinc finger region:ZZ-type	3	0.470957614	1.E-01	74287, 17966, 12914	618	14	16021	6.E+00	1.E+00	9.E-01	8.E+01
INTERPRO	IPR000433:Zinc finger, ZZ-type	3	0.470957614	1.E-01	74287, 17966, 12914	630	17	17763	5.E+00	1.E+00	8.E-01	9.E+01
SMART	SM00291:ZnF_ZZ	3	0.470957614	2.E-01	74287, 17966, 12914	418	17	9131	4.E+00	1.E+00	7.E-01	9.E+01



Annotation Cluster 153	Enrichment Score: 0.8687426308321204													
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR		
GOTERM_CC_FAT	GO:0042641~actomyosin	4	0.627943485		7.E-02 77579, 11459, 208727, 19200		434	27	12504	4.E+00	1.E+00	3.E-01	6.E+01	
GOTERM_CC_FAT	GO:0001725~stress fiber	3	0.470957614		2.E-01 77579, 11459, 19200		434	23	12504	4.E+00	1.E+00	5.E-01	9.E+01	
GOTERM_CC_FAT	GO:0032432~actin filament bundle	3	0.470957614		2.E-01 77579, 11459, 19200		434	24	12504	4.E+00	1.E+00	6.E-01	1.E+02	
Annotation Cluster 154	Enrichment Score: 0.8648120743591324													
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR		
GOTERM_BP_FAT	GO:0043010~camera-type eye development	11	1.726844584		5.E-02 18771, 12955, 232906, 77579, 12028, 120		572	130	13588	2.E+00	1.E+00	3.E-01	6.E+01	
GOTERM_BP_FAT	GO:0001654~eye development	12	1.883830455		7.E-02 17536, 18771, 12955, 232906, 77579, 120		572	157	13588	2.E+00	1.E+00	4.E-01	7.E+01	
GOTERM_BP_FAT	GO:0007423~sensory organ development	17	2.668759812		8.E-02 17536, 73750, 12955, 232906, 19378, 178		572	257	13588	2.E+00	1.E+00	4.E-01	8.E+01	
GOTERM_BP_FAT	GO:0048593~camera-type eye morphogenesis	4	0.627943485		3.E-01 12028, 12018, 56847, 17268		572	48	13588	2.E+00	1.E+00	9.E-01	1.E+02	
GOTERM_BP_FAT	GO:0048592~eye morphogenesis	4	0.627943485		6.E-01 12028, 12018, 56847, 17268		572	73	13588	1.E+00	1.E+00	1.E+00	1.E+02	
Annotation Cluster 155	Enrichment Score: 0.8636406827771825													
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR		
SP_PIR_KEYWORDS	translation regulation	7	1.098901099		2.E-02 13684, 13685, 19317, 13665, 11651, 6809		629	63	17854	3.E+00	1.E+00	1.E-01	3.E+01	
GOTERM_BP_FAT	GO:0006446~regulation of translational initiation	3	0.470957614		2.E-01 13685, 13665, 68092		572	21	13588	3.E+00	1.E+00	8.E-01	1.E+02	
GOTERM_BP_FAT	GO:0006417~regulation of translation	7	1.098901099		2.E-01 13684, 13685, 19317, 13665, 11651, 6809		572	100	13588	2.E+00	1.E+00	8.E-01	1.E+02	
GOTERM_BP_FAT	GO:0010608~posttranscriptional regulation of gene expression	9	1.412872841		3.E-01 13684, 13685, 19317, 13665, 11651, 1204		572	148	13588	1.E+00	1.E+00	8.E-01	1.E+02	
Annotation Cluster 156	Enrichment Score: 0.8535220565823248													
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR		
GOTERM_BP_FAT	GO:0009954~proximal/distal pattern formation	4	0.627943485		9.E-02 15438, 15405, 19378, 15430		572	25	13588	4.E+00	1.E+00	5.E-01	8.E+01	
GOTERM_BP_FAT	GO:0035136~forelimb morphogenesis	4	0.627943485		1.E-01 15438, 15405, 19378, 15430		572	27	13588	4.E+00	1.E+00	5.E-01	9.E+01	
GOTERM_BP_FAT	GO:0035107~appendage morphogenesis	9	1.412872841		1.E-01 15438, 12028, 12018, 15405, 19378, 1543		572	115	13588	2.E+00	1.E+00	5.E-01	9.E+01	
GOTERM_BP_FAT	GO:0035108~limb morphogenesis	9	1.412872841		1.E-01 15438, 12028, 12018, 15405, 19378, 1543		572	115	13588	2.E+00	1.E+00	5.E-01	9.E+01	
GOTERM_BP_FAT	GO:0060173~limb development	9	1.412872841		1.E-01 15438, 12028, 12018, 15405, 19378, 1543		572	119	13588	2.E+00	1.E+00	6.E-01	9.E+01	
GOTERM_BP_FAT	GO:0048736~appendage development	9	1.412872841		1.E-01 15438, 12028, 12018, 15405, 19378, 1543		572	119	13588	2.E+00	1.E+00	6.E-01	9.E+01	
GOTERM_BP_FAT	GO:0030326~embryonic limb morphogenesis	7	1.098901099		2.E-01 15438, 15405, 19378, 15430, 20481, 1467		572	97	13588	2.E+00	1.E+00	8.E-01	1.E+02	
GOTERM_BP_FAT	GO:0035113~embryonic appendage morphogenesis	7	1.098901099		2.E-01 15438, 15405, 19378, 15430, 20481, 1467		572	97	13588	2.E+00	1.E+00	8.E-01	1.E+02	
GOTERM_BP_FAT	GO:0035115~embryonic forelimb morphogenesis	3	0.470957614		2.E-01 15438, 15405, 19378		572	22	13588	3.E+00	1.E+00	8.E-01	1.E+02	
Annotation Cluster 157	Enrichment Score: 0.8529733819609358													
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR		
GOTERM_BP_FAT	GO:0033059~cellular pigmentation	3	0.470957614		9.E-02 12043, 11891, 171531		572	12	13588	6.E+00	1.E+00	5.E-01	8.E+01	
GOTERM_BP_FAT	GO:0048066~pigmentation during development	4	0.627943485		1.E-01 12043, 11891, 14682, 171531		572	30	13588	3.E+00	1.E+00	6.E-01	9.E+01	
GOTERM_BP_FAT	GO:0030318~melanocyte differentiation	3	0.470957614		1.E-01 12043, 11891, 171531		572	16	13588	4.E+00	1.E+00	6.E-01	9.E+01	
GOTERM_BP_FAT	GO:0050931~pigment cell differentiation	3	0.470957614		2.E-01 12043, 11891, 171531		572	17	13588	4.E+00	1.E+00	7.E-01	1.E+02	
GOTERM_BP_FAT	GO:0043473~pigmentation	5	0.784929356		2.E-01 12043, 17869, 11891, 14682, 171531		572	56	13588	2.E+00	1.E+00	7.E-01	1.E+02	
Annotation Cluster 158	Enrichment Score: 0.850679632393856													
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR		
SP_PIR_KEYWORDS	actin-binding	13	2.040816327		1.E-01 22323, 227753, 215280, 76448, 224014, 2		629	226	17854	2.E+00	1.E+00	3.E-01	8.E+01	
GOTERM_MF_FAT	GO:0003779~actin binding	17	2.668759812		1.E-01 22323, 215280, 227753, 19894, 94190, 76		550	288	13288	1.E+00	1.E+00	6.E-01	9.E+01	
GOTERM_MF_FAT	GO:0008092~cytoskeletal protein binding	22	3.453689168		2.E-01 22323, 215280, 227753, 26934, 19894, 94		550	414	13288	1.E+00	1.E+00	7.E-01	1.E+02	
Annotation Cluster 159	Enrichment Score: 0.8504511441100686													
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR		
GOTERM_BP_FAT	GO:0008544~epidermis development	11	1.726844584		4.E-02 16994, 12831, 13649, 12842, 14178, 2639		572	125	13588	2.E+00	1.E+00	3.E-01	5.E+01	
GOTERM_BP_FAT	GO:0007398~ectoderm development	11	1.726844584		5.E-02 16994, 12831, 13649, 12842, 14178, 2639		572	133	13588	2.E+00	1.E+00	4.E-01	6.E+01	
GOTERM_BP_FAT	GO:0043588~skin development	4	0.627943485		1.E-01 16994, 12831, 12842, 24069		572	30	13588	3.E+00	1.E+00	6.E-01	9.E+01	
GOTERM_BP_FAT	GO:0001942~hair follicle development	5	0.784929356		2.E-01 13649, 14178, 11651, 12043, 19225		572	50	13588	2.E+00	1.E+00	7.E-01	1.E+02	
GOTERM_BP_FAT	GO:0022405~hair cycle process	5	0.784929356		2.E-01 13649, 14178, 11651, 12043, 19225		572	50	13588	2.E+00	1.E+00	7.E-01	1.E+02	
GOTERM_BP_FAT	GO:0022404~molting cycle process	5	0.784929356		2.E-01 13649, 14178, 11651, 12043, 19225		572	50	13588	2.E+00	1.E+00	7.E-01	1.E+02	
GOTERM_BP_FAT	GO:0042633~hair cycle	5	0.784929356		2.E-01 13649, 14178, 11651, 12043, 19225		572	52	13588	2.E+00	1.E+00	7.E-01	1.E+02	
GOTERM_BP_FAT	GO:0042303~molting cycle	5	0.784929356		2.E-01 13649, 14178, 11651, 12043, 19225		572	52	13588	2.E+00	1.E+00	7.E-01	1.E+02	
BIOCARTA	m_telPathway:Telomeres, Telomerase, Cellular Aging and Immortal	5	0.784929356		2.E-01 13649, 11651, 12043, 17869, 16001		167	18	1171	2.E+00	1.E+00	6.E-01	1.E+02	
GOTERM_BP_FAT	GO:0048589~developmental growth	6	0.941915228		4.E-01 14432, 11651, 12043, 19225, 17979, 1600		572	100	13588	1.E+00	1.E+00	9.E-01	1.E+02	
Annotation Cluster 160	Enrichment Score: 0.8483750429859115													
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR		
GOTERM_CC_FAT	GO:0000775~chromosome, centromeric region	11	1.726844584		5.E-03 67052, 19053, 20871, 12236, 18005, 2277		434	111	12504	3.E+00	8.E-01	5.E-02	7.E+00	
GOTERM_CC_FAT	GO:0000793~condensed chromosome	7	1.098901099		2.E-01 13006, 67052, 12236, 18005, 12566, 5615		434	107	12504	2.E+00	1.E+00	5.E-01	9.E+01	
SP_PIR_KEYWORDS	kinetochore	5	0.784929356		2.E-01 67052, 18817, 12236, 18005, 56150		629	61	17854	2.E+00	1.E+00	4.E-01	9.E+01	



GOTERM_CC_FAT	GO:0000776~kinetochore	5	0.784929356	2.E-01	67052	12236	56150	20466	12914	434	62	12504	2.E+00	1.E+00	5.E-01	9.E+01		
GOTERM_CC_FAT	GO:0000777~condensed chromosome kinetochore	4	0.627943485	3.E-01	67052	12236	56150	12914		434	53	12504	2.E+00	1.E+00	7.E-01	1.E+02		
GOTERM_CC_FAT	GO:0000779~condensed chromosome, centromeric region	4	0.627943485	3.E-01	67052	12236	56150	12914		434	60	12504	2.E+00	1.E+00	8.E-01	1.E+02		
GOTERM_BP_FAT	GO:0007059~chromosome segregation	4	0.627943485	5.E-01	67052	30939	18005	56150		572	64	13588	1.E+00	1.E+00	1.E+00	1.E+02		
Annotation Cluster 161	Enrichment Score: 0.8454274672043486																	
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR						
KEGG_PATHWAY	mmu00270:Cysteine and methionine metabolism	7	1.098901099		3.E-02	16828	232087	13436	16833	16832	229	409	33	5738	3.E+00	1.E+00	7.E-02	3.E+01
SP_PIR_KEYWORDS	one-carbon metabolism	3	0.470957614		1.E-01	232087	229709	11720				629	15	17854	6.E+00	1.E+00	3.E-01	8.E+01
KEGG_PATHWAY	mmu00450:Selenoamino acid metabolism	4	0.627943485		2.E-01	232087	229709	11720	23971			409	23	5738	2.E+00	1.E+00	4.E-01	1.E+02
GOTERM_BP_FAT	GO:0006730~one-carbon metabolic process	5	0.784929356		7.E-01	232087	15278	13436	229709	11720		572	117	13588	1.E+00	1.E+00	1.E+00	1.E+02
Annotation Cluster 162	Enrichment Score: 0.8420451164433566																	
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR						
GOTERM_BP_FAT	GO:0031349~positive regulation of defense response	9	1.412872841		2.E-03	19370	14127	17874	16179	21898	2700	572	57	13588	4.E+00	1.E+00	4.E-02	4.E+00
GOTERM_BP_FAT	GO:0050729~positive regulation of inflammatory response	3	0.470957614		3.E-01	14127	16803	21937				572	24	13588	3.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0050727~regulation of inflammatory response	4	0.627943485		4.E-01	14127	11486	16803	21937			572	57	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0032101~regulation of response to external stimulus	6	0.941915228		4.E-01	56717	14127	11486	21898	16803	2193	572	103	13588	1.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0032103~positive regulation of response to external stimulus	3	0.470957614		5.E-01	14127	16803	21937				572	39	13588	2.E+00	1.E+00	1.E+00	1.E+02
Annotation Cluster 163	Enrichment Score: 0.8266985896621962																	
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR						
KEGG_PATHWAY	mmu03420:Nucleotide excision repair	9	1.412872841		1.E-02	13872	19891	19358	68240	17420	1488	409	43	5738	3.E+00	8.E-01	3.E-02	1.E+01
KEGG_PATHWAY	mmu03430:Mismatch repair	3	0.470957614		5.E-01	19891	68240	18538				409	22	5738	2.E+00	1.E+00	7.E-01	1.E+02
KEGG_PATHWAY	mmu03030:DNA replication	3	0.470957614		7.E-01	19891	68240	18538				409	35	5738	1.E+00	1.E+00	9.E-01	1.E+02
Annotation Cluster 164	Enrichment Score: 0.8248147868912022																	
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR						
GOTERM_BP_FAT	GO:0043086~negative regulation of catalytic activity	11	1.726844584		1.E-02	15170	24064	11806	11807	14678	1319	572	101	13588	3.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0006469~negative regulation of protein kinase activity	4	0.627943485		4.E-01	15170	24064	13197	12576			572	51	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0033673~negative regulation of kinase activity	4	0.627943485		4.E-01	15170	24064	13197	12576			572	51	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0051348~negative regulation of transferase activity	4	0.627943485		4.E-01	15170	24064	13197	12576			572	53	13588	2.E+00	1.E+00	9.E-01	1.E+02
Annotation Cluster 165	Enrichment Score: 0.8195238514011826																	
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR						
GOTERM_CC_FAT	GO:0000775~chromosome, centromeric region	11	1.726844584		5.E-03	67052	19053	20871	12236	18005	2277	434	111	12504	3.E+00	8.E-01	5.E-02	7.E+00
GOTERM_CC_FAT	GO:0044427~chromosomal part	20	3.139717425		1.E-02	19891	621893	67052	20871	18005	122	434	318	12504	2.E+00	1.E+00	9.E-02	2.E+01
GOTERM_CC_FAT	GO:0005694~chromosome	20	3.139717425		7.E-02	19891	621893	67052	20871	18005	122	434	378	12504	2.E+00	1.E+00	3.E-01	6.E+01
GOTERM_CC_FAT	GO:0000793~condensed chromosome	7	1.098901099		2.E-01	13006	67052	12236	18005	12566	5615	434	107	12504	2.E+00	1.E+00	5.E-01	9.E+01
GOTERM_CC_FAT	GO:0000785~chromatin	7	1.098901099		5.E-01	319168	621893	319169	216848	22778		434	165	12504	1.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0051276~chromosome organization	15	2.354788069		8.E-01	621893	57376	22130	18005	22778	561	572	404	13588	9.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0006325~chromatin organization	11	1.726844584		9.E-01	319168	621893	319169	57376	22130	2	572	315	13588	8.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0016568~chromatin modification	7	1.098901099		9.E-01	57376	22130	20220	22778	13436	2087	572	236	13588	7.E-01	1.E+00	1.E+00	1.E+02
Annotation Cluster 166	Enrichment Score: 0.8157233086600313																	
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR						
GOTERM_BP_FAT	GO:0006606~protein import into nucleus	6	0.941915228		9.E-02	11865	19384	231103	12953	70572	164	572	56	13588	3.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0051170~nuclear import	6	0.941915228		1.E-01	11865	19384	231103	12953	70572	164	572	58	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0034504~protein localization in nucleus	6	0.941915228		1.E-01	11865	19384	231103	12953	70572	164	572	61	13588	2.E+00	1.E+00	5.E-01	9.E+01
GOTERM_BP_FAT	GO:0017038~protein import	7	1.098901099		1.E-01	11865	19384	12122	231103	12953	705	572	82	13588	2.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0000060~protein import into nucleus translocation	3	0.470957614		2.E-01	11865	231103	16452				572	18	13588	4.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0006605~protein targeting	9	1.412872841		2.E-01	11865	19384	12122	231103	12953	118	572	133	13588	2.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0006913~nucleocytoplasmic transport	7	1.098901099		2.E-01	11865	19384	231103	68092	12953	705	572	96	13588	2.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0033365~protein localization in organelle	7	1.098901099		2.E-01	11865	19384	12122	231103	12953	705	572	97	13588	2.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0051169~nuclear transport	7	1.098901099		2.E-01	11865	19384	231103	68092	12953	705	572	98	13588	2.E+00	1.E+00	8.E-01	1.E+02
Annotation Cluster 167	Enrichment Score: 0.8117057210646591																	
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR						
SP_PIR_KEYWORDS	Initiation factor	6	0.941915228		4.E-02	13684	54709	13665	13681	208643	136	629	55	17854	3.E+00	1.E+00	2.E-01	5.E+01
GOTERM_MF_FAT	GO:0003743~translation initiation factor activity	6	0.941915228		1.E-01	13684	54709	13665	13681	208643	136	550	62	13288	2.E+00	1.E+00	6.E-01	8.E+01
SP_PIR_KEYWORDS	protein biosynthesis	9	1.412872841		1.E-01	13684	78294	13628	54709	13665	1998	629	139	17854	2.E+00	1.E+00	4.E-01	8.E+01
GOTERM_MF_FAT	GO:0008135~translation factor activity, nucleic acid binding	7	1.098901099		2.E-01	13684	13628	54709	13665	13681	2086	550	98	13288	2.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0006412~translation	13	2.040816327		7.E-01	78294	13684	13628	13665	19989	7425	572	319	13588	1.E+00	1.E+00	1.E+00	1.E+02
Annotation Cluster 168	Enrichment Score: 0.7949887616154814																	



Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0043113~receptor clustering	3	0.470957614		1E-01 192176, 18479, 12568		572	13	13588	5.E+00	1.E+00	5.E-01
GOTERM_BP_FAT	GO:0007172~signal complex assembly	3	0.470957614		1E-01 192176, 18479, 12568		572	15	13588	5.E+00	1.E+00	6.E-01
GOTERM_BP_FAT	GO:0043623~cellular protein complex assembly	8	1.25588697		2.E-01 22142, 227753, 192176, 18479, 12568, 67		572	108	13588	2.E+00	1.E+00	7.E-01
GOTERM_BP_FAT	GO:0043112~receptor metabolic process	3	0.470957614		3.E-01 192176, 18479, 12568		572	26	13588	3.E+00	1.E+00	9.E-01
Annotation Cluster 169	Enrichment Score: 0.7938960185020366											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_SEQ_FEATURE	metal ion-binding site:Potassium	4	0.627943485		1.E-03 18746, 18770, 232087, 11720		618	6	16021	2.E+01	8.E-01	5.E-02
SP_PIR_KEYWORDS	potassium	4	0.627943485		8.E-01 18746, 18770, 232087, 11720		629	118	17854	1.E+00	1.E+00	1.E+00
GOTERM_MF_FAT	GO:0030955~potassium ion binding	4	0.627943485		9.E-01 18746, 18770, 232087, 11720		550	118	13288	8.E-01	1.E+00	1.E+00
GOTERM_MF_FAT	GO:0031420~alkali metal ion binding	6	0.941915228		9.E-01 18746, 18770, 232087, 20505, 20504, 117		550	206	13288	7.E-01	1.E+00	1.E+00
Annotation Cluster 170	Enrichment Score: 0.786514267102255											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	DNA binding	19	2.982731554		5.E-03 78294, 15430, 20375, 22778, 14281, 1428		629	258	17854	2.E+00	9.E-01	3.E-02
INTERPRO	IPR001827:Homeobox protein, antennapedia type, conserved site	5	0.784929356		9.E-03 15402, 15415, 15407, 15416, 18609		630	24	17763	6.E+00	1.E+00	2.E-01
INTERPRO	IPR017995:Homeobox protein, antennapedia type	4	0.627943485		1.E-02 15402, 15415, 15416, 18609		630	14	17763	8.E+00	1.E+00	2.E-01
UP_SEQ_FEATURE	short sequence motif:Atp-type hexapeptide	5	0.784929356		1.E-02 15402, 15415, 15407, 15416, 18609		618	24	16021	5.E+00	1.E+00	3.E-01
GOTERM_BP_FAT	GO:0048705~skeletal system morphogenesis	10	1.569858713		1.E-01 15402, 18596, 15438, 12842, 15415, 1540		572	130	13588	2.E+00	1.E+00	5.E-01
INTERPRO	IPR017970:Homeobox, conserved site	13	2.040816327		1.E-01 17536, 15430, 13799, 15402, 15438, 1877		630	222	17763	2.E+00	1.E+00	7.E-01
GOTERM_BP_FAT	GO:0048704~embryonic skeletal system morphogenesis	6	0.941915228		1.E-01 15402, 15438, 15415, 15407, 15416, 1543		572	64	13588	2.E+00	1.E+00	6.E-01
GOTERM_BP_FAT	GO:0048706~embryonic skeletal system development	7	1.098901099		1.E-01 15402, 15438, 15415, 15407, 15416, 1540		572	83	13588	2.E+00	1.E+00	6.E-01
GOTERM_BP_FAT	GO:0048562~embryonic organ morphogenesis	10	1.569858713		2.E-01 15402, 13836, 15438, 24064, 15415, 1540		572	161	13588	1.E+00	1.E+00	8.E-01
INTERPRO	IPR001356:Homeobox	12	1.883830455		3.E-01 15402, 17536, 15438, 18771, 15415, 1540		630	254	17763	1.E+00	1.E+00	1.E+00
INTERPRO	IPR012287:Homeodomain-related	12	1.883830455		3.E-01 15402, 17536, 15438, 18771, 15415, 1540		630	259	17763	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0009952~anterior/posterior pattern formation	9	1.412872841		3.E-01 15402, 15438, 15415, 15407, 15416, 1192		572	153	13588	1.E+00	1.E+00	9.E-01
SP_PIR_KEYWORDS	Homeobox	12	1.883830455		3.E-01 15402, 17536, 15438, 18771, 15415, 1540		629	263	17854	1.E+00	1.E+00	7.E-01
UP_SEQ_FEATURE	DNA-binding region:Homeobox	9	1.412872841		4.E-01 15402, 15438, 15415, 15407, 15416, 1860		618	180	16021	1.E+00	1.E+00	1.E+00
GOTERM_MF_FAT	GO:0043565~sequence-specific DNA binding	25	3.924646782		4.E-01 17536, 17869, 22778, 12912, 17135, 1801		550	556	13288	1.E+00	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0003002~regionalization	10	1.569858713		5.E-01 15402, 15438, 15415, 15407, 15416, 1192		572	214	13588	1.E+00	1.E+00	1.E+00
GOTERM_MF_FAT	GO:0003700~transcription factor activity	32	5.023547881		6.E-01 17536, 69890, 17869, 22778, 12912, 1713		550	776	13288	1.E+00	1.E+00	1.E+00
SMART	SM00389:HOX	12	1.883830455		6.E-01 15402, 17536, 15438, 18771, 15415, 1540		418	254	9131	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0007389~pattern specification process	12	1.883830455		7.E-01 15402, 15438, 14674, 15415, 15407, 1541		572	284	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0008344~adult locomotory behavior	3	0.470957614		7.E-01 15438, 15416, 15430		572	62	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0030534~adult behavior	4	0.627943485		8.E-01 15438, 15416, 15430, 12568		572	93	13588	1.E+00	1.E+00	1.E+00
Annotation Cluster 171	Enrichment Score: 0.7843555319988303											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0046883~regulation of hormone secretion	5	0.784929356		6.E-02 14661, 18413, 18576, 12912, 103988		572	36	13588	3.E+00	1.E+00	4.E-01
GOTERM_BP_FAT	GO:0050796~regulation of insulin secretion	3	0.470957614		2.E-01 14661, 18576, 103988		572	22	13588	3.E+00	1.E+00	8.E-01
GOTERM_BP_FAT	GO:0002791~regulation of peptide secretion	3	0.470957614		3.E-01 14661, 18576, 103988		572	26	13588	3.E+00	1.E+00	9.E-01
Annotation Cluster 172	Enrichment Score: 0.778568100189028											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR004825:Insulin/IGF/relaxin	3	0.470957614		6.E-02 16333, 16334, 16000		630	11	17763	8.E+00	1.E+00	6.E-01
SMART	SM00078:IGF	3	0.470957614		9.E-02 16333, 16334, 16000		418	11	9131	6.E+00	1.E+00	5.E-01
GOTERM_MF_FAT	GO:0005179~hormone activity	3	0.470957614		1.E+00 16333, 16334, 16000		550	113	13288	6.E-01	1.E+00	1.E+00
Annotation Cluster 173	Enrichment Score: 0.7730958602444785											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0042060~wound healing	9	1.412872841		1.E-01 14060, 14674, 14432, 77579, 74145, 1406		572	112	13588	2.E+00	1.E+00	5.E-01
SP_PIR_KEYWORDS	blood coagulation	4	0.627943485		1.E-01 14060, 74145, 14065, 14064		629	37	17854	3.E+00	1.E+00	4.E-01
GOTERM_BP_FAT	GO:0007596~blood coagulation	6	0.941915228		2.E-01 14060, 14674, 74145, 14065, 11891, 1406		572	70	13588	2.E+00	1.E+00	7.E-01
GOTERM_BP_FAT	GO:0050817~coagulation	6	0.941915228		2.E-01 14060, 14674, 74145, 14065, 11891, 1406		572	70	13588	2.E+00	1.E+00	7.E-01
GOTERM_BP_FAT	GO:0007599~hemostasis	6	0.941915228		2.E-01 14060, 14674, 74145, 14065, 11891, 1406		572	71	13588	2.E+00	1.E+00	7.E-01
GOTERM_BP_FAT	GO:0050878~regulation of body fluid levels	6	0.941915228		3.E-01 14060, 14674, 74145, 14065, 11891, 1406		572	89	13588	2.E+00	1.E+00	9.E-01
Annotation Cluster 174	Enrichment Score: 0.7677267390353827											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
BIOCARTA	m_cardiacegfPathway:Role of EGF Receptor Transactivation by GPCl	6	0.941915228		8.E-02 13649, 18803, 15461, 17869, 14281, 1184		167	17	1171	2.E+00	1.E+00	3.E-01
BIOCARTA	m_cdMacPathway:Cadmium induces DNA synthesis and proliferatio	5	0.784929356		1.E-01 26395, 15461, 17869, 14281, 18795		167	14	1171	3.E+00	1.E+00	4.E-01
KEGG_PATHWAY	mmu05216:Thyroid cancer	5	0.784929356		1.E-01 19713, 21787, 26395, 15461, 17869		409	29	5738	2.E+00	1.E+00	3.E-01
KEGG_PATHWAY	mmu05219:Bladder cancer	4	0.627943485		6.E-01 13649, 26395, 15461, 17869		409	42	5738	1.E+00	1.E+00	8.E-01



Annotation Cluster 175	Enrichment Score: 0.7643520292406943													
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR		
SP_PIR_KEYWORDS	cytolysis	5	0.784929356		1.E-03 14939, 14941, 14940, 14944, 14943	629	14	17854	1.E+01	4.E-01	9.E-03	2.E+00		
SP_PIR_KEYWORDS	serine proteinase	7	1.098901099		4.E-03 14939, 14941, 14940, 13035, 12263, 1494	629	43	17854	5.E+00	8.E-01	2.E-02	5.E+00		
GOTERM_BP_FAT	GO:0019835~cytolysis	5	0.784929356		1.E-02 14939, 14941, 14940, 14944, 14943	572	23	13588	5.E+00	1.E+00	1.E-01	2.E+01		
PIR_SUPERFAMILY	PIRSF001135:trypsin	8	1.25588697		5.E-02 18048, 14939, 14941, 14940, 13035, 1722	400	68	8136	2.E+00	1.E+00	8.E-01	5.E+01		
UP_SEQ_FEATURE	domain:Peptidase S1	9	1.412872841		6.E-02 18048, 14939, 14941, 14940, 13035, 1722	618	111	16021	2.E+00	1.E+00	8.E-01	7.E+01		
SP_PIR_KEYWORDS	T-cell	4	0.627943485		9.E-02 14939, 14941, 14940, 14943	629	31	17854	4.E+00	1.E+00	3.E-01	8.E+01		
INTERPRO	IPR001314:Peptidase S1A, chymotrypsin	9	1.412872841		1.E-01 18048, 14939, 14941, 14940, 13035, 1722	630	143	17763	2.E+00	1.E+00	8.E-01	9.E+01		
INTERPRO	IPR018114:Peptidase S1/S6, chymotrypsin/Hap, active site	9	1.412872841		2.E-01 18048, 14939, 14941, 14940, 13035, 1722	630	151	17763	2.E+00	1.E+00	9.E-01	9.E+01		
INTERPRO	IPR001254:Peptidase S1 and S6, chymotrypsin/Hap	9	1.412872841		2.E-01 18048, 14939, 14941, 14940, 13035, 1722	630	159	17763	2.E+00	1.E+00	9.E-01	1.E+02		
UP_SEQ_FEATURE	propeptide:Activation peptide	5	0.784929356		4.E-01 14939, 74145, 13035, 17227, 14944	618	78	16021	2.E+00	1.E+00	1.E+00	1.E+02		
SP_PIR_KEYWORDS	Serine protease	8	1.25588697		4.E-01 14939, 14941, 14940, 13035, 17227, 1226	629	164	17854	1.E+00	1.E+00	7.E-01	1.E+02		
GOTERM_MF_FAT	GO:0004252~serine-type endopeptidase activity	10	1.569858713		4.E-01 18048, 14939, 14941, 14940, 18195, 1303	550	189	13288	1.E+00	1.E+00	9.E-01	1.E+02		
SP_PIR_KEYWORDS	zymogen	9	1.412872841		4.E-01 14939, 74145, 14941, 14940, 13035, 1722	629	199	17854	1.E+00	1.E+00	7.E-01	1.E+02		
SMART	SM00020:Tryp_SpC	9	1.412872841		4.E-01 18048, 14939, 14941, 14940, 13035, 1722	418	159	9131	1.E+00	1.E+00	9.E-01	1.E+02		
UP_SEQ_FEATURE	active site:Charge relay system	9	1.412872841		5.E-01 669888, 14939, 14941, 14940, 13035, 172	618	198	16021	1.E+00	1.E+00	1.E+00	1.E+02		
GOTERM_MF_FAT	GO:0008236~serine-type peptidase activity	10	1.569858713		5.E-01 18048, 14939, 14941, 14940, 18195, 1303	550	212	13288	1.E+00	1.E+00	1.E+00	1.E+02		
GOTERM_MF_FAT	GO:0017171~serine hydrolase activity	10	1.569858713		5.E-01 18048, 14939, 14941, 14940, 18195, 1303	550	213	13288	1.E+00	1.E+00	1.E+00	1.E+02		
GOTERM_MF_FAT	GO:0004175~endopeptidase activity	12	1.883830455		1.E+00 18048, 14939, 14941, 14940, 18195, 1303	550	421	13288	7.E-01	1.E+00	1.E+00	1.E+02		
SP_PIR_KEYWORDS	Protease	11	1.726844584		1.E+00 14939, 14941, 14940, 13035, 59029, 1722	629	509	17854	6.E-01	1.E+00	1.E+00	1.E+02		
GOTERM_MF_FAT	GO:0070011~peptidase activity, acting on L-amino acid peptides	13	2.040816327		1.E+00 14939, 14941, 18195, 14940, 59029, 1303	550	603	13288	5.E-01	1.E+00	1.E+00	1.E+02		
GOTERM_MF_FAT	GO:0008233~peptidase activity	13	2.040816327		1.E+00 14939, 14941, 18195, 14940, 59029, 1303	550	629	13288	5.E-01	1.E+00	1.E+00	1.E+02		
Annotation Cluster 176	Enrichment Score: 0.7546579950537358													
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR		
GOTERM_BP_FAT	GO:0042743~hydrogen peroxide metabolic process	5	0.784929356		9.E-03 672195, 50493, 13063, 17969, 13077, 130	572	20	13588	6.E+00	1.E+00	1.E-01	1.E+01		
SP_PIR_KEYWORDS	metalloprotein	7	1.098901099		1.E-02 18746, 672195, 11486, 13087, 13063, 130	629	56	17854	4.E+00	1.E+00	7.E-02	2.E+01		
SP_PIR_KEYWORDS	electron transfer	5	0.784929356		1.E-02 672195, 13087, 13063, 13077, 13106, 130	629	27	17854	5.E+00	1.E+00	7.E-02	2.E+01		
SP_PIR_KEYWORDS	microsome	9	1.412872841		2.E-02 56615, 76279, 13087, 98238, 66447, 1307	629	100	17854	3.E+00	1.E+00	1.E-01	3.E+01		
SP_PIR_KEYWORDS	chromoprotein	5	0.784929356		5.E-02 672195, 13087, 13063, 13077, 13106, 130	629	40	17854	4.E+00	1.E+00	2.E-01	5.E+01		
KEGG_PATHWAY	mmu00982:Drug metabolism	10	1.569858713		8.E-02 56615, 76279, 14863, 13087, 56847, 6644	409	75	5738	2.E+00	1.E+00	2.E-01	6.E+01		
UP_SEQ_FEATURE	metal ion-binding site:Iron (heme axial ligand)	8	1.25588697		9.E-02 18126, 672195, 76279, 13087, 13063, 130	618	99	16021	2.E+00	1.E+00	9.E-01	8.E+01		
GOTERM_MF_FAT	GO:0009055~electron carrier activity	13	2.040816327		1.E-01 672195, 76279, 14782, 13382, 99586, 181	550	202	13288	2.E+00	1.E+00	6.E-01	9.E+01		
SP_PIR_KEYWORDS	heme	8	1.25588697		2.E-01 18126, 672195, 76279, 13087, 13063, 130	629	142	17854	2.E+00	1.E+00	6.E-01	1.E+02		
PIR_SUPERFAMILY	PIRSF000045:cytochrome P450 CYP2D6	4	0.627943485		3.E-01 76279, 13087, 13077, 13106	400	36	8136	2.E+00	1.E+00	1.E+00	1.E+02		
BIOCARTA	m_AcetaminophenPathway:Mechanism of Acetaminophen Activity a	3	0.470957614		3.E-01 13077, 19225, 13106	167	7	1171	3.E+00	1.E+00	6.E-01	1.E+02		
GOTERM_MF_FAT	GO:0016712~oxidoreductase activity, acting on paired donors, with	4	0.627943485		3.E-01 76279, 13087, 13077, 13106	550	44	13288	2.E+00	1.E+00	8.E-01	1.E+02		
SP_PIR_KEYWORDS	iron	14	2.197802198		3.E-01 382985, 672195, 76279, 99586, 18126, 19	629	321	17854	1.E+00	1.E+00	7.E-01	1.E+02		
GOTERM_MF_FAT	GO:0020037~heme binding	8	1.25588697		4.E-01 18126, 672195, 76279, 13087, 13063, 130	550	144	13288	1.E+00	1.E+00	9.E-01	1.E+02		
GOTERM_MF_FAT	GO:0070330~aromatase activity	3	0.470957614		4.E-01 76279, 13087, 13077	550	34	13288	2.E+00	1.E+00	9.E-01	1.E+02		
GOTERM_MF_FAT	GO:0046906~tetrapyrrole binding	8	1.25588697		4.E-01 18126, 672195, 76279, 13087, 13063, 130	550	151	13288	1.E+00	1.E+00	9.E-01	1.E+02		
INTERPRO	IPR002401:Cytochrome P450, E-class, group I	4	0.627943485		5.E-01 76279, 13087, 13077, 13106	630	70	17763	2.E+00	1.E+00	1.E+00	1.E+02		
COG_ONTOLOGY	Secondary metabolites biosynthesis transport, and catabolism	4	0.627943485		5.E-01 76279, 13087, 13077, 13106	50	109	2040	1.E+00	1.E+00	1.E+00	1.E+02		
INTERPRO	IPR017973:Cytochrome P450, C-terminal region	4	0.627943485		6.E-01 76279, 13087, 13077, 13106	630	81	17763	1.E+00	1.E+00	1.E+00	1.E+02		
INTERPRO	IPR001128:Cytochrome P450	4	0.627943485		6.E-01 76279, 13087, 13077, 13106	630	87	17763	1.E+00	1.E+00	1.E+00	1.E+02		
INTERPRO	IPR017972:Cytochrome P450, conserved site	4	0.627943485		6.E-01 76279, 13087, 13077, 13106	630	89	17763	1.E+00	1.E+00	1.E+00	1.E+02		
GOTERM_MF_FAT	GO:0005506~iron ion binding	14	2.197802198		7.E-01 382985, 672195, 76279, 99586, 18126, 19	550	343	13288	1.E+00	1.E+00	1.E+00	1.E+02		
SP_PIR_KEYWORDS	Monoxygenase	4	0.627943485		7.E-01 76279, 13087, 13077, 13106	629	108	17854	1.E+00	1.E+00	9.E-01	1.E+02		
Annotation Cluster 177	Enrichment Score: 0.7511217561703423													
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR		
GOTERM_BP_FAT	GO:0006461~protein complex assembly	16	2.51177394		6.E-02 22142, 227753, 22130, 18416, 17869, 184	572	227	13588	2.E+00	1.E+00	4.E-01	6.E+01		
GOTERM_BP_FAT	GO:0070271~protein complex biogenesis	16	2.51177394		6.E-02 22142, 227753, 22130, 18416, 17869, 184	572	227	13588	2.E+00	1.E+00	4.E-01	6.E+01		
GOTERM_BP_FAT	GO:0043623~cellular protein complex assembly	8	1.25588697		2.E-01 22142, 227753, 192176, 18479, 12568, 67	572	108	13588	2.E+00	1.E+00	7.E-01	1.E+02		
GOTERM_BP_FAT	GO:0065003~macromolecular complex assembly	19	2.982731554		2.E-01 22142, 621893, 227753, 22130, 18416, 17	572	338	13588	1.E+00	1.E+00	7.E-01	1.E+02		
GOTERM_BP_FAT	GO:0051259~protein oligomerization	6	0.941915228		2.E-01 18416, 72269, 12028, 20133, 16001, 2013	572	72	13588	2.E+00	1.E+00	7.E-01	1.E+02		
GOTERM_BP_FAT	GO:0043933~macromolecular complex subunit organization	20	3.139717425		2.E-01 22142, 621893, 227753, 22130, 18416, 11	572	367	13588	1.E+00	1.E+00	7.E-01	1.E+02		
GOTERM_BP_FAT	GO:0051258~protein polymerization	4	0.627943485		2.E-01 22142, 227753, 67141, 22376	572	40	13588	2.E+00	1.E+00	8.E-01	1.E+02		
GOTERM_BP_FAT	GO:0034622~cellular macromolecular complex assembly	11	1.726844584		4.E-01 319168, 22142, 621893, 319169, 227753,	572	217	13588	1.E+00	1.E+00	9.E-01	1.E+02		
GOTERM_BP_FAT	GO:0034621~cellular macromolecular complex subunit organization	12	1.883830455		5.E-01 621893, 22142, 227753, 22130, 18479, 67	572	245	13588	1.E+00	1.E+00	9.E-01	1.E+02		
Annotation Cluster 178	Enrichment Score: 0.7500462914082131													
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR		
BIOCARTA	m_mitochondriaPathway:Role of Mitochondria in Apoptotic Signali	8	1.25588697		2.E-02 672195, 66593, 12048, 12028, 12122, 120	167	21	1171	3.E+00	1.E+00	1.E-01	2.E+01		



BIOCARTA	m_ceramidePathway:Ceramide Signaling Pathway	7	1.098901099	8.E-02 672195, 12015, 12028, 26395, 12043, 130	167	22	1171	2.E+00	1.E+00	3.E-01	6.E+01
BIOCARTA	m_HivnefPathway:HIV-I Nef: negative effector of Fas and TNF	7	1.098901099	8.E-01 22029, 672195, 218397, 12122, 12043, 11	167	52	1171	9.E-01	1.E+00	1.E+00	1.E+02
BIOCARTA	m_deathPathway:Induction of apoptosis through DR3 and DR4/5 D	4	0.627943485	8.E-01 672195, 12122, 12043, 13063, 12370	167	29	1171	1.E+00	1.E+00	1.E+00	1.E+02

Annotation Cluster 179	Enrichment Score: 0.7447376234546411											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0005581~collagen	5	0.784929356		4.E-03 12843, 12831, 12842, 16948, 12815	434	19	12504	8.E+00	7.E-01	4.E-02	5.E+00
UP_SEQ_FEATURE	domain:Fibrillar collagen NC1	4	0.627943485		6.E-03 12843, 12831, 12842, 12815	618	10	16021	1.E+01	1.E+00	2.E-01	9.E+00
INTERPRO	IPR000885:Fibrillar collagen C-terminal	4	0.627943485		6.E-03 12843, 12831, 12842, 12815	630	11	17763	1.E+01	1.E+00	1.E-01	9.E+00
SMART	SM00038:COLF	4	0.627943485		1.E-02 12843, 12831, 12842, 12815	418	11	9131	8.E+00	9.E-01	1.E-01	1.E+01
UP_SEQ_FEATURE	propeptide:C-terminal propeptide	3	0.470957614		3.E-02 12843, 12842, 12815	618	7	16021	1.E+01	1.E+00	5.E-01	4.E+01
GOTERM_MF_FAT	GO:0048407~platelet-derived growth factor binding	3	0.470957614		5.E-02 12843, 12831, 12842	550	9	13288	8.E+00	1.E+00	4.E-01	5.E+01
GOTERM_CC_FAT	GO:0044420~extracellular matrix part	7	1.098901099		1.E-01 12843, 12831, 11657, 12842, 20692, 1694	434	92	12504	2.E+00	1.E+00	4.E-01	8.E+01
GOTERM_MF_FAT	GO:0005201~extracellular matrix structural constituent	4	0.627943485		1.E-01 12843, 12831, 12842, 12815	550	30	13288	3.E+00	1.E+00	6.E-01	9.E+01
UP_SEQ_FEATURE	region of interest:Triple-helical region	3	0.470957614		2.E-01 12831, 12842, 12815	618	18	16021	4.E+00	1.E+00	1.E+00	9.E+01
GOTERM_MF_FAT	GO:0019838~growth factor binding	6	0.941915228		2.E-01 12843, 12831, 16195, 12842, 16001, 1708	550	72	13288	2.E+00	1.E+00	7.E-01	9.E+01
GOTERM_BP_FAT	GO:0030199~collagen fibril organization	3	0.470957614		2.E-01 12831, 16948, 12815	572	21	13588	3.E+00	1.E+00	8.E-01	1.E+02
SP_PIR_KEYWORDS	hydroxylation	4	0.627943485		4.E-01 12843, 12831, 12842, 12815	629	64	17854	2.E+00	1.E+00	7.E-01	1.E+02
SP_PIR_KEYWORDS	copper	3	0.470957614		5.E-01 11657, 20692, 16948	629	49	17854	2.E+00	1.E+00	8.E-01	1.E+02
KEGG_PATHWAY	mmu04512:ECM-receptor interaction	7	1.098901099		5.E-01 12843, 12831, 12842, 20969, 12505, 1641	409	83	5738	1.E+00	1.E+00	7.E-01	1.E+02
INTERPRO	IPR008160:Collagen triple helix repeat	4	0.627943485		6.E-01 12843, 12831, 12842, 12815	630	81	17763	1.E+00	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	collagen	4	0.627943485		6.E-01 12843, 12831, 12842, 12815	629	84	17854	1.E+00	1.E+00	9.E-01	1.E+02
GOTERM_MF_FAT	GO:0005507~copper ion binding	3	0.470957614		7.E-01 11657, 20692, 16948	550	61	13288	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_CC_FAT	GO:0005604~basement membrane	3	0.470957614		7.E-01 12831, 11657, 20692	434	73	12504	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0043062~extracellular structure organization	6	0.941915228		8.E-01 12051, 12831, 16948, 18479, 12815, 1338	572	149	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0030198~extracellular matrix organization	4	0.627943485		8.E-01 12051, 12831, 16948, 12815	572	101	13588	9.E-01	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	extracellular matrix	5	0.784929356		9.E-01 12843, 12831, 12842, 20692, 12815	629	213	17854	7.E-01	1.E+00	1.E+00	1.E+02
GOTERM_CC_FAT	GO:0005578~proteinaceous extracellular matrix	7	1.098901099		9.E-01 12843, 12831, 11657, 12842, 20692, 1694	434	297	12504	7.E-01	1.E+00	1.E+00	1.E+02
GOTERM_CC_FAT	GO:0031012~extracellular matrix	7	1.098901099		1.E+00 12843, 12831, 11657, 12842, 20692, 1694	434	309	12504	7.E-01	1.E+00	1.E+00	1.E+02
GOTERM_MF_FAT	GO:0005198~structural molecule activity	12	1.883830455		1.E+00 22142, 12843, 78294, 12831, 67891, 1284	550	450	13288	6.E-01	1.E+00	1.E+00	1.E+02

Annotation Cluster 180		Enrichment Score: 0.7358406119930417										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0022612~gland morphogenesis	9	1.412872841	2.E-02	13649, 20779, 14178, 12043, 12505, 1600	572	84	13588	3.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0060740~prostate gland epithelium morphogenesis	3	0.470957614	3.E-01	12505, 16001, 16000	572	26	13588	3.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0060512~prostate gland morphogenesis	3	0.470957614	3.E-01	12505, 16001, 16000	572	27	13588	3.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0030850~prostate gland development	3	0.470957614	5.E-01	12505, 16001, 16000	572	39	13588	2.E+00	1.E+00	1.E+00	1.E+02

Annotation Cluster 181	Enrichment Score: 0.6957111420970774											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0051329~interphase of mitotic cell cycle	5	0.784929356		1.E-01 13197, 12043, 16412, 20466, 69581	572	49	13588	2.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0051325~interphase	5	0.784929356		2.E-01 13197, 12043, 16412, 20466, 69581	572	51	13588	2.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0000082~G1/S transition of mitotic cell cycle	3	0.470957614		3.E-01 12043, 16412, 69581	572	28	13588	3.E+00	1.E+00	9.E-01	1.E+02

Annotation Cluster 182		Enrichment Score: 0.6852673828589726										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0032318~regulation of Ras GTPase activity	8	1.25588697		5.E-02 56717, 24064, 71709, 228998, 19765, 194	572	80	13588	2.E+00	1.E+00	3.E-01	6.E+01
UP_SEQ_FEATURE	domain:Arf-GAP	3	0.470957614		2.E-01 228998, 212285, 106952	618	21	16021	4.E+00	1.E+00	1.E+00	1.E+02
INTERPRO	IPR001164:Arf GTPase activating protein	3	0.470957614		2.E-01 228998, 212285, 106952	630	23	17763	4.E+00	1.E+00	9.E-01	1.E+02
GOTERM_MF_FAT	GO:0008060~ARF GTPase activator activity	3	0.470957614		2.E-01 228998, 212285, 106952	550	23	13288	3.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0032312~regulation of ARF GTPase activity	3	0.470957614		3.E-01 228998, 212285, 106952	572	23	13588	3.E+00	1.E+00	8.E-01	1.E+02
SMART	SM00105:ArfGap	3	0.470957614		3.E-01 228998, 212285, 106952	418	23	9131	3.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0032012~regulation of ARF protein signal transduction	3	0.470957614		5.E-01 228998, 212285, 106952	572	38	13588	2.E+00	1.E+00	1.E+00	1.E+02

Annotation Cluster 183		Enrichment Score: 0.6675632875659951										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0033043~regulation of organelle organization	13	2.040816327	3.E-02	227753, 16800, 56150, 11848, 16994, 567	572	154	13588	2.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0032535~regulation of cellular component size	11	1.726844584	1.E-01	56717, 227753, 16197, 218397, 72269, 11	572	161	13588	2.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0032271~regulation of protein polymerization	5	0.784929356	2.E-01	56717, 227753, 218397, 19684, 12576	572	57	13588	2.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0051493~regulation of cytoskeleton organization	7	1.098901099	2.E-01	56717, 227753, 218397, 16800, 19684, 11	572	99	13588	2.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0032956~regulation of actin cytoskeleton organization	5	0.784929356	2.E-01	56717, 227753, 218397, 19684, 11848	572	60	13588	2.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0032970~regulation of actin filament-based process	5	0.784929356	3.E-01	56717, 227753, 218397, 19684, 11848	572	61	13588	2.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0043254~regulation of protein complex assembly	5	0.784929356	3.E-01	56717, 227753, 218397, 19684, 12576	572	65	13588	2.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0030833~regulation of actin filament polymerization	4	0.627943485	3.E-01	56717, 227753, 218397, 19684	572	45	13588	2.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0044087~regulation of cellular component biogenesis	6	0.941915228	3.E-01	56717, 227753, 218397, 19684, 11848, 12	572	89	13588	2.E+00	1.E+00	9.E-01	1.E+02



GOTERM_BP_FAT	GO:0008064~regulation of actin polymerization or depolymerization	4	0.627943485	4.E-01	56717, 227753, 218397, 19684	572	50	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0030832~regulation of actin filament length	4	0.627943485	4.E-01	56717, 227753, 218397, 19684	572	51	13588	2.E+00	1.E+00	9.E-01	1.E+02
Annotation Cluster 184	Enrichment Score: 0.6671572820140248											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR006186:Serine/threonine-specific protein phosphatase and bis(5-	3	0.470957614		1.E-01 19053, 19056, 19057	630	15	17763	6.E+00	1.E+00	7.E-01	8.E+01
SMART	SM00156:PP2Ac	3	0.470957614		1.E-01 19053, 19056, 19057	418	15	9131	4.E+00	1.E+00	6.E-01	9.E+01
INTERPRO	IPR004843:Metallophosphoesterase	3	0.470957614		3.E-01 19053, 19056, 19057	630	29	17763	3.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	metal ion-binding site:Iron	3	0.470957614		5.E-01 19053, 19056, 19057	618	47	16021	2.E+00	1.E+00	1.E+00	1.E+02
Annotation Cluster 185	Enrichment Score: 0.6645602172110462											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0016410~N-acyltransferase activity	6	0.941915228		1.E-01 18108, 18107, 12753, 217214, 17979, 129	550	67	13288	2.E+00	1.E+00	6.E-01	9.E+01
SP_PIR_KEYWORDS	Acytransferase	9	1.412872841		2.E-01 18108, 18107, 108672, 12753, 235339, 27	629	155	17854	2.E+00	1.E+00	5.E-01	9.E+01
GOTERM_MF_FAT	GO:0004402~histone acetyltransferase activity	3	0.470957614		2.E-01 12753, 17979, 12914	550	20	13288	4.E+00	1.E+00	7.E-01	1.E+02
GOTERM_MF_FAT	GO:0004468~lysine N-acetyltransferase activity	3	0.470957614		2.E-01 12753, 17979, 12914	550	20	13288	4.E+00	1.E+00	7.E-01	1.E+02
UP_SEQ_FEATURE	compositionally biased region:Poly-Gln	8	1.25588697		2.E-01 12753, 16367, 53610, 17869, 76448, 1797	618	130	16021	2.E+00	1.E+00	1.E+00	1.E+02
GOTERM_MF_FAT	GO:0016407~acetyltransferase activity	5	0.784929356		3.E-01 12753, 235339, 217214, 17979, 12914	550	63	13288	2.E+00	1.E+00	8.E-01	1.E+02
GOTERM_MF_FAT	GO:0008080~N-acetyltransferase activity	4	0.627943485		4.E-01 12753, 217214, 17979, 12914	550	51	13288	2.E+00	1.E+00	9.E-01	1.E+02
Annotation Cluster 186	Enrichment Score: 0.6626874911088445											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
BIOCARTA	m_gpccrPathway:Signaling Pathway from G-Protein Families	7	1.098901099		1.E-01 18803, 12315, 12314, 26395, 12313, 1546	167	25	1171	2.E+00	1.E+00	4.E-01	8.E+01
BIOCARTA	m_Ccr5Pathway:Pertussis toxin-insensitive CCR5 Signaling in Macro	5	0.784929356		2.E-01 18803, 12315, 12314, 26416, 12313, 1428	167	16	1171	2.E+00	1.E+00	5.E-01	9.E+01
BIOCARTA	m_vipPathway:Neuropeptides VIP and PACAP inhibit the apoptosis	5	0.784929356		2.E-01 18019, 18803, 12315, 12314, 12313, 1786	167	16	1171	2.E+00	1.E+00	5.E-01	9.E+01
BIOCARTA	m_calcineurinPathway:Effects of calcineurin in Keratinocyte Differen	3	0.470957614		5.E-01 18803, 12315, 12314, 12313, 14682	167	12	1171	2.E+00	1.E+00	9.E-01	1.E+02
Annotation Cluster 187	Enrichment Score: 0.6556797969956717											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0003006~reproductive developmental process	20	3.139717425		2.E-02 11651, 12043, 72508, 13382, 67141, 5671	572	264	13588	2.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0007281~germ cell development	10	1.569858713		3.E-02 56717, 12048, 12028, 72508, 11651, 1204	572	101	13588	2.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0048609~reproductive process in a multicellular organism	23	3.610675039		1.E-01 19317, 26934, 11651, 238055, 12043, 725	572	409	13588	1.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0032504~multicellular organism reproduction	23	3.610675039		1.E-01 19317, 26934, 11651, 238055, 12043, 725	572	409	13588	1.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0007276~gamete generation	19	2.982731554		2.E-01 19317, 26934, 11651, 238055, 12043, 725	572	331	13588	1.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0048610~reproductive cellular process	11	1.726844584		2.E-01 56717, 12048, 12028, 72508, 11651, 1204	572	173	13588	2.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0019953~sexual reproduction	19	2.982731554		4.E-01 19317, 26934, 11651, 238055, 12043, 725	572	386	13588	1.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0009566~fertilization	3	0.470957614		8.E-01 12048, 12028, 238055	572	73	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0007283~spermatogenesis	8	1.25588697		9.E-01 110957, 19317, 26934, 12048, 12028, 238	572	255	13588	7.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0048232~male gamete generation	8	1.25588697		9.E-01 110957, 19317, 26934, 12048, 12028, 238	572	255	13588	7.E-01	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	spermatogenesis	3	0.470957614		9.E-01 110957, 26934, 67402	629	123	17854	7.E-01	1.E+00	1.E+00	1.E+02
Annotation Cluster 188	Enrichment Score: 0.6399486696869626											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0006690~icosanoid metabolic process	4	0.627943485		2.E-01 17969, 19225, 20963, 21937	572	34	13588	3.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0033559~unsaturated fatty acid metabolic process	4	0.627943485		2.E-01 17969, 19225, 20963, 21937	572	36	13588	3.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0006631~fatty acid metabolic process	10	1.569858713		4.E-01 19317, 15107, 11807, 26416, 19088, 2199	572	184	13588	1.E+00	1.E+00	9.E-01	1.E+02
Annotation Cluster 189	Enrichment Score: 0.6373287413441967											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_SEQ_FEATURE	domain:Sushi 1	4	0.627943485		1.E-01 14060, 20343, 20339, 12263	618	33	16021	3.E+00	1.E+00	9.E-01	9.E+01
UP_SEQ_FEATURE	domain:Sushi 2	4	0.627943485		1.E-01 14060, 20343, 20339, 12263	618	33	16021	3.E+00	1.E+00	9.E-01	9.E+01
SP_PIR_KEYWORDS	sushi	4	0.627943485		2.E-01 14060, 20343, 20339, 12263	629	46	17854	2.E+00	1.E+00	5.E-01	1.E+02
UP_SEQ_FEATURE	domain:Sushi 3	3	0.470957614		2.E-01 14060, 20339, 12263	618	24	16021	3.E+00	1.E+00	1.E+00	1.E+02
INTERPRO	IPR000436:Sushi/SCR/CCP	4	0.627943485		3.E-01 14060, 20343, 20339, 12263	630	53	17763	2.E+00	1.E+00	1.E+00	1.E+02
INTERPRO	IPR016060:Complement control module	4	0.627943485		3.E-01 14060, 20343, 20339, 12263	630	54	17763	2.E+00	1.E+00	1.E+00	1.E+02
SMART	SM00032:CCP	4	0.627943485		4.E-01 14060, 20343, 20339, 12263	418	53	9131	2.E+00	1.E+00	9.E-01	1.E+02
Annotation Cluster 190	Enrichment Score: 0.627214216295615											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
BIOCARTA	m_cdMacPathway:Cadmium induces DNA synthesis and proliferatio	5	0.784929356		1.E-01 26395, 15461, 17869, 14281, 18795	167	14	1171	3.E+00	1.E+00	4.E-01	8.E+01
BIOCARTA	m_bArrestin-srcPathway:Roles of ???-arrestin-dependent Recruitmei	5	0.784929356		3.E-01 14191, 20779, 26395, 15461, 18795	167	19	1171	2.E+00	1.E+00	7.E-01	1.E+02
BIOCARTA	m_CCR3Pathway:CCR3 signaling in Eosinophils	5	0.784929356		4.E-01 26395, 15461, 14682, 11848, 18795	167	22	1171	2.E+00	1.E+00	8.E-01	1.E+02
Annotation Cluster 191	Enrichment Score: 0.5838320956909692											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR



UP_SEQ_FEATURE	domain:SAM	7	1.098901099	5.E-02 13836, 54383, 50768, 243362, 16822, 212	618	68	16021	3.E+00	1.E+00	7.E-01	6.E+01	
INTERPRO	IPR001660:Sterile alpha motif SAM	5	0.784929356	4.E-01 13836, 54383, 16822, 212285, 106952	630	87	17763	2.E+00	1.E+00	1.E+00	1.E+02	
INTERPRO	IPR013761:Sterile alpha motif-type	4	0.627943485	5.E-01 13836, 54383, 212285, 106952	630	72	17763	2.E+00	1.E+00	1.E+00	1.E+02	
SMART	SM00454:SAM	5	0.784929356	6.E-01 13836, 54383, 16822, 212285, 106952	418	87	9131	1.E+00	1.E+00	1.E+00	1.E+02	
Annotation Cluster 192												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_SEQ_FEATURE	domain:N-terminal Ras-GEF	3	0.470957614	1.E-01 20662, 20663, 19417	618	17	16021	5.E+00	1.E+00	9.E-01	9.E+01	
INTERPRO	IPR019804:Ras guanine-nucleotide exchange factor, conserved site	3	0.470957614	2.E-01 20662, 20663, 19417	630	24	17763	4.E+00	1.E+00	9.E-01	1.E+02	
UP_SEQ_FEATURE	domain:Ras-GEF	3	0.470957614	2.E-01 20662, 20663, 19417	618	24	16021	3.E+00	1.E+00	1.E+00	1.E+02	
INTERPRO	IPR001895:Guanine-nucleotide dissociation stimulator CDC25	3	0.470957614	3.E-01 20662, 20663, 19417	630	28	17763	3.E+00	1.E+00	9.E-01	1.E+02	
INTERPRO	IPR000651:Guanine nucleotide exchange factor for Ras-like GTPase:	3	0.470957614	3.E-01 20662, 20663, 19417	630	30	17763	3.E+00	1.E+00	1.E+00	1.E+02	
INTERPRO	IPR008937:Ras guanine nucleotide exchange factor	3	0.470957614	3.E-01 20662, 20663, 19417	630	31	17763	3.E+00	1.E+00	1.E+00	1.E+02	
SMART	SM00147:RasGEF	3	0.470957614	4.E-01 20662, 20663, 19417	418	28	9131	2.E+00	1.E+00	9.E-01	1.E+02	
SMART	SM00229:RasGEFN	3	0.470957614	4.E-01 20662, 20663, 19417	418	30	9131	2.E+00	1.E+00	9.E-01	1.E+02	
Annotation Cluster 193												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0006790~sulfur metabolic process	8	1.25588697	1.E-01 56615, 22017, 232087, 54200, 14782, 143	572	94	13588	2.E+00	1.E+00	5.E-01	8.E+01	
GOTERM_BP_FAT	GO:0006749~glutathione metabolic process	3	0.470957614	3.E-01 56615, 14782, 14381	572	24	13588	3.E+00	1.E+00	8.E-01	1.E+02	
GOTERM_BP_FAT	GO:0006575~cellular amino acid derivative metabolic process	8	1.25588697	4.E-01 56615, 18453, 22017, 232087, 14462, 147	572	141	13588	1.E+00	1.E+00	9.E-01	1.E+02	
GOTERM_BP_FAT	GO:0006518~peptide metabolic process	3	0.470957614	5.E-01 56615, 14782, 14381	572	38	13588	2.E+00	1.E+00	1.E+00	1.E+02	
Annotation Cluster 194												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0051271~negative regulation of cell motion	4	0.627943485	1.E-01 11486, 12043, 106952, 12576	572	32	13588	3.E+00	1.E+00	6.E-01	9.E+01	
GOTERM_BP_FAT	GO:0030336~negative regulation of cell migration	3	0.470957614	3.E-01 11486, 12043, 106952	572	28	13588	3.E+00	1.E+00	9.E-01	1.E+02	
GOTERM_BP_FAT	GO:0040013~negative regulation of locomotion	3	0.470957614	5.E-01 11486, 12043, 106952	572	31	13588	2.E+00	1.E+00	9.E-01	1.E+02	
Annotation Cluster 195												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0006357~regulation of transcription from RNA polymerase II pr	39	6.12244898	1.E-02 17536, 22130, 19720, 17869, 22778, 1291	572	616	13588	2.E+00	1.E+00	1.E-01	2.E+01	
GOTERM_BP_FAT	GO:0010605~negative regulation of macromolecule metabolic proc	27	4.238618524	2.E-01 13685, 22130, 19720, 17869, 22778, 6714	572	506	13588	1.E+00	1.E+00	7.E-01	1.E+02	
GOTERM_BP_FAT	GO:0000122~negative regulation of transcription from RNA polyme	14	2.197802198	2.E-01 19720, 17869, 22778, 20481, 20466, 2406	572	231	13588	1.E+00	1.E+00	7.E-01	1.E+02	
GOTERM_BP_FAT	GO:0045892~negative regulation of transcription, DNA-dependent	16	2.51177394	3.E-01 19720, 17869, 22778, 20481, 20467, 2046	572	308	13588	1.E+00	1.E+00	9.E-01	1.E+02	
GOTERM_BP_FAT	GO:0051253~negative regulation of RNA metabolic process	16	2.51177394	3.E-01 19720, 17869, 22778, 20481, 20467, 2046	572	310	13588	1.E+00	1.E+00	9.E-01	1.E+02	
GOTERM_BP_FAT	GO:0031327~negative regulation of cellular biosynthetic process	20	3.139717425	5.E-01 13685, 22130, 19720, 17869, 22778, 2048	572	430	13588	1.E+00	1.E+00	9.E-01	1.E+02	
GOTERM_BP_FAT	GO:0009890~negative regulation of biosynthetic process	20	3.139717425	5.E-01 13685, 22130, 19720, 17869, 22778, 2048	572	434	13588	1.E+00	1.E+00	1.E+00	1.E+02	
GOTERM_BP_FAT	GO:0010558~negative regulation of macromolecule biosynthetic pr	19	2.982731554	5.E-01 13685, 22130, 19720, 17869, 22778, 2048	572	418	13588	1.E+00	1.E+00	1.E+00	1.E+02	
GOTERM_BP_FAT	GO:0045934~negative regulation of nucleobase, nucleoside, nucleoc	18	2.825745683	5.E-01 22130, 19720, 17869, 22778, 20481, 2046	572	397	13588	1.E+00	1.E+00	1.E+00	1.E+02	
GOTERM_BP_FAT	GO:0051172~negative regulation of nitrogen compound metabolic	18	2.825745683	5.E-01 22130, 19720, 17869, 22778, 20481, 2046	572	401	13588	1.E+00	1.E+00	1.E+00	1.E+02	
GOTERM_BP_FAT	GO:0016481~negative regulation of transcription	16	2.51177394	6.E-01 19720, 17869, 22778, 20481, 20467, 2046	572	372	13588	1.E+00	1.E+00	1.E+00	1.E+02	
GOTERM_BP_FAT	GO:0010629~negative regulation of gene expression	17	2.668759812	7.E-01 19720, 17869, 68092, 22778, 20481, 2046	572	410	13588	1.E+00	1.E+00	1.E+00	1.E+02	
Annotation Cluster 196												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
BIOCARTA	m_d4gdiPathway:D4-GDI Signaling Pathway	5	0.784929356	6.E-02 672195, 14939, 11855, 11857, 13063, 123	167	11	1171	3.E+00	1.E+00	3.E-01	5.E+01	
BIOCARTA	m_caspasePathway:Caspase Cascade in Apoptosis	4	0.627943485	6.E-01 672195, 14939, 11857, 13063, 12370	167	21	1171	1.E+00	1.E+00	9.E-01	1.E+02	
BIOCARTA	m_HivnefPathway:HIV-I Nef: negative effector of Fas and TNF	7	1.098901099	8.E-01 22029, 672195, 218397, 12122, 12043, 11	167	52	1171	9.E-01	1.E+00	1.E+00	1.E+02	
Annotation Cluster 197												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	manganese	9	1.412872841	1.E-01 11350, 23920, 19053, 14208, 18534, 1184	629	145	17854	2.E+00	1.E+00	4.E-01	9.E+01	
UP_SEQ_FEATURE	metal ion-binding site:Manganese	3	0.470957614	3.E-01 19053, 18534, 74551	618	31	16021	3.E+00	1.E+00	1.E+00	1.E+02	
GOTERM_MF_FAT	GO:0030145~manganese ion binding	7	1.098901099	6.E-01 11350, 19053, 14208, 18534, 11847, 1436	550	148	13288	1.E+00	1.E+00	1.E+00	1.E+02	
Annotation Cluster 198												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0060541~respiratory system development	8	1.25588697	3.E-01 15402, 24064, 14178, 11486, 19378, 1694	572	124	13588	2.E+00	1.E+00	8.E-01	1.E+02	
GOTERM_BP_FAT	GO:0030324~lung development	7	1.098901099	3.E-01 15402, 24064, 14178, 11486, 19378, 1694	572	111	13588	1.E+00	1.E+00	9.E-01	1.E+02	
GOTERM_BP_FAT	GO:0030323~respiratory tube development	7	1.098901099	3.E-01 15402, 24064, 14178, 11486, 19378, 1694	572	113	13588	1.E+00	1.E+00	9.E-01	1.E+02	
Annotation Cluster 199												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0006511~ubiquitin-dependent protein catabolic process	9	1.412872841	2.E-01 19053, 19358, 26965, 99152, 16396, 6610	572	141	13588	2.E+00	1.E+00	8.E-01	1.E+02	



GOTERM_BP_FAT	GO:0010498~proteasomal protein catabolic process	3	0.470957614	4.E-01	19053, 19358, 66105	572	30	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0043161~proteasomal ubiquitin-dependent protein catabolic process	3	0.470957614	4.E-01	19053, 19358, 66105	572	30	13588	2.E+00	1.E+00	9.E-01	1.E+02
Annotation Cluster 200	Enrichment Score: 0.48069223980377196											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0042770~DNA damage response, signal transduction	5	0.784929356	2.E-01	12051, 11920, 26416, 12534, 170770	572	57	13588	2.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0000077~DNA damage checkpoint	3	0.470957614	4.E-01	11920, 26416, 12534	572	30	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0000075~cell cycle checkpoint	4	0.627943485	4.E-01	11920, 26416, 56150, 12534	572	52	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0031570~DNA integrity checkpoint	3	0.470957614	4.E-01	11920, 26416, 12534	572	33	13588	2.E+00	1.E+00	9.E-01	1.E+02
Annotation Cluster 201	Enrichment Score: 0.4608462012834763											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0051493~regulation of cytoskeleton organization	7	1.098901099	2.E-01	56717, 227753, 218397, 16800, 19684, 11	572	99	13588	2.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0051495~positive regulation of cytoskeleton organization	3	0.470957614	3.E-01	56717, 11848, 12576	572	26	13588	3.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0044087~regulation of cellular component biogenesis	6	0.941915228	3.E-01	56717, 227753, 218397, 19684, 11848, 12	572	89	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0010638~positive regulation of organelle organization	4	0.627943485	4.E-01	16994, 56717, 11848, 12576	572	52	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0051130~positive regulation of cellular component organization	6	0.941915228	6.E-01	16994, 56717, 14127, 21844, 11848, 1257	572	122	13588	1.E+00	1.E+00	1.E+00	1.E+02
Annotation Cluster 202	Enrichment Score: 0.4478209263351998											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0008361~regulation of cell size	8	1.25588697	2.E-01	56717, 16197, 72269, 11651, 12043, 1185	572	108	13588	2.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0045792~negative regulation of cell size	5	0.784929356	2.E-01	56717, 72269, 11651, 12043, 170770	572	53	13588	2.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0045926~negative regulation of growth	5	0.784929356	3.E-01	17874, 72269, 12043, 24088, 170770	572	71	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0030308~negative regulation of cell growth	3	0.470957614	6.E-01	72269, 12043, 170770	572	47	13588	2.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0001558~regulation of cell growth	3	0.470957614	9.E-01	72269, 12043, 170770	572	92	13588	8.E-01	1.E+00	1.E+00	1.E+02
Annotation Cluster 203	Enrichment Score: 0.44399014136925957											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0051327~M phase of meiotic cell cycle	6	0.941915228	3.E-01	13006, 209091, 30939, 18005, 12531, 671	572	88	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0007126~meiosis	6	0.941915228	3.E-01	13006, 209091, 30939, 18005, 12531, 671	572	88	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0051321~meiotic cell cycle	6	0.941915228	3.E-01	13006, 209091, 30939, 18005, 12531, 671	572	90	13588	2.E+00	1.E+00	9.E-01	1.E+02
SP_PIR_KEYWORDS	meiosis	3	0.470957614	5.E-01	13006, 209091, 18005	629	50	17854	2.E+00	1.E+00	8.E-01	1.E+02
Annotation Cluster 204	Enrichment Score: 0.4410021419720743											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0003712~transcription cofactor activity	11	1.726844584	2.E-01	20481, 22601, 15278, 12815, 17978, 2688	550	180	13288	1.E+00	1.E+00	8.E-01	1.E+02
GOTERM_MF_FAT	GO:0003714~transcription corepressor activity	5	0.784929356	3.E-01	20481, 26885, 20467, 20466, 208727	550	72	13288	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_MF_FAT	GO:0016564~transcription repressor activity	9	1.412872841	6.E-01	69890, 22778, 20481, 17978, 26885, 2046	550	211	13288	1.E+00	1.E+00	1.E+00	1.E+02
Annotation Cluster 205	Enrichment Score: 0.4387239480176077											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0044057~regulation of system process	12	1.883830455	2.E-01	16994, 11486, 11806, 11807, 14678, 1546	572	201	13588	1.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0048168~regulation of neuronal synaptic plasticity	3	0.470957614	3.E-01	15461, 19417, 13385	572	27	13588	3.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0048167~regulation of synaptic plasticity	4	0.627943485	3.E-01	15461, 12568, 19417, 13385	572	48	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0050804~regulation of synaptic transmission	6	0.941915228	4.E-01	16994, 14678, 15461, 12568, 19417, 1338	572	100	13588	1.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0051969~regulation of transmission of nerve impulse	6	0.941915228	5.E-01	16994, 14678, 15461, 12568, 19417, 1338	572	107	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0031644~regulation of neurological system process	6	0.941915228	5.E-01	16994, 14678, 15461, 12568, 19417, 1338	572	113	13588	1.E+00	1.E+00	1.E+00	1.E+02
Annotation Cluster 206	Enrichment Score: 0.43766673253504357											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	EF hand	6	0.941915228	3.E-03	18826, 12315, 12314, 12313, 20692, 2020	629	28	17854	6.E+00	7.E-01	2.E-02	4.E+00
SP_PIR_KEYWORDS	calcium binding	5	0.784929356	8.E-02	16952, 20692, 20202, 19059, 20201	629	47	17854	3.E+00	1.E+00	3.E-01	7.E+01
INTERPRO	IPR018247:EF-HAND 1	10	1.569858713	3.E-01	18803, 18826, 12315, 12314, 12313, 2069	630	211	17763	1.E+00	1.E+00	1.E+00	1.E+02
INTERPRO	IPR011992:EF-Hand type	10	1.569858713	4.E-01	18826, 12315, 12314, 12313, 20692, 2020	630	227	17763	1.E+00	1.E+00	1.E+00	1.E+02
INTERPRO	IPR018248:EF hand	6	0.941915228	5.E-01	18826, 12315, 12314, 12313, 20202, 1905	630	132	17763	1.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	domain:EF-hand 2	7	1.098901099	6.E-01	18826, 12315, 12314, 12313, 20202, 1905	618	160	16021	1.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	domain:EF-hand 1	7	1.098901099	6.E-01	18826, 12315, 12314, 12313, 20202, 1905	618	161	16021	1.E+00	1.E+00	1.E+00	1.E+02
INTERPRO	IPR018249:EF-HAND 2	8	1.25588697	6.E-01	18803, 18826, 12315, 12314, 12313, 2020	630	205	17763	1.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	calcium-binding region:2	5	0.784929356	6.E-01	18826, 12315, 12314, 12313, 19059, 5904	618	110	16021	1.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	calcium-binding region:1	5	0.784929356	7.E-01	18826, 12315, 12314, 12313, 19059, 5904	618	120	16021	1.E+00	1.E+00	1.E+00	1.E+02
INTERPRO	IPR002048:Calcium-binding EF-hand	5	0.784929356	7.E-01	18826, 12315, 12314, 12313, 19059, 5904	630	137	17763	1.E+00	1.E+00	1.E+00	1.E+02
SMART	SM00054:EFh	5	0.784929356	9.E-01	18826, 12315, 12314, 12313, 19059, 5904	418	137	9131	8.E-01	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	calcium	21	3.296703297	9.E-01	227753, 16952, 238055, 18797, 214952, 2	629	731	17854	8.E-01	1.E+00	1.E+00	1.E+02
GOTERM_MF_FAT	GO:0005509~calcium ion binding	21	3.296703297	1.E+00	227753, 16952, 18797, 214952, 21881, 18	550	840	13288	6.E-01	1.E+00	1.E+00	1.E+02



Annotation Cluster 207		Enrichment Score: 0.4334399530359315										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_SEQ_FEATURE	domain:PDZ 1	4	0.627943485		1.E-01 277360, 73750, 170761, 13385	618	34	16021	3.E+00	1.E+00	9.E-01	9.E+01
UP_SEQ_FEATURE	domain:PDZ 3	3	0.470957614		2.E-01 73750, 170761, 13385	618	24	16021	3.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	domain:PDZ 2	3	0.470957614		4.E-01 73750, 170761, 13385	618	33	16021	2.E+00	1.E+00	1.E+00	1.E+02
INTERPRO	IPR001478:PDZ/DHR/GLGF	7	1.098901099		4.E-01 277360, 73750, 170761, 70231, 21844, 13	630	148	17763	1.E+00	1.E+00	1.E+00	1.E+02
SMART	SM00228:PDZ	7	1.098901099		7.E-01 277360, 73750, 170761, 70231, 21844, 13	418	148	9131	1.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	domain:PDZ	4	0.627943485		7.E-01 70231, 21844, 74498, 24001	618	95	16021	1.E+00	1.E+00	1.E+00	1.E+02
Annotation Cluster 208		Enrichment Score: 0.4167866517700656										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0051493~regulation of cytoskeleton organization	7	1.098901099		2.E-01 56717, 227753, 218397, 16800, 19684, 11	572	99	13588	2.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0010639~negative regulation of organelle organization	5	0.784929356		3.E-01 227753, 11920, 16800, 56150, 19684	572	62	13588	2.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0051129~negative regulation of cellular component organization	6	0.941915228		4.E-01 227753, 11920, 104215, 16800, 56150, 19	572	93	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0043242~negative regulation of protein complex disassembly	3	0.470957614		4.E-01 227753, 16800, 19684	572	35	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0043244~regulation of protein complex disassembly	3	0.470957614		5.E-01 227753, 16800, 19684	572	43	13588	2.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0051494~negative regulation of cytoskeleton organization	3	0.470957614		6.E-01 227753, 16800, 19684	572	48	13588	1.E+00	1.E+00	1.E+00	1.E+02
Annotation Cluster 209		Enrichment Score: 0.4109238004126499										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0001822~kidney development	8	1.25588697		2.E-01 382985, 18596, 19713, 12028, 109900, 12	572	107	13588	2.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0001894~tissue homeostasis	4	0.627943485		4.E-01 18596, 12028, 12043, 12815	572	50	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0048871~multicellular organismal homeostasis	4	0.627943485		6.E-01 18596, 12028, 12043, 12815	572	71	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0060249~anatomical structure homeostasis	4	0.627943485		7.E-01 18596, 12028, 12043, 12815	572	83	13588	1.E+00	1.E+00	1.E+00	1.E+02
Annotation Cluster 210		Enrichment Score: 0.4037540726033223										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0001822~kidney development	8	1.25588697		2.E-01 382985, 18596, 19713, 12028, 109900, 12	572	107	13588	2.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0001657~ureteric bud development	3	0.470957614		5.E-01 19713, 12043, 12505	572	42	13588	2.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0001656~metanephros development	3	0.470957614		7.E-01 19713, 12043, 12505	572	58	13588	1.E+00	1.E+00	1.E+00	1.E+02
Annotation Cluster 211		Enrichment Score: 0.39034193978698										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0005543~phospholipid binding	9	1.412872841		1.E-01 18416, 16952, 17972, 27359, 17969, 2330	550	119	13288	2.E+00	1.E+00	6.E-01	9.E+01
UP_SEQ_FEATURE	domain:PX	3	0.470957614		5.E-01 17972, 17969, 58240	618	42	16021	2.E+00	1.E+00	1.E+00	1.E+02
INTERPRO	IPR001683:Phox-like	3	0.470957614		5.E-01 17972, 17969, 58240	630	47	17763	2.E+00	1.E+00	1.E+00	1.E+02
GOTERM_MF_FAT	GO:0035091~phosphoinositide binding	4	0.627943485		6.E-01 17972, 17969, 233071, 58240	550	75	13288	1.E+00	1.E+00	1.E+00	1.E+02
SMART	SM00312:PX	3	0.470957614		6.E-01 17972, 17969, 58240	418	47	9131	1.E+00	1.E+00	1.E+00	1.E+02
Annotation Cluster 212		Enrichment Score: 0.3850919470715316										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0016192~vesicle-mediated transport	26	4.081632653		1.E-01 22324, 227753, 269589, 11852, 94190, 13	572	466	13588	1.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0016044~membrane organization	15	2.354788069		3.E-01 22324, 94190, 12122, 13430, 12043, 5725	572	272	13588	1.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0006897~endocytosis	9	1.412872841		5.E-01 14127, 22324, 108672, 94190, 13430, 154	572	188	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0010324~membrane invagination	9	1.412872841		5.E-01 14127, 22324, 108672, 94190, 13430, 154	572	188	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0006909~phagocytosis	3	0.470957614		6.E-01 14127, 22324, 16803	572	49	13588	1.E+00	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	Endocytosis	3	0.470957614		8.E-01 94190, 13430, 17533	629	93	17854	9.E-01	1.E+00	1.E+00	1.E+02
Annotation Cluster 213		Enrichment Score: 0.3733729508907291										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0006470~protein amino acid dephosphorylation	9	1.412872841		1.E-01 15170, 218294, 19253, 14208, 12043, 125	572	114	13588	2.E+00	1.E+00	5.E-01	9.E+01
GOTERM_MF_FAT	GO:0004725~protein tyrosine phosphatase activity	7	1.098901099		2.E-01 15170, 218294, 19253, 26395, 12532, 125	550	101	13288	2.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0016311~dephosphorylation	9	1.412872841		2.E-01 15170, 218294, 19253, 14208, 12043, 125	572	141	13588	2.E+00	1.E+00	8.E-01	1.E+02
INTERPRO	IPR000387:Protein-tyrosine phosphatase	3	0.470957614		8.E-01 15170, 218294, 19253	630	78	17763	1.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	active site:Phosphocysteine intermediate	3	0.470957614		8.E-01 15170, 218294, 19253	618	75	16021	1.E+00	1.E+00	1.E+00	1.E+02
INTERPRO	IPR000387:Dual-specific/protein-tyrosine phosphatase, conserved r	3	0.470957614		8.E-01 15170, 218294, 19253	630	82	17763	1.E+00	1.E+00	1.E+00	1.E+02
INTERPRO	IPR016130:Protein-tyrosine phosphatase, active site	3	0.470957614		8.E-01 15170, 218294, 19253	630	87	17763	1.E+00	1.E+00	1.E+00	1.E+02
Annotation Cluster 214		Enrichment Score: 0.36719820743008097										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0031406~carboxylic acid binding	6	0.941915228		3.E-01 18126, 235339, 17999, 18416, 27402, 162	550	85	13288	2.E+00	1.E+00	8.E-01	1.E+02
GOTERM_MF_FAT	GO:0016597~amino acid binding	3	0.470957614		4.E-01 18126, 17999, 18416	550	33	13288	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_MF_FAT	GO:0043176~amine binding	3	0.470957614		7.E-01 18126, 17999, 18416	550	61	13288	1.E+00	1.E+00	1.E+00	1.E+02
Annotation Cluster 215		Enrichment Score: 0.3586977002956306										



Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0040018~positive regulation of multicellular organism growth	3	0.470957614		3.E-01 12043, 22778, 12912		572	27	13588	3.E+00	1.E+00	9.E-01 1.E+02
GOTERM_BP_FAT	GO:0040014~regulation of multicellular organism growth	5	0.784929356		4.E-01 11816, 12043, 22778, 12912, 14381		572	75	13588	2.E+00	1.E+00	9.E-01 1.E+02
GOTERM_BP_FAT	GO:0045927~positive regulation of growth	3	0.470957614		7.E-01 12043, 22778, 12912		572	56	13588	1.E+00	1.E+00	1.E+00 1.E+02
Annotation Cluster 216												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR007125:Histone core	5	0.784929356		6.E-02 319168, 621893, 319169, 20662, 20663, 3		630	42	17763	3.E+00	1.E+00	6.E-01 6.E+01
SP_PIR_KEYWORDS	citrullination	3	0.470957614		1.E-01 319168, 621893, 319169, 319191		629	16	17854	5.E+00	1.E+00	3.E-01 8.E+01
PIR_SUPERFAMILY	PIRSF002048:histone H2A	3	0.470957614		1.E-01 319168, 621893, 319169, 319191		400	13	8136	5.E+00	1.E+00	1.E+00 9.E+01
INTERPRO	IPR002119:Histone H2A	3	0.470957614		2.E-01 319168, 621893, 319169, 319191		630	25	17763	3.E+00	1.E+00	9.E-01 1.E+02
SMART	SM00414:H2A	3	0.470957614		3.E-01 319168, 621893, 319169, 319191		418	25	9131	3.E+00	1.E+00	8.E-01 1.E+02
SP_PIR_KEYWORDS	nucleosome core	3	0.470957614		5.E-01 319168, 621893, 319169, 319191		629	44	17854	2.E+00	1.E+00	8.E-01 1.E+02
GOTERM_CC_FAT	GO:0032993~protein-DNA complex	4	0.627943485		5.E-01 319168, 621893, 19891, 319169, 319191		434	75	12504	2.E+00	1.E+00	9.E-01 1.E+02
GOTERM_CC_FAT	GO:0000785~chromatin	7	1.098901099		5.E-01 319168, 621893, 319169, 216848, 22778,		434	165	12504	1.E+00	1.E+00	9.E-01 1.E+02
GOTERM_CC_FAT	GO:0000786~nucleosome	3	0.470957614		6.E-01 319168, 621893, 319169, 319191		434	62	12504	1.E+00	1.E+00	9.E-01 1.E+02
GOTERM_BP_FAT	GO:0006334~nucleosome assembly	3	0.470957614		8.E-01 319168, 621893, 319169, 319191		572	73	13588	1.E+00	1.E+00	1.E+00 1.E+02
GOTERM_BP_FAT	GO:0031497~chromatin assembly	3	0.470957614		8.E-01 319168, 621893, 319169, 319191		572	75	13588	1.E+00	1.E+00	1.E+00 1.E+02
GOTERM_BP_FAT	GO:0034728~nucleosome organization	3	0.470957614		8.E-01 319168, 621893, 319169, 319191		572	76	13588	9.E-01	1.E+00	1.E+00 1.E+02
GOTERM_BP_FAT	GO:0065004~protein-DNA complex assembly	3	0.470957614		8.E-01 319168, 621893, 319169, 319191		572	76	13588	9.E-01	1.E+00	1.E+00 1.E+02
GOTERM_BP_FAT	GO:0006333~chromatin assembly or disassembly	4	0.627943485		8.E-01 319168, 621893, 319169, 216848, 319191		572	109	13588	9.E-01	1.E+00	1.E+00 1.E+02
SP_PIR_KEYWORDS	chromosomal protein	4	0.627943485		9.E-01 319168, 621893, 319169, 20877, 319191		629	136	17854	8.E-01	1.E+00	1.E+00 1.E+02
GOTERM_BP_FAT	GO:0006323~DNA packaging	3	0.470957614		9.E-01 319168, 621893, 319169, 319191		572	101	13588	7.E-01	1.E+00	1.E+00 1.E+02
KEGG_PATHWAY	mmu05322:Systemic lupus erythematosus	5	0.784929356		9.E-01 319168, 621893, 319169, 13035, 319191,		409	103	5738	7.E-01	1.E+00	1.E+00 1.E+02
Annotation Cluster 217												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0005615~extracellular space	24	3.767660911		1.E-01 11657, 11813, 11814, 11806, 11807, 1181		434	511	12504	1.E+00	1.E+00	4.E-01 8.E+01
GOTERM_CC_FAT	GO:0044421~extracellular region part	29	4.552590267		4.E-01 12831, 11657, 11813, 11814, 11816, 6604		434	774	12504	1.E+00	1.E+00	8.E-01 1.E+02
SP_PIR_KEYWORDS	Secreted	43	6.750392465		9.E-01 227753, 12831, 11813, 11657, 11814, 141		629	1420	17854	9.E-01	1.E+00	1.E+00 1.E+02
GOTERM_CC_FAT	GO:0005576~extracellular region	44	6.907378336		1.E+00 227753, 12831, 11813, 11657, 14178, 118		434	1680	12504	8.E-01	1.E+00	1.E+00 1.E+02
Annotation Cluster 218												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0021537~telencephalon development	5	0.784929356		4.E-01 13649, 77579, 12028, 56847, 12568		572	72	13588	2.E+00	1.E+00	9.E-01 1.E+02
GOTERM_BP_FAT	GO:0021987~cerebral cortex development	3	0.470957614		5.E-01 13649, 12028, 12568		572	37	13588	2.E+00	1.E+00	1.E+00 1.E+02
GOTERM_BP_FAT	GO:0021543~pallium development	3	0.470957614		7.E-01 13649, 12028, 12568		572	53	13588	1.E+00	1.E+00	1.E+00 1.E+02
Annotation Cluster 219												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0030030~cell projection organization	21	3.296703297		5.E-02 22323, 100044475, 73750, 17973, 11651,		572	319	13588	2.E+00	1.E+00	3.E-01 6.E+01
GOTERM_BP_FAT	GO:0022037~metencephalon development	4	0.627943485		2.E-01 77579, 15407, 12043, 12568		572	41	13588	2.E+00	1.E+00	8.E-01 1.E+02
GOTERM_BP_FAT	GO:0048666~neuron development	16	2.51177394		2.E-01 22323, 73750, 12043, 15430, 18479, 1379		572	292	13588	1.E+00	1.E+00	8.E-01 1.E+02
GOTERM_BP_FAT	GO:0032989~cellular component morphogenesis	18	2.825745683		3.E-01 22323, 13649, 13605, 12043, 16800, 1641		572	351	13588	1.E+00	1.E+00	9.E-01 1.E+02
GOTERM_BP_FAT	GO:0030182~neuron differentiation	20	3.139717425		3.E-01 22323, 73750, 19378, 12043, 15430, 1847		572	399	13588	1.E+00	1.E+00	9.E-01 1.E+02
GOTERM_BP_FAT	GO:0031175~neuron projection development	10	1.569858713		6.E-01 22323, 14432, 77579, 12043, 18479, 1256		572	218	13588	1.E+00	1.E+00	1.E+00 1.E+02
GOTERM_BP_FAT	GO:0000902~cell morphogenesis	13	2.040816327		7.E-01 22323, 13649, 12043, 13605, 16800, 1291		572	309	13588	1.E+00	1.E+00	1.E+00 1.E+02
GOTERM_BP_FAT	GO:0007411~axon guidance	4	0.627943485		8.E-01 22323, 14432, 77579, 12568		572	98	13588	1.E+00	1.E+00	1.E+00 1.E+02
GOTERM_BP_FAT	GO:0032990~cell part morphogenesis	8	1.25588697		8.E-01 22323, 14432, 77579, 12028, 12018, 1204		572	212	13588	9.E-01	1.E+00	1.E+00 1.E+02
GOTERM_BP_FAT	GO:0007409~axonogenesis	6	0.941915228		8.E-01 22323, 14432, 77579, 12043, 12568, 1291		572	163	13588	9.E-01	1.E+00	1.E+00 1.E+02
GOTERM_BP_FAT	GO:0048812~neuron projection morphogenesis	6	0.941915228		9.E-01 22323, 14432, 77579, 12043, 12568, 1291		572	176	13588	8.E-01	1.E+00	1.E+00 1.E+02
GOTERM_BP_FAT	GO:0048667~cell morphogenesis involved in neuron differentiation	6	0.941915228		9.E-01 22323, 14432, 77579, 12043, 12568, 1291		572	182	13588	8.E-01	1.E+00	1.E+00 1.E+02
GOTERM_BP_FAT	GO:0048858~cell projection morphogenesis	6	0.941915228		9.E-01 22323, 14432, 77579, 12043, 12568, 1291		572	202	13588	7.E-01	1.E+00	1.E+00 1.E+02
GOTERM_BP_FAT	GO:0000904~cell morphogenesis involved in differentiation	6	0.941915228		9.E-01 22323, 14432, 77579, 12043, 12568, 1291		572	212	13588	7.E-01	1.E+00	1.E+00 1.E+02
Annotation Cluster 220												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0030247~polysaccharide binding	7	1.098901099		4.E-01 12831, 669888, 11816, 12505, 13035, 775		550	128	13288	1.E+00	1.E+00	9.E-01 1.E+02
GOTERM_MF_FAT	GO:0001871~pattern binding	7	1.098901099		4.E-01 12831, 669888, 11816, 12505, 13035, 775		550	128	13288	1.E+00	1.E+00	9.E-01 1.E+02
GOTERM_MF_FAT	GO:0008201~heparin binding	5	0.784929356		5.E-01 12831, 669888, 11816, 13035, 16409		550	83	13288	1.E+00	1.E+00	9.E-01 1.E+02
GOTERM_MF_FAT	GO:0005539~glycosaminoglycan binding	6	0.941915228		5.E-01 12831, 669888, 11816, 12505, 13035, 164		550	114	13288	1.E+00	1.E+00	1.E+00 1.E+02
GOTERM_MF_FAT	GO:0030246~carbohydrate binding	14	2.197802198		6.E-01 17159, 12831, 11816, 27007, 13035, 1039		550	317	13288	1.E+00	1.E+00	1.E+00 1.E+02
SP_PIR_KEYWORDS	heparin-binding	3	0.470957614		6.E-01 12831, 669888, 11816		629	53	17854	2.E+00	1.E+00	9.E-01 1.E+02
Annotation Cluster 221												
Enrichment Score: 0.3080134989707941												



Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0035257~nuclear hormone receptor binding	3	0.470957614	4	E-01 12815, 17978, 17979	550	34	13288	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_MF_FAT	GO:0051427~hormone receptor binding	3	0.470957614	5	E-01 12815, 17978, 17979	550	39	13288	2.E+00	1.E+00	1.E+00	1.E+02
GOTERM_MF_FAT	GO:0003713~transcription coactivator activity	5	0.784929356	6	E-01 22601, 12815, 17978, 17979, 12914	550	100	13288	1.E+00	1.E+00	1.E+00	1.E+02
Annotation Cluster 222	Enrichment Score: 0.2985386187255895											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0002683~negative regulation of immune system process	6	0.941915228	2	E-01 15170, 16197, 11486, 16396, 16190, 1905	572	76	13588	2.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0050868~negative regulation of T cell activation	3	0.470957614	5	E-01 15170, 16396, 16190	572	42	13588	2.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0051250~negative regulation of lymphocyte activation	3	0.470957614	6	E-01 15170, 16396, 16190	572	52	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0002695~negative regulation of leukocyte activation	3	0.470957614	7	E-01 15170, 16396, 16190	572	53	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0050866~negative regulation of cell activation	3	0.470957614	7	E-01 15170, 16396, 16190	572	53	13588	1.E+00	1.E+00	1.E+00	1.E+02
Annotation Cluster 223	Enrichment Score: 0.297102456918567											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0060485~mesenchyme development	4	0.627943485	4	E-01 15402, 19713, 19378, 12043	572	50	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0014031~mesenchymal cell development	3	0.470957614	6	E-01 19713, 19378, 12043	572	47	13588	2.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0048762~mesenchymal cell differentiation	3	0.470957614	6	E-01 19713, 19378, 12043	572	49	13588	1.E+00	1.E+00	1.E+00	1.E+02
Annotation Cluster 224	Enrichment Score: 0.2904962157623705											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	s-adenosyl-L-methionine	5	0.784929356	4	E-01 18113, 22017, 15278, 13436, 12846	629	88	17854	2.E+00	1.E+00	7.E-01	1.E+02
UP_SEQ_FEATURE	binding site:S-adenosyl-L-methionine	3	0.470957614	5	E-01 18113, 22017, 12846	618	42	16021	2.E+00	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	methyltransferase	5	0.784929356	7	E-01 18113, 22017, 15278, 13436, 12846	629	142	17854	1.E+00	1.E+00	9.E-01	1.E+02
Annotation Cluster 225	Enrichment Score: 0.281765115647306											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR001609:Myosin head, motor region	3	0.470957614	4	E-01 17925, 77579, 270163	630	38	17763	2.E+00	1.E+00	1.E+00	1.E+02
INTERPRO	IPR000048:IQ calmodulin-binding region	5	0.784929356	4	E-01 14432, 17925, 77579, 270163, 19417	630	92	17763	2.E+00	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	motor protein	6	0.941915228	4	E-01 17925, 77579, 19348, 270163, 13430, 718	629	123	17854	1.E+00	1.E+00	8.E-01	1.E+02
SP_PIR_KEYWORDS	myosin	3	0.470957614	5	E-01 17925, 77579, 270163	629	47	17854	2.E+00	1.E+00	8.E-01	1.E+02
SMART	SM00242:MYSc	3	0.470957614	5	E-01 17925, 77579, 270163	418	38	9131	2.E+00	1.E+00	9.E-01	1.E+02
UP_SEQ_FEATURE	domain:IQ	3	0.470957614	6	E-01 14432, 77579, 19417	618	53	16021	1.E+00	1.E+00	1.E+00	1.E+02
SMART	SM00015:IQ	5	0.784929356	6	E-01 14432, 17925, 77579, 270163, 19417	418	92	9131	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_CC_FAT	GO:0016459~myosin complex	3	0.470957614	6	E-01 17925, 77579, 270163	434	61	12504	1.E+00	1.E+00	9.E-01	1.E+02
GOTERM_MF_FAT	GO:0003774~motor activity	6	0.941915228	7	E-01 17925, 77579, 19348, 270163, 13430, 718	550	138	13288	1.E+00	1.E+00	1.E+00	1.E+02
Annotation Cluster 226	Enrichment Score: 0.268051840533494											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0005911~cell-cell junction	9	1.412872841	3	E-01 18669, 18671, 16456, 18670, 69524, 1305	434	173	12504	1.E+00	1.E+00	6.E-01	1.E+02
SP_PIR_KEYWORDS	Tight junction	4	0.627943485	4	E-01 16456, 69524, 13052, 16800	629	61	17854	2.E+00	1.E+00	7.E-01	1.E+02
GOTERM_CC_FAT	GO:0005923~tight junction	4	0.627943485	5	E-01 16456, 69524, 13052, 16800	434	76	12504	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_CC_FAT	GO:0070160~occluding junction	4	0.627943485	5	E-01 16456, 69524, 13052, 16800	434	76	12504	2.E+00	1.E+00	9.E-01	1.E+02
INTERPRO	IPR003598:Immunoglobulin subtype 2	8	1.25588697	5	E-01 18596, 16456, 69524, 13052, 83964, 1297	630	187	17763	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_CC_FAT	GO:0043296~apical junction complex	4	0.627943485	7	E-01 16456, 69524, 13052, 16800	434	101	12504	1.E+00	1.E+00	9.E-01	1.E+02
GOTERM_CC_FAT	GO:0016327~apicolateral plasma membrane	4	0.627943485	7	E-01 16456, 69524, 13052, 16800	434	103	12504	1.E+00	1.E+00	1.E+00	1.E+02
SMART	SM004081Gc2	8	1.25588697	8	E-01 18596, 16456, 69524, 13052, 83964, 1297	418	187	9131	9.E-01	1.E+00	1.E+00	1.E+02
INTERPRO	IPR013106:Immunoglobulin V-set	8	1.25588697	1	E+00 270152, 16456, 69524, 13052, 83964, 129	630	364	17763	6.E-01	1.E+00	1.E+00	1.E+02
Annotation Cluster 227	Enrichment Score: 0.25627551847600705											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR000626:Ubiquitin	3	0.470957614	5	E-01 78294, 19358, 22218	630	47	17763	2.E+00	1.E+00	1.E+00	1.E+02
INTERPRO	IPR019955:Ubiquitin supergroup	3	0.470957614	5	E-01 78294, 19358, 22218	630	50	17763	2.E+00	1.E+00	1.E+00	1.E+02
SMART	SM00213:UBQ	3	0.470957614	6	E-01 78294, 19358, 22218	418	47	9131	1.E+00	1.E+00	1.E+00	1.E+02
Annotation Cluster 228	Enrichment Score: 0.24878426381227497											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR017892:Protein kinase, C-terminal	3	0.470957614	4	E-01 72508, 11651, 20112	630	40	17763	2.E+00	1.E+00	1.E+00	1.E+02
INTERPRO	IPR000961:AGC-kinase, C-terminal	3	0.470957614	6	E-01 72508, 11651, 20112	630	53	17763	2.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	domain:AGC-kinase C-terminal	3	0.470957614	6	E-01 72508, 11651, 20112	618	53	16021	1.E+00	1.E+00	1.E+00	1.E+02
SMART	SM00133:S_TK_X	3	0.470957614	7	E-01 72508, 11651, 20112	418	53	9131	1.E+00	1.E+00	1.E+00	1.E+02
Annotation Cluster 229	Enrichment Score: 0.24237307818190784											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0007051~spindle organization	3	0.470957614	3	E-01 13006, 67052, 67141	572	28	13588	3.E+00	1.E+00	9.E-01	1.E+02



GOTERM_BP_FAT	GO:0007017~microtubule-based process	9	1.412872841	7.E-01	22142, 13006, 67052, 19348, 13197, 7181	572	211	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0000226~microtubule cytoskeleton organization	4	0.627943485	9.E-01	13006, 67052, 13197, 67141	572	111	13588	9.E-01	1.E+00	1.E+00	1.E+02
Annotation Cluster 230	Enrichment Score: 0.23540968364291415											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0030017~sarcomere	4	0.627943485	5.E-01	12955, 11464, 11459, 208727	434	80	12504	1.E+00	1.E+00	9.E-01	1.E+02
GOTERM_CC_FAT	GO:0031674~I band	3	0.470957614	6.E-01	12955, 11464, 208727	434	53	12504	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_CC_FAT	GO:0044449~contractile fiber part	4	0.627943485	6.E-01	12955, 11464, 11459, 208727	434	86	12504	1.E+00	1.E+00	9.E-01	1.E+02
GOTERM_CC_FAT	GO:0030016~myofibril	4	0.627943485	6.E-01	12955, 11464, 11459, 208727	434	91	12504	1.E+00	1.E+00	9.E-01	1.E+02
GOTERM_CC_FAT	GO:0043292~contractile fiber	4	0.627943485	6.E-01	12955, 11464, 11459, 208727	434	95	12504	1.E+00	1.E+00	9.E-01	1.E+02
Annotation Cluster 231	Enrichment Score: 0.2341019342306107											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR000629:RNA helicase, ATP-dependent, DEAD-box, conserved site	3	0.470957614	3.E-01	110957, 13681, 13682	630	31	17763	3.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	short sequence motif:DEAD box	3	0.470957614	3.E-01	110957, 13681, 13682	618	30	16021	3.E+00	1.E+00	1.E+00	1.E+02
INTERPRO	IPR014014:RNA helicase, DEAD-box type, Q motif	3	0.470957614	4.E-01	110957, 13681, 13682	630	35	17763	2.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	short sequence motif:Q motif	3	0.470957614	4.E-01	110957, 13681, 13682	618	33	16021	2.E+00	1.E+00	1.E+00	1.E+02
INTERPRO	IPR011545:DNA/RNA helicase, DEAD/DEAH box type, N-terminal	3	0.470957614	6.E-01	110957, 13681, 13682	630	55	17763	2.E+00	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	helicase	5	0.784929356	6.E-01	13872, 110957, 27041, 13681, 13682	629	120	17854	1.E+00	1.E+00	9.E-01	1.E+02
UP_SEQ_FEATURE	domain:Helicase C-terminal	4	0.627943485	6.E-01	13872, 110957, 13681, 13682	618	86	16021	1.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	domain:Helicase ATP-binding	4	0.627943485	7.E-01	13872, 110957, 13681, 13682	618	89	16021	1.E+00	1.E+00	1.E+00	1.E+02
INTERPRO	IPR014021:Helicase, superfamily 1 and 2, ATP-binding	4	0.627943485	7.E-01	13872, 110957, 13681, 13682	630	99	17763	1.E+00	1.E+00	1.E+00	1.E+02
INTERPRO	IPR001650:DNA/RNA helicase, C-terminal	4	0.627943485	7.E-01	13872, 110957, 13681, 13682	630	100	17763	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_MF_FAT	GO:0070035~purine NTP-dependent helicase activity	4	0.627943485	7.E-01	13872, 110957, 13681, 13682	550	86	13288	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_MF_FAT	GO:008026~ATP-dependent helicase activity	4	0.627943485	7.E-01	13872, 110957, 13681, 13682	550	86	13288	1.E+00	1.E+00	1.E+00	1.E+02
INTERPRO	IPR014001:DEAD-like helicase, N-terminal	4	0.627943485	7.E-01	13872, 110957, 13681, 13682	630	103	17763	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_MF_FAT	GO:0043386~helicase activity	5	0.784929356	8.E-01	13872, 110957, 27041, 13681, 13682	550	129	13288	9.E-01	1.E+00	1.E+00	1.E+02
SMART	SM00490:HELICc	4	0.627943485	8.E-01	13872, 110957, 13681, 13682	418	99	9131	9.E-01	1.E+00	1.E+00	1.E+02
SMART	SM00487:DEXDc	4	0.627943485	9.E-01	13872, 110957, 13681, 13682	418	103	9131	8.E-01	1.E+00	1.E+00	1.E+02
Annotation Cluster 232	Enrichment Score: 0.22724474721028554											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0060284~regulation of cell development	8	1.25588697	5.E-01	12028, 11853, 12043, 108138, 17268, 218	572	159	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0010720~positive regulation of cell development	3	0.470957614	6.E-01	12043, 108138, 21844	572	47	13588	2.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0051960~regulation of nervous system development	7	1.098901099	6.E-01	11853, 12043, 108138, 17268, 21844, 160	572	148	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0045664~regulation of neuron differentiation	5	0.784929356	6.E-01	11853, 12043, 17268, 21844, 11848	572	102	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0050767~regulation of neurogenesis	6	0.941915228	7.E-01	11853, 12043, 108138, 17268, 21844, 118	572	132	13588	1.E+00	1.E+00	1.E+00	1.E+02
Annotation Cluster 233	Enrichment Score: 0.19098435976279735											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0019932~second-messenger-mediated signaling	8	1.25588697	2.E-01	16994, 18126, 14678, 30955, 192176, 146	572	118	13588	2.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0007187~G-protein signaling, coupled to cyclic nucleotide secc	4	0.627943485	5.E-01	18126, 14678, 192176, 14682	572	60	13588	2.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0019935~cyclic-nucleotide-mediated signaling	4	0.627943485	5.E-01	18126, 14678, 192176, 14682	572	66	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0006140~regulation of nucleotide metabolic process	4	0.627943485	6.E-01	72269, 14678, 192176, 14682	572	75	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0007188~G-protein signaling, coupled to cAMP nucleotide secc	3	0.470957614	7.E-01	14678, 192176, 14682	572	55	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0045761~regulation of adenylate cyclase activity	3	0.470957614	7.E-01	14678, 192176, 14682	572	60	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0019933~cAMP-mediated signaling	3	0.470957614	7.E-01	14678, 192176, 14682	572	61	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0031279~regulation of cyclase activity	3	0.470957614	7.E-01	14678, 192176, 14682	572	62	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0051339~regulation of lyase activity	3	0.470957614	7.E-01	14678, 192176, 14682	572	62	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0030817~regulation of cAMP biosynthetic process	3	0.470957614	8.E-01	14678, 192176, 14682	572	65	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0030814~regulation of cAMP metabolic process	3	0.470957614	8.E-01	14678, 192176, 14682	572	67	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0030802~regulation of cyclic nucleotide biosynthetic process	3	0.470957614	8.E-01	14678, 192176, 14682	572	70	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0030808~regulation of nucleotide biosynthetic process	3	0.470957614	8.E-01	14678, 192176, 14682	572	70	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0030799~regulation of cyclic nucleotide metabolic process	3	0.470957614	8.E-01	14678, 192176, 14682	572	73	13588	1.E+00	1.E+00	1.E+00	1.E+02
Annotation Cluster 234	Enrichment Score: 0.18730757170517445											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	metal-binding	107	16.79748823	1.E-01	18746, 22324, 19744, 22778, 16800, 1715	629	2682	17854	1.E+00	1.E+00	3.E-01	8.E+01
SP_PIR_KEYWORDS	zinc-finger	46	7.221350078	4.E-01	22324, 74287, 19720, 54354, 22778, 1680	629	1204	17854	1.E+00	1.E+00	7.E-01	1.E+02
SP_PIR_KEYWORDS	zinc	60	9.419152276	9.E-01	22324, 54354, 22778, 16800, 171531, 129	629	1886	17854	9.E-01	1.E+00	1.E+00	1.E+02
GOTERM_MF_FAT	GO:0046914~transition metal ion binding	83	13.02982732	1.E+00	22324, 672195, 54354, 22778, 16800, 171	550	2608	13288	8.E-01	1.E+00	1.E+00	1.E+02
GOTERM_MF_FAT	GO:0046872~metal ion binding	130	20.40816327	1.E+00	18746, 22324, 19744, 16952, 16800, 2277	550	3850	13288	8.E-01	1.E+00	1.E+00	1.E+02
GOTERM_MF_FAT	GO:0043169~cation binding	130	20.40816327	1.E+00	18746, 22324, 19744, 16952, 16800, 2277	550	3885	13288	8.E-01	1.E+00	1.E+00	1.E+02
GOTERM_MF_FAT	GO:0043167~ion binding	131	20.56514914	1.E+00	18746, 22324, 19744, 18416, 16952, 1680	550	3934	13288	8.E-01	1.E+00	1.E+00	1.E+02
GOTERM_MF_FAT	GO:0008270~zinc ion binding	62	9.733124019	1.E+00	22324, 54354, 22778, 16800, 171531, 129	550	2105	13288	7.E-01	1.E+00	1.E+00	1.E+02



Annotation Cluster 235		Enrichment Score: 0.1787160172622403										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0003713~transcription coactivator activity	5	0.784929356		6.E-01 22601, 12815, 17978, 17979, 12914		550	100	13288	1.E+00	1.E+00	1.E+00
GOTERM_MF_FAT	GO:0003682~chromatin binding	7	1.098901099		6.E-01 22130, 216848, 15430, 17978, 20466, 179		550	155	13288	1.E+00	1.E+00	1.E+00
BIOCARTA	m_vdrPathway:Control of Gene Expression by Vitamin D Receptor	4	0.627943485		8.E-01 57376, 17978, 17979, 12914		167	28	1171	1.E+00	1.E+00	1.E+00
Annotation Cluster 236		Enrichment Score: 0.17328372526008654										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_SEQ_FEATURE	domain:Ig-like C2-type 1	7	1.098901099		4.E-01 15896, 18596, 21687, 13052, 12978, 1472		618	130	16021	1.E+00	1.E+00	1.E+00
UP_SEQ_FEATURE	domain:Ig-like C2-type 2	7	1.098901099		4.E-01 15896, 18596, 21687, 13052, 12978, 1472		618	131	16021	1.E+00	1.E+00	1.E+00
SP_PIR_KEYWORDS	Immunoglobulin domain	17	2.668759812		5.E-01 21687, 69524, 16456, 17123, 545156, 120		629	443	17854	1.E+00	1.E+00	8.E-01
INTERPRO	IPR003598Immunoglobulin subtype 2	8	1.25588697		5.E-01 18596, 16456, 69524, 13052, 83964, 1297		630	187	17763	1.E+00	1.E+00	1.E+00
INTERPRO	IPR013783Immunoglobulin-like fold	23	3.610675039		6.E-01 15007, 18729, 14972, 21687, 15018, 6952		630	644	17763	1.E+00	1.E+00	1.E+00
INTERPRO	IPR013151Immunoglobulin	7	1.098901099		6.E-01 18729, 18596, 16456, 18724, 83964, 1297		630	178	17763	1.E+00	1.E+00	1.E+00
SMART	SM00408IGc2	8	1.25588697		8.E-01 18596, 16456, 69524, 13052, 83964, 1297		418	187	9131	9.E-01	1.E+00	1.E+00
UP_SEQ_FEATURE	domain:Ig-like C2-type 3	3	0.470957614		9.E-01 18596, 12978, 17082		618	87	16021	9.E-01	1.E+00	1.E+00
INTERPRO	IPR007110Immunoglobulin-like	18	2.825745683		9.E-01 15007, 18729, 14972, 21687, 15018, 6952		630	604	17763	8.E-01	1.E+00	1.E+00
INTERPRO	IPR003599Immunoglobulin subtype	9	1.412872841		9.E-01 270152, 18729, 18596, 69524, 18724, 130		630	313	17763	8.E-01	1.E+00	1.E+00
UP_SEQ_FEATURE	domain:Ig-like V-type	3	0.470957614		9.E-01 69524, 83964, 57781		618	104	16021	7.E-01	1.E+00	1.E+00
INTERPRO	IPR013106Immunoglobulin V-set	8	1.25588697		1.E+00 270152, 16456, 69524, 13052, 83964, 129		630	364	17763	6.E-01	1.E+00	1.E+00
SMART	SM00409IG	9	1.412872841		1.E+00 270152, 18729, 18596, 69524, 18724, 130		418	313	9131	6.E-01	1.E+00	1.E+00
Annotation Cluster 237		Enrichment Score: 0.16756957724715496										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	viral nucleoprotein	3	0.470957614		2.E-01 15387, 15381, 20639		629	27	17854	3.E+00	1.E+00	6.E-01
SP_PIR_KEYWORDS	mRNA transport	4	0.627943485		4.E-01 19317, 231042, 68092, 66441		629	60	17854	2.E+00	1.E+00	7.E-01
GOTERM_BP_FAT	GO:0051028~mRNA transport	4	0.627943485		5.E-01 19317, 231042, 68092, 66441		572	62	13588	2.E+00	1.E+00	1.E+00
SP_PIR_KEYWORDS	mrna splicing	8	1.25588697		5.E-01 15387, 19317, 15381, 53610, 75062, 6809		629	191	17854	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0051236~establishment of RNA localization	4	0.627943485		5.E-01 19317, 231042, 68092, 66441		572	66	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0050658~RNA transport	4	0.627943485		5.E-01 19317, 231042, 68092, 66441		572	66	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0050657~nucleic acid transport	4	0.627943485		5.E-01 19317, 231042, 68092, 66441		572	66	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0006403~RNA localization	4	0.627943485		5.E-01 19317, 231042, 68092, 66441		572	67	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0015931~nucleobase, nucleoside, nucleotide and nucleic acid ti	4	0.627943485		6.E-01 19317, 231042, 68092, 66441		572	74	13588	1.E+00	1.E+00	1.E+00
GOTERM_CC_FAT	GO:0005681~spliceosome	5	0.784929356		6.E-01 15387, 19744, 15381, 75062, 20639		434	124	12504	1.E+00	1.E+00	9.E-01
SP_PIR_KEYWORDS	rna-binding	16	2.51177394		7.E-01 13684, 15387, 19317, 27041, 15381, 5361		629	485	17854	9.E-01	1.E+00	9.E-01
SP_PIR_KEYWORDS	mrna processing	8	1.25588697		7.E-01 15387, 19317, 15381, 53610, 75062, 6809		629	240	17854	9.E-01	1.E+00	9.E-01
GOTERM_BP_FAT	GO:0008380~RNA splicing	8	1.25588697		7.E-01 15387, 19317, 15381, 53610, 75062, 6809		572	201	13588	9.E-01	1.E+00	1.E+00
SP_PIR_KEYWORDS	Spliceosome	4	0.627943485		8.E-01 15387, 15381, 75062, 20639		629	111	17854	1.E+00	1.E+00	1.E+00
UP_SEQ_FEA TURE	domain:RRM	3	0.470957614		9.E-01 27041, 15381, 68092		618	99	16021	8.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0006397~mRNA processing	8	1.25588697		9.E-01 15387, 19317, 15381, 53610, 75062, 6809		572	262	13588	7.E-01	1.E+00	1.E+00
INTERPRO	IPR000504:RNA recognition motif, RNP-1	5	0.784929356		9.E-01 27041, 15381, 53610, 68092, 20639		630	212	17763	7.E-01	1.E+00	1.E+00
INTERPRO	IPR012677:Nucleotide-binding, alpha-beta plait	5	0.784929356		9.E-01 27041, 15381, 53610, 68092, 20639		630	213	17763	7.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0016071~mRNA metabolic process	8	1.25588697		1.E+00 15387, 19317, 15381, 53610, 75062, 6809		572	302	13588	6.E-01	1.E+00	1.E+00
KEGG_PATHWAY	mmu03040:Spliceosome	5	0.784929356		1.E+00 15387, 15381, 75062, 68092, 20639		409	124	5738	6.E-01	1.E+00	1.E+00
SMART	SM00360:RRM	5	0.784929356		1.E+00 27041, 15381, 53610, 68092, 20639		418	212	9131	5.E-01	1.E+00	1.E+00
GOTERM_MF_FAT	GO:0003723~RNA binding	16	2.51177394		1.E+00 13684, 15387, 19317, 27041, 15381, 5361		550	672	13288	6.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0006396~RNA processing	9	1.412872841		1.E+00 15387, 19317, 15381, 53610, 75062, 6809		572	437	13588	5.E-01	1.E+00	1.E+00
Annotation Cluster 238		Enrichment Score: 0.1538680852193244										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0030216~keratinocyte differentiation	3	0.470957614		6.E-01 26395, 19225, 17123		572	48	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0009913~epidermal cell differentiation	3	0.470957614		6.E-01 26395, 19225, 17123		572	51	13588	1.E+00	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0030855~epithelial cell differentiation	4	0.627943485		9.E-01 16456, 26395, 19225, 17123		572	123	13588	8.E-01	1.E+00	1.E+00
Annotation Cluster 239		Enrichment Score: 0.15004150190674312										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_SEQ_FEATURE	repeat:TPR 7	3	0.470957614		6.E-01 56317, 52563, 69957		618	49	16021	2.E+00	1.E+00	1.E+00
UP_SEQ_FEATURE	repeat:TPR 4	4	0.627943485		6.E-01 56317, 52563, 59008, 69957		618	82	16021	1.E+00	1.E+00	1.E+00
UP_SEQ_FEATURE	repeat:TPR 6	3	0.470957614		6.E-01 56317, 52563, 69957		618	55	16021	1.E+00	1.E+00	1.E+00
INTERPRO	IPR001440:Tetratricopeptide TPR-1	4	0.627943485		7.E-01 17970, 56317, 52563, 69957		630	95	17763	1.E+00	1.E+00	1.E+00
UP_SEQ_FEATURE	repeat:TPR 3	5	0.784929356		7.E-01 17970, 56317, 52563, 59008, 69957		618	118	16021	1.E+00	1.E+00	1.E+00
UP_SEQ_FEATURE	repeat:TPR 5	3	0.470957614		7.E-01 56317, 52563, 69957		618	61	16021	1.E+00	1.E+00	1.E+00
SP_PIR_KEYWORDS	tptr repeat	5	0.784929356		7.E-01 17970, 56317, 52563, 59008, 69957		629	141	17854	1.E+00	1.E+00	9.E-01
UP_SEQ_FEATURE	repeat:TPR 1	5	0.784929356		7.E-01 17970, 56317, 52563, 59008, 69957		618	130	16021	1.E+00	1.E+00	1.E+00



UP_SEQ_FEATURE	repeat:TPR 2	5	0.784929356	7.E-01	17970, 56317, 52563, 59008, 69957	618	130	16021	1.E+00	1.E+00	1.E+00	1.E+02
INTERPRO	IPR019734:Tetratricopeptide repeat	4	0.627943485	8.E-01	17970, 56317, 52563, 69957	630	112	17763	1.E+00	1.E+00	1.E+00	1.E+02
INTERPRO	IPR013026:Tetratricopeptide region	4	0.627943485	8.E-01	17970, 56317, 52563, 69957	630	114	17763	1.E+00	1.E+00	1.E+00	1.E+02
INTERPRO	IPR011990:Tetratricopeptide-like helical	5	0.784929356	8.E-01	17970, 56317, 52563, 59008, 69957	630	150	17763	9.E-01	1.E+00	1.E+00	1.E+02
SMART	SM00028:TPR	4	0.627943485	9.E-01	17970, 56317, 52563, 69957	418	112	9131	8.E-01	1.E+00	1.E+00	1.E+02
Annotation Cluster 240	Enrichment Score: 0.1474604128468198											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0050954~sensory perception of mechanical stimulus	6	0.941915228	3.E-01	24064, 73750, 17869, 14360, 12815, 1257	572	92	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0007605~sensory perception of sound	5	0.784929356	5.E-01	24064, 73750, 17869, 12815, 12576	572	84	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0043583~ear development	5	0.784929356	6.E-01	24064, 73750, 12043, 17869, 12576	572	104	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0048839~inner ear development	3	0.470957614	9.E-01	24064, 73750, 12576	572	88	13588	8.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0050877~neurological system process	21	3.296703297	1.E+00	17159, 19317, 73750, 19894, 19088, 1543	572	1681	13588	3.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0050890~cognition	15	2.354788069	1.E+00	17159, 73750, 19088, 17869, 12815, 1466	572	1480	13588	2.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0007600~sensory perception	10	1.569858713	1.E+00	216869, 24064, 73750, 15416, 17869, 143	572	1402	13588	2.E-01	1.E+00	1.E+00	1.E+02
Annotation Cluster 241	Enrichment Score: 0.14026072641679252											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	respiratory chain	3	0.470957614	6.E-01	672195, 13063, 13067, 68342	629	62	17854	1.E+00	1.E+00	9.E-01	1.E+02
GOTERM_CC_FAT	GO:0070469~respiratory chain	3	0.470957614	7.E-01	672195, 13063, 13067, 68342	434	65	12504	1.E+00	1.E+00	9.E-01	1.E+02
SP_PIR_KEYWORDS	electron transport	4	0.627943485	7.E-01	672195, 93692, 13063, 13067, 68342	629	100	17854	1.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0022900~electron transport chain	5	0.784929356	7.E-01	672195, 93692, 13382, 13063, 13067, 683	572	112	13588	1.E+00	1.E+00	1.E+00	1.E+02
KEGG_PATHWAY	mmu05012:Parkinson's disease	6	0.941915228	1.E+00	78294, 672195, 13063, 67942, 11740, 130	409	133	5738	6.E-01	1.E+00	1.E+00	1.E+02
Annotation Cluster 242	Enrichment Score: 0.12589089142378884											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0070279~vitamin B6 binding	3	0.470957614	7.E-01	110095, 11657, 76282	550	54	13288	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_MF_FAT	GO:0030170~pyridoxal phosphate binding	3	0.470957614	7.E-01	110095, 11657, 76282	550	54	13288	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_MF_FAT	GO:0019842~vitamin binding	3	0.470957614	1.E+00	110095, 11657, 76282	550	121	13288	6.E-01	1.E+00	1.E+00	1.E+02
Annotation Cluster 243	Enrichment Score: 0.11225285315604605											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0034754~cellular hormone metabolic process	3	0.470957614	6.E-01	11806, 19378, 56847	572	52	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0010817~regulation of hormone levels	5	0.784929356	8.E-01	19894, 16367, 11806, 19378, 56847	572	128	13588	9.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0042445~hormone metabolic process	3	0.470957614	9.E-01	11806, 19378, 56847	572	90	13588	8.E-01	1.E+00	1.E+00	1.E+02
Annotation Cluster 244	Enrichment Score: 0.10928699860659556											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0045202~synapse	12	1.883830455	5.E-01	245049, 19894, 14432, 94190, 77579, 206	434	319	12504	1.E+00	1.E+00	9.E-01	1.E+02
SP_PIR_KEYWORDS	synapse	6	0.941915228	9.E-01	19894, 14432, 94190, 13430, 72508, 1338	629	213	17854	8.E-01	1.E+00	1.E+00	1.E+02
GOTERM_CC_FAT	GO:0044456~synapse part	4	0.627943485	1.E+00	19894, 20662, 13430, 13385	434	212	12504	5.E-01	1.E+00	1.E+00	1.E+02
Annotation Cluster 245	Enrichment Score: 0.09948652728320478											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	disulfide bond	96	15.07064364	2.E-01	12475, 15018, 69524, 18414, 14782, 1201	629	2469	17854	1.E+00	1.E+00	5.E-01	9.E+01
SP_PIR_KEYWORDS	signal	106	16.64050235	5.E-01	12475, 15018, 69524, 14178, 69121, 1841	629	2970	17854	1.E+00	1.E+00	8.E-01	1.E+02
UP_SEQ_FEATURE	disulfide bond	92	14.44270016	5.E-01	12765, 12475, 15018, 69524, 18414, 1478	618	2379	16021	1.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	signal peptide	106	16.64050235	8.E-01	12475, 15018, 69524, 14178, 69121, 1841	618	2963	16021	9.E-01	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	membrane	176	27.62951334	1.E+00	23232, 19744, 12475, 15018, 69524, 1695	629	5507	17854	9.E-01	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	glycoprotein	104	16.32653061	1.E+00	12475, 15018, 69524, 14178, 69121, 1695	629	3600	17854	8.E-01	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	topological domain:Extracellular	62	9.733124019	1.E+00	12765, 15018, 69524, 18414, 21937, 1640	618	2174	16021	7.E-01	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	98	15.38461538	1.E+00	12475, 15018, 69524, 14178, 69121, 1841	618	3444	16021	7.E-01	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	receptor	51	8.006279435	1.E+00	12765, 18414, 12952, 12953, 21937, 1640	629	2465	17854	6.E-01	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	topological domain:Cytoplasmic	67	10.51805338	1.E+00	12765, 69524, 18414, 21937, 16994, 1640	618	2780	16021	6.E-01	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	transmembrane region	88	13.81475667	1.E+00	12765, 15018, 69524, 18414, 21937, 1699	618	4113	16021	6.E-01	1.E+00	1.E+00	1.E+02
GOTERM_CC_FAT	GO:0016021~integral to membrane	93	14.59968603	1.E+00	12765, 12475, 15018, 69524, 18414, 2193	434	5709	12504	5.E-01	1.E+00	1.E+00	1.E+02
GOTERM_CC_FAT	GO:0031224~intrinsic to membrane	107	16.79748823	1.E+00	12475, 15018, 69524, 18414, 170758, 164	434	5914	12504	5.E-01	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	transmembrane	88	13.81475667	1.E+00	12765, 15018, 69524, 18414, 21937, 1699	629	5237	17854	5.E-01	1.E+00	1.E+00	1.E+02
Annotation Cluster 246	Enrichment Score: 0.09413860271532883											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR016186:C-type lectin-like	5	0.784929356	7.E-01	20343, 27007, 12505, 20339, 17533	630	127	17763	1.E+00	1.E+00	1.E+00	1.E+02
INTERPRO	IPR018378:C-type lectin conserved site	4	0.627943485	7.E-01	20343, 27007, 20339, 17533	630	104	17763	1.E+00	1.E+00	1.E+00	1.E+02
INTERPRO	IPR001304:C-type lectin	4	0.627943485	8.E-01	20343, 27007, 20339, 17533	630	118	17763	1.E+00	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	Lectin	5	0.784929356	8.E-01	20345, 20343, 27007, 20339, 17533	629	167	17854	8.E-01	1.E+00	1.E+00	1.E+02



UP_SEQ_FEATURE	domain:C-type lectin	3	0.470957614	9.E-01	20343, 27007, 20339	618	90	16021	9.E-01	1.E+00	1.E+00	1.E+02
GOTERM_MF_FAT	GO:0005529--sugar binding	6	0.941915228	9.E-01	20345, 20343, 27007, 20339, 17533, 1039	550	181	13288	8.E-01	1.E+00	1.E+00	1.E+02
SMART	SM00034:CLECT	4	0.627943485	9.E-01	20343, 27007, 20339, 17533	418	118	9131	7.E-01	1.E+00	1.E+00	1.E+02
Annotation Cluster 247												
Category	Enrichment Score: 0.0681196033018973											
	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0005840--ribosome	7	1.098901099		7.E-01 78294, 67891, 72508, 19989, 20112, 7425	434	192	12504	1.E+00	1.E+00	9.E-01	1.E+02
GOTERM_CC_FAT	GO:0030529--ribonucleoprotein complex	14	2.197802198		8.E-01 15387, 78294, 19744, 15381, 72508, 1998	434	462	12504	9.E-01	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	ribosomal protein	5	0.784929356		9.E-01 78294, 67891, 72508, 19989, 20112	629	177	17854	8.E-01	1.E+00	1.E+00	1.E+02
GOTERM_MF_FAT	GO:0003735--structural constituent of ribosome	5	0.784929356		9.E-01 78294, 67891, 19989, 74256, 16409	550	151	13288	8.E-01	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	ribonucleoprotein	6	0.941915228		1.E+00 15387, 78294, 67891, 15381, 19989, 2063	629	266	17854	6.E-01	1.E+00	1.E+00	1.E+02
KEGG_PATHWAY	mmu03010:Ribosome	3	0.470957614		1.E+00 78294, 67891, 19989	409	89	5738	5.E-01	1.E+00	1.E+00	1.E+02
Annotation Cluster 248												
Category	Enrichment Score: 0.03033258522164936											
	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_SEQ_FEATURE	domain:EGF-like	3	0.470957614		7.E-01 20343, 20339, 19225	618	68	16021	1.E+00	1.E+00	1.E+00	1.E+02
INTERPRO	IPR013032:EGF-like region, conserved site	8	1.25588697		9.E-01 13836, 21687, 20343, 16414, 16412, 2033	630	310	17763	7.E-01	1.E+00	1.E+00	1.E+02
INTERPRO	IPR006209:EGF	3	0.470957614		9.E-01 20343, 20339, 19225	630	128	17763	7.E-01	1.E+00	1.E+00	1.E+02
INTERPRO	IPR000742:EGF-like, type 3	4	0.627943485		1.E+00 21687, 20343, 20339, 19225	630	199	17763	6.E-01	1.E+00	1.E+00	1.E+02
INTERPRO	IPR006210:EGF-like	4	0.627943485		1.E+00 21687, 20343, 20339, 19225	630	203	17763	6.E-01	1.E+00	1.E+00	1.E+02
SMART	SM00181:EGF	4	0.627943485		1.E+00 21687, 20343, 20339, 19225	418	203	9131	4.E-01	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	egf-like domain	3	0.470957614		1.E+00 21687, 20343, 20339	629	222	17854	4.E-01	1.E+00	1.E+00	1.E+02
Annotation Cluster 249												
Category	Enrichment Score: 0.025453816857916468											
	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR011333:BTB/POZ fold	5	0.784929356		9.E-01 69288, 246710, 192192, 21402, 22724	630	180	17763	8.E-01	1.E+00	1.E+00	1.E+02
INTERPRO	IPR013069:BTB/POZ	3	0.470957614		9.E-01 69288, 246710, 22724	630	128	17763	7.E-01	1.E+00	1.E+00	1.E+02
INTERPRO	IPR000210:BTB/POZ-like	4	0.627943485		1.E+00 69288, 246710, 192192, 22724	630	180	17763	6.E-01	1.E+00	1.E+00	1.E+02
SMART	SM00225:BTB	4	0.627943485		1.E+00 69288, 246710, 192192, 22724	418	180	9131	5.E-01	1.E+00	1.E+00	1.E+02
Annotation Cluster 250												
Category	Enrichment Score: 0.024657895086977976											
	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0042277--peptide binding	6	0.941915228		8.E-01 14972, 12765, 15018, 14065, 16847, 1406	550	160	13288	9.E-01	1.E+00	1.E+00	1.E+02
GOTERM_MF_FAT	GO:0008528--peptide receptor activity, G-protein coupled	3	0.470957614		9.E-01 12765, 14065, 14064	550	110	13288	7.E-01	1.E+00	1.E+00	1.E+02
GOTERM_MF_FAT	GO:0001653--peptide receptor activity	3	0.470957614		9.E-01 12765, 14065, 14064	550	110	13288	7.E-01	1.E+00	1.E+00	1.E+02
INTERPRO	IPR017452:GPCR, rhodopsin-like superfamily	3	0.470957614		1.E+00 12765, 14065, 14064	630	1575	17763	5.E-02	1.E+00	1.E+00	1.E+02
INTERPRO	IPR000276:7TM GPCR, rhodopsin-like	3	0.470957614		1.E+00 12765, 14065, 14064	630	1458	17763	6.E-02	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	g-protein coupled receptor	3	0.470957614		1.E+00 12765, 14065, 14064	629	1411	17854	6.E-02	1.E+00	1.E+00	1.E+02
Annotation Cluster 251												
Category	Enrichment Score: 0.024284932331927096											
	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR019775:WD40 repeat, conserved site	7	1.098901099		9.E-01 107995, 54709, 56371, 103583, 192192, 1	630	258	17763	8.E-01	1.E+00	1.E+00	1.E+02
INTERPRO	IPR001680:WD40 repeat	7	1.098901099		9.E-01 107995, 54709, 56371, 103583, 192192, 1	630	259	17763	8.E-01	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	wd repeat	7	1.098901099		9.E-01 107995, 54709, 56371, 103583, 192192, 1	629	263	17854	8.E-01	1.E+00	1.E+00	1.E+02
INTERPRO	IPR017986:WD40 repeat, region	6	0.941915228		9.E-01 107995, 54709, 56371, 103583, 12234, 74	630	228	17763	7.E-01	1.E+00	1.E+00	1.E+02
INTERPRO	IPR015943:WD40/YVTN repeat-like	8	1.25588697		9.E-01 52206, 107995, 54709, 56371, 103583, 19	630	305	17763	7.E-01	1.E+00	1.E+00	1.E+02
INTERPRO	IPR019781:WD40 repeat, subgroup	6	0.941915228		9.E-01 107995, 54709, 56371, 103583, 12234, 74	630	235	17763	7.E-01	1.E+00	1.E+00	1.E+02
INTERPRO	IPR019782:WD40 repeat 2	5	0.784929356		9.E-01 107995, 54709, 56371, 103583, 12234	630	214	17763	7.E-01	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:WD 7	3	0.470957614		1.E+00 107995, 56371, 74370	618	124	16021	6.E-01	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:WD 5	5	0.784929356		1.E+00 107995, 54709, 56371, 192192, 74370	618	202	16021	6.E-01	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:WD 4	5	0.784929356		1.E+00 107995, 54709, 56371, 192192, 74370	618	218	16021	6.E-01	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:WD 3	5	0.784929356		1.E+00 107995, 54709, 56371, 192192, 74370	618	231	16021	6.E-01	1.E+00	1.E+00	1.E+02
SMART	SM00320:WD40	7	1.098901099		1.E+00 107995, 54709, 56371, 103583, 192192, 1	418	259	9131	6.E-01	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:WD 1	5	0.784929356		1.E+00 107995, 54709, 56371, 192192, 74370	618	235	16021	6.E-01	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:WD 2	5	0.784929356		1.E+00 107995, 54709, 56371, 192192, 74370	618	235	16021	6.E-01	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:WD 6	3	0.470957614		1.E+00 107995, 56371, 74370	618	161	16021	5.E-01	1.E+00	1.E+00	1.E+02
Annotation Cluster 252												
Category	Enrichment Score: 0.023410013653434203											
	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0005773--vacuole	5	0.784929356		9.E-01 17159, 56722, 230163, 11891, 13382	434	204	12504	7.E-01	1.E+00	1.E+00	1.E+02
GOTERM_CC_FAT	GO:0005764--lysosome	4	0.627943485		9.E-01 17159, 56722, 230163, 11891	434	178	12504	6.E-01	1.E+00	1.E+00	1.E+02
GOTERM_CC_FAT	GO:000323--lytic vacuole	4	0.627943485		1.E+00 17159, 56722, 230163, 11891	434	179	12504	6.E-01	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	lysosome	3	0.470957614		1.E+00 17159, 56722, 11891	629	144	17854	6.E-01	1.E+00	1.E+00	1.E+02
Annotation Cluster 253												
Enrichment Score: 0.010494151335358113												



Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR001841:Zinc finger, RING-type	7	1.098901099	9.E-01	66156, 20128, 216848, 19720, 17420, 273	630	286	286	17763	7.E-01	1.E+00	1.E+00
UP_SEQ_FEATURE	zinc finger region:RING-type	4	0.627943485	1.E+00	66156, 20128, 19720, 17420	618	176	176	16021	6.E-01	1.E+00	1.E+00
INTERPRO	IPR018957:Zinc finger, C3HC4 RING-type	4	0.627943485	1.E+00	20128, 19720, 17420, 74126	630	219	219	17763	5.E-01	1.E+00	1.E+00
SMART	SM00184:RING	7	1.098901099	1.E+00	66156, 20128, 216848, 19720, 17420, 273	418	286	286	9131	5.E-01	1.E+00	1.E+00
INTERPRO	IPR017907:Zinc finger, RING-type, conserved site	4	0.627943485	1.E+00	20128, 19720, 17420, 74126	630	254	254	17763	4.E-01	1.E+00	1.E+00
Annotation Cluster 254	Enrichment Score: 0.0032730115694397347											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0019226~transmission of nerve impulse	5	0.784929356	1.E+00	19317, 19894, 14360, 12568, 12846	572	226	226	13588	5.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0007267~cell-cell signaling	6	0.941915228	1.E+00	19894, 14178, 16367, 12568, 20963, 1284	572	290	290	13588	5.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0007268~synaptic transmission	3	0.470957614	1.E+00	19894, 12568, 12846	572	178	178	13588	4.E-01	1.E+00	1.E+00
Annotation Cluster 255	Enrichment Score: 0.0032335854864088214											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0006813~potassium ion transport	4	0.627943485	1.E+00	12566, 18195, 192192, 12576	572	160	160	13588	6.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0015672~monovalent inorganic cation transport	7	1.098901099	1.E+00	20505, 12566, 18195, 192192, 67942, 205	572	303	303	13588	5.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0030001~metal ion transport	7	1.098901099	1.E+00	16818, 20505, 12566, 18195, 192192, 205	572	442	442	13588	4.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0006812~cation transport	8	1.25588697	1.E+00	16818, 20505, 12566, 18195, 192192, 679	572	515	515	13588	4.E-01	1.E+00	1.E+00
SP_PIR_KEYWORDS	ion transport	5	0.784929356	1.E+00	28253, 26934, 20505, 67942, 20504	629	543	543	17854	3.E-01	1.E+00	1.E+00
GOTERM_BP_FAT	GO:0006811~ion transport	10	1.569858713	1.E+00	28253, 16818, 26934, 20505, 12566, 1819	572	712	712	13588	3.E-01	1.E+00	1.E+00
Annotation Cluster 256	Enrichment Score: 2.5380003269168238E-8											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR013087:Zinc finger, C2H2-type/integrase, DNA-binding	3	0.470957614	1.E+00	69890, 74287, 75062, 22778, 22724	630	514	514	17763	2.E-01	1.E+00	1.E+00
INTERPRO	IPR015880:Zinc finger, C2H2-like	5	0.784929356	1.E+00	69890, 74287, 75062, 22778, 22724	630	676	676	17763	2.E-01	1.E+00	1.E+00
INTERPRO	IPR007087:Zinc finger, C2H2-type	5	0.784929356	1.E+00	14163, 69890, 74287, 22778, 22724	630	681	681	17763	2.E-01	1.E+00	1.E+00
SMART	SM00355:ZnF_C2H2	5	0.784929356	1.E+00	69890, 74287, 75062, 22778, 22724	418	676	676	9131	2.E-01	1.E+00	1.E+00



TH/SH-PPI-DAVID-Lung

Mus musculus (942)

Unknown (12)

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0060691~generation of precursor metabolites and energy	96	10.93394077	2.E-50	18746, 226646, 66377, 11676, 56012, 116	809	261	13588	6.E+00	6.E-47	6.E-47	4.E-47
GOTERM_BP_FAT	GO:006412~translation	96	10.93394077	9.E-42	666899, 100048462, 13669, 100044516, 2	809	319	13588	5.E+00	3.E-38	1.E-38	2.E-38
GOTERM_BP_FAT	GO:0022900~electron transport chain	54	6.150341686	2.E-35	70316, 672195, 226646, 100041273, 6637	809	112	13588	8.E+00	7.E-32	2.E-32	4.E-32
GOTERM_BP_FAT	GO:0060606~glucose metabolic process	52	5.922551253	2.E-27	18746, 68263, 18679, 11676, 56012, 1167	809	140	13588	6.E+00	6.E-24	2.E-24	4.E-24
GOTERM_BP_FAT	GO:0060607~glucose catabolic process	32	3.644646925	3.E-25	18746, 68263, 100042746, 15275, 15277,	809	52	13588	1.E+01	1.E-21	2.E-22	6.E-22
GOTERM_BP_FAT	GO:0019320~hexose catabolic process	32	3.644646925	3.E-25	18746, 68263, 100042746, 15275, 15277,	809	52	13588	1.E+01	1.E-21	2.E-22	6.E-22
GOTERM_BP_FAT	GO:0046365~monosaccharide catabolic process	32	3.644646925	2.E-24	18746, 68263, 100042746, 15275, 15277,	809	54	13588	1.E+01	5.E-21	8.E-22	3.E-21
GOTERM_BP_FAT	GO:0060696~glycolysis	29	3.302961276	5.E-24	18746, 68263, 100042746, 15275, 15277,	809	44	13588	1.E+01	1.E-20	2.E-21	9.E-21
GOTERM_BP_FAT	GO:0019318~hexose metabolic process	53	6.036446469	6.E-24	18746, 68263, 18679, 11676, 56012, 1167	809	169	13588	5.E+00	2.E-20	2.E-21	1.E-20
GOTERM_BP_FAT	GO:0044275~cellular carbohydrate catabolic process	32	3.644646925	1.E-22	18746, 68263, 100042746, 15275, 15277,	809	60	13588	9.E+00	4.E-19	4.E-20	2.E-19
GOTERM_BP_FAT	GO:0046164~alcohol catabolic process	33	3.758542141	2.E-22	18746, 68263, 100042746, 15275, 15277,	809	65	13588	9.E+00	5.E-19	5.E-20	3.E-19
GOTERM_BP_FAT	GO:0055996~monosaccharide metabolic process	53	6.036446469	3.E-21	18746, 68263, 18679, 11676, 56012, 1167	809	191	13588	5.E+00	9.E-18	8.E-19	5.E-18
GOTERM_BP_FAT	GO:0007049~cell cycle	97	11.04783599	4.E-19	12190, 16952, 243362, 59008, 16800, 182	809	611	13588	3.E+00	1.E-15	1.E-16	7.E-16
GOTERM_BP_FAT	GO:0016052~carbohydrate catabolic process	32	3.644646925	7.E-18	18746, 68263, 100042746, 15275, 15277,	809	81	13588	7.E+00	2.E-14	2.E-15	1.E-14
GOTERM_BP_FAT	GO:0007242~intracellular signaling cascade	122	13.8952164	1.E-17	12190, 22324, 19744, 192662, 14815, 168	809	915	13588	2.E+00	3.E-14	2.E-15	2.E-14
GOTERM_BP_FAT	GO:0051301~cell division	57	6.492027335	6.E-16	12190, 59008, 16800, 56150, 18221, 1721	809	281	13588	3.E+00	2.E-12	1.E-13	1.E-12
GOTERM_BP_FAT	GO:0051726~regulation of cell cycle	49	5.580865604	6.E-16	12190, 56150, 16994, 13555, 52563, 1355	809	214	13588	4.E+00	2.E-12	1.E-13	1.E-12
GOTERM_BP_FAT	GO:0035023~regulation of Rho protein signal transduction	30	3.416856492	5.E-15	22324, 13605, 442801, 16800, 53972, 218	809	86	13588	6.E+00	1.E-11	8.E-13	8.E-12
GOTERM_BP_FAT	GO:0000278~mitotic cell cycle	51	5.808656036	7.E-15	16800, 59008, 56150, 18221, 13006, 5256	809	244	13588	4.E+00	2.E-11	1.E-12	1.E-11
GOTERM_BP_FAT	GO:0055114~oxidation reduction	90	10.25056948	4.E-13	66885, 226646, 66377, 14782, 22273, 698	809	672	13588	2.E+00	7.E-11	8.E-10	8.E-10
GOTERM_BP_FAT	GO:0022402~cell cycle process	61	6.9476082	1.E-11	12190, 59008, 16800, 56150, 18221, 1300	809	393	13588	3.E+00	3.E-08	2.E-09	2.E-08
GOTERM_BP_FAT	GO:006260~DNA replication	35	3.986332574	1.E-11	12190, 80905, 68240, 50793, 23834, 1721	809	152	13588	4.E+00	4.E-08	2.E-09	2.E-08
GOTERM_BP_FAT	GO:0022403~cell cycle phase	54	6.150341686	2.E-11	12190, 16800, 59008, 56150, 18221, 1300	809	328	13588	3.E+00	6.E-08	3.E-09	4.E-08
GOTERM_BP_FAT	GO:0030029~actin filament-based process	37	4.214123007	5.E-11	22323, 215280, 227753, 94190, 11856, 16	809	176	13588	4.E+00	1.E-07	6.E-09	9.E-08
GOTERM_BP_FAT	GO:0000087~M phase of mitotic cell cycle	39	4.44191344	5.E-11	12454, 12236, 16800, 59008, 56150, 2383	809	194	13588	3.E+00	2.E-07	7.E-09	1.E-07
GOTERM_BP_FAT	GO:0016310~phosphorylation	88	10.02277904	1.E-10	18747, 13665, 12912, 16543, 22273, 2392	809	718	13588	2.E+00	3.E-07	1.E-08	2.E-07
GOTERM_BP_FAT	GO:0007067~mitosis	38	4.328018223	1.E-10	12454, 12236, 16800, 59008, 56150, 2383	809	190	13588	3.E+00	3.E-07	1.E-08	2.E-07
GOTERM_BP_FAT	GO:0000280~nuclear division	38	4.328018223	1.E-10	12454, 12236, 16800, 59008, 56150, 2383	809	190	13588	3.E+00	3.E-07	1.E-08	2.E-07
GOTERM_BP_FAT	GO:0048285~organelle fission	38	4.328018223	3.E-10	12454, 12236, 16800, 59008, 56150, 2383	809	197	13588	3.E+00	1.E-06	4.E-08	6.E-07
GOTERM_BP_FAT	GO:0015980~energy derivation by oxidation of organic compound	26	2.961275626	3.E-10	66416, 11651, 17721, 17722, 18679, 2227	809	98	13588	4.E+00	1.E-06	4.E-08	6.E-07
GOTERM_BP_FAT	GO:0001775~cell activation	43	4.897494305	5.E-10	22324, 19934, 16803, 14026, 22376, 5824	809	246	13588	3.E+00	1.E-06	5.E-08	9.E-07
GOTERM_BP_FAT	GO:0042773~ATP synthesis coupled electron transport	12	1.366742597	7.E-10	66416, 17719, 675851, 17721, 13382, 177	809	18	13588	1.E+01	2.E-06	7.E-08	1.E-06
GOTERM_BP_FAT	GO:0042325~regulation of phosphorylation	47	5.353075171	9.E-10	13649, 14151, 20416, 16543, 15163, 1870	809	290	13588	3.E+00	3.E-06	8.E-08	2.E-06
GOTERM_BP_FAT	GO:006413~translational initiation	16	1.822323462	2.E-09	13684, 66235, 13669, 56347, 53356, 2690	809	38	13588	7.E+00	5.E-06	1.E-07	3.E-06
GOTERM_BP_FAT	GO:0022904~respiratory electron transport chain	14	1.59453303	2.E-09	66416, 17719, 675851, 17721, 13382, 177	809	28	13588	8.E+00	5.E-06	2.E-07	3.E-06
GOTERM_BP_FAT	GO:0045321~leukocyte activation	39	4.44191344	2.E-09	22324, 19934, 16803, 22376, 58240, 1205	809	219	13588	3.E+00	6.E-06	2.E-07	4.E-06
GOTERM_BP_FAT	GO:0030036~actin cytoskeleton organization	33	3.758542141	2.E-09	22323, 227753, 94190, 11856, 16800, 204	809	165	13588	3.E+00	7.E-06	2.E-07	4.E-06
GOTERM_BP_FAT	GO:006796~phosphate metabolic process	96	10.93394077	3.E-09	18747, 13665, 12912, 16543, 22273, 2392	809	866	13588	2.E+00	9.E-06	2.E-07	5.E-06
GOTERM_BP_FAT	GO:006793~phosphorus metabolic process	96	10.93394077	3.E-09	18747, 13665, 12912, 16543, 22273, 2392	809	866	13588	2.E+00	9.E-06	2.E-07	5.E-06
GOTERM_BP_FAT	GO:0051174~regulation of phosphorus metabolic process	47	5.353075171	3.E-09	13649, 14151, 20416, 16543, 15163, 1870	809	301	13588	3.E+00	9.E-06	2.E-07	5.E-06
GOTERM_BP_FAT	GO:0019220~regulation of phosphate metabolic process	47	5.353075171	3.E-09	13649, 14151, 20416, 16543, 15163, 1870	809	301	13588	3.E+00	9.E-06	2.E-07	5.E-06
GOTERM_BP_FAT	GO:0066270~DNA replication initiation	9	1.025056948	6.E-09	17218, 17217, 17220, 12448, 17216, 1244	809	10	13588	2.E+01	2.E-05	5.E-07	1.E-05
GOTERM_BP_FAT	GO:0046578~regulation of Ras protein signal transduction	34	3.872437358	7.E-09	22324, 13605, 442801, 16800, 53972, 218	809	181	13588	3.E+00	2.E-05	5.E-07	1.E-05
GOTERM_BP_FAT	GO:0007264~small GTPase mediated signal transduction	42	4.783599089	7.E-09	117600, 228543, 19744, 232906, 11852, 1	809	258	13588	2.E+00	2.E-05	5.E-07	1.E-05
GOTERM_BP_FAT	GO:0001932~regulation of protein amino acid phosphorylation	27	3.0751170843	8.E-09	13649, 14151, 16543, 15163, 56717, 1859	809	121	13588	4.E+00	2.E-05	6.E-07	1.E-05
GOTERM_BP_FAT	GO:0042110~T cell activation	26	2.961275626	1.E-08	22324, 19934, 22376, 58240, 16408, 1205	809	116	13588	4.E+00	4.E-05	1.E-06	3.E-05
GOTERM_BP_FAT	GO:0031399~regulation of protein modification process	31	3.530751708	3.E-08	13649, 14151, 67141, 16543, 15163, 5671	809	165	13588	3.E+00	1.E-04	2.E-06	6.E-05
GOTERM_BP_FAT	GO:0000279~M phase	43	4.897494305	3.E-08	12190, 12454, 12236, 16800, 59008, 5615	809	283	13588	3.E+00	1.E-04	2.E-06	6.E-05
GOTERM_BP_FAT	GO:0046649~lymphocyte activation	33	3.758542141	9.E-08	22324, 19934, 22376, 58240, 12051, 1640	809	191	13588	3.E+00	3.E-04	6.E-06	2.E-04
GOTERM_BP_FAT	GO:0044093~positive regulation of molecular function	44	5.011389522	1.E-07	672195, 66593, 11856, 17869, 14852, 204	809	306	13588	2.E+00	4.E-04	8.E-06	2.E-04
GOTERM_BP_FAT	GO:006259~DNA metabolic process	54	6.150341686	2.E-07	12190, 50793, 17218, 17217, 17216, 1300	809	421	13588	2.E+00	5.E-04	1.E-05	3.E-04
GOTERM_BP_FAT	GO:008283~cell proliferation	38	4.328018223	2.E-07	12190, 19206, 665032, 26965, 12234, 129	809	247	13588	3.E+00	5.E-04	1.E-05	3.E-04
GOTERM_BP_FAT	GO:0048534~hemopoietic or lymphoid organ development	41	4.669703872	2.E-07	12190, 22324, 14151, 19934, 21934, 5824	809	281	13588	2.E+00	7.E-04	1.E-05	4.E-04
GOTERM_BP_FAT	GO:0030097~hemopoiesis	38	4.328018223	3.E-07	12190, 22324, 14151, 19934, 15163, 1590	809	251	13588	3.E+00	8.E-04	2.E-05	5.E-04
GOTERM_BP_FAT	GO:0042775~mitochondrial ATP synthesis coupled electron transport	9	1.025056948	3.E-07	67530, 17719, 675851, 67264, 17717, 133	809	14	13588	1.E+01	1.E-03	2.E-05	6.E-04
GOTERM_BP_FAT	GO:0042157~lipoprotein metabolic process	19	2.164009112	3.E-07	18108, 18107, 11814, 11806, 276846, 118	809	76	13588	4.E+00	1.E-03	2.E-05	6.E-04
GOTERM_BP_FAT	GO:0032268~regulation of cellular protein metabolic process	40	4.555808656	6.E-07	13684, 13649, 13685, 14151, 13665, 1165	809	280	13588	2.E+00	2.E-03	3.E-05	1.E-03
GOTERM_BP_FAT	GO:0002520~immune system development	41	4.669703872	8.E-07	12190, 22324, 14151, 19934, 21934, 5824	809	295	13588	2.E+00	3.E-03	5.E-05	2.E-03
GOTERM_BP_FAT	GO:006468~protein amino acid phosphorylation	70	7.972665148	1.E-06	18747, 13665, 12912, 16543, 23920, 1681	809	640	13588	2.E+00	3.E-03	5.E-05	2.E-03
GOTERM_BP_FAT	GO:0045333~cellular respiration	16	1.822323462	1.E-06	66416, 17719, 675851, 17721, 13382, 177	809	59	13588	5.E+00	4.E-03	7.E-05	2.E-03



GOTERM_BP_FAT	GO:0010627~regulation of protein kinase cascade	27	3.075170843	1.E-06	12234, 16543, 15163, 16994, 12703, 1478	809	155	13588	3.E+00	4.E-03	7.E-05	3.E-03
GOTERM_BP_FAT	GO:0051056~regulation of small GTPase mediated signal transduc	34	3.872437358	2.E-06	22324, 13605, 442801, 16800, 53972, 218	809	228	13588	3.E+00	5.E-03	9.E-05	3.E-03
GOTERM_BP_FAT	GO:0043085~positive regulation of catalytic activity	37	4.214123007	2.E-06	672195, 66593, 11856, 17869, 14852, 204	809	261	13588	2.E+00	6.E-03	1.E-04	4.E-03
GOTERM_BP_FAT	GO:0043009~chordate embryonic development	50	5.69476082	5.E-06	12190, 23223, 19206, 238055, 18803, 114	809	421	13588	2.E+00	1.E-02	2.E-04	9.E-03
GOTERM_BP_FAT	GO:0019637~organophosphate metabolic process	28	3.189066059	5.E-06	68262, 14178, 276846, 329777, 52123, 21	809	176	13588	3.E+00	2.E-02	3.E-04	9.E-03
GOTERM_BP_FAT	GO:0009792~embryonic development ending in birth or egg hatching	50	5.69476082	6.E-06	12190, 23223, 19206, 238055, 18803, 114	809	425	13588	2.E+00	2.E-02	3.E-04	1.E-02
GOTERM_BP_FAT	GO:0042592~homeostatic process	62	7.061503417	1.E-05	19206, 238055, 14782, 20191, 12815, 159	809	584	13588	2.E+00	3.E-02	5.E-04	2.E-02
GOTERM_BP_FAT	GO:0043068~positive regulation of programmed cell death	34	3.872437358	1.E-05	12190, 672195, 66593, 67184, 11816, 149	809	250	13588	2.E+00	4.E-02	6.E-04	2.E-02
GOTERM_BP_FAT	GO:0042158~lipoprotein biosynthetic process	14	1.59453303	1.E-05	18108, 18107, 276846, 11806, 11816, 329	809	55	13588	4.E+00	4.E-02	7.E-04	3.E-02
GOTERM_BP_FAT	GO:0010942~positive regulation of cell death	34	3.872437358	2.E-05	12190, 672195, 66593, 67184, 11816, 149	809	252	13588	2.E+00	5.E-02	7.E-04	3.E-02
GOTERM_BP_FAT	GO:0002757~immune response-activating signal transduction	13	1.480637813	2.E-05	15170, 27007, 16818, 17874, 18803, 1412	809	48	13588	5.E+00	5.E-02	8.E-04	3.E-02
GOTERM_BP_FAT	GO:0051338~regulation of transferase activity	29	3.302961276	2.E-05	20416, 16543, 56717, 16367, 19164, 1254	809	199	13588	2.E+00	5.E-02	8.E-04	3.E-02
GOTERM_BP_FAT	GO:0006261~DNA-dependent DNA replication	11	1.25284738	2.E-05	382985, 17218, 12190, 17217, 17220, 124	809	34	13588	5.E+00	5.E-02	8.E-04	3.E-02
GOTERM_BP_FAT	GO:0043549~regulation of kinase activity	28	3.189066059	3.E-05	20416, 16543, 56717, 16367, 19164, 1254	809	192	13588	2.E+00	8.E-02	1.E-03	5.E-02
GOTERM_BP_FAT	GO:0043065~positive regulation of apoptosis	33	3.758542141	3.E-05	12190, 672195, 66593, 67184, 11816, 149	809	248	13588	2.E+00	8.E-02	1.E-03	5.E-02
GOTERM_BP_FAT	GO:0045786~negative regulation of cell cycle	12	1.366742597	3.E-05	11785, 57441, 19645, 11852, 11920, 1204	809	43	13588	5.E+00	9.E-02	1.E-03	5.E-02
GOTERM_BP_FAT	GO:0006644~phospholipid metabolic process	25	2.84738041	3.E-05	68262, 14178, 276846, 329777, 52123, 21	809	163	13588	3.E+00	1.E-01	1.E-03	6.E-02
GOTERM_BP_FAT	GO:0048872~homeostasis of number of cells	20	2.277904328	3.E-05	14151, 11651, 12043, 20375, 12183, 6827	809	113	13588	3.E+00	1.E-01	1.E-03	6.E-02
GOTERM_BP_FAT	GO:0002684~positive regulation of immune system process	29	3.302961276	4.E-05	14972, 15018, 16396, 16803, 12010, 1640	809	206	13588	2.E+00	1.E-01	1.E-03	6.E-02
GOTERM_BP_FAT	GO:0010033~response to organic substance	54	6.150341686	4.E-05	12475, 14815, 20191, 16803, 12912, 1464	809	505	13588	2.E+00	1.E-01	1.E-03	7.E-02
GOTERM_BP_FAT	GO:0051336~regulation of hydrolase activity	28	3.189066059	4.E-05	23234, 672195, 66593, 17869, 11856, 148	809	196	13588	2.E+00	1.E-01	1.E-03	7.E-02
GOTERM_BP_FAT	GO:0030879~mammary gland development	17	1.936218679	4.E-05	12190, 19206, 14815, 11855, 15277, 2193	809	86	13588	3.E+00	1.E-01	2.E-03	7.E-02
GOTERM_BP_FAT	GO:0002764~immune response-regulating signal transduction	13	1.480637813	4.E-05	15170, 27007, 16818, 17874, 18803, 1412	809	52	13588	4.E+00	1.E-01	2.E-03	7.E-02
GOTERM_BP_FAT	GO:0008219~cell death	54	6.150341686	4.E-05	12765, 672195, 54354, 14852, 100046871	809	507	13588	2.E+00	1.E-01	2.E-03	8.E-02
GOTERM_BP_FAT	GO:0051347~positive regulation of transferase activity	22	2.505694761	5.E-05	11806, 14678, 21899, 21898, 57257, 2041	809	135	13588	3.E+00	1.E-01	2.E-03	8.E-02
GOTERM_BP_FAT	GO:0050778~positive regulation of immune response	22	2.505694761	5.E-05	19370, 14972, 15170, 15018, 27007, 2189	809	136	13588	3.E+00	1.E-01	2.E-03	9.E-02
GOTERM_BP_FAT	GO:0006120~mitochondrial electron transport, NADH to ubiquinone	5	0.569476082	6.E-05	17719, 675851, 67264, 17717, 13382, 681	809	5	13588	2.E+01	2.E-01	2.E-03	1.E-01
GOTERM_BP_FAT	GO:0007243~protein kinase cascade	31	3.530751708	7.E-05	11651, 20416, 16543, 55979, 12703, 1636	809	236	13588	2.E+00	2.E-01	2.E-03	1.E-01
GOTERM_BP_FAT	GO:0008360~regulation of cell shape	12	1.366742597	7.E-05	80837, 14163, 14674, 232906, 77579, 104	809	47	13588	4.E+00	2.E-01	3.E-03	1.E-01
GOTERM_BP_FAT	GO:0016265~death	54	6.150341686	8.E-05	12765, 672195, 54354, 14852, 100046871	809	519	13588	2.E+00	2.E-01	3.E-03	1.E-01
GOTERM_BP_FAT	GO:0033674~positive regulation of kinase activity	21	2.391799544	8.E-05	14678, 21899, 21898, 57257, 20416, 1338	809	130	13588	3.E+00	2.E-01	3.E-03	1.E-01
GOTERM_BP_FAT	GO:0006739~NADP metabolic process	7	0.797266515	9.E-05	17970, 21991, 21351, 17969, 66171, 1039	809	14	13588	8.E+00	2.E-01	3.E-03	2.E-01
GOTERM_BP_FAT	GO:0007015~actin filament organization	13	1.480637813	9.E-05	227753, 13800, 12043, 11856, 16800, 140	809	56	13588	4.E+00	2.E-01	3.E-03	2.E-01
GOTERM_BP_FAT	GO:0006119~oxidative phosphorylation	13	1.480637813	9.E-05	66416, 17719, 675851, 17721, 13382, 177	809	56	13588	4.E+00	2.E-01	3.E-03	2.E-01
GOTERM_BP_FAT	GO:0030705~cytoskeleton-dependent intracellular transport	10	1.138952164	9.E-05	11785, 245049, 215280, 17925, 77579, 14	809	33	13588	5.E+00	2.E-01	3.E-03	2.E-01
GOTERM_BP_FAT	GO:0051240~positive regulation of multicellular organismal process	24	2.733485194	1.E-04	12475, 15018, 16803, 12912, 12051, 1699	809	163	13588	2.E+00	3.E-01	3.E-03	2.E-01
GOTERM_BP_FAT	GO:0048584~positive regulation of response to stimulus	26	2.961275626	1.E-04	14972, 15018, 16803, 12010, 21937, 1880	809	186	13588	2.E+00	3.E-01	4.E-03	2.E-01
GOTERM_BP_FAT	GO:0007010~cytoskeleton organization	38	4.328018223	1.E-04	23232, 227753, 94190, 11856, 16800, 204	809	326	13588	2.E+00	3.E-01	4.E-03	2.E-01
GOTERM_BP_FAT	GO:0009725~response to hormone stimulus	24	2.733485194	1.E-04	13685, 12842, 109900, 232087, 11651, 12	809	165	13588	2.E+00	3.E-01	4.E-03	2.E-01
GOTERM_BP_FAT	GO:0001568~blood vessel development	31	3.530751708	1.E-04	12831, 11852, 11816, 11651, 238055, 204	809	244	13588	2.E+00	3.E-01	4.E-03	2.E-01
GOTERM_BP_FAT	GO:0030098~lymphocyte differentiation	19	2.164009112	1.E-04	22324, 19934, 12043, 20375, 74734, 1081	809	114	13588	3.E+00	3.E-01	4.E-03	2.E-01
GOTERM_BP_FAT	GO:0006915~apoptosis	49	5.580865604	1.E-04	672195, 12765, 54354, 14852, 100046871	809	465	13588	2.E+00	3.E-01	4.E-03	2.E-01
GOTERM_BP_FAT	GO:0030048~actin filament-based movement	7	0.797266515	1.E-04	11785, 245049, 215280, 17925, 77579, 14	809	15	13588	8.E+00	3.E-01	4.E-03	2.E-01
GOTERM_BP_FAT	GO:0032760~positive regulation of tumor necrosis factor product	7	0.797266515	1.E-04	14127, 17874, 12475, 21898, 24088, 1680	809	15	13588	8.E+00	3.E-01	4.E-03	2.E-01
GOTERM_BP_FAT	GO:0033554~cellular response to stress	44	5.011389522	1.E-04	12190, 80905, 245000, 12649, 22209, 136	809	404	13588	2.E+00	4.E-01	4.E-03	3.E-01
GOTERM_BP_FAT	GO:0002253~activation of immune response	16	1.822323462	1.E-04	15170, 27007, 21898, 16818, 17874, 1880	809	86	13588	3.E+00	4.E-01	4.E-03	3.E-01
GOTERM_BP_FAT	GO:0007265~Ras protein signal transduction	13	1.480637813	2.E-04	117600, 14674, 192662, 69581, 11848, 80	809	59	13588	4.E+00	4.E-01	4.E-03	3.E-01
GOTERM_BP_FAT	GO:0007346~regulation of mitotic cell cycle	17	1.936218679	2.E-04	12190, 17869, 12043, 56150, 67141, 1338	809	96	13588	3.E+00	4.E-01	5.E-03	3.E-01
GOTERM_BP_FAT	GO:0007169~transmembrane receptor protein tyrosine kinase signaling	26	2.961275626	2.E-04	13649, 13685, 14178, 11651, 21844, 1870	809	192	13588	2.E+00	4.E-01	5.E-03	3.E-01
GOTERM_BP_FAT	GO:0001944~vasculature development	31	3.530751708	2.E-04	12831, 11852, 11816, 11651, 238055, 204	809	250	13588	2.E+00	4.E-01	5.E-03	3.E-01
GOTERM_BP_FAT	GO:0012501~programmed cell death	49	5.580865604	2.E-04	672195, 12765, 54354, 14852, 100046871	809	473	13588	2.E+00	4.E-01	6.E-03	3.E-01
GOTERM_BP_FAT	GO:0001836~release of cytochrome c from mitochondria	7	0.797266515	2.E-04	12048, 12028, 12122, 12018, 12043, 1786	809	16	13588	7.E+00	5.E-01	6.E-03	4.E-01
GOTERM_BP_FAT	GO:0043507~positive regulation of JUN kinase activity	7	0.797266515	2.E-04	16179, 16334, 21899, 117149, 20963, 165	809	16	13588	7.E+00	5.E-01	6.E-03	4.E-01
GOTERM_BP_FAT	GO:0031960~response to corticosteroid stimulus	8	0.911161731	3.E-04	12039, 20779, 12842, 11409, 109900, 263	809	23	13588	6.E+00	6.E-01	8.E-03	5.E-01
GOTERM_BP_FAT	GO:0002521~leukocyte differentiation	21	2.391799544	3.E-04	22324, 19934, 12043, 20375, 74734, 1081	809	142	13588	2.E+00	6.E-01	8.E-03	5.E-01
GOTERM_BP_FAT	GO:0043067~regulation of programmed cell death	55	6.264236902	3.E-04	12190, 672195, 13628, 14815, 14852, 120	809	560	13588	2.E+00	6.E-01	8.E-03	5.E-01
GOTERM_BP_FAT	GO:0010941~regulation of cell death	55	6.264236902	3.E-04	12190, 672195, 13628, 14815, 14852, 120	809	563	13588	2.E+00	6.E-01	9.E-03	6.E-01
GOTERM_BP_FAT	GO:0002366~leukocyte activation during immune response	9	1.025056948	3.E-04	12051, 11486, 18826, 234779, 19164, 118	809	31	13588	5.E+00	6.E-01	9.E-03	6.E-01
GOTERM_BP_FAT	GO:0002263~cell activation during immune response	9	1.025056948	3.E-04	12051, 11486, 18826, 234779, 19164, 118	809	31	13588	5.E+00	6.E-01	9.E-03	6.E-01
GOTERM_BP_FAT	GO:0006800~oxygen and reactive oxygen species metabolic process	11	1.25284738	4.E-04	18126, 672195, 17970, 68349, 50493, 120	809	47	13588	4.E+00	7.E-01	1.E-02	7.E-01
GOTERM_BP_FAT	GO:0043408~regulation of MAPKKK cascade	16	1.822323462	4.E-04	15170, 21899, 21898, 14180, 224014, 165	809	93	13588	3.E+00	7.E-01	1.E-02	7.E-01
GOTERM_BP_FAT	GO:0043603~cellular amide metabolic process	10	1.138952164	4.E-04	18416, 17970, 109900, 11847, 21991, 213	809	39	13588	4.E+00	7.E-01	1.E-02	7.E-01
GOTERM_BP_FAT	GO:0050798~activated T cell proliferation	5	0.569476082	4.E-04	16408, 16411, 16414, 14360, 16409	809	7	13588	1.E+01	7.E-01	1.E-02	7.E-01
GOTERM_BP_FAT	GO:0042981~regulation of apoptosis	54	6.150341686	4.E-04	12190, 672195, 13628, 14815, 14852, 120	809	553	13588	2.E+00	7.E-01	1.E-02	7.E-01
GOTERM_BP_FAT	GO:0034637~cellular carbohydrate biosynthetic process	12	1.366742597	4.E-04	18682, 14751, 234779, 18534, 11651, 219	809	56	13588	4.E+00	7.E-01	1.E-02	7.E-01



GOTERM_BP_FAT	GO:0009611~response to wounding	38	4.328018223	4.E-04 12475, 11651, 18793, 16803, 14026, 2193	809	347	13588	2.E+00	7.E-01	1.E-02	7.E-01
GOTERM_BP_FAT	GO:0051094~positive regulation of developmental process	27	3.0751170843	4.E-04 11852, 15376, 21844, 15902, 16818, 1201	809	214	13588	2.E+00	7.E-01	1.E-02	7.E-01
GOTERM_BP_FAT	GO:0030218~erythrocyte differentiation	11	1.25284738	4.E-04 14151, 19645, 18771, 21349, 20085, 2037	809	48	13588	4.E+00	7.E-01	1.E-02	8.E-01
GOTERM_BP_FAT	GO:0006974~response to DNA damage stimulus	33	3.758542141	5.E-04 12190, 80905, 245000, 12649, 22209, 120	809	287	13588	2.E+00	7.E-01	1.E-02	8.E-01
GOTERM_BP_FAT	GO:0043122~regulation of I-kappaB kinase/NF-kappaB cascade	10	1.138952164	5.E-04 16994, 17874, 21899, 21898, 56722, 1921	809	40	13588	4.E+00	7.E-01	1.E-02	8.E-01
GOTERM_BP_FAT	GO:0043434~response to peptide hormone stimulus	16	1.822323462	5.E-04 13685, 12842, 109900, 12043, 11651, 384	809	95	13588	3.E+00	7.E-01	1.E-02	8.E-01
GOTERM_BP_FAT	GO:0008637~apoptotic mitochondrial changes	8	0.911161731	5.E-04 12048, 12028, 12122, 12018, 11651, 1204	809	25	13588	5.E+00	8.E-01	1.E-02	9.E-01
GOTERM_BP_FAT	GO:0035295~tube development	31	3.530751708	5.E-04 23233, 14178, 19206, 232906, 15376, 148	809	264	13588	2.E+00	8.E-01	1.E-02	9.E-01
GOTERM_BP_FAT	GO:0030099~myeloid cell differentiation	16	1.822323462	5.E-04 14151, 20375, 12183, 15902, 15163, 2134	809	96	13588	3.E+00	8.E-01	1.E-02	9.E-01
GOTERM_BP_FAT	GO:0002237~response to molecule of bacterial origin	11	1.25284738	5.E-04 17874, 12475, 16179, 17087, 234779, 264	809	49	13588	4.E+00	8.E-01	1.E-02	9.E-01
GOTERM_BP_FAT	GO:0051329~interphase of mitotic cell cycle	11	1.25284738	5.E-04 104394, 19645, 13559, 12649, 12443, 131	809	49	13588	4.E+00	8.E-01	1.E-02	9.E-01
GOTERM_BP_FAT	GO:0006073~cellular glucan metabolic process	9	1.025056948	6.E-04 18682, 110095, 16195, 102093, 110094, 1	809	33	13588	5.E+00	8.E-01	1.E-02	1.E+00
GOTERM_BP_FAT	GO:0044042~glucan metabolic process	9	1.025056948	6.E-04 18682, 110095, 16195, 102093, 110094, 1	809	33	13588	5.E+00	8.E-01	1.E-02	1.E+00
GOTERM_BP_FAT	GO:0005977~glycogen metabolic process	9	1.025056948	6.E-04 18682, 110095, 16195, 102093, 110094, 1	809	33	13588	5.E+00	8.E-01	1.E-02	1.E+00
GOTERM_BP_FAT	GO:0006919~activation of caspase activity	9	1.025056948	6.E-04 16818, 672195, 66593, 12028, 12018, 178	809	33	13588	5.E+00	8.E-01	1.E-02	1.E+00
GOTERM_BP_FAT	GO:0002429~immune response-activating cell surface receptor si	10	1.138952164	6.E-04 14127, 15170, 18803, 16818, 234779, 270	809	41	13588	4.E+00	8.E-01	1.E-02	1.E+00
GOTERM_BP_FAT	GO:0009719~response to endogenous stimulus	24	2.733485194	6.E-04 13685, 12842, 109900, 232087, 11651, 12	809	184	13588	2.E+00	8.E-01	1.E-02	1.E+00
GOTERM_BP_FAT	GO:0002009~morphogenesis of an epithelium	23	2.619589977	6.E-04 22323, 13649, 13800, 19206, 232906, 169	809	173	13588	2.E+00	8.E-01	1.E-02	1.E+00
GOTERM_BP_FAT	GO:0002285~lymphocyte activation during immune response	7	0.797266515	6.E-04 12051, 11486, 18826, 234779, 19164, 118	809	19	13588	6.E+00	8.E-01	1.E-02	1.E+00
GOTERM_BP_FAT	GO:0045428~regulation of nitric oxide biosynthetic process	7	0.797266515	6.E-04 19370, 21898, 27007, 11847, 16414, 3790	809	19	13588	6.E+00	8.E-01	1.E-02	1.E+00
GOTERM_BP_FAT	GO:0006497~protein amino acid lipidation	11	1.25284738	6.E-04 18108, 18107, 14731, 56703, 108672, 177	809	50	13588	4.E+00	8.E-01	1.E-02	1.E+00
GOTERM_BP_FAT	GO:0042127~regulation of cell proliferation	52	5.922551253	6.E-04 14178, 19206, 16952, 16408, 16994, 1812	809	538	13588	2.E+00	8.E-01	1.E-02	1.E+00
GOTERM_BP_FAT	GO:0046651~lymphocyte proliferation	10	1.138952164	7.E-04 16408, 12445, 16197, 16411, 14226, 1202	809	42	13588	4.E+00	9.E-01	1.E-02	1.E+00
GOTERM_BP_FAT	GO:0045859~regulation of protein kinase activity	24	2.733485194	7.E-04 15170, 21899, 14678, 21898, 20416, 1338	809	186	13588	2.E+00	9.E-01	1.E-02	1.E+00
GOTERM_BP_FAT	GO:0010522~regulation of calcium ion transport into cytosol	5	0.569476082	7.E-04 14226, 12028, 12018, 12043, 20191	809	8	13588	1.E+01	9.E-01	2.E-02	1.E+00
GOTERM_BP_FAT	GO:0043550~regulation of lipid kinase activity	5	0.569476082	7.E-04 18048, 19645, 16367, 57257, 12540	809	8	13588	1.E+01	9.E-01	2.E-02	1.E+00
GOTERM_BP_FAT	GO:0051325~interphase	11	1.25284738	7.E-04 104394, 19645, 13559, 12649, 12443, 131	809	51	13588	4.E+00	9.E-01	2.E-02	1.E+00
GOTERM_BP_FAT	GO:0034101~erythrocyte homeostasis	11	1.25284738	7.E-04 14151, 19645, 18771, 21349, 20085, 2037	809	51	13588	4.E+00	9.E-01	2.E-02	1.E+00
GOTERM_BP_FAT	GO:0007266~Rho protein signal transduction	8	0.911161731	8.E-04 80837, 117600, 57874, 14674, 192662, 12	809	27	13588	5.E+00	9.E-01	2.E-02	1.E+00
GOTERM_BP_FAT	GO:0032680~regulation of tumor necrosis factor production	8	0.911161731	8.E-04 12051, 14127, 17874, 12475, 21898, 2408	809	27	13588	5.E+00	9.E-01	2.E-02	1.E+00
GOTERM_BP_FAT	GO:0032869~cellular response to insulin stimulus	10	1.138952164	8.E-04 18709, 18708, 13685, 16367, 16334, 1042	809	43	13588	4.E+00	9.E-01	2.E-02	1.E+00
GOTERM_BP_FAT	GO:0032943~mononuclear cell proliferation	10	1.138952164	8.E-04 16408, 12445, 16197, 16411, 14226, 1202	809	43	13588	4.E+00	9.E-01	2.E-02	1.E+00
GOTERM_BP_FAT	GO:0070661~leukocyte proliferation	10	1.138952164	8.E-04 16408, 12445, 16197, 16411, 14226, 1202	809	43	13588	4.E+00	9.E-01	2.E-02	1.E+00
GOTERM_BP_FAT	GO:0060562~epithelial tube morphogenesis	17	1.936218679	8.E-04 22323, 13800, 19206, 232906, 16911, 148	809	111	13588	3.E+00	9.E-01	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0043086~negative regulation of catalytic activity	16	1.822323462	9.E-04 15170, 11806, 11807, 14678, 11847, 6714	809	101	13588	3.E+00	9.E-01	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0012502~induction of programmed cell death	22	2.505694761	9.E-04 382985, 12190, 15170, 66593, 67184, 118	809	167	13588	2.E+00	9.E-01	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0006917~induction of apoptosis	22	2.505694761	9.E-04 382985, 12190, 15170, 66593, 67184, 118	809	167	13588	2.E+00	9.E-01	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0051345~positive regulation of hydrolase activity	14	1.59453303	9.E-04 672195, 66593, 17869, 11856, 14852, 168	809	81	13588	3.E+00	9.E-01	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0002218~activation of innate immune response	6	0.683371298	9.E-04 17874, 16179, 21898, 27007, 24088, 1067	809	14	13588	7.E+00	9.E-01	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0048729~tissue morphogenesis	28	3.189066059	9.E-04 23233, 13649, 18747, 14178, 19206, 2329	809	238	13588	2.E+00	9.E-01	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0002768~immune response-regulating cell surface receptor si	10	1.138952164	1.E-03 14127, 15170, 18803, 16818, 234779, 270	809	44	13588	4.E+00	9.E-01	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0001819~positive regulation of cytokine production	12	1.366742597	1.E-03 19370, 12475, 15018, 27007, 21898, 1446	809	62	13588	3.E+00	9.E-01	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0042098~T cell proliferation	8	0.911161731	1.E-03 16408, 12445, 16411, 14226, 12028, 1641	809	28	13588	5.E+00	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0009617~response to bacterium	21	2.391799544	1.E-03 14972, 12475, 239081, 21898, 13035, 168	809	157	13588	2.E+00	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0010952~positive regulation of peptidase activity	9	1.025056948	1.E-03 16818, 672195, 66593, 12028, 12018, 178	809	36	13588	4.E+00	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0043280~positive regulation of caspase activity	9	1.025056948	1.E-03 16818, 672195, 66593, 12028, 12018, 178	809	36	13588	4.E+00	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0043506~regulation of JUN kinase activity	7	0.797266515	1.E-03 16179, 16334, 21899, 117149, 20963, 165	809	21	13588	6.E+00	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0046328~regulation of JNK cascade	10	1.138952164	1.E-03 17874, 16179, 16334, 21899, 21898, 1171	809	45	13588	4.E+00	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0010564~regulation of cell cycle process	13	1.480637813	1.E-03 12190, 56150, 67141, 11785, 16994, 5256	809	73	13588	3.E+00	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0008654~phospholipid biosynthetic process	14	1.59453303	1.E-03 14178, 68262, 276846, 329777, 52123, 10	809	83	13588	3.E+00	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0048009~insulin-like growth factor receptor signaling pathwa	5	0.569476082	1.E-03 18708, 16367, 11651, 16001, 16000	809	9	13588	9.E+00	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0035239~tube morphogenesis	22	2.505694761	1.E-03 22323, 14674, 13800, 19206, 232906, 169	809	171	13588	2.E+00	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0018108~peptidyl-tyrosine phosphorylation	9	1.025056948	1.E-03 11350, 16818, 12229, 20779, 18413, 1436	809	37	13588	4.E+00	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0006112~energy reserve metabolic process	9	1.025056948	1.E-03 18682, 110095, 16195, 102093, 110094, 1	809	37	13588	4.E+00	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0018212~peptidyl-tyrosine modification	9	1.025056948	1.E-03 11350, 16818, 12229, 20779, 18413, 1436	809	37	13588	4.E+00	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0045429~positive regulation of nitric oxide biosynthetic proce	6	0.683371298	1.E-03 19370, 21898, 27007, 16414, 379043, 240	809	15	13588	7.E+00	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0070302~regulation of stress-activated protein kinase signalin	10	1.138952164	1.E-03 17874, 16179, 16334, 21899, 21898, 1171	809	46	13588	4.E+00	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0080135~regulation of cellular response to stress	13	1.480637813	1.E-03 14151, 21899, 21898, 224014, 16543, 117	809	75	13588	3.E+00	1.E+00	3.E-02	3.E+00
GOTERM_BP_FAT	GO:0048732~gland development	24	2.733485194	1.E-03 12190, 13649, 14178, 11806, 19206, 1481	809	197	13588	2.E+00	1.E+00	3.E-02	3.E+00
GOTERM_BP_FAT	GO:0032496~response to lipopolysaccharide	9	1.025056948	1.E-03 17874, 12475, 16179, 17087, 234779, 264	809	38	13588	4.E+00	1.E+00	3.E-02	3.E+00
GOTERM_BP_FAT	GO:0060429~epithelium development	30	3.416856492	2.E-03 22323, 13649, 19206, 232906, 15376, 148	809	271	13588	2.E+00	1.E+00	3.E-02	3.E+00
GOTERM_BP_FAT	GO:0008284~positive regulation of cell proliferation	31	3.530751708	2.E-03 13649, 14178, 17869, 11855, 15163, 1640	809	284	13588	2.E+00	1.E+00	3.E-02	3.E+00
GOTERM_BP_FAT	GO:0046777~protein amino acid autophosphorylation	12	1.366742597	2.E-03 56717, 18747, 13649, 16818, 23920, 1617	809	66	13588	3.E+00	1.E+00	3.E-02	3.E+00
GOTERM_BP_FAT	GO:0030217~T cell differentiation	13	1.480637813	2.E-03 22324, 19934, 12043, 74734, 108138, 100	809	76	13588	3.E+00	1.E+00	3.E-02	3.E+00
GOTERM_BP_FAT	GO:0045597~positive regulation of cell differentiation	22	2.505694761	2.E-03 15376, 12043, 108138, 21844, 15902, 118	809	175	13588	2.E+00	1.E+00	3.E-02	3.E+00



GOTERM_BP_FAT	GO:0010959~regulation of metal ion transport	10	1.138952164	2.E-03 17999, 234779, 14226, 14678, 12028, 120	809	48	13588	3.E+00	1.E+00	3.E-02	3.E+00
GOTERM_BP_FAT	GO:0051402~neuron apoptosis	6	0.683371298	2.E-03 11920, 12028, 19164, 12043, 12568, 1000	809	16	13588	6.E+00	1.E+00	3.E-02	3.E+00
GOTERM_BP_FAT	GO:0070391~response to lipoteichoic acid	4	0.455580866	2.E-03 12475, 21898, 24088, 16803	809	5	13588	1.E+01	1.E+00	3.E-02	3.E+00
GOTERM_BP_FAT	GO:0010740~positive regulation of protein kinase cascade	14	1.59453303	2.E-03 21899, 21898, 14180, 11848, 15163, 1699	809	88	13588	3.E+00	1.E+00	3.E-02	4.E+00
GOTERM_BP_FAT	GO:0032870~cellular response to hormone stimulus	11	1.25284738	2.E-03 18709, 18708, 13685, 16367, 16334, 1042	809	58	13588	3.E+00	1.E+00	3.E-02	4.E+00
GOTERM_BP_FAT	GO:0044092~negative regulation of molecular function	18	2.050113895	2.E-03 15170, 11806, 11807, 14678, 17869, 1184	809	132	13588	2.E+00	1.E+00	4.E-02	4.E+00
GOTERM_BP_FAT	GO:0032868~response to insulin stimulus	11	1.25284738	2.E-03 18709, 18708, 56717, 13685, 16367, 1633	809	59	13588	3.E+00	1.E+00	4.E-02	4.E+00
GOTERM_BP_FAT	GO:0009820~alkaloid metabolic process	7	0.797266515	2.E-03 17970, 21991, 21351, 17969, 66171, 1039	809	24	13588	5.E+00	1.E+00	4.E-02	4.E+00
GOTERM_BP_FAT	GO:0006769~nicotinamide metabolic process	7	0.797266515	2.E-03 17970, 21991, 21351, 17969, 66171, 1039	809	24	13588	5.E+00	1.E+00	4.E-02	4.E+00
GOTERM_BP_FAT	GO:0046496~nicotinamide nucleotide metabolic process	7	0.797266515	2.E-03 17970, 21991, 21351, 17969, 66171, 1039	809	24	13588	5.E+00	1.E+00	4.E-02	4.E+00
GOTERM_BP_FAT	GO:0052548~regulation of endopeptidase activity	10	1.138952164	2.E-03 16818, 672195, 12015, 66593, 12028, 120	809	50	13588	3.E+00	1.E+00	4.E-02	4.E+00
GOTERM_BP_FAT	GO:0043281~regulation of caspase activity	10	1.138952164	2.E-03 16818, 672195, 12015, 66593, 12028, 120	809	50	13588	3.E+00	1.E+00	4.E-02	4.E+00
GOTERM_BP_FAT	GO:0001701~in utero embryonic development	29	3.302961276	3.E-03 12190, 13649, 18107, 22209, 11651, 2380	809	267	13588	2.E+00	1.E+00	4.E-02	4.E+00
GOTERM_BP_FAT	GO:0032844~regulation of homeostatic process	11	1.25284738	3.E-03 14127, 16818, 21349, 11486, 14226, 1202	809	60	13588	3.E+00	1.E+00	4.E-02	5.E+00
GOTERM_BP_FAT	GO:0045860~positive regulation of protein kinase activity	17	1.936218679	3.E-03 14678, 21899, 21898, 20416, 13383, 2240	809	124	13588	2.E+00	1.E+00	4.E-02	5.E+00
GOTERM_BP_FAT	GO:0031570~DNA integrity checkpoint	8	0.911161731	3.E-03 245000, 11920, 67177, 26416, 12649, 124	809	33	13588	4.E+00	1.E+00	5.E-02	5.E+00
GOTERM_BP_FAT	GO:0043123~positive regulation of I-kappaB kinase/NF-kappaB c	8	0.911161731	3.E-03 16994, 17874, 21899, 21898, 56722, 1921	809	33	13588	4.E+00	1.E+00	5.E-02	5.E+00
GOTERM_BP_FAT	GO:0052547~regulation of peptidase activity	10	1.138952164	3.E-03 16818, 672195, 12015, 66593, 12028, 120	809	51	13588	3.E+00	1.E+00	5.E-02	5.E+00
GOTERM_BP_FAT	GO:0006090~pyruvate metabolic process	7	0.797266515	3.E-03 14751, 235339, 18534, 21991, 230163, 18	809	25	13588	5.E+00	1.E+00	5.E-02	5.E+00
GOTERM_BP_FAT	GO:0008156~negative regulation of DNA replication	5	0.569476082	3.E-03 12190, 57441, 22130, 67177, 269582	809	11	13588	8.E+00	1.E+00	5.E-02	5.E+00
GOTERM_BP_FAT	GO:0001914~regulation of T cell mediated cytotoxicity	5	0.569476082	3.E-03 14972, 15018, 16197, 19056, 12010	809	11	13588	8.E+00	1.E+00	5.E-02	5.E+00
GOTERM_BP_FAT	GO:0000075~cell cycle checkpoint	10	1.138952164	3.E-03 245000, 11920, 67177, 26416, 12649, 124	809	52	13588	3.E+00	1.E+00	5.E-02	6.E+00
GOTERM_BP_FAT	GO:0006275~regulation of DNA replication	6	0.683371298	3.E-03 12190, 57441, 22130, 67177, 18538, 2695	809	18	13588	6.E+00	1.E+00	5.E-02	6.E+00
GOTERM_BP_FAT	GO:0043087~regulation of GTPase activity	14	1.59453303	3.E-03 22324, 228359, 57257, 11856, 14567, 145	809	93	13588	3.E+00	1.E+00	5.E-02	6.E+00
GOTERM_BP_FAT	GO:0043269~regulation of ion transport	11	1.25284738	3.E-03 16994, 17999, 234779, 14226, 14678, 120	809	62	13588	3.E+00	1.E+00	5.E-02	6.E+00
GOTERM_BP_FAT	GO:0001816~cytokine production	9	1.025056948	3.E-03 18019, 17874, 21898, 16822, 13383, 1680	809	43	13588	4.E+00	1.E+00	5.E-02	6.E+00
GOTERM_BP_FAT	GO:0044264~cellular polysaccharide metabolic process	9	1.025056948	3.E-03 18682, 110095, 16195, 102093, 110094, 1	809	43	13588	4.E+00	1.E+00	5.E-02	6.E+00
GOTERM_BP_FAT	GO:0050900~leukocyte migration	9	1.025056948	3.E-03 20310, 14127, 20345, 56744, 12490, 1641	809	43	13588	4.E+00	1.E+00	5.E-02	6.E+00
GOTERM_BP_FAT	GO:0046907~intracellular transport	41	4.669703872	3.E-03 215280, 269589, 11852, 14026, 171531, 2	809	431	13588	2.E+00	1.E+00	5.E-02	6.E+00
GOTERM_BP_FAT	GO:0007167~enzyme linked receptor protein signaling pathway	29	3.302961276	3.E-03 13649, 13685, 14178, 11651, 21844, 1870	809	273	13588	2.E+00	1.E+00	5.E-02	6.E+00
GOTERM_BP_FAT	GO:0032469~endoplasmic reticulum calcium ion homeostasis	4	0.455580866	4.E-03 12028, 12018, 19164, 12043	809	6	13588	1.E+01	1.E+00	6.E-02	6.E+00
GOTERM_BP_FAT	GO:0006122~mitochondrial electron transport, ubiquinol to cytoc	4	0.455580866	4.E-03 67530, 66594, 66576, 22273	809	6	13588	1.E+01	1.E+00	6.E-02	6.E+00
GOTERM_BP_FAT	GO:0043551~regulation of phosphoinositide 3-kinase activity	4	0.455580866	4.E-03 18048, 16367, 57257, 12540	809	6	13588	1.E+01	1.E+00	6.E-02	6.E+00
GOTERM_BP_FAT	GO:0042159~lipoprotein catabolic process	4	0.455580866	4.E-03 11816, 11920, 12491, 238055	809	6	13588	1.E+01	1.E+00	6.E-02	6.E+00
GOTERM_BP_FAT	GO:0043552~positive regulation of phosphoinositide 3-kinase act	4	0.455580866	4.E-03 18048, 16367, 57257, 12540	809	6	13588	1.E+01	1.E+00	6.E-02	6.E+00
GOTERM_BP_FAT	GO:0050730~regulation of peptidyl-tyrosine phosphorylation	10	1.138952164	4.E-03 56717, 18596, 15170, 13649, 12703, 1841	809	53	13588	3.E+00	1.E+00	6.E-02	6.E+00
GOTERM_BP_FAT	GO:0031098~stress-activated protein kinase signaling pathway	8	0.911161731	4.E-03 17874, 57874, 16334, 74155, 117149, 209	809	35	13588	4.E+00	1.E+00	6.E-02	7.E+00
GOTERM_BP_FAT	GO:0002274~myeloid leukocyte activation	8	0.911161731	4.E-03 23880, 14127, 21898, 20375, 74734, 1682	809	35	13588	4.E+00	1.E+00	6.E-02	7.E+00
GOTERM_BP_FAT	GO:0046486~glycerolipid metabolic process	17	1.936218679	4.E-03 11814, 276846, 329777, 18534, 238055, 1	809	129	13588	2.E+00	1.E+00	6.E-02	7.E+00
GOTERM_BP_FAT	GO:0002758~innate immune response-activating signal transduct	5	0.569476082	4.E-03 17874, 16179, 27007, 24088, 106759	809	12	13588	7.E+00	1.E+00	6.E-02	7.E+00
GOTERM_BP_FAT	GO:0051384~response to glucocorticoid stimulus	6	0.683371298	4.E-03 12039, 11409, 109900, 26395, 12043, 230	809	19	13588	5.E+00	1.E+00	6.E-02	7.E+00
GOTERM_BP_FAT	GO:0045087~innate immune response	15	1.708428246	4.E-03 15170, 239081, 21899, 21898, 16803, 178	809	107	13588	2.E+00	1.E+00	6.E-02	8.E+00
GOTERM_BP_FAT	GO:0030595~leukocyte chemotaxis	7	0.797266515	4.E-03 20310, 14127, 56744, 16414, 20202, 1680	809	27	13588	4.E+00	1.E+00	6.E-02	8.E+00
GOTERM_BP_FAT	GO:0060326~cell chemotaxis	7	0.797266515	4.E-03 20310, 14127, 56744, 16414, 20202, 1680	809	27	13588	4.E+00	1.E+00	6.E-02	8.E+00
GOTERM_BP_FAT	GO:0019725~cellular homeostasis	34	3.872437358	4.E-03 11816, 14782, 20191, 103988, 214952, 16	809	343	13588	2.E+00	1.E+00	6.E-02	8.E+00
GOTERM_BP_FAT	GO:0045089~positive regulation of innate immune response	8	0.911161731	5.E-03 19370, 17874, 16179, 21898, 27007, 3790	809	36	13588	4.E+00	1.E+00	7.E-02	8.E+00
GOTERM_BP_FAT	GO:0022604~regulation of cell morphogenesis	14	1.59453303	5.E-03 14163, 14674, 232906, 76117, 21844, 102	809	97	13588	2.E+00	1.E+00	7.E-02	8.E+00
GOTERM_BP_FAT	GO:0006979~response to oxidative stress	13	1.480637813	5.E-03 382985, 226646, 12842, 56338, 11816, 12	809	87	13588	3.E+00	1.E+00	7.E-02	9.E+00
GOTERM_BP_FAT	GO:0008286~insulin receptor signaling pathway	7	0.797266515	5.E-03 18709, 18708, 13685, 16367, 16334, 1165	809	28	13588	4.E+00	1.E+00	7.E-02	9.E+00
GOTERM_BP_FAT	GO:0000082~G1/S transition of mitotic cell cycle	7	0.797266515	5.E-03 104394, 19645, 13559, 12443, 12043, 164	809	28	13588	4.E+00	1.E+00	7.E-02	9.E+00
GOTERM_BP_FAT	GO:0019362~pyridine nucleotide metabolic process	7	0.797266515	5.E-03 17970, 21991, 21351, 17969, 66171, 1039	809	28	13588	4.E+00	1.E+00	7.E-02	9.E+00
GOTERM_BP_FAT	GO:0006094~gluconeogenesis	6	0.683371298	5.E-03 14751, 18534, 21991, 230163, 18563, 745	809	20	13588	5.E+00	1.E+00	8.E-02	9.E+00
GOTERM_BP_FAT	GO:0044242~cellular lipid catabolic process	10	1.138952164	5.E-03 18783, 18803, 11814, 669888, 74147, 234	809	56	13588	3.E+00	1.E+00	8.E-02	9.E+00
GOTERM_BP_FAT	GO:0019221~cytokine-mediated signaling pathway	10	1.138952164	5.E-03 15170, 17874, 16195, 12703, 12983, 1201	809	56	13588	3.E+00	1.E+00	8.E-02	9.E+00
GOTERM_BP_FAT	GO:0046165~alcohol biosynthetic process	8	0.911161731	6.E-03 14751, 234779, 18534, 21991, 230163, 18	809	37	13588	4.E+00	1.E+00	8.E-02	9.E+00
GOTERM_BP_FAT	GO:0030335~positive regulation of cell migration	8	0.911161731	6.E-03 18708, 16367, 73167, 12043, 11855, 2033	809	37	13588	4.E+00	1.E+00	8.E-02	9.E+00
GOTERM_BP_FAT	GO:0006955~immune response	43	4.897494305	6.E-03 14972, 12475, 22324, 15018, 16803, 1201	809	471	13588	2.E+00	1.E+00	8.E-02	1.E+01
GOTERM_BP_FAT	GO:0007257~activation of JUN kinase activity	5	0.569476082	6.E-03 16334, 117149, 20963, 16543, 224014	809	13	13588	6.E+00	1.E+00	8.E-02	1.E+01
GOTERM_BP_FAT	GO:0031349~positive regulation of defense response	10	1.138952164	6.E-03 19370, 14127, 17874, 16179, 21898, 2700	809	57	13588	3.E+00	1.E+00	8.E-02	1.E+01
GOTERM_BP_FAT	GO:0002224~toll-like receptor signaling pathway	4	0.455580866	6.E-03 17874, 16179, 24088, 106759	809	7	13588	1.E+01	1.E+00	8.E-02	1.E+01
GOTERM_BP_FAT	GO:0016331~morphogenesis of embryonic epithelium	12	1.366742597	6.E-03 22323, 13800, 16911, 232906, 19206, 197	809	78	13588	3.E+00	1.E+00	8.E-02	1.E+01
GOTERM_BP_FAT	GO:0006281~DNA repair	24	2.733485194	7.E-03 382985, 12190, 80905, 11546, 245000, 12	809	222	13588	2.E+00	1.E+00	9.E-02	1.E+01
GOTERM_BP_FAT	GO:0009967~positive regulation of signal transduction	20	2.277904328	7.E-03 21899, 21898, 14180, 56847, 15163, 1184	809	172	13588	2.E+00	1.E+00	9.E-02	1.E+01
GOTERM_BP_FAT	GO:0060537~muscle tissue development	17	1.936218679	7.E-03 15430, 18479, 16412, 13383, 20467, 1136	809	136	13588	2.E+00	1.E+00	9.E-02	1.E+01
GOTERM_BP_FAT	GO:0045017~glycerolipid biosynthetic process	10	1.138952164	7.E-03 14731, 56703, 276846, 13350, 19012, 329	809	58	13588	3.E+00	1.E+00	9.E-02	1.E+01



GOTERM_BP_FAT	GO:0051098--regulation of binding	13	1.480637813	7.E-03 245000, 21898, 17869, 16414, 12914, 178	809	90	13588	2.E+00	1.E+00	9.E-02	1.E+01
GOTERM_BP_FAT	GO:0007507--heart development	24	2.733485194	7.E-03 12831, 19206, 19378, 16412, 20416, 2046	809	223	13588	2.E+00	1.E+00	9.E-02	1.E+01
GOTERM_BP_FAT	GO:0032535--regulation of cellular component size	19	2.164009112	7.E-03 227753, 104394, 67184, 68349, 11651, 12	809	161	13588	2.E+00	1.E+00	9.E-02	1.E+01
GOTERM_BP_FAT	GO:0010604--positive regulation of macromolecule metabolic pro	54	6.150341686	7.E-03 22130, 21869, 12912, 12914, 16543, 2193	809	633	13588	1.E+00	1.E+00	9.E-02	1.E+01
GOTERM_BP_FAT	GO:0019748--secondary metabolic process	11	1.25284738	7.E-03 17970, 19378, 12043, 21991, 21351, 5684	809	69	13588	3.E+00	1.E+00	9.E-02	1.E+01
GOTERM_BP_FAT	GO:0006506--GPI anchor biosynthetic process	7	0.797266515	8.E-03 14731, 56703, 276846, 329777, 18701, 22	809	30	13588	4.E+00	1.E+00	1.E-01	1.E+01
GOTERM_BP_FAT	GO:0002260--lymphocyte homeostasis	7	0.797266515	8.E-03 12442, 12028, 12018, 11651, 12043, 1905	809	30	13588	4.E+00	1.E+00	1.E-01	1.E+01
GOTERM_BP_FAT	GO:0001910--regulation of leukocyte mediated cytotoxicity	7	0.797266515	8.E-03 19370, 14972, 15018, 16197, 27007, 3790	809	30	13588	4.E+00	1.E+00	1.E-01	1.E+01
GOTERM_BP_FAT	GO:0031341--regulation of cell killing	7	0.797266515	8.E-03 19370, 14972, 15018, 16197, 27007, 3790	809	30	13588	4.E+00	1.E+00	1.E-01	1.E+01
GOTERM_BP_FAT	GO:0000165--MAPKKK cascade	15	1.708428246	8.E-03 14678, 20416, 224014, 16543, 17873, 178	809	114	13588	2.E+00	1.E+00	1.E-01	1.E+01
GOTERM_BP_FAT	GO:0043406--positive regulation of MAP kinase activity	10	1.138952164	8.E-03 16179, 16334, 21899, 26395, 19164, 2041	809	59	13588	3.E+00	1.E+00	1.E-01	1.E+01
GOTERM_BP_FAT	GO:0002286--T cell activation during immune response	5	0.569476082	8.E-03 12051, 18826, 19164, 11891, 23882	809	14	13588	6.E+00	1.E+00	1.E-01	1.E+01
GOTERM_BP_FAT	GO:0002252--immune effector process	16	1.822323462	8.E-03 15170, 15018, 108138, 13035, 16803, 133	809	126	13588	2.E+00	1.E+00	1.E-01	1.E+01
GOTERM_BP_FAT	GO:0030334--regulation of cell migration	13	1.480637813	8.E-03 14674, 73167, 12043, 11855, 384783, 187	809	92	13588	2.E+00	1.E+00	1.E-01	1.E+01
GOTERM_BP_FAT	GO:0048598--embryonic morphogenesis	34	3.872437358	9.E-03 22323, 18747, 232906, 19206, 15376, 178	809	359	13588	2.E+00	1.E+00	1.E-01	1.E+01
GOTERM_BP_FAT	GO:0046364--monosaccharide biosynthetic process	7	0.797266515	9.E-03 14751, 18534, 21991, 230163, 18563, 143	809	31	13588	4.E+00	1.E+00	1.E-01	1.E+01
GOTERM_BP_FAT	GO:0046489--phosphoinositide biosynthetic process	7	0.797266515	9.E-03 14731, 56703, 276846, 329777, 18701, 22	809	31	13588	4.E+00	1.E+00	1.E-01	1.E+01
GOTERM_BP_FAT	GO:0046902--regulation of mitochondrial membrane permeability	4	0.455580866	9.E-03 12028, 12122, 12018, 12043	809	8	13588	8.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0051272--positive regulation of cell motion	8	0.911161731	1.E-02 18708, 16367, 73167, 12043, 11855, 2033	809	41	13588	3.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0016051--carbohydrate biosynthetic process	12	1.366742597	1.E-02 18682, 14751, 234779, 18534, 11651, 219	809	83	13588	2.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0006469--negative regulation of protein kinase activity	9	1.025056948	1.E-02 17873, 15170, 19645, 24064, 13197, 1916	809	51	13588	3.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0033673--negative regulation of kinase activity	9	1.025056948	1.E-02 17873, 15170, 19645, 24064, 13197, 1916	809	51	13588	3.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0045576--mast cell activation	5	0.569476082	1.E-02 23880, 14127, 21898, 74734, 16822	809	15	13588	6.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0050830--defense response to Gram-positive bacterium	6	0.683371298	1.E-02 17874, 14191, 13035, 17969, 24088, 1680	809	23	13588	4.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0019835--cytolysis	6	0.683371298	1.E-02 14939, 14941, 230558, 14940, 14944, 149	809	23	13588	4.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0051654--establishment of mitochondrion localization	3	0.341685649	1.E-02 59040, 16561, 214952	809	3	13588	2.E+01	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0010882--regulation of cardiac muscle contraction by calcium	3	0.341685649	1.E-02 14226, 20191, 208727	809	3	13588	2.E+01	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0047497--mitochondrion transport along microtubule	3	0.341685649	1.E-02 59040, 16561, 214952	809	3	13588	2.E+01	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0034643--mitochondrion localization, microtubule-mediated	3	0.341685649	1.E-02 59040, 16561, 214952	809	3	13588	2.E+01	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0006505--GPI anchor metabolic process	7	0.797266515	1.E-02 14731, 56703, 276846, 329777, 18701, 22	809	32	13588	4.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0007254--JNK cascade	7	0.797266515	1.E-02 17874, 57874, 16334, 117149, 20963, 165	809	32	13588	4.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0045454--cell redox homeostasis	10	1.138952164	1.E-02 18453, 12304, 93692, 26462, 50493, 1482	809	62	13588	3.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0043405--regulation of MAP kinase activity	12	1.366742597	1.E-02 15170, 24064, 16179, 16334, 21899, 2639	809	84	13588	2.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0051270--regulation of cell motion	14	1.59453303	1.E-02 14674, 73167, 12043, 11855, 384783, 187	809	107	13588	2.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0042108--positive regulation of cytokine biosynthetic process	8	0.911161731	1.E-02 12051, 16994, 17874, 11807, 21899, 2189	809	42	13588	3.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0032386--regulation of intracellular transport	8	0.911161731	1.E-02 18747, 18826, 14226, 68092, 192176, 125	809	42	13588	3.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0043388--positive regulation of DNA binding	8	0.911161731	1.E-02 17874, 16179, 12315, 12314, 12313, 2189	809	42	13588	3.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0008361--regulation of cell size	14	1.59453303	1.E-02 104394, 67184, 68349, 12043, 11651, 118	809	108	13588	2.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0030384--phosphoinositide metabolic process	10	1.138952164	1.E-02 18708, 14731, 56703, 276846, 329777, 30	809	63	13588	3.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0051050--positive regulation of transport	16	1.822323462	1.E-02 18747, 68092, 11651, 12912, 103988, 169	809	132	13588	2.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0051348--negative regulation of transferase activity	9	1.025056948	1.E-02 17873, 15170, 19645, 24064, 13197, 1916	809	53	13588	3.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0045792--negative regulation of cell size	9	1.025056948	1.E-02 11785, 56717, 67184, 72269, 68349, 1165	809	53	13588	3.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0051247--positive regulation of protein metabolic process	14	1.59453303	1.E-02 17999, 12043, 11651, 16396, 216080, 151	809	109	13588	2.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0031328--positive regulation of cellular biosynthetic process	47	5.353075171	1.E-02 17536, 22130, 15376, 17869, 12912, 2186	809	552	13588	1.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0006525--arginine metabolic process	4	0.455580866	1.E-02 18126, 18416, 109900, 11847	809	9	13588	7.E+00	1.E+00	2.E-01	2.E+01
GOTERM_BP_FAT	GO:0051640--organelle localization	9	1.025056948	1.E-02 245049, 77579, 19164, 12540, 11891, 171	809	54	13588	3.E+00	1.E+00	2.E-01	2.E+01
GOTERM_BP_FAT	GO:0001838--embryonic epithelial tube formation	9	1.025056948	1.E-02 22323, 13800, 16911, 232906, 19206, 197	809	54	13588	3.E+00	1.E+00	2.E-01	2.E+01
GOTERM_BP_FAT	GO:0051924--regulation of calcium ion transport	7	0.797266515	1.E-02 234779, 14226, 14678, 12028, 12018, 120	809	34	13588	3.E+00	1.E+00	2.E-01	2.E+01
GOTERM_BP_FAT	GO:0051091--positive regulation of transcription factor activity	7	0.797266515	1.E-02 17874, 16179, 21898, 16414, 24088, 1067	809	34	13588	3.E+00	1.E+00	2.E-01	2.E+01
GOTERM_BP_FAT	GO:0051656--establishment of organelle localization	7	0.797266515	1.E-02 77579, 19164, 12540, 11891, 59040, 1656	809	34	13588	3.E+00	1.E+00	2.E-01	2.E+01
GOTERM_BP_FAT	GO:0048514--blood vessel morphogenesis	21	2.391799544	1.E-02 19317, 14674, 11852, 11816, 238055, 141	809	198	13588	2.E+00	1.E+00	2.E-01	2.E+01
GOTERM_BP_FAT	GO:0002696--positive regulation of leukocyte activation	13	1.480637813	1.E-02 19370, 21898, 16408, 16818, 17874, 1412	809	99	13588	2.E+00	1.E+00	2.E-01	2.E+01
GOTERM_BP_FAT	GO:0040017--positive regulation of locomotion	8	0.911161731	1.E-02 18708, 16367, 73167, 12043, 11855, 2033	809	44	13588	3.E+00	1.E+00	2.E-01	2.E+01
GOTERM_BP_FAT	GO:0019319--hexose biosynthetic process	6	0.683371298	1.E-02 14751, 18534, 21991, 230163, 18563, 745	809	25	13588	4.E+00	1.E+00	2.E-01	2.E+01
GOTERM_BP_FAT	GO:0008624--induction of apoptosis by extracellular signals	6	0.683371298	1.E-02 12015, 67184, 14939, 12028, 26885, 1067	809	25	13588	4.E+00	1.E+00	2.E-01	2.E+01
GOTERM_BP_FAT	GO:0031032--actomyosin structure organization	6	0.683371298	1.E-02 26934, 77579, 11464, 71994, 16412, 1145	809	25	13588	4.E+00	1.E+00	2.E-01	2.E+01
GOTERM_BP_FAT	GO:0051092--positive regulation of NF-kappaB transcription facto	6	0.683371298	1.E-02 17874, 16179, 21898, 16414, 24088, 1067	809	25	13588	4.E+00	1.E+00	2.E-01	2.E+01
GOTERM_BP_FAT	GO:0009891--positive regulation of biosynthetic process	47	5.353075171	1.E-02 17536, 22130, 15376, 17869, 12912, 2186	809	557	13588	1.E+00	1.E+00	2.E-01	2.E+01
GOTERM_BP_FAT	GO:0010648--negative regulation of cell communication	20	2.277904328	1.E-02 15170, 69121, 380714, 66042, 14678, 141	809	186	13588	2.E+00	1.E+00	2.E-01	2.E+01
GOTERM_BP_FAT	GO:0002697--regulation of immune effector process	12	1.366742597	1.E-02 19370, 15170, 14972, 15018, 27007, 1680	809	88	13588	2.E+00	1.E+00	2.E-01	2.E+01
GOTERM_BP_FAT	GO:0048599--oocyte development	5	0.569476082	2.E-02 12190, 12043, 12531, 20112, 67141	809	17	13588	5.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0010332--response to gamma radiation	5	0.569476082	2.E-02 12190, 12028, 12018, 12043, 108138	809	17	13588	5.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0002474--antigen processing and presentation of peptide ant	5	0.569476082	2.E-02 15007, 14972, 14127, 15018, 12010	809	17	13588	5.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0009156--ribonucleoside monophosphate biosynthetic proces	5	0.569476082	2.E-02 11486, 56749, 11717, 11566, 99586	809	17	13588	5.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0008629--induction of apoptosis by intracellular signals	7	0.797266515	2.E-02 12051, 12190, 66593, 11920, 12028, 1786	809	35	13588	3.E+00	1.E+00	2.E-01	3.E+01



GOTERM_BP_FAT	GO:0051099~positive regulation of binding	8	0.911161731	2E-02 17874, 16179, 12315, 12314, 12313, 2189	809	45	13588	3E+00	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0002443~leukocyte mediated immunity	12	1.366742597	2E-02 12051, 14127, 15170, 17874, 230558, 118	809	89	13588	2E+00	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0016477~cell migration	24	2.733485194	2E-02 117600, 13649, 11806, 16414, 57257, 187	809	240	13588	2E+00	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0050867~positive regulation of cell activation	13	1.480637813	2E-02 19370, 21898, 16408, 16818, 17874, 1412	809	101	13588	2E+00	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0002819~regulation of adaptive immune response	9	1.025056948	2E-02 14972, 14127, 15170, 15018, 16197, 1148	809	56	13588	3E+00	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0002822~regulation of adaptive immune response based on :	9	1.025056948	2E-02 14972, 14127, 15170, 15018, 16197, 1148	809	56	13588	3E+00	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0010647~positive regulation of cell communication	20	2.277904328	2E-02 21899, 21898, 14180, 56847, 15163, 1184	809	189	13588	2E+00	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0032880~regulation of protein localization	12	1.366742597	2E-02 16994, 18747, 18826, 14570, 104215, 192	809	90	13588	2E+00	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0045088~regulation of innate immune response	8	0.911161731	2E-02 19370, 17874, 16179, 21898, 27007, 3790	809	46	13588	3E+00	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0002699~positive regulation of immune effector process	8	0.911161731	2E-02 19370, 14972, 14127, 15018, 27007, 3790	809	46	13588	3E+00	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0001817~regulation of cytokine production	16	1.822323462	2E-02 19370, 12475, 15018, 11807, 21899, 2700	809	139	13588	2E+00	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0040008~regulation of growth	25	2.84738041	2E-02 67184, 19206, 11816, 20416, 22193, 1291	809	256	13588	2E+00	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0050851~antigen receptor-mediated signaling pathway	7	0.797266515	2E-02 15170, 18803, 16818, 234779, 19164, 209	809	36	13588	3E+00	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0001556~oocyte maturation	4	0.455580866	2E-02 12190, 12531, 20112, 67141	809	10	13588	7E+00	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0002221~pattern recognition receptor signaling pathway	4	0.455580866	2E-02 17874, 16179, 24088, 106759	809	10	13588	7E+00	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0046626~regulation of insulin receptor signaling pathway	4	0.455580866	2E-02 12703, 20779, 12702, 11625	809	10	13588	7E+00	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0014706~striated muscle tissue development	15	1.708428246	2E-02 15430, 18479, 16412, 20467, 11364, 1184	809	127	13588	2E+00	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0042770~DNA damage response, signal transduction	9	1.025056948	2E-02 12051, 12190, 245000, 11920, 26416, 126	809	57	13588	3E+00	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0048870~cell motility	27	3.075170843	2E-02 117600, 13649, 238055, 18792, 21869, 16	809	284	13588	2E+00	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0051674~localization of cell	27	3.075170843	2E-02 117600, 13649, 238055, 18792, 21869, 16	809	284	13588	2E+00	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0006928~cell motion	33	3.758542141	2E-02 117600, 22323, 13649, 11658, 238055, 18	809	367	13588	2E+00	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0043029~T cell homeostasis	5	0.569476082	2E-02 12442, 12028, 11651, 12043, 19056	809	18	13588	5E+00	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0009994~oocyte differentiation	5	0.569476082	2E-02 12190, 12043, 12531, 20112, 67141	809	18	13588	5E+00	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0060674~placenta blood vessel development	5	0.569476082	2E-02 12702, 18815, 26395, 11651, 16477	809	18	13588	5E+00	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0002709~regulation of T cell mediated immunity	5	0.569476082	2E-02 14972, 15018, 16197, 19056, 12010	809	18	13588	5E+00	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0032755~positive regulation of interleukin-6 production	5	0.569476082	2E-02 14127, 17874, 21898, 24088, 106759	809	18	13588	5E+00	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0030300~regulation of intestinal cholesterol absorption	3	0.341685649	2E-02 11806, 11807, 11808	809	4	13588	1E+01	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0000089~mitotic metaphase	3	0.341685649	2E-02 67052, 20112, 67141	809	4	13588	1E+01	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0070059~apoptosis in response to endoplasmic reticulum str	3	0.341685649	2E-02 12028, 12018, 12043	809	4	13588	1E+01	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0050670~regulation of lymphocyte proliferation	11	1.25284738	2E-02 16408, 15170, 17874, 246779, 11486, 218	809	80	13588	2E+00	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0032944~regulation of mononuclear cell proliferation	11	1.25284738	2E-02 16408, 15170, 17874, 246779, 11486, 218	809	80	13588	2E+00	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0042326~negative regulation of phosphorylation	6	0.683371298	2E-02 15170, 12703, 12028, 12018, 19164, 2023	809	27	13588	4E+00	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0000910~cytokinesis	6	0.683371298	2E-02 12190, 26934, 77579, 20877, 233406, 192	809	27	13588	4E+00	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0002694~regulation of leukocyte activation	17	1.936218679	2E-02 19370, 15170, 21898, 16396, 13383, 1640	809	154	13588	2E+00	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0030900~forebrain development	18	2.050113895	2E-02 13649, 232906, 433759, 19378, 56847, 14	809	167	13588	2E+00	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0030031~cell projection assembly	10	1.138952164	2E-02 19354, 104394, 77579, 30938, 57257, 125	809	70	13588	2E+00	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0002703~regulation of leukocyte mediated immunity	10	1.138952164	2E-02 19370, 14972, 14127, 15170, 15018, 1619	809	70	13588	2E+00	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0048608~reproductive structure development	15	1.708428246	2E-02 12190, 12043, 14180, 13383, 21869, 2077	809	130	13588	2E+00	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0018904~organic ether metabolic process	8	0.911161731	2E-02 17777, 11814, 669888, 13350, 19012, 185	809	48	13588	3E+00	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0035148~tube lumen formation	9	1.025056948	2E-02 22323, 13800, 16911, 232906, 19206, 197	809	59	13588	3E+00	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0009314~response to radiation	16	1.822323462	2E-02 12190, 14151, 232087, 17869, 12043, 108	809	143	13588	2E+00	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0055007~cardiac muscle cell differentiation	6	0.683371298	2E-02 77579, 14465, 11464, 16412, 11364, 1420	809	28	13588	4E+00	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0070663~regulation of leukocyte proliferation	11	1.25284738	2E-02 16408, 15170, 17874, 246779, 11486, 218	809	82	13588	2E+00	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0050865~regulation of cell activation	17	1.936218679	2E-02 19370, 15170, 21898, 16396, 13383, 1640	809	156	13588	2E+00	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0051251~positive regulation of lymphocyte activation	12	1.366742597	2E-02 19370, 21898, 16408, 16818, 17874, 1201	809	94	13588	2E+00	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0006733~oxidoreduction coenzyme metabolic process	7	0.797266515	2E-02 17970, 21991, 21351, 17969, 66171, 1039	809	38	13588	3E+00	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0031400~negative regulation of protein modification process	7	0.797266515	2E-02 15170, 12703, 12028, 12018, 19164, 1256	809	38	13588	3E+00	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0043525~positive regulation of neuron apoptosis	5	0.569476082	2E-02 16994, 11920, 12028, 14815, 12568	809	19	13588	4E+00	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0009161~ribonucleoside monophosphate metabolic process	5	0.569476082	2E-02 11486, 56749, 11717, 11566, 99586	809	19	13588	4E+00	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0046632~alpha-beta T cell differentiation	5	0.569476082	2E-02 12051, 19934, 12043, 20963, 100047372,	809	19	13588	4E+00	1E+00	2E-01	3E+01
GOTERM_BP_FAT	GO:0032494~response to peptidoglycan	4	0.455580866	2E-02 17874, 16179, 26416, 24088	809	11	13588	6E+00	1E+00	2E-01	4E+01
GOTERM_BP_FAT	GO:0009250~glucan biosynthetic process	4	0.455580866	2E-02 18682, 11651, 27357, 77559	809	11	13588	6E+00	1E+00	2E-01	4E+01
GOTERM_BP_FAT	GO:0043393~regulation of protein binding	4	0.455580866	2E-02 245000, 19164, 17869, 106759	809	11	13588	6E+00	1E+00	2E-01	4E+01
GOTERM_BP_FAT	GO:0033135~regulation of peptidyl-serine phosphorylation	4	0.455580866	2E-02 12028, 12018, 18413, 12043	809	11	13588	6E+00	1E+00	2E-01	4E+01
GOTERM_BP_FAT	GO:0006268~DNA unwinding during replication	4	0.455580866	2E-02 17217, 17220, 17216, 17219	809	11	13588	6E+00	1E+00	2E-01	4E+01
GOTERM_BP_FAT	GO:0051591~response to cAMP	4	0.455580866	2E-02 12039, 12842, 109900, 232087	809	11	13588	6E+00	1E+00	2E-01	4E+01
GOTERM_BP_FAT	GO:0007090~regulation of S phase of mitotic cell cycle	4	0.455580866	2E-02 11785, 12190, 67177, 27214	809	11	13588	6E+00	1E+00	2E-01	4E+01
GOTERM_BP_FAT	GO:0005978~glycogen biosynthetic process	4	0.455580866	2E-02 18682, 11651, 27357, 77559	809	11	13588	6E+00	1E+00	2E-01	4E+01
GOTERM_BP_FAT	GO:0045926~negative regulation of growth	10	1.138952164	2E-02 11785, 17874, 67184, 19206, 72269, 6834	809	71	13588	2E+00	1E+00	2E-01	4E+01
GOTERM_BP_FAT	GO:0051249~regulation of lymphocyte activation	16	1.822323462	2E-02 19370, 15170, 21898, 16396, 13383, 1640	809	144	13588	2E+00	1E+00	2E-01	4E+01
GOTERM_BP_FAT	GO:0048545~response to steroid hormone stimulus	9	1.025056948	2E-02 12039, 20779, 12842, 11409, 109900, 263	809	60	13588	3E+00	1E+00	2E-01	4E+01
GOTERM_BP_FAT	GO:0021915~neural tube development	11	1.25284738	2E-02 22323, 13836, 13800, 16911, 232906, 192	809	83	13588	2E+00	1E+00	2E-01	4E+01
GOTERM_BP_FAT	GO:0006631~fatty acid metabolic process	19	2.164009112	3E-02 70316, 66885, 19317, 15107, 11807, 1908	809	184	13588	2E+00	1E+00	2E-01	4E+01
GOTERM_BP_FAT	GO:0009968~negative regulation of signal transduction	18	2.050113895	3E-02 15170, 69121, 380714, 66042, 14180, 202	809	171	13588	2E+00	1E+00	2E-01	4E+01
GOTERM_BP_FAT	GO:0009628~response to abiotic stimulus	24	2.733485194	3E-02 12190, 14151, 12842, 12955, 232087, 178	809	251	13588	2E+00	1E+00	2E-01	4E+01



GOTERM_BP_FAT	GO:0021537~telencephalon development	10	1.138952164	3.E-02 13649, 77579, 433759, 12028, 19164, 148	809	72	13588	2.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0051051~negative regulation of transport	10	1.138952164	3.E-02 16994, 11486, 17999, 14678, 104215, 184	809	72	13588	2.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0001843~neural tube closure	7	0.797266515	3.E-02 22323, 13800, 16911, 232906, 19206, 507	809	39	13588	3.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0060606~tube closure	7	0.797266515	3.E-02 22323, 13800, 16911, 232906, 19206, 507	809	39	13588	3.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0001776~leukocyte homeostasis	7	0.797266515	3.E-02 12442, 12028, 12018, 11651, 12043, 1905	809	39	13588	3.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0009119~ribonucleoside metabolic process	7	0.797266515	3.E-02 22017, 11486, 72269, 232087, 56749, 222	809	39	13588	3.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0045936~negative regulation of phosphate metabolic process	6	0.683371298	3.E-02 15170, 12703, 12028, 12018, 19164, 2023	809	29	13588	3.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0010563~negative regulation of phosphorus metabolic process	6	0.683371298	3.E-02 15170, 12703, 12028, 12018, 19164, 2023	809	29	13588	3.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0009991~response to extracellular stimulus	15	1.708428246	3.E-02 12190, 12842, 109900, 12043, 100040331	809	133	13588	2.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0002460~adaptive immune response based on somatic recombination	11	1.25284738	3.E-02 12051, 14127, 17874, 21899, 230558, 118	809	84	13588	2.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0002250~adaptive immune response	11	1.25284738	3.E-02 12051, 14127, 17874, 21899, 230558, 118	809	84	13588	2.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0022612~gland morphogenesis	11	1.25284738	3.E-02 13649, 20779, 14178, 19206, 12043, 1481	809	84	13588	2.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0006954~inflammatory response	22	2.505694761	3.E-02 12475, 239081, 21899, 21898, 11651, 164	809	225	13588	2.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0009894~regulation of catabolic process	8	0.911161731	3.E-02 56717, 17999, 14447, 282663, 11651, 192	809	50	13588	3.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0051053~negative regulation of DNA metabolic process	5	0.569476082	3.E-02 12190, 57441, 22130, 67177, 269582	809	20	13588	4.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0042743~hydrogen peroxide metabolic process	5	0.569476082	3.E-02 672195, 50493, 13063, 13077, 17969, 130	809	20	13588	4.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0042593~glucose homeostasis	7	0.797266515	3.E-02 12015, 19206, 380714, 18609, 231103, 18	809	40	13588	3.E+00	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0033500~carbohydrate homeostasis	7	0.797266515	3.E-02 12015, 19206, 380714, 18609, 231103, 18	809	40	13588	3.E+00	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0040012~regulation of locomotion	13	1.480637813	3.E-02 14674, 73167, 12043, 11855, 384783, 187	809	110	13588	2.E+00	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0060341~regulation of cellular localization	17	1.936218679	3.E-02 18747, 380714, 14226, 68092, 20191, 129	809	161	13588	2.E+00	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0001841~neural tube formation	8	0.911161731	3.E-02 22323, 13800, 16911, 232906, 19206, 507	809	51	13588	3.E+00	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0000077~DNA damage checkpoint	6	0.683371298	3.E-02 245000, 11920, 26416, 12649, 12443, 125	809	30	13588	3.E+00	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0043279~response to alkaloid	6	0.683371298	3.E-02 12043, 17869, 12568, 16847, 20191, 1338	809	30	13588	3.E+00	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0001909~leukocyte mediated cytotoxicity	4	0.455580866	3.E-02 15170, 11891, 13035, 17969	809	12	13588	6.E+00	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0002244~hemopoietic progenitor cell differentiation	4	0.455580866	3.E-02 19164, 20375, 12043, 108138	809	12	13588	6.E+00	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0033261~regulation of S phase	4	0.455580866	3.E-02 11785, 12190, 67177, 27214	809	12	13588	6.E+00	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0070227~lymphocyte apoptosis	4	0.455580866	3.E-02 12028, 12018, 11651, 17869	809	12	13588	6.E+00	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0032508~DNA duplex unwinding	4	0.455580866	3.E-02 17217, 17220, 17216, 17219	809	12	13588	6.E+00	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0031663~lipopolysaccharide-mediated signaling pathway	4	0.455580866	3.E-02 17874, 16179, 26416, 106759	809	12	13588	6.E+00	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0051101~regulation of DNA binding	10	1.138952164	3.E-02 17874, 16179, 12315, 12314, 12313, 2189	809	74	13588	2.E+00	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0051279~regulation of release of sequestered calcium ion into cytosol	3	0.341685649	3.E-02 14226, 12028, 20191	809	5	13588	1.E+01	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0032374~regulation of cholesterol transport	3	0.341685649	3.E-02 11806, 11807, 11808	809	5	13588	1.E+01	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0008635~activation of caspase activity by cytochrome c	3	0.341685649	3.E-02 672195, 12028, 12018, 13063	809	5	13588	1.E+01	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0002312~B cell activation during immune response	3	0.341685649	3.E-02 12051, 11486, 234779	809	5	13588	1.E+01	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0002313~mature B cell differentiation during immune response	3	0.341685649	3.E-02 12051, 11486, 234779	809	5	13588	1.E+01	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0032371~regulation of sterol transport	3	0.341685649	3.E-02 11806, 11807, 11808	809	5	13588	1.E+01	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0007517~muscle organ development	18	2.050113895	3.E-02 12955, 15430, 18479, 16412, 13383, 2046	809	176	13588	2.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0001501~skeletal system development	26	2.961275626	3.E-02 69121, 17869, 21934, 12815, 15402, 1859	809	285	13588	2.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0043069~negative regulation of programmed cell death	23	2.619589977	3.E-02 13628, 11651, 17869, 12043, 108138, 204	809	244	13588	2.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0042060~wound healing	13	1.480637813	3.E-02 14674, 18793, 14026, 14060, 14432, 5674	809	112	13588	2.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0010557~positive regulation of macromolecule biosynthetic process	43	4.897494305	3.E-02 17536, 22130, 15376, 17869, 21869, 1291	809	530	13588	1.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0001763~morphogenesis of a branching structure	14	1.59453303	3.E-02 14674, 14178, 15376, 12043, 13383, 1223	809	125	13588	2.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0032270~positive regulation of cellular protein metabolic process	12	1.366742597	4.E-02 56717, 18413, 12567, 19164, 11651, 1204	809	100	13588	2.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0042035~regulation of cytokine biosynthetic process	9	1.025056948	4.E-02 12051, 16994, 17874, 11807, 21899, 2189	809	64	13588	2.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0060548~negative regulation of cell death	23	2.619589977	4.E-02 13628, 11651, 17869, 12043, 108138, 204	809	245	13588	2.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0002449~lymphocyte mediated immunity	10	1.138952164	4.E-02 12051, 14127, 15170, 17874, 230558, 118	809	76	13588	2.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0014020~primary neural tube formation	7	0.797266515	4.E-02 22323, 13800, 16911, 232906, 19206, 507	809	42	13588	3.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0021700~developmental maturation	12	1.366742597	4.E-02 12190, 108672, 12229, 19713, 19164, 116	809	101	13588	2.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0002706~regulation of lymphocyte mediated immunity	9	1.025056948	4.E-02 19370, 14972, 14127, 15170, 15018, 1619	809	65	13588	2.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0043547~positive regulation of GTPase activity	4	0.455580866	4.E-02 71709, 11856, 19765, 19417	809	13	13588	5.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0032392~DNA geometric change	4	0.455580866	4.E-02 17217, 17220, 17216, 17219	809	13	13588	5.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0008154~actin polymerization or depolymerization	4	0.455580866	4.E-02 227753, 13800, 14026, 22376	809	13	13588	5.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0032675~regulation of interleukin-6 production	6	0.683371298	4.E-02 14127, 17874, 21899, 21898, 24088, 1067	809	32	13588	3.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0045582~positive regulation of T cell differentiation	6	0.683371298	4.E-02 16818, 12015, 16197, 11486, 16190, 2096	809	32	13588	3.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0006639~acylglycerol metabolic process	7	0.797266515	4.E-02 17777, 11814, 669888, 13350, 19012, 185	809	43	13588	3.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0031667~response to nutrient levels	13	1.480637813	4.E-02 12190, 12842, 109900, 12043, 100040331	809	115	13588	2.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0042113~B cell activation	10	1.138952164	4.E-02 12051, 18708, 16197, 11486, 234779, 120	809	78	13588	2.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0031401~positive regulation of protein modification process	10	1.138952164	4.E-02 56717, 18413, 19164, 12043, 216080, 209	809	78	13588	2.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0003006~reproductive developmental process	24	2.733485194	4.E-02 12190, 11651, 14180, 12043, 13382, 6714	809	264	13588	2.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0035051~cardiac cell differentiation	6	0.683371298	4.E-02 77579, 14465, 11464, 16412, 11364, 1420	809	33	13588	3.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0030902~hindbrain development	9	1.025056948	4.E-02 77579, 15407, 50768, 15376, 19378, 1204	809	67	13588	2.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0046631~alpha-beta T cell activation	5	0.569476082	4.E-02 12051, 19934, 12043, 20963, 100047372	809	23	13588	4.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0001912~positive regulation of leukocyte mediated cytotoxicity	5	0.569476082	4.E-02 19370, 14972, 15018, 27007, 379043, 120	809	23	13588	4.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0031343~positive regulation of cell killing	5	0.569476082	4.E-02 19370, 14972, 15018, 27007, 379043, 120	809	23	13588	4.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0031099~regeneration	5	0.569476082	4.E-02 14432, 18815, 12043, 18793, 11625	809	23	13588	4.E+00	1.E+00	3.E-01	6.E+01



GOTERM_BP_FAT	GO:0001933~negative regulation of protein amino acid phosphor	5	0.569476082	4.E-02 15170, 12703, 12028, 12018, 19164	809	23	13588	4.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0048878~chemical homeostasis	31	3.530751708	4.E-02 14151, 19206, 11816, 238055, 20191, 103	809	365	13588	1.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0009164~nucleoside catabolic process	3	0.341685649	5.E-02 11486, 72269, 99586	809	6	13588	8.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0060068~vagina development	3	0.341685649	5.E-02 12028, 12018, 17979	809	6	13588	8.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0045123~cellular extravasation	3	0.341685649	5.E-02 20345, 16414, 16409	809	6	13588	8.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0046503~glycerolipid catabolic process	3	0.341685649	5.E-02 11814, 669888, 238055	809	6	13588	8.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0055117~regulation of cardiac muscle contraction	3	0.341685649	5.E-02 14226, 20191, 208727	809	6	13588	8.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0044058~regulation of digestive system process	3	0.341685649	5.E-02 11806, 11807, 11808	809	6	13588	8.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0031365~N-terminal protein amino acid modification	3	0.341685649	5.E-02 18108, 18107, 12914	809	6	13588	8.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0032368~regulation of lipid transport	3	0.341685649	5.E-02 11806, 11807, 11808	809	6	13588	8.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0046464~acylglycerol catabolic process	3	0.341685649	5.E-02 11814, 669888, 238055	809	6	13588	8.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0001783~B cell apoptosis	3	0.341685649	5.E-02 12028, 12018, 17869	809	6	13588	8.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0019433~triglyceride catabolic process	3	0.341685649	5.E-02 11814, 669888, 238055	809	6	13588	8.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0044269~glycerol ether catabolic process	3	0.341685649	5.E-02 11814, 669888, 238055	809	6	13588	8.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0042692~muscle cell differentiation	13	1.480637813	5.E-02 19317, 18479, 16412, 11364, 19645, 1305	809	117	13588	2.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0007159~leukocyte adhesion	4	0.455580866	5.E-02 16408, 20345, 16414, 16409	809	14	13588	5.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0032319~regulation of Rho GTPase activity	4	0.455580866	5.E-02 56717, 71709, 19765, 19417	809	14	13588	5.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0010906~regulation of glucose metabolic process	4	0.455580866	5.E-02 14447, 14815, 103988, 208727	809	14	13588	5.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0050853~B cell receptor signaling pathway	4	0.455580866	5.E-02 15170, 16818, 20963, 17096	809	14	13588	5.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0001101~response to acid	4	0.455580866	5.E-02 56717, 20779, 12028, 12043	809	14	13588	5.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0009116~nucleoside metabolic process	8	0.911161731	5.E-02 22017, 11486, 72269, 232087, 56749, 708	809	56	13588	2.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0007292~female gamete generation	8	0.911161731	5.E-02 12190, 20779, 11920, 12043, 12531, 1684	809	56	13588	2.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0001934~positive regulation of protein amino acid phosphor	8	0.911161731	5.E-02 56717, 18413, 19164, 12043, 20963, 1645	809	56	13588	2.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0043066~negative regulation of apoptosis	22	2.505694761	5.E-02 13628, 11651, 17869, 12043, 108138, 204	809	239	13588	2.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0043523~regulation of neuron apoptosis	10	1.138952164	5.E-02 16994, 12048, 11920, 12028, 15461, 1204	809	80	13588	2.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0045621~positive regulation of lymphocyte differentiation	6	0.683371298	5.E-02 16818, 12015, 16197, 11486, 16190, 2096	809	34	13588	3.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0006638~neutral lipid metabolic process	7	0.797266515	5.E-02 17777, 11814, 669888, 13350, 19012, 185	809	45	13588	3.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0006662~glycerol ether metabolic process	7	0.797266515	5.E-02 17777, 11814, 669888, 13350, 19012, 185	809	45	13588	3.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0048754~branching morphogenesis of a tube	11	1.25284738	5.E-02 15402, 14674, 20779, 24064, 15376, 1204	809	93	13588	2.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0007093~mitotic cell cycle checkpoint	5	0.569476082	5.E-02 11920, 12443, 56150, 68193, 12534	809	24	13588	3.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0045834~positive regulation of lipid metabolic process	5	0.569476082	5.E-02 18048, 16367, 11816, 57257, 12540	809	24	13588	3.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0048738~cardiac muscle tissue development	8	0.911161731	5.E-02 13052, 77579, 14465, 11464, 16412, 2046	809	57	13588	2.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0031589~cell-substrate adhesion	8	0.911161731	5.E-02 19944, 665032, 50768, 12043, 16414, 118	809	57	13588	2.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0046474~glycerophospholipid biosynthetic process	7	0.797266515	5.E-02 14731, 56703, 276846, 329777, 18701, 22	809	46	13588	3.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0030183~B cell differentiation	7	0.797266515	5.E-02 12051, 18708, 11486, 234779, 12028, 120	809	46	13588	3.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0008610~lipid biosynthetic process	25	2.84738041	5.E-02 70316, 14178, 68262, 276846, 329777, 52	809	285	13588	1.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0009411~response to UV	6	0.683371298	5.E-02 13872, 12190, 14151, 12028, 12043, 1257	809	35	13588	3.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0050731~positive regulation of peptidyl-tyrosine phosphoryla	6	0.683371298	5.E-02 56717, 18413, 20963, 16452, 15163, 1709	809	35	13588	3.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0060711~labyrinthine layer development	6	0.683371298	5.E-02 12702, 14784, 18815, 26395, 11651, 1647	809	35	13588	3.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0050817~coagulation	9	1.025056948	6.E-02 14060, 14674, 56744, 18815, 74145, 1406	809	70	13588	2.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0007596~blood coagulation	9	1.025056948	6.E-02 14060, 14674, 56744, 18815, 74145, 1406	809	70	13588	2.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0019216~regulation of lipid metabolic process	8	0.911161731	6.E-02 18048, 19645, 16367, 11816, 57257, 2380	809	58	13588	2.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0016042~lipid catabolic process	14	1.59453303	6.E-02 11813, 11814, 11816, 238055, 18797, 113	809	134	13588	2.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0042509~regulation of tyrosine phosphorylation of STAT prot	4	0.455580866	6.E-02 12703, 16452, 15163, 17096	809	15	13588	4.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0051648~vesicle localization	4	0.455580866	6.E-02 245049, 19164, 11891, 171531	809	15	13588	4.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0001782~B cell homeostasis	4	0.455580866	6.E-02 12028, 12018, 12043, 18707	809	15	13588	4.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0000186~activation of MAPKK activity	4	0.455580866	6.E-02 17873, 14678, 19164, 23882	809	15	13588	4.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0010675~regulation of cellular carbohydrate metabolic proces	4	0.455580866	6.E-02 14447, 14815, 103988, 208727	809	15	13588	4.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0006109~regulation of carbohydrate metabolic process	4	0.455580866	6.E-02 14447, 14815, 103988, 208727	809	15	13588	4.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0046131~pyrimidine ribonucleoside metabolic process	4	0.455580866	6.E-02 72269, 56749, 22271, 99586	809	15	13588	4.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0045944~positive regulation of transcription from RNA polym	30	3.416856492	6.E-02 17536, 22130, 15376, 17869, 21869, 1291	809	358	13588	1.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0042742~defense response to bacterium	12	1.366742597	6.E-02 12051, 14972, 14127, 17874, 18126, 1419	809	108	13588	2.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0010741~negative regulation of protein kinase cascade	5	0.569476082	6.E-02 15170, 12703, 24064, 16001, 17082	809	25	13588	3.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0030308~negative regulation of cell growth	7	0.797266515	6.E-02 11785, 67184, 72269, 68349, 12043, 1162	809	47	13588	3.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0030258~lipid modification	7	0.797266515	6.E-02 18708, 74147, 26416, 30955, 11364, 1870	809	47	13588	3.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0001649~osteoblast differentiation	7	0.797266515	6.E-02 78294, 12842, 12161, 14180, 208727, 160	809	47	13588	3.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0007599~hemostasis	9	1.025056948	6.E-02 14060, 14674, 56744, 18815, 74145, 1406	809	71	13588	2.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0051090~regulation of transcription factor activity	8	0.911161731	6.E-02 17874, 16179, 21898, 16414, 192176, 240	809	59	13588	2.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0051783~regulation of nuclear division	6	0.683371298	6.E-02 16994, 11920, 52563, 12540, 56150, 6899	809	36	13588	3.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0034656~nucleobase, nucleoside and nucleotide catabolic prc	6	0.683371298	6.E-02 11486, 17970, 72269, 17969, 22271, 9958	809	36	13588	3.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0006641~triglyceride metabolic process	6	0.683371298	6.E-02 17777, 11814, 669888, 13350, 18534, 238	809	36	13588	3.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0007088~regulation of mitosis	6	0.683371298	6.E-02 16994, 11920, 52563, 12540, 56150, 6899	809	36	13588	3.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0034655~nucleobase, nucleoside, nucleotide and nucleic acid	6	0.683371298	6.E-02 11486, 17970, 72269, 17969, 22271, 9958	809	36	13588	3.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0060428~lung epithelium development	3	0.341685649	6.E-02 15402, 14465, 21869	809	7	13588	7.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0046627~negative regulation of insulin receptor signaling pat	3	0.341685649	6.E-02 12703, 12702, 11625	809	7	13588	7.E+00	1.E+00	4.E-01	7.E+01



GOTERM_BP_FAT	GO:0033205--cytokinesis during cell cycle	3	0.341685649	6.E-02 12190, 26934, 77579	809	7	13588	7.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0042953--lipoprotein transport	3	0.341685649	6.E-02 17777, 12491, 238055	809	7	13588	7.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0002335--mature B cell differentiation	3	0.341685649	6.E-02 12051, 11486, 234779	809	7	13588	7.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0051323--metaphase	3	0.341685649	6.E-02 67052, 20112, 67141	809	7	13588	7.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0046461--neutral lipid catabolic process	3	0.341685649	6.E-02 11814, 669888, 238055	809	7	13588	7.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0007005--mitochondrion organization	11	1.25284738	6.E-02 382985, 18181, 12048, 13052, 12028, 121	809	97	13588	2.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0030030--cell projection organization	27	3.075170843	6.E-02 22323, 11658, 11651, 21869, 14026, 1707	809	319	13588	1.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0042327--positive regulation of phosphorylation	8	0.911161731	6.E-02 56717, 18413, 19164, 12043, 20963, 1645	809	60	13588	2.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0051173--positive regulation of nitrogen compound metabolis	41	4.669703872	6.E-02 17536, 22130, 15376, 17869, 21869, 1291	809	526	13588	1.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0060541--respiratory system development	13	1.480637813	7.E-02 14178, 15376, 14180, 19378, 16948, 5684	809	124	13588	2.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0060603--mammary gland duct morphogenesis	5	0.569476082	7.E-02 20779, 19206, 14815, 17979, 12234	809	26	13588	3.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0030324--lung development	12	1.366742597	7.E-02 15402, 24064, 14178, 11486, 14465, 7431	809	111	13588	2.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0030071--regulation of mitotic metaphase/anaphase transitor	4	0.455580866	7.E-02 11920, 52563, 56150, 68999	809	16	13588	4.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0001906--cell killing	4	0.455580866	7.E-02 15170, 11891, 13035, 17969	809	16	13588	4.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0021795--cerebral cortex cell migration	4	0.455580866	7.E-02 13649, 19164, 12568, 21869	809	16	13588	4.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0009416--response to light stimulus	11	1.25284738	7.E-02 13872, 11785, 12190, 14151, 12028, 2320	809	98	13588	2.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0021987--cerebral cortex development	6	0.683371298	7.E-02 13649, 12028, 19164, 12568, 21869, 1162	809	37	13588	3.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0050871--positive regulation of B cell activation	6	0.683371298	7.E-02 12015, 11486, 21898, 106759, 12575, 209	809	37	13588	3.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0031016--pancreas development	6	0.683371298	7.E-02 15376, 18609, 19378, 16001, 18576, 1600	809	37	13588	3.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0030323--respiratory tube development	12	1.366742597	7.E-02 15402, 24064, 14178, 11486, 14465, 7431	809	113	13588	2.E+00	1.E+00	5.E-01	7.E+01
GOTERM_BP_FAT	GO:0001890--placenta development	10	1.138952164	7.E-02 13649, 12702, 11486, 13857, 14784, 1881	809	87	13588	2.E+00	1.E+00	5.E-01	7.E+01
GOTERM_BP_FAT	GO:0010562--positive regulation of phosphorus metabolic proces	8	0.911161731	7.E-02 56717, 18413, 19164, 12043, 20963, 1645	809	62	13588	2.E+00	1.E+00	5.E-01	7.E+01
GOTERM_BP_FAT	GO:0045937--positive regulation of phosphate metabolic process	8	0.911161731	7.E-02 56717, 18413, 19164, 12043, 20963, 1645	809	62	13588	2.E+00	1.E+00	5.E-01	7.E+01
GOTERM_BP_FAT	GO:0033043--regulation of organelle organization	15	1.708428246	7.E-02 227753, 16800, 56150, 13383, 14026, 123	809	154	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0032946--positive regulation of mononuclear cell proliferation	7	0.797266515	7.E-02 16408, 17874, 11486, 21898, 106759, 125	809	50	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0007160--cell-matrix adhesion	7	0.797266515	7.E-02 50768, 12043, 16414, 11856, 16412, 1256	809	50	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0050671--positive regulation of lymphocyte proliferation	7	0.797266515	7.E-02 16408, 17874, 11486, 21898, 106759, 125	809	50	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0000187--activation of MAPK activity	7	0.797266515	7.E-02 16334, 26395, 20416, 117149, 20963, 165	809	50	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0009395--phospholipid catabolic process	4	0.455580866	8.E-02 18783, 18803, 234779, 18797	809	17	13588	4.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0009620--response to fungus	4	0.455580866	8.E-02 17874, 12018, 17969, 24088	809	17	13588	4.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0030593--neutrophil chemotaxis	4	0.455580866	8.E-02 20310, 14127, 16414, 16409	809	17	13588	4.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0032729--positive regulation of interferon-gamma production	4	0.455580866	8.E-02 12051, 19370, 15018, 27007, 379043	809	17	13588	4.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0006650--glycerophospholipid metabolic process	10	1.138952164	8.E-02 18708, 14731, 56703, 276846, 329777, 30	809	88	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0032321--positive regulation of Rho GTPase activity	3	0.341685649	8.E-02 71709, 19765, 19417	809	8	13588	6.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0009263--deoxyribonucleotide biosynthetic process	3	0.341685649	8.E-02 382985, 20133, 20135	809	8	13588	6.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0048857--neural nucleus development	3	0.341685649	8.E-02 15407, 12043, 56847	809	8	13588	6.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0031017--exocrine pancreas development	3	0.341685649	8.E-02 18609, 16001, 16000	809	8	13588	6.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0006098--pentose-phosphate shunt	3	0.341685649	8.E-02 21991, 21351, 66171	809	8	13588	6.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0051881--regulation of mitochondrial membrane potential	3	0.341685649	8.E-02 12018, 12043, 227197	809	8	13588	6.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0002685--regulation of leukocyte migration	3	0.341685649	8.E-02 11486, 20339, 24088	809	8	13588	6.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0042088--T-helper 1 type immune response	3	0.341685649	8.E-02 12051, 21899, 23882	809	8	13588	6.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0002320--lymphoid progenitor cell differentiation	3	0.341685649	8.E-02 20375, 12043, 108138	809	8	13588	6.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0048041--focal adhesion formation	3	0.341685649	8.E-02 50768, 12043, 11856	809	8	13588	6.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0051646--mitochondrion localization	3	0.341685649	8.E-02 59040, 16561, 214952	809	8	13588	6.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0045893--positive regulation of transcription, DNA-dependent	33	3.758542141	8.E-02 17536, 22130, 15376, 17869, 21869, 1291	809	416	13588	1.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0008584--male gonad development	6	0.683371298	8.E-02 12048, 12028, 12043, 14180, 21869, 1162	809	39	13588	3.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0048477--oogenesis	6	0.683371298	8.E-02 12190, 20779, 12043, 12531, 20112, 6714	809	39	13588	3.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0032147--activation of protein kinase activity	7	0.797266515	8.E-02 17873, 21899, 14678, 21898, 19164, 1338	809	51	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0007229--integrin-mediated signaling pathway	9	1.025056948	8.E-02 16408, 23234, 16411, 232906, 57257, 164	809	76	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0007259--JAK-STAT cascade	5	0.569476082	8.E-02 55979, 12703, 18413, 12568, 16452	809	28	13588	3.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0007249--I-kappaB kinase/NF-kappaB cascade	5	0.569476082	8.E-02 57874, 12229, 21899, 21898, 117149	809	28	13588	3.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0015758--glucose transport	5	0.569476082	8.E-02 16333, 20525, 16334, 22612, 11651	809	28	13588	3.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0007611--learning or memory	10	1.138952164	8.E-02 17159, 11785, 14661, 11514, 19085, 1916	809	89	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0051146--striated muscle cell differentiation	10	1.138952164	8.E-02 19645, 13052, 77579, 14465, 11464, 1641	809	89	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0034613--cellular protein localization	25	2.84738041	8.E-02 269589, 171531, 236643, 320051, 231103	809	299	13588	1.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0048568--embryonic organ development	21	2.391799544	8.E-02 13649, 19378, 11651, 17869, 14180, 1543	809	241	13588	1.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0006952--defense response	35	3.986332574	8.E-02 14972, 12475, 15018, 11651, 16803, 1201	809	448	13588	1.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0051254--positive regulation of RNA metabolic process	33	3.758542141	9.E-02 17536, 22130, 15376, 17869, 21869, 1291	809	419	13588	1.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0002705--positive regulation of leukocyte mediated immunity	6	0.683371298	9.E-02 19370, 14972, 14127, 15018, 27007, 3790	809	40	13588	3.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0002708--positive regulation of lymphocyte mediated immuni	6	0.683371298	9.E-02 19370, 14972, 14127, 15018, 27007, 3790	809	40	13588	3.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0070665--positive regulation of leukocyte proliferation	7	0.797266515	9.E-02 16408, 17874, 11486, 21898, 106759, 125	809	52	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0010948--negative regulation of cell cycle process	4	0.455580866	9.E-02 11785, 11920, 18413, 56150	809	18	13588	4.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0022029--telencephalon cell migration	4	0.455580866	9.E-02 13649, 19164, 12568, 21869	809	18	13588	4.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0070727--cellular macromolecule localization	25	2.84738041	9.E-02 269589, 171531, 236643, 320051, 231103	809	301	13588	1.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0048585--negative regulation of response to stimulus	8	0.911161731	9.E-02 56717, 15170, 12703, 16197, 12702, 1148	809	65	13588	2.E+00	1.E+00	5.E-01	8.E+01



GOTERM_BP_FAT	GO:0044057~regulation of system process	18	2.050113895	9.E-02 18747, 11806, 11807, 14678, 14226, 1484	809	201	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0006874~cellular calcium ion homeostasis	10	1.138952164	9.E-02 18751, 16818, 13857, 11816, 14226, 1202	809	91	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0051248~negative regulation of protein metabolic process	9	1.025056948	9.E-02 15170, 13685, 12703, 12028, 12018, 1916	809	78	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0051047~positive regulation of secretion	7	0.797266515	9.E-02 14127, 14661, 12568, 12912, 83671, 1039	809	53	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0021543~pallium development	7	0.797266515	9.E-02 13649, 433759, 12028, 19164, 12568, 218	809	53	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0010035~response to inorganic substance	10	1.138952164	1.E-01 12842, 19053, 12443, 26462, 17420, 5049	809	92	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0042531~positive regulation of tyrosine phosphorylation of S	3	0.341685649	1.E-01 16452, 15163, 17096	809	9	13588	6.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0002902~regulation of B cell apoptosis	3	0.341685649	1.E-01 11486, 12028, 17869	809	9	13588	6.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0000050~urea cycle	3	0.341685649	1.E-01 18416, 109900, 11847	809	9	13588	6.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0019627~urea metabolic process	3	0.341685649	1.E-01 18416, 109900, 11847	809	9	13588	6.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0046112~nucleobase biosynthetic process	3	0.341685649	1.E-01 11486, 56749, 99586	809	9	13588	6.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0001916~positive regulation of T cell mediated cytotoxicity	3	0.341685649	1.E-01 14972, 15018, 12010	809	9	13588	6.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0007398~ectoderm development	13	1.480637813	1.E-01 12831, 13649, 14178, 12842, 19206, 1537	809	133	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0001525~angiogenesis	13	1.480637813	1.E-01 14674, 11852, 14180, 20416, 18771, 1475	809	133	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0001503~ossification	11	1.25284738	1.E-01 78294, 12842, 12161, 69121, 12043, 1418	809	106	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0051592~response to calcium ion	4	0.455580866	1.E-01 12443, 17420, 18575, 11704	809	19	13588	4.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0021885~forebrain cell migration	4	0.455580866	1.E-01 13649, 19164, 12568, 21869	809	19	13588	4.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0030239~myofibril assembly	4	0.455580866	1.E-01 77579, 11464, 16412, 11459	809	19	13588	4.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0043271~negative regulation of ion transport	4	0.455580866	1.E-01 16994, 17999, 14678, 12043	809	19	13588	4.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0051693~actin filament capping	4	0.455580866	1.E-01 227753, 14026, 12345, 19684	809	19	13588	4.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0046425~regulation of JAK-STAT cascade	4	0.455580866	1.E-01 12703, 16452, 15163, 17096	809	19	13588	4.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0048535~lymph node development	4	0.455580866	1.E-01 16994, 16197, 21934, 15902	809	19	13588	4.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0009112~nucleobase metabolic process	4	0.455580866	1.E-01 11486, 56749, 11717, 99586	809	19	13588	4.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0033157~regulation of intracellular protein transport	5	0.569476082	1.E-01 18747, 18826, 192176, 12568, 24069	809	30	13588	3.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0008645~hexose transport	5	0.569476082	1.E-01 16333, 20525, 16334, 22612, 11651	809	30	13588	3.E+00	1.E+00	5.E-01	8.E+01
GOTERM_CC_FAT	GO:0070469~respiratory chain	49	5.580865604	1.E-48 70316, 672195, 226646, 100041273, 6637	636	65	12504	1.E+01	4.E-46	4.E-46	2.E-45
GOTERM_CC_FAT	GO:0005840~ribosome	68	7.744874715	9.E-39 666899, 100048462, 20103, 100044516, 1	636	192	12504	7.E+00	4.E-36	2.E-36	1.E-35
GOTERM_CC_FAT	GO:0044429~mitochondrial part	88	10.02277904	1.E-23 226646, 66885, 672195, 100041273, 6826	636	524	12504	3.E+00	5.E-21	2.E-21	2.E-20
GOTERM_CC_FAT	GO:0031966~mitochondrial membrane	68	7.744874715	1.E-20 226646, 100041273, 66377, 18416, 59513	636	368	12504	4.E+00	6.E-18	1.E-18	2.E-17
GOTERM_CC_FAT	GO:0005740~mitochondrial envelope	70	7.972665148	2.E-20 226646, 100041273, 66377, 18416, 59513	636	391	12504	4.E+00	9.E-18	2.E-18	3.E-17
GOTERM_CC_FAT	GO:0030529~ribonucleoprotein complex	76	8.656036446	7.E-20 666899, 100048462, 19744, 20103, 10004	636	462	12504	3.E+00	3.E-17	5.E-18	1.E-16
GOTERM_CC_FAT	GO:0005743~mitochondrial inner membrane	59	6.719817768	2.E-19 226646, 100041273, 66377, 18416, 59513	636	296	12504	4.E+00	7.E-17	1.E-17	2.E-16
GOTERM_CC_FAT	GO:0019866~organelle inner membrane	60	6.833712984	5.E-19 226646, 100041273, 66377, 18416, 59513	636	312	12504	4.E+00	2.E-16	2.E-17	7.E-16
GOTERM_CC_FAT	GO:0031967~organelle envelope	81	9.225512528	1.E-18 226646, 100041273, 66377, 18416, 59513	636	540	12504	3.E+00	5.E-16	5.E-17	2.E-15
GOTERM_CC_FAT	GO:0031975~envelope	81	9.225512528	1.E-18 226646, 100041273, 66377, 18416, 59513	636	542	12504	3.E+00	6.E-16	6.E-17	2.E-15
GOTERM_CC_FAT	GO:0043232~intracellular non-membrane-bounded organelle	182	20.72892938	2.E-18 666899, 22130, 94190, 100039355, 16800	636	1919	12504	2.E+00	6.E-16	6.E-17	2.E-15
GOTERM_CC_FAT	GO:0043228~non-membrane-bounded organelle	182	20.72892938	2.E-18 666899, 22130, 94190, 100039355, 16800	636	1919	12504	2.E+00	6.E-16	6.E-17	2.E-15
GOTERM_CC_FAT	GO:0005739~mitochondrion	136	15.48974943	5.E-16 18746, 18747, 226646, 66885, 66377, 100	636	1322	12504	2.E+00	2.E-13	1.E-14	6.E-13
GOTERM_CC_FAT	GO:0005852~eukaryotic translation initiation factor 3 complex	11	1.25284738	6.E-12 27979, 66085, 13669, 16341, 53356, 5634	636	12	12504	2.E+01	3.E-09	2.E-10	9.E-09
GOTERM_CC_FAT	GO:0005829~cytosol	68	7.744874715	1.E-11 100048462, 18747, 672195, 20103, 14815	636	549	12504	2.E+00	6.E-09	4.E-10	2.E-08
GOTERM_CC_FAT	GO:0031090~organelle membrane	87	9.908883827	3.E-11 226646, 100041273, 66377, 18416, 59513	636	809	12504	2.E+00	1.E-08	7.E-10	4.E-08
GOTERM_CC_FAT	GO:0022626~cytosolic ribosome	12	1.366742597	1.E-10 100048462, 19944, 100042832, 20103, 19	636	18	12504	1.E+01	5.E-08	3.E-09	2.E-07
GOTERM_CC_FAT	GO:0033279~ribosomal subunit	20	2.277904328	4.E-10 100048462, 20103, 100039355, 10004339	636	66	12504	6.E+00	1.E-07	8.E-09	5.E-07
GOTERM_CC_FAT	GO:0044445~cytosolic part	19	2.164009112	1.E-09 100048462, 20103, 100043391, 18709, 18	636	63	12504	6.E+00	5.E-07	3.E-08	2.E-06
GOTERM_CC_FAT	GO:0030027~lamellipodium	17	1.936218679	6.E-08 22323, 14163, 227753, 13800, 54519, 116	636	63	12504	5.E+00	3.E-05	1.E-06	9.E-05
GOTERM_CC_FAT	GO:0005819~spindle	21	2.391799544	5.E-07 26934, 20871, 18005, 11651, 17869, 2087	636	109	12504	4.E+00	2.E-04	1.E-05	7.E-04
GOTERM_CC_FAT	GO:0005759~mitochondrial matrix	26	2.961275626	7.E-07 66885, 672195, 68263, 18416, 231086, 11	636	163	12504	3.E+00	3.E-04	1.E-05	9.E-04
GOTERM_CC_FAT	GO:0031980~mitochondrial lumen	26	2.961275626	7.E-07 66885, 672195, 68263, 18416, 231086, 11	636	163	12504	3.E+00	3.E-04	1.E-05	9.E-04
GOTERM_CC_FAT	GO:0015935~small ribosomal subunit	11	1.25284738	9.E-07 20103, 100039355, 677113, 20102, 20088	636	29	12504	7.E+00	3.E-04	2.E-05	1.E-03
GOTERM_CC_FAT	GO:0045271~respiratory chain complex I	6	0.683371298	2.E-06 226646, 67264, 68349, 227197, 17993, 17	636	6	12504	2.E+01	8.E-04	3.E-05	3.E-03
GOTERM_CC_FAT	GO:0030964~NADH dehydrogenase complex	6	0.683371298	2.E-06 226646, 67264, 68349, 227197, 17993, 17	636	6	12504	2.E+01	8.E-04	3.E-05	3.E-03
GOTERM_CC_FAT	GO:0005747~mitochondrial respiratory chain complex I	6	0.683371298	2.E-06 226646, 67264, 68349, 227197, 17993, 17	636	6	12504	2.E+01	8.E-04	3.E-05	3.E-03
GOTERM_CC_FAT	GO:0031252~cell leading edge	20	2.277904328	3.E-06 22323, 14163, 227753, 13800, 54519, 228	636	112	12504	4.E+00	1.E-03	5.E-05	5.E-03
GOTERM_CC_FAT	GO:0022625~cytosolic large ribosomal subunit	6	0.683371298	6.E-06 100048462, 20005, 110954, 100042832, 1	636	7	12504	2.E+01	3.E-03	1.E-04	9.E-03
GOTERM_CC_FAT	GO:0031974~membrane-enclosed lumen	92	10.47835991	2.E-05 18747, 66885, 672195, 68263, 22130, 184	636	1174	12504	2.E+00	9.E-03	4.E-04	3.E-02
GOTERM_CC_FAT	GO:0000808~origin recognition complex	5	0.569476082	3.E-05 18393, 17216, 50793, 26428, 56452	636	5	12504	2.E+01	1.E-02	5.E-04	4.E-02
GOTERM_CC_FAT	GO:0043233~organelle lumen	89	10.13667426	3.E-05 18747, 66885, 672195, 68263, 22130, 184	636	1136	12504	2.E+00	1.E-02	5.E-04	5.E-02
GOTERM_CC_FAT	GO:0000307~cyclin-dependent protein kinase holoenzyme compl	6	0.683371298	4.E-05 12447, 12443, 12567, 12566, 18538, 1257	636	9	12504	1.E+01	1.E-02	5.E-04	5.E-02
GOTERM_CC_FAT	GO:0070013~intracellular organelle lumen	88	10.02277904	5.E-05 18747, 66885, 672195, 68263, 22130, 184	636	1133	12504	2.E+00	2.E-02	7.E-04	7.E-02
GOTERM_CC_FAT	GO:0005746~mitochondrial respiratory chain	7	0.797266515	6.E-05 226646, 67184, 67264, 68349, 227197, 17	636	15	12504	9.E+00	2.E-02	7.E-04	8.E-02
GOTERM_CC_FAT	GO:0005856~cytoskeleton	85	9.681093394	2.E-04 22323, 13669, 94190, 54519, 54354, 7181	636	1122	12504	1.E+00	7.E-02	2.E-03	2.E-01
GOTERM_CC_FAT	GO:0030427~site of polarized growth	11	1.25284738	2.E-04 11785, 73750, 77579, 19164, 18479, 1256	636	51	12504	4.E+00	8.E-02	2.E-03	3.E-01
GOTERM_CC_FAT	GO:0030426~growth cone	11	1.25284738	2.E-04 11785, 73750, 77579, 19164, 18479, 1256	636	51	12504	4.E+00	8.E-02	2.E-03	3.E-01
GOTERM_CC_FAT	GO:0042470~melanosome	14	1.59453303	3.E-04 269589, 14674, 18453, 20525, 54401, 148	636	85	12504	3.E+00	1.E-01	4.E-03	5.E-01
GOTERM_CC_FAT	GO:0048770~pigment granule	14	1.59453303	3.E-04 269589, 14674, 18453, 20525, 54401, 148	636	85	12504	3.E+00	1.E-01	4.E-03	5.E-01



GOTERM_CC_FAT	GO:0005667~transcription factor complex	26	2.961275626	4.E-04	18181, 21869, 12912, 12914, 13872, 1355	636	234	12504	2.E+00	1.E-01	4.E-03	5.E-01
GOTERM_CC_FAT	GO:0042627~chylomicron	5	0.569476082	4.E-04	11813, 11814, 669888, 11816, 11808	636	8	12504	1.E+01	1.E-01	4.E-03	5.E-01
GOTERM_CC_FAT	GO:0042995~cell projection	49	5.580865604	5.E-04	22323, 18746, 94190, 16952, 54519, 1680	636	575	12504	2.E+00	2.E-01	5.E-03	7.E-01
GOTERM_CC_FAT	GO:0042765~GPI-anchor transamidase complex	4	0.455580866	5.E-04	14731, 329777, 228812, 100046871, 7892	636	4	12504	2.E+01	2.E-01	5.E-03	7.E-01
GOTERM_CC_FAT	GO:0005664~nuclear origin of replication recognition complex	4	0.455580866	5.E-04	18393, 17216, 50793, 56452	636	4	12504	2.E+01	2.E-01	5.E-03	7.E-01
GOTERM_CC_FAT	GO:0015934~large ribosomal subunit	9	1.025056948	6.E-04	100048462, 100042832, 19921, 10004339	636	39	12504	5.E+00	2.E-01	6.E-03	9.E-01
GOTERM_CC_FAT	GO:0005675~holo TFIIH complex	5	0.569476082	1.E-03	13872, 17420, 14884, 14885, 66671	636	10	12504	1.E+01	3.E-01	1.E-02	1.E+00
GOTERM_CC_FAT	GO:0044427~chromosomal part	30	3.416856492	2.E-03	60406, 245000, 12649, 433759, 22209, 50	636	318	12504	2.E+00	5.E-01	2.E-02	2.E+00
GOTERM_CC_FAT	GO:0015629~actin cytoskeleton	22	2.505694761	2.E-03	215280, 73750, 19894, 13800, 232906, 94	636	205	12504	2.E+00	5.E-01	2.E-02	2.E+00
GOTERM_CC_FAT	GO:0009897~external side of plasma membrane	22	2.505694761	2.E-03	19370, 14972, 15018, 11658, 11816, 2700	636	206	12504	2.E+00	5.E-01	2.E-02	3.E+00
GOTERM_CC_FAT	GO:0032994~protein-lipid complex	7	0.797266515	2.E-03	11813, 11814, 669888, 11806, 11807, 118	636	27	12504	5.E+00	5.E-01	2.E-02	3.E+00
GOTERM_CC_FAT	GO:0034358~plasma lipoprotein particle	7	0.797266515	2.E-03	11813, 11814, 669888, 11806, 11807, 118	636	27	12504	5.E+00	5.E-01	2.E-02	3.E+00
GOTERM_CC_FAT	GO:0005925~focal adhesion	10	1.138952164	2.E-03	22323, 12549, 13800, 22793, 236920, 545	636	57	12504	3.E+00	6.E-01	2.E-02	3.E+00
GOTERM_CC_FAT	GO:0022627~cytosolic small ribosomal subunit	4	0.455580866	3.E-03	20103, 20085, 677113, 20088, 20068	636	6	12504	1.E+01	6.E-01	2.E-02	3.E+00
GOTERM_CC_FAT	GO:0044455~mitochondrial membrane part	9	1.025056948	2.E-03	226646, 67184, 67264, 68349, 227197, 17	636	49	12504	4.E+00	7.E-01	3.E-02	4.E+00
GOTERM_CC_FAT	GO:0005924~cell-substrate adherens junction	10	1.138952164	3.E-03	22323, 12549, 13800, 22793, 236920, 545	636	61	12504	3.E+00	7.E-01	3.E-02	5.E+00
GOTERM_CC_FAT	GO:0009986~cell surface	28	3.189066059	4.E-03	14972, 15018, 11658, 11816, 14782, 5778	636	305	12504	2.E+00	8.E-01	3.E-02	5.E+00
GOTERM_CC_FAT	GO:0030175~filopodium	6	0.683371298	4.E-03	22323, 13800, 12568, 19684, 224014, 240	636	22	12504	5.E+00	8.E-01	3.E-02	6.E+00
GOTERM_CC_FAT	GO:0031594~neuromuscular junction	6	0.683371298	4.E-03	18747, 77579, 16412, 12568, 13383, 2087	636	22	12504	5.E+00	8.E-01	3.E-02	6.E+00
GOTERM_CC_FAT	GO:0000267~cell fraction	46	5.239179954	5.E-03	672195, 12955, 665032, 238055, 21869, 1	636	596	12504	2.E+00	9.E-01	4.E-02	7.E+00
GOTERM_CC_FAT	GO:0016323~basolateral plasma membrane	16	1.822323462	5.E-03	22323, 13649, 13800, 20525, 22793, 2369	636	141	12504	2.E+00	9.E-01	4.E-02	7.E+00
GOTERM_CC_FAT	GO:0030055~cell-substrate junction	10	1.138952164	6.E-03	22323, 12549, 13800, 22793, 236920, 545	636	66	12504	3.E+00	9.E-01	4.E-02	8.E+00
GOTERM_CC_FAT	GO:0019897~extrinsic to plasma membrane	9	1.025056948	6.E-03	269589, 14674, 14675, 11816, 14673, 836	636	55	12504	3.E+00	9.E-01	4.E-02	8.E+00
GOTERM_CC_FAT	GO:0005912~adherens junction	13	1.480637813	7.E-03	22323, 69524, 13800, 22793, 236920, 545	636	106	12504	2.E+00	9.E-01	5.E-02	1.E+01
GOTERM_CC_FAT	GO:0045251~electron transfer flavoprotein complex	3	0.341685649	7.E-03	110826, 110842, 66841	636	3	12504	2.E+01	9.E-01	5.E-02	1.E+01
GOTERM_CC_FAT	GO:0017133~mitochondrial electron transfer flavoprotein comple	3	0.341685649	7.E-03	110826, 110842, 66841	636	3	12504	2.E+01	9.E-01	5.E-02	1.E+01
GOTERM_CC_FAT	GO:0005654~nucleoplasm	45	5.125284738	9.E-03	60406, 18747, 18181, 67184, 12649, 4337	636	599	12504	1.E+00	1.E+00	6.E-02	1.E+01
GOTERM_CC_FAT	GO:0043235~receptor complex	11	1.25284738	9.E-03	16408, 15170, 12475, 16411, 21898, 1641	636	83	12504	3.E+00	1.E+00	6.E-02	1.E+01
GOTERM_CC_FAT	GO:0005694~chromosome	31	3.530751708	1.E-02	60406, 245000, 12649, 433759, 22209, 50	636	378	12504	2.E+00	1.E+00	7.E-02	1.E+01
GOTERM_CC_FAT	GO:0000151~ubiquitin ligase complex	9	1.025056948	1.E-02	17999, 26965, 52563, 99152, 16396, 2140	636	60	12504	3.E+00	1.E+00	7.E-02	1.E+01
GOTERM_CC_FAT	GO:0045121~membrane raft	11	1.25284738	1.E-02	14127, 12475, 16818, 14678, 104215, 124	636	85	12504	3.E+00	1.E+00	7.E-02	1.E+01
GOTERM_CC_FAT	GO:0034385~triglyceride-rich lipoprotein particle	4	0.455580866	1.E-02	11813, 11814, 669888, 11816	636	10	12504	8.E+00	1.E+00	7.E-02	2.E+01
GOTERM_CC_FAT	GO:0034361~very-low-density lipoprotein particle	4	0.455580866	1.E-02	11813, 11814, 669888, 11816	636	10	12504	8.E+00	1.E+00	7.E-02	2.E+01
GOTERM_CC_FAT	GO:0005626~insoluble fraction	40	4.555808656	1.E-02	269589, 11852, 12955, 665032, 238055, 1	636	528	12504	1.E+00	1.E+00	7.E-02	2.E+01
GOTERM_CC_FAT	GO:0015630~microtubule cytoskeleton	35	3.986332574	1.E-02	13669, 66214, 13430, 11651, 17869, 5435	636	450	12504	2.E+00	1.E+00	8.E-02	2.E+01
GOTERM_CC_FAT	GO:0005581~collagen	5	0.569476082	1.E-02	12843, 12831, 12842, 16948, 12815	636	19	12504	5.E+00	1.E+00	8.E-02	2.E+01
GOTERM_CC_FAT	GO:0000015~phosphopyruvate hydratase complex	3	0.341685649	1.E-02	433182, 13807, 13806, 13808, 100044223	636	4	12504	1.E+01	1.E+00	8.E-02	2.E+01
GOTERM_CC_FAT	GO:0005853~eukaryotic translation elongation factor 1 complex	3	0.341685649	1.E-02	13628, 66656, 55949	636	4	12504	1.E+01	1.E+00	8.E-02	2.E+01
GOTERM_CC_FAT	GO:0044454~nuclear chromosome part	12	1.366742597	2.E-02	60406, 18393, 19891, 17216, 13006, 2450	636	103	12504	2.E+00	1.E+00	9.E-02	2.E+01
GOTERM_CC_FAT	GO:0000228~nuclear chromosome	13	1.480637813	2.E-02	19891, 60406, 245000, 50793, 22209, 180	636	121	12504	2.E+00	1.E+00	1.E-01	2.E+01
GOTERM_CC_FAT	GO:0005942~phosphoinositide 3-kinase complex	4	0.455580866	2.E-02	18709, 18708, 30955, 18707	636	12	12504	7.E+00	1.E+00	1.E-01	2.E+01
GOTERM_CC_FAT	GO:0070161~anchoring junction	13	1.480637813	2.E-02	22323, 69524, 13800, 22793, 236920, 545	636	123	12504	2.E+00	1.E+00	1.E-01	3.E+01
GOTERM_CC_FAT	GO:0031988~membrane-bounded vesicle	32	3.644646925	2.E-02	215280, 13649, 269589, 100046871, 1167	636	420	12504	1.E+00	1.E+00	1.E-01	3.E+01
GOTERM_CC_FAT	GO:0000775~chromosome, centromeric region	12	1.366742597	3.E-02	18393, 67052, 19053, 20871, 12236, 1800	636	111	12504	2.E+00	1.E+00	1.E-01	3.E+01
GOTERM_CC_FAT	GO:0001772~immunological synapse	4	0.455580866	3.E-02	16408, 192662, 74734, 13383	636	13	12504	6.E+00	1.E+00	1.E-01	3.E+01
GOTERM_CC_FAT	GO:0005625~soluble fraction	11	1.25284738	3.E-02	110095, 672195, 269589, 12955, 11852, 1	636	99	12504	2.E+00	1.E+00	1.E-01	3.E+01
GOTERM_CC_FAT	GO:0005624~membrane fraction	37	4.214123007	3.E-02	269589, 11852, 665032, 238055, 16396, 1	636	510	12504	1.E+00	1.E+00	1.E-01	3.E+01
GOTERM_CC_FAT	GO:0031968~organelle outer membrane	10	1.138952164	3.E-02	56717, 12015, 14732, 12048, 12028, 1916	636	87	12504	2.E+00	1.E+00	2.E-01	4.E+01
GOTERM_CC_FAT	GO:0044430~cytoskeletal part	52	5.922551253	3.E-02	13669, 54354, 16800, 71819, 56150, 1707	636	774	12504	1.E+00	1.E+00	2.E-01	4.E+01
GOTERM_CC_FAT	GO:0031981~nuclear lumen	58	6.605922551	4.E-02	18747, 22130, 101206, 21869, 12912, 129	636	883	12504	1.E+00	1.E+00	2.E-01	4.E+01
GOTERM_CC_FAT	GO:0009898~internal side of plasma membrane	23	2.619589977	4.E-02	228543, 19744, 102093, 11853, 243362, 7	636	287	12504	2.E+00	1.E+00	2.E-01	4.E+01
GOTERM_CC_FAT	GO:0031982~vesicle	37	4.214123007	4.E-02	215280, 13649, 269589, 16396, 10004687	636	519	12504	1.E+00	1.E+00	2.E-01	4.E+01
GOTERM_CC_FAT	GO:0019867~outer membrane	10	1.138952164	4.E-02	56717, 12015, 14732, 12048, 12028, 1916	636	90	12504	2.E+00	1.E+00	2.E-01	4.E+01
GOTERM_CC_FAT	GO:0031965~nuclear membrane	6	0.683371298	4.E-02	19720, 19164, 12043, 23897, 18538, 2221	636	38	12504	3.E+00	1.E+00	2.E-01	4.E+01
GOTERM_CC_FAT	GO:0034364~high-density lipoprotein particle	4	0.455580866	4.E-02	11806, 11807, 11816, 11808	636	16	12504	5.E+00	1.E+00	2.E-01	5.E+01
GOTERM_CC_FAT	GO:0042641~actomyosin	5	0.569476082	5.E-02	13800, 77579, 11459, 208727, 19200	636	27	12504	4.E+00	1.E+00	2.E-01	5.E+01
GOTERM_CC_FAT	GO:0044451~nucleoplasm part	36	4.10022779	5.E-02	60406, 18181, 433759, 101206, 17869, 21	636	513	12504	1.E+00	1.E+00	2.E-01	5.E+01
GOTERM_CC_FAT	GO:0005741~mitochondrial outer membrane	9	1.025056948	5.E-02	56717, 12015, 14732, 12048, 12028, 1527	636	80	12504	2.E+00	1.E+00	2.E-01	5.E+01
GOTERM_CC_FAT	GO:0016023~cytoplasmic membrane-bounded vesicle	30	3.416856492	5.E-02	13649, 215280, 269589, 100046871, 1715	636	414	12504	1.E+00	1.E+00	2.E-01	5.E+01
GOTERM_CC_FAT	GO:0008305~integrin complex	5	0.569476082	5.E-02	16408, 16411, 16414, 16412, 16409	636	28	12504	4.E+00	1.E+00	2.E-01	5.E+01
GOTERM_CC_FAT	GO:0044459~plasma membrane part	98	11.16173121	5.E-02	22323, 19744, 15018, 69524, 19206, 9419	636	1633	12504	1.E+00	1.E+00	2.E-01	5.E+01
GOTERM_CC_FAT	GO:0031410~cytoplasmic vesicle	35	3.986332574	6.E-02	215280, 13649, 269589, 16396, 10004687	636	508	12504	1.E+00	1.E+00	2.E-01	6.E+01
GOTERM_CC_FAT	GO:0005884~actin filament	5	0.569476082	6.E-02	73750, 18826, 11459, 170758, 66440, 668	636	30	12504	3.E+00	1.E+00	2.E-01	6.E+01
GOTERM_CC_FAT	GO:0016605~PML body	4	0.455580866	7.E-02	19645, 22218, 12914, 68275	636	19	12504	4.E+00	1.E+00	3.E-01	6.E+01
GOTERM_CC_FAT	GO:0001726~ruffle	6	0.683371298	9.E-02	14163, 18826, 228359, 19159, 19684, 106	636	47	12504	3.E+00	1.E+00	3.E-01	7.E+01



GOTERM_CC_FAT	GO:0000793--condensed chromosome	10	1.138952164	9.E-02 18393, 13006, 67052, 12236, 18005, 1712	636	107	12504	2.E+00	1.E+00	3.E-01	7.E+01
GOTERM_CC_FAT	GO:0000776--kinetochore	7	0.797266515	9.E-02 18393, 67052, 12236, 17120, 56150, 2046	636	62	12504	2.E+00	1.E+00	3.E-01	7.E+01
GOTERM_CC_FAT	GO:0000803--sex chromosome	4	0.455580866	1.E-01 245000, 22209, 12566, 20467	636	22	12504	4.E+00	1.E+00	3.E-01	8.E+01
GOTERM_CC_FAT	GO:0000806--Y chromosome	2	0.227790433	1.E-01 12566, 20467	636	2	12504	2.E+01	1.E+00	3.E-01	8.E+01
GOTERM_CC_FAT	GO:0005584--collagen type I	2	0.227790433	1.E-01 12843, 12842	636	2	12504	2.E+01	1.E+00	3.E-01	8.E+01
GOTERM_MF_FAT	GO:0003735--structural constituent of ribosome	64	7.28929385	5.E-39 666899, 100048462, 20103, 100044516, 1	754	151	13288	7.E+00	4.E-36	4.E-36	7.E-36
GOTERM_MF_FAT	GO:0030695--GTPase regulator activity	83	9.453302961	2.E-28 22324, 228482, 94190, 192662, 243362, 1	754	361	13288	4.E+00	1.E-25	6.E-26	2.E-25
GOTERM_MF_FAT	GO:0060589--nucleoside-triphosphatase regulator activity	83	9.453302961	5.E-28 22324, 228482, 94190, 192662, 243362, 1	754	367	13288	4.E+00	4.E-25	1.E-25	8.E-25
GOTERM_MF_FAT	GO:0050136--NADH dehydrogenase (quinone) activity	22	2.505694761	9.E-24 226646, 100041273, 66416, 67184, 17721	754	24	13288	2.E+01	6.E-21	2.E-21	1.E-20
GOTERM_MF_FAT	GO:0008137--NADH dehydrogenase (ubiquinone) activity	22	2.505694761	9.E-24 226646, 100041273, 66416, 67184, 17721	754	24	13288	2.E+01	6.E-21	2.E-21	1.E-20
GOTERM_MF_FAT	GO:0003954--NADH dehydrogenase activity	22	2.505694761	9.E-24 226646, 100041273, 66416, 67184, 17721	754	24	13288	2.E+01	6.E-21	2.E-21	1.E-20
GOTERM_MF_FAT	GO:0016651--oxidoreductase activity, acting on NADH or NADPH	29	3.302961276	4.E-22 226646, 100041273, 66416, 67184, 14782	754	51	13288	1.E+01	3.E-19	6.E-20	6.E-19
GOTERM_MF_FAT	GO:0016655--oxidoreductase activity, acting on NADH or NADPH,	22	2.505694761	1.E-21 226646, 100041273, 66416, 67184, 17721	754	27	13288	1.E+01	8.E-19	1.E-19	2.E-18
GOTERM_MF_FAT	GO:0005083--small GTPase regulator activity	55	6.264236902	2.E-20 22324, 192662, 16800, 171531, 16801, 22	754	223	13288	4.E+00	1.E-17	2.E-18	3.E-17
GOTERM_MF_FAT	GO:0005096--GTPase activator activity	48	5.466970387	4.E-18 117600, 94190, 232906, 228482, 192662,	754	192	13288	4.E+00	3.E-15	3.E-16	6.E-15
GOTERM_MF_FAT	GO:0008047--enzyme activator activity	52	5.922551253	5.E-16 94190, 228482, 243362, 192662, 14270, 2	754	249	13288	4.E+00	4.E-13	5.E-14	8.E-13
GOTERM_MF_FAT	GO:0005198--structural molecule activity	73	8.314350797	6.E-16 666899, 100048462, 20103, 100044516, 1	754	450	13288	3.E+00	5.E-13	5.E-14	1.E-12
GOTERM_MF_FAT	GO:0008135--translation factor activity, nucleic acid binding	31	3.530751708	8.E-15 13684, 66235, 13669, 56347, 53356, 2690	754	98	13288	6.E+00	6.E-12	6.E-13	1.E-11
GOTERM_MF_FAT	GO:0005089--Rho guanyl-nucleotide exchange factor activity	26	2.961275626	4.E-14 22324, 13605, 16800, 442801, 53972, 218	754	71	13288	6.E+00	3.E-11	2.E-12	6.E-11
GOTERM_MF_FAT	GO:0003743--translation initiation factor activity	24	2.733485194	1.E-13 13684, 66235, 13669, 53356, 56347, 2690	754	62	13288	7.E+00	8.E-11	6.E-12	2.E-11
GOTERM_MF_FAT	GO:0005088--Ras guanyl-nucleotide exchange factor activity	26	2.961275626	2.E-12 22324, 13605, 16800, 442801, 53972, 218	754	83	13288	6.E+00	2.E-09	1.E-10	3.E-09
GOTERM_MF_FAT	GO:0017076--purine nucleotide binding	174	19.81776765	9.E-12 18746, 18747, 19744, 66885, 26905, 7181	754	1871	13288	2.E+00	7.E-09	4.E-10	1.E-08
GOTERM_MF_FAT	GO:0000166--nucleotide binding	194	22.09567198	2.E-11 18746, 18747, 19744, 26905, 14782, 1707	754	2183	13288	2.E+00	2.E-08	1.E-09	3.E-08
GOTERM_MF_FAT	GO:0032553--ribonucleotide binding	162	18.45102506	7.E-10 18746, 18747, 19744, 26905, 71819, 1707	754	1796	13288	2.E+00	5.E-07	3.E-08	1.E-06
GOTERM_MF_FAT	GO:0005255--purine ribonucleotide binding	162	18.45102506	7.E-10 18746, 18747, 19744, 26905, 71819, 1707	754	1796	13288	2.E+00	5.E-07	3.E-08	1.E-06
GOTERM_MF_FAT	GO:0005085--guanyl-nucleotide exchange factor activity	28	3.189066059	5.E-08 22324, 13605, 16800, 442801, 53972, 218	754	147	13288	3.E+00	4.E-05	2.E-06	8.E-05
GOTERM_MF_FAT	GO:0017016--Ras GTPase binding	17	1.936218679	6.E-08 117600, 269589, 19894, 17970, 380714, 1	754	57	13288	5.E+00	5.E-05	2.E-06	1.E-04
GOTERM_MF_FAT	GO:0031267--small GTPase binding	17	1.936218679	1.E-07 117600, 269589, 19894, 17970, 380714, 1	754	59	13288	5.E+00	8.E-05	4.E-06	2.E-04
GOTERM_MF_FAT	GO:0005100--Rho GTPase activator activity	10	1.138952164	2.E-07 117600, 71709, 17925, 50768, 228359, 76	754	18	13288	1.E+01	1.E-04	6.E-06	3.E-04
GOTERM_MF_FAT	GO:0001882--nucleoside binding	136	15.48974943	2.E-07 18746, 18747, 66885, 71819, 14782, 1721	754	1558	13288	2.E+00	1.E-04	6.E-06	3.E-04
GOTERM_MF_FAT	GO:0001883--purine nucleoside binding	135	15.37585421	2.E-07 18746, 18747, 66885, 71819, 14782, 1721	754	1548	13288	2.E+00	2.E-04	7.E-06	3.E-04
GOTERM_MF_FAT	GO:0051020--GTPase binding	17	1.936218679	2.E-07 117600, 269589, 19894, 17970, 380714, 1	754	62	13288	5.E+00	2.E-04	7.E-06	3.E-04
GOTERM_MF_FAT	GO:0030554--adenyl nucleotide binding	134	15.261959	2.E-07 18746, 18747, 66885, 71819, 14782, 1721	754	1535	13288	2.E+00	2.E-04	7.E-06	3.E-04
GOTERM_MF_FAT	GO:0017137--Rab GTPase binding	10	1.138952164	3.E-07 245049, 269589, 19894, 320051, 380714,	754	19	13288	9.E+00	2.E-04	9.E-06	5.E-04
GOTERM_MF_FAT	GO:0004715--non-membrane spanning protein tyrosine kinase ac	13	1.480637813	1.E-06 11350, 12229, 16818, 14191, 22390, 2077	754	40	13288	6.E+00	1.E-03	4.E-05	2.E-03
GOTERM_MF_FAT	GO:0003924--GTPase activity	23	2.619589977	3.E-06 22142, 14674, 14675, 26905, 13627, 1467	754	128	13288	3.E+00	2.E-03	7.E-05	4.E-03
GOTERM_MF_FAT	GO:0019843--rRNA binding	10	1.138952164	3.E-06 26961, 100042832, 20102, 268449, 10004	754	24	13288	7.E+00	3.E-03	9.E-05	5.E-03
GOTERM_MF_FAT	GO:0019899--enzyme binding	32	3.6444646925	6.E-06 117600, 269589, 26965, 12649, 13605, 16	754	229	13288	2.E+00	4.E-03	1.E-04	9.E-03
GOTERM_MF_FAT	GO:0032559--adenyl ribonucleotide binding	122	13.8952164	8.E-06 18746, 18747, 71819, 17218, 23920, 1721	754	1460	13288	1.E+00	6.E-03	2.E-04	1.E-02
GOTERM_MF_FAT	GO:0004672--protein kinase activity	59	6.719817768	2.E-05 18747, 16818, 23920, 20779, 14884, 1256	754	583	13288	2.E+00	1.E-02	4.E-04	3.E-02
GOTERM_MF_FAT	GO:0005524--ATP binding	119	13.55353075	2.E-05 18746, 18747, 71819, 17218, 23920, 1721	754	1443	13288	1.E+00	2.E-02	5.E-04	3.E-02
GOTERM_MF_FAT	GO:0008353--RNA polymerase II carboxy-terminal domain kinase	7	0.797266515	2.E-05 13872, 107951, 17420, 14884, 14885, 125	754	12	13288	1.E+01	2.E-02	5.E-04	3.E-02
GOTERM_MF_FAT	GO:0005525--GTP binding	41	4.669703872	2.E-05 228543, 19744, 232906, 11852, 26905, 13	754	354	13288	2.E+00	2.E-02	5.E-04	4.E-02
GOTERM_MF_FAT	GO:0009055--electron carrier activity	28	3.189066059	3.E-05 66885, 672195, 226646, 14782, 66414, 11	754	202	13288	2.E+00	2.E-02	6.E-04	4.E-02
GOTERM_MF_FAT	GO:0032561--guanyl ribonucleotide binding	41	4.669703872	4.E-05 228543, 19744, 232906, 11852, 26905, 13	754	363	13288	2.E+00	3.E-02	8.E-04	6.E-02
GOTERM_MF_FAT	GO:0019001--guanyl nucleotide binding	41	4.669703872	4.E-05 228543, 19744, 232906, 11852, 26905, 13	754	363	13288	2.E+00	3.E-02	8.E-04	6.E-02
GOTERM_MF_FAT	GO:0005092--GDP-dissociation inhibitor activity	5	0.569476082	5.E-05 14570, 192662, 14567, 11857, 14569	754	5	13288	2.E+01	4.E-02	1.E-03	7.E-02
GOTERM_MF_FAT	GO:0019207--kinase regulator activity	15	1.708428246	5.E-05 66214, 19085, 19088, 100039474, 66197,	754	73	13288	4.E+00	4.E-02	1.E-03	8.E-02
GOTERM_MF_FAT	GO:0016624--oxidoreductase activity, acting on the aldehyde or c	6	0.683371298	6.E-05 12039, 68263, 18597, 18598, 100048676,	754	9	13288	1.E+01	4.E-02	1.E-03	9.E-02
GOTERM_MF_FAT	GO:0050662--coenzyme binding	23	2.619589977	1.E-04 226646, 66885, 100042746, 56847, 14782	754	160	13288	3.E+00	7.E-02	2.E-03	2.E-01
GOTERM_MF_FAT	GO:0016538--cyclin-dependent protein kinase regulator activity	7	0.797266515	1.E-04 12448, 12447, 12443, 100044764, 54124,	754	15	13288	8.E+00	7.E-02	2.E-03	2.E-01
GOTERM_MF_FAT	GO:0016411--acylglycerol O-acyltransferase activity	6	0.683371298	2.E-04 55979, 28169, 68262, 67512, 13350, 5212	754	11	13288	1.E+01	1.E-01	3.E-03	2.E-01
GOTERM_MF_FAT	GO:0042043--neurexin binding	5	0.569476082	3.E-04 269589, 27359, 83671, 13385, 83672	754	7	13288	1.E+01	2.E-01	5.E-03	5.E-01
GOTERM_MF_FAT	GO:0003841--1-acylglycerol-3-phosphate O-acyltransferase activit	5	0.569476082	3.E-04 55979, 28169, 68262, 67512, 52123	754	7	13288	1.E+01	2.E-01	5.E-03	5.E-01
GOTERM_MF_FAT	GO:0004713--protein tyrosine kinase activity	22	2.505694761	4.E-04 11350, 13649, 12229, 23920, 16818, 1859	754	164	13288	2.E+00	2.E-01	6.E-03	6.E-01
GOTERM_MF_FAT	GO:0019887--protein kinase regulator activity	12	1.366742597	4.E-04 66214, 19085, 19088, 100039474, 66197,	754	59	13288	4.E+00	3.E-01	7.E-03	6.E-01
GOTERM_MF_FAT	GO:0019992--diacylglycerol binding	12	1.366742597	4.E-04 18751, 22324, 26934, 78816, 13350, 1792	754	59	13288	4.E+00	3.E-01	7.E-03	6.E-01
GOTERM_MF_FAT	GO:0017124--SH3 domain binding	14	1.59453303	5.E-04 22323, 20401, 15170, 19317, 13800, 2283	754	79	13288	3.E+00	3.E-01	7.E-03	7.E-01
GOTERM_MF_FAT	GO:0048037--cofactor binding	27	3.075170843	5.E-04 70316, 66885, 226646, 100042746, 14782	754	226	13288	2.E+00	3.E-01	7.E-03	7.E-01
GOTERM_MF_FAT	GO:0019904--protein domain specific binding	24	2.733485194	5.E-04 22323, 11350, 15170, 20401, 19317, 1380	754	192	13288	2.E+00	3.E-01	8.E-03	8.E-01
GOTERM_MF_FAT	GO:0008289--lipid binding	36	4.10022779	6.E-04 22324, 11814, 18416, 19206, 11816, 1695	754	345	13288	2.E+00	4.E-01	9.E-03	9.E-01
GOTERM_MF_FAT	GO:0003923--GPI-anchor transamidase activity	4	0.455580866	7.E-04 14731, 276846, 329777, 100046871, 7892	754	4	13288	2.E+01	4.E-01	1.E-02	1.E+00
GOTERM_MF_FAT	GO:004896--cytokine receptor activity	11	1.25284738	9.E-04 12765, 16195, 12983, 16197, 50498, 1385	754	55	13288	4.E+00	5.E-01	1.E-02	1.E+00
GOTERM_MF_FAT	GO:0030675--Rac GTPase activator activity	5	0.569476082	1.E-03 228359, 76117, 19765, 233071, 106952	754	9	13288	1.E+01	5.E-01	1.E-02	2.E+00
GOTERM_MF_FAT	GO:0019955--cytokine binding	14	1.59453303	1.E-03 12765, 18414, 21937, 16195, 18824, 1298	754	88	13288	3.E+00	6.E-01	2.E-02	2.E+00



GOTERM_MF_FAT	GO:0051539--4 iron, 4 sulfur cluster binding	7	0.797266515	1.E-03 226646, 17995, 227197, 225887, 66841, 7	754	23	13288	5.E+00	7.E-01	2.E-02	2.E+00
GOTERM_MF_FAT	GO:0003995--acyl-CoA dehydrogenase activity	6	0.683371298	1.E-03 11370, 66885, 11409, 229211, 11364, 113	754	16	13288	7.E+00	7.E-01	2.E-02	2.E+00
GOTERM_MF_FAT	GO:0051540--metal cluster binding	10	1.138952164	2.E-03 66694, 226646, 14151, 17995, 227197, 22	754	50	13288	4.E+00	7.E-01	2.E-02	3.E+00
GOTERM_MF_FAT	GO:0051536--iron-sulfur cluster binding	10	1.138952164	2.E-03 66694, 226646, 14151, 17995, 227197, 22	754	50	13288	4.E+00	7.E-01	2.E-02	3.E+00
GOTERM_MF_FAT	GO:0050660--FAD binding	12	1.366742597	2.E-03 11370, 66885, 18126, 11409, 110842, 264	754	71	13288	3.E+00	8.E-01	3.E-02	3.E+00
GOTERM_MF_FAT	GO:0035004--phosphoinositide 3-kinase activity	5	0.569476082	2.E-03 18709, 18708, 11920, 30955, 18707	754	11	13288	8.E+00	8.E-01	3.E-02	4.E+00
GOTERM_MF_FAT	GO:0016303--1-phosphatidylinositol-3-kinase activity	5	0.569476082	2.E-03 18709, 18708, 11920, 30955, 18707	754	11	13288	8.E+00	8.E-01	3.E-02	4.E+00
GOTERM_MF_FAT	GO:0016681--oxidoreductase activity, acting on diphenols and rel.	4	0.455580866	3.E-03 66694, 67530, 66594, 66576	754	6	13288	1.E+01	9.E-01	4.E-02	5.E+00
GOTERM_MF_FAT	GO:0016668--oxidoreductase activity, acting on sulfur group of di	4	0.455580866	3.E-03 26462, 50493, 14782, 13382	754	6	13288	1.E+01	9.E-01	4.E-02	5.E+00
GOTERM_MF_FAT	GO:0004396--hexokinase activity	4	0.455580866	3.E-03 15275, 15277, 103988, 212032	754	6	13288	1.E+01	9.E-01	4.E-02	5.E+00
GOTERM_MF_FAT	GO:0016679--oxidoreductase activity, acting on diphenols and rel.	4	0.455580866	3.E-03 66694, 67530, 66594, 66576	754	6	13288	1.E+01	9.E-01	4.E-02	5.E+00
GOTERM_MF_FAT	GO:0008121--ubiquinol-cytochrome-c reductase activity	4	0.455580866	3.E-03 66694, 67530, 66594, 66576	754	6	13288	1.E+01	9.E-01	4.E-02	5.E+00
GOTERM_MF_FAT	GO:0005099--Ras GTPase activator activity	11	1.25284738	3.E-03 117600, 71709, 17925, 50768, 228359, 76	754	65	13288	3.E+00	9.E-01	4.E-02	5.E+00
GOTERM_MF_FAT	GO:0004674--protein serine/threonine kinase activity	38	4.328018223	5.E-03 107951, 18747, 245000, 12649, 11651, 12	754	421	13288	2.E+00	1.E+00	6.E-02	8.E+00
GOTERM_MF_FAT	GO:0004693--cyclin-dependent protein kinase activity	7	0.797266515	6.E-03 12445, 107951, 12567, 12566, 12568, 125	754	30	13288	4.E+00	1.E+00	7.E-02	9.E+00
GOTERM_MF_FAT	GO:0001530--lipopolysaccharide binding	4	0.455580866	8.E-03 12475, 17087, 21898, 16803	754	8	13288	9.E+00	1.E+00	9.E-02	1.E+01
GOTERM_MF_FAT	GO:0004083--2,3-bisphospho-D-glycerate 2-phosphohydrolase ac	3	0.341685649	9.E-03 18648, 12183, 56012	754	3	13288	2.E+01	1.E+00	1.E-01	1.E+01
GOTERM_MF_FAT	GO:0034416--bisphosphoglycerate phosphatase activity	3	0.341685649	9.E-03 18648, 12183, 56012	754	3	13288	2.E+01	1.E+00	1.E-01	1.E+01
GOTERM_MF_FAT	GO:0004082--bisphosphoglycerate mutase activity	3	0.341685649	9.E-03 18648, 12183, 56012	754	3	13288	2.E+01	1.E+00	1.E-01	1.E+01
GOTERM_MF_FAT	GO:0004738--pyruvate dehydrogenase activity	3	0.341685649	9.E-03 68263, 18597, 18598	754	3	13288	2.E+01	1.E+00	1.E-01	1.E+01
GOTERM_MF_FAT	GO:0004619--phosphoglycerate mutase activity	3	0.341685649	9.E-03 18648, 12183, 56012	754	3	13288	2.E+01	1.E+00	1.E-01	1.E+01
GOTERM_MF_FAT	GO:0004748--ribonucleoside-diphosphate reductase activity	3	0.341685649	9.E-03 382985, 20133, 20135	754	3	13288	2.E+01	1.E+00	1.E-01	1.E+01
GOTERM_MF_FAT	GO:0003863--3-methyl-2-oxobutanoate dehydrogenase (2-methyl	3	0.341685649	9.E-03 12039, 100048676, 12040, 13171	754	3	13288	2.E+01	1.E+00	1.E-01	1.E+01
GOTERM_MF_FAT	GO:0004739--pyruvate dehydrogenase (acetyl-transferring) activity	3	0.341685649	9.E-03 68263, 18597, 18598	754	3	13288	2.E+01	1.E+00	1.E-01	1.E+01
GOTERM_MF_FAT	GO:0016728--oxidoreductase activity, acting on CH or CH2 group:	3	0.341685649	9.E-03 382985, 20133, 20135	754	3	13288	2.E+01	1.E+00	1.E-01	1.E+01
GOTERM_MF_FAT	GO:0005094--Rho GDP-dissociation inhibitor activity	3	0.341685649	9.E-03 14570, 192662, 11857	754	3	13288	2.E+01	1.E+00	1.E-01	1.E+01
GOTERM_MF_FAT	GO:0008374--O-acyltransferase activity	7	0.797266515	1.E-02 55979, 28169, 68262, 14732, 67512, 1335	754	35	13288	4.E+00	1.E+00	1.E-01	2.E+01
GOTERM_MF_FAT	GO:0004842--ubiquitin-protein ligase activity	13	1.480637813	1.E-02 56550, 74287, 218793, 17999, 26965, 222	754	104	13288	2.E+00	1.E+00	1.E-01	2.E+01
GOTERM_MF_FAT	GO:0019205--nucleobase, nucleoside, nucleotide kinase activity	7	0.797266515	1.E-02 80914, 68556, 22245, 14923, 11636, 6658	754	36	13288	3.E+00	1.E+00	1.E-01	2.E+01
GOTERM_MF_FAT	GO:0016868--intramolecular transferase activity, phosphotransfera	4	0.455580866	2.E-02 18648, 72157, 12183, 56012	754	10	13288	7.E+00	1.E+00	2.E-01	2.E+01
GOTERM_MF_FAT	GO:0004634--phosphopyruvate hydratase activity	3	0.341685649	2.E-02 433182, 13807, 13806, 13808, 100044223	754	4	13288	1.E+01	1.E+00	2.E-01	2.E+01
GOTERM_MF_FAT	GO:0004849--uridine kinase activity	3	0.341685649	2.E-02 80914, 68556, 22245	754	4	13288	1.E+01	1.E+00	2.E-01	2.E+01
GOTERM_MF_FAT	GO:0004459--L-lactate dehydrogenase activity	3	0.341685649	2.E-02 16828, 16833, 16832	754	4	13288	1.E+01	1.E+00	2.E-01	2.E+01
GOTERM_MF_FAT	GO:0019200--carbohydrate kinase activity	5	0.569476082	2.E-02 56421, 15275, 15277, 103988, 212032	754	20	13288	4.E+00	1.E+00	2.E-01	3.E+01
GOTERM_MF_FAT	GO:0019787--small conjugating protein ligase activity	14	1.59453303	2.E-02 56550, 74287, 218793, 17999, 26965, 222	754	125	13288	2.E+00	1.E+00	2.E-01	3.E+01
GOTERM_MF_FAT	GO:0005516--calmodulin binding	13	1.480637813	3.E-02 102093, 18679, 18682, 18126, 14432, 775	754	114	13288	2.E+00	1.E+00	3.E-01	3.E+01
GOTERM_MF_FAT	GO:0008034--lipoprotein binding	5	0.569476082	3.E-02 11806, 11807, 11816, 21899, 12491	754	21	13288	4.E+00	1.E+00	3.E-01	4.E+01
GOTERM_MF_FAT	GO:0004332--fructose-bisphosphate aldolase activity	3	0.341685649	3.E-02 230163, 11676, 11674	754	5	13288	1.E+01	1.E+00	3.E-01	4.E+01
GOTERM_MF_FAT	GO:0030676--Rac guanyl-nucleotide exchange factor activity	3	0.341685649	3.E-02 22324, 57257, 16800	754	5	13288	1.E+01	1.E+00	3.E-01	4.E+01
GOTERM_MF_FAT	GO:0004457--lactate dehydrogenase activity	3	0.341685649	3.E-02 16828, 16833, 16832	754	5	13288	1.E+01	1.E+00	3.E-01	4.E+01
GOTERM_MF_FAT	GO:0043548--phosphoinositide 3-kinase binding	3	0.341685649	3.E-02 16367, 16001, 384783	754	5	13288	1.E+01	1.E+00	3.E-01	4.E+01
GOTERM_MF_FAT	GO:0031405--lipoic acid binding	3	0.341685649	3.E-02 235339, 27402, 13171	754	5	13288	1.E+01	1.E+00	3.E-01	4.E+01
GOTERM_MF_FAT	GO:0016725--oxidoreductase activity, acting on CH or CH2 group:	3	0.341685649	3.E-02 382985, 20133, 20135	754	5	13288	1.E+01	1.E+00	3.E-01	4.E+01
GOTERM_MF_FAT	GO:0032403--protein complex binding	10	1.138952164	3.E-02 12039, 18708, 14127, 16367, 245000, 272	754	78	13288	2.E+00	1.E+00	3.E-01	4.E+01
GOTERM_MF_FAT	GO:0019201--nucleotide kinase activity	4	0.455580866	4.E-02 14923, 11636, 66588, 11637	754	14	13288	5.E+00	1.E+00	3.E-01	5.E+01
GOTERM_MF_FAT	GO:0048365--Rac GTPase binding	3	0.341685649	4.E-02 17970, 16800, 192176	754	6	13288	9.E+00	1.E+00	3.E-01	5.E+01
GOTERM_MF_FAT	GO:0008035--high-density lipoprotein binding	3	0.341685649	4.E-02 11806, 11807, 12491	754	6	13288	9.E+00	1.E+00	3.E-01	5.E+01
GOTERM_MF_FAT	GO:0017048--Rho GTPase binding	5	0.569476082	4.E-02 117600, 17970, 13605, 16800, 192176	754	24	13288	4.E+00	1.E+00	3.E-01	5.E+01
GOTERM_MF_FAT	GO:0008201--heparin binding	10	1.138952164	4.E-02 19944, 12831, 19206, 19934, 11816, 6650	754	83	13288	2.E+00	1.E+00	3.E-01	5.E+01
GOTERM_MF_FAT	GO:0004435--phosphoinositide phospholipase C activity	4	0.455580866	5.E-02 18803, 234779, 18797, 18795	754	15	13288	5.E+00	1.E+00	4.E-01	5.E+01
GOTERM_MF_FAT	GO:0031406--carboxylic acid binding	10	1.138952164	5.E-02 70316, 18126, 11409, 235339, 17999, 184	754	85	13288	2.E+00	1.E+00	4.E-01	5.E+01
GOTERM_MF_FAT	GO:0019900--kinase binding	10	1.138952164	5.E-02 19645, 16179, 16367, 12649, 12443, 1600	754	85	13288	2.E+00	1.E+00	4.E-01	5.E+01
GOTERM_MF_FAT	GO:0005159--insulin-like growth factor receptor binding	3	0.341685649	6.E-02 18708, 16367, 16000	754	7	13288	8.E+00	1.E+00	4.E-01	6.E+01
GOTERM_MF_FAT	GO:0016832--aldehyde-lyase activity	3	0.341685649	6.E-02 230163, 11676, 11674	754	7	13288	8.E+00	1.E+00	4.E-01	6.E+01
GOTERM_MF_FAT	GO:0000287--magnesium ion binding	32	3.644646925	6.E-02 228543, 80905, 18746, 19744, 232087, 54	754	409	13288	1.E+00	1.E+00	4.E-01	6.E+01
GOTERM_MF_FAT	GO:0016860--intramolecular oxidoreductase activity	6	0.683371298	6.E-02 18453, 12304, 14751, 74147, 21991, 1482	754	38	13288	3.E+00	1.E+00	4.E-01	6.E+01
GOTERM_MF_FAT	GO:0001727--lipid kinase activity	5	0.569476082	6.E-02 18709, 18708, 11920, 30955, 18707	754	27	13288	3.E+00	1.E+00	4.E-01	6.E+01
GOTERM_MF_FAT	GO:0005158--insulin receptor binding	4	0.455580866	7.E-02 18708, 16367, 27261, 384783	754	17	13288	4.E+00	1.E+00	5.E-01	7.E+01
GOTERM_MF_FAT	GO:0003756--protein disulfide isomerase activity	3	0.341685649	7.E-02 18453, 12304, 14827	754	8	13288	7.E+00	1.E+00	5.E-01	7.E+01
GOTERM_MF_FAT	GO:0016864--intramolecular oxidoreductase activity, transposing t	3	0.341685649	7.E-02 18453, 12304, 14827	754	8	13288	7.E+00	1.E+00	5.E-01	7.E+01
GOTERM_MF_FAT	GO:0016836--hydro-lyase activity	6	0.683371298	9.E-02 22276, 74147, 433182, 13807, 13806, 937	754	42	13288	3.E+00	1.E+00	5.E-01	8.E+01
GOTERM_MF_FAT	GO:0003705--RNA polymerase II transcription factor activity, enha	5	0.569476082	9.E-02 18771, 14465, 15376, 21869, 17268	754	30	13288	3.E+00	1.E+00	5.E-01	8.E+01
GOTERM_MF_FAT	GO:0005201--extracellular matrix structural constituent	5	0.569476082	9.E-02 12843, 12831, 12842, 12815, 11704	754	30	13288	3.E+00	1.E+00	5.E-01	8.E+01
GOTERM_MF_FAT	GO:0048407--platelet-derived growth factor binding	3	0.341685649	9.E-02 12843, 12831, 12842	754	9	13288	6.E+00	1.E+00	5.E-01	8.E+01
GOTERM_MF_FAT	GO:0016862--intramolecular oxidoreductase activity, interconvertir	3	0.341685649	9.E-02 18453, 12304, 14827	754	9	13288	6.E+00	1.E+00	5.E-01	8.E+01



GOTERM_MF_FAT	GO:0019206--nucleoside kinase activity	3	0.341685649	9.E-02 80914, 68556, 22245	754	9	13288	6.E+00	1.E+00	5.E-01	8.E+01
GOTERM_MF_FAT	GO:0004629--phospholipase C activity	4	0.455580866	9.E-02 18803, 234779, 18797, 18795	754	19	13288	4.E+00	1.E+00	5.E-01	8.E+01
GOTERM_MF_FAT	GO:0051537--2 iron, 2 sulfur cluster binding	4	0.455580866	9.E-02 66694, 14151, 227197, 72900	754	19	13288	4.E+00	1.E+00	5.E-01	8.E+01
GOTERM_MF_FAT	GO:0003746--translation elongation factor activity	5	0.569476082	1.E-01 13627, 13628, 13629, 66656, 55949	754	31	13288	3.E+00	1.E+00	6.E-01	8.E+01
GOTERM_MF_FAT	GO:0004714--transmembrane receptor protein tyrosine kinase act	7	0.797266515	1.E-01 13836, 18596, 13649, 23920, 19713, 1600	754	56	13288	2.E+00	1.E+00	5.E-01	8.E+01
BIOCARTA	m_p53Pathway:p53 Signaling Pathway	12	1.366742597	3.E-06 13555, 19645, 12447, 11920, 12028, 1244	188	16	1171	5.E+00	6.E-04	6.E-04	4.E-03
BIOCARTA	m_fcer1Pathway:Fc Epsilon Receptor 1 Signaling in Mast Cells	16	1.822323462	3.E-05 22324, 12229, 14281, 20416, 18751, 1412	188	32	1171	3.E+00	7.E-03	3.E-03	4.E-02
BIOCARTA	m_il2rbPathway:IL-2 Receptor Beta Chain in T cell Activation	17	1.936218679	4.E-05 15170, 11651, 17869, 12043, 14281, 2041	188	36	1171	3.E+00	8.E-03	3.E-03	5.E-02
BIOCARTA	m_RacCycDPathway:Influence of Ras and Rho proteins on G1 to S	13	1.480637813	9.E-05 11651, 18479, 11848, 18708, 13555, 1964	188	24	1171	3.E+00	2.E-02	5.E-03	1.E-01
BIOCARTA	m_ghPathway:Growth Hormone Signaling Pathway	13	1.480637813	2.E-04 15170, 20416, 18751, 18708, 18803, 1270	188	25	1171	3.E+00	3.E-02	7.E-03	2.E-01
BIOCARTA	m_g1Pathway:Cell Cycle: G1/S Check Point	13	1.480637813	2.E-04 11350, 245000, 13555, 19645, 12447, 119	188	25	1171	3.E+00	3.E-02	7.E-03	2.E-01
BIOCARTA	m_bcrPathway:BCR Signaling Pathway	14	1.59453303	2.E-04 22324, 12229, 14281, 20416, 18751, 1880	188	29	1171	3.E+00	4.E-02	7.E-03	2.E-01
BIOCARTA	m_jgf1rPathway:Multiple antiapoptotic pathways from IGF-1R sigr	11	1.25284738	2.E-04 18708, 18747, 12015, 16367, 14784, 2066	188	19	1171	4.E+00	5.E-02	7.E-03	3.E-01
BIOCARTA	m_trkaPathway:Trka Receptor Signaling Pathway	9	1.025056948	2.E-04 18048, 18751, 18708, 18803, 14784, 2066	188	13	1171	4.E+00	5.E-02	6.E-03	3.E-01
BIOCARTA	m_cellcyclePathway:Cyclins and Cell Cycle Regulation	12	1.366742597	3.E-04 12445, 13555, 19645, 12447, 12443, 1256	188	23	1171	3.E+00	7.E-02	8.E-03	4.E-01
BIOCARTA	m_rbPathway:RB Tumor Suppressor/Checkpoint Signaling in resp	8	0.911161731	4.E-04 19645, 22390, 11920, 12649, 12567, 1253	188	11	1171	5.E+00	1.E-01	1.E-02	6.E-01
BIOCARTA	m_tffPathway:Trefoil Factors Initiate Mucosal Healing	11	1.25284738	1.E-03 18708, 13649, 672195, 12015, 14784, 206	188	23	1171	3.E+00	3.E-01	3.E-02	2.E+00
BIOCARTA	m_il3Pathway:IL 3 signaling pathway	9	1.025056948	1.E-03 15170, 12983, 14784, 20662, 26395, 1546	188	16	1171	4.E+00	3.E-01	3.E-02	2.E+00
BIOCARTA	m_mcmPathway:CDK Regulation of DNA Replication	6	0.683371298	2.E-03 17217, 12447, 26429, 12566, 23834, 1257	188	7	1171	5.E+00	3.E-01	3.E-02	2.E+00
BIOCARTA	m_plcPathway:Phospholipase C Signaling Pathway	6	0.683371298	2.E-03 18751, 18708, 22324, 18803, 11651, 1879	188	7	1171	5.E+00	3.E-01	3.E-02	2.E+00
BIOCARTA	m_pyk2Pathway:Links between Pyk2 and Map Kinases	12	1.366742597	2.E-03 18479, 20416, 18751, 18803, 20779, 1478	188	27	1171	3.E+00	3.E-01	3.E-02	2.E+00
BIOCARTA	m_chemicalPathway:Apoptotic Signaling in Response to DNA Dan	10	1.138952164	2.E-03 18751, 672195, 12015, 12048, 11920, 120	188	20	1171	3.E+00	3.E-01	3.E-02	2.E+00
BIOCARTA	m_jgf1mrtorPathway:Skeletal muscle hypertrophy is regulated via /	10	1.138952164	2.E-03 13684, 18708, 56717, 13685, 26905, 1366	188	20	1171	3.E+00	3.E-01	3.E-02	2.E+00
BIOCARTA	m_Par1Pathway:Thrombin signaling and protease-activated recept	9	1.025056948	2.E-03 18751, 18708, 14674, 14065, 14682, 1680	188	17	1171	3.E+00	4.E-01	3.E-02	3.E+00
BIOCARTA	m_jgf1PathwayJGF-1 Signaling Pathway	10	1.138952164	3.E-03 18708, 16367, 14784, 20662, 26395, 1546	188	21	1171	3.E+00	5.E-01	4.E-02	4.E+00
BIOCARTA	m_epoPathway:EPO Signaling Pathway	10	1.138952164	3.E-03 15170, 18803, 13857, 14784, 20662, 2639	188	21	1171	3.E+00	5.E-01	4.E-02	4.E+00
BIOCARTA	m_monocytePathway:Monocyte and its Surface Molecules	7	0.797266515	4.E-03 16408, 20343, 16414, 12505, 16412, 2033	188	11	1171	4.E+00	5.E-01	4.E-02	4.E+00
BIOCARTA	m_neutrophilPathway:Neutrophil and Its Surface Molecules	6	0.683371298	4.E-03 16408, 20343, 16414, 12505, 20339, 1640	188	8	1171	5.E+00	6.E-01	4.E-02	5.E+00
BIOCARTA	m_badPathway:Regulation of BAD phosphorylation	9	1.025056948	4.E-03 18708, 18747, 12015, 12048, 12028, 1165	188	18	1171	3.E+00	6.E-01	4.E-02	5.E+00
BIOCARTA	m_gleevecPathway:Inhibition of Cellular Proliferation by Gleevec	10	1.138952164	4.E-03 18708, 12015, 14784, 20662, 26395, 1546	188	22	1171	3.E+00	6.E-01	4.E-02	5.E+00
BIOCARTA	m_ngfPathway:Nerve growth factor pathway (NGF)	9	1.025056948	6.E-03 18048, 18708, 18803, 14784, 20662, 2639	188	19	1171	3.E+00	7.E-01	6.E-02	7.E+00
BIOCARTA	m_ecmPathway:Erk and PI-3 Kinase Are Necessary for Collagen Bi	9	1.025056948	6.E-03 18708, 20779, 26395, 15461, 11855, 1436	188	19	1171	3.E+00	7.E-01	6.E-02	7.E+00
BIOCARTA	m_TPOPathway:TPO Signaling Pathway	10	1.138952164	6.E-03 18751, 18708, 18803, 14784, 20662, 2639	188	23	1171	3.E+00	7.E-01	6.E-02	7.E+00
BIOCARTA	m_p27Pathway:Regulation of p27 Phosphorylation during Cell Cyt	7	0.797266515	6.E-03 13555, 19645, 12447, 26965, 12566, 5412	188	12	1171	4.E+00	7.E-01	6.E-02	8.E+00
BIOCARTA	m_tcrPathway:T Cell Receptor Signaling Pathway	13	1.480637813	7.E-03 22324, 14281, 20416, 18751, 16818, 1870	188	36	1171	2.E+00	8.E-01	6.E-02	9.E+00
BIOCARTA	m_lymphocytePathway:Adhesion Molecules on Lymphocyte	6	0.683371298	7.E-03 16408, 20343, 16414, 12505, 16412, 2033	188	9	1171	4.E+00	8.E-01	6.E-02	9.E+00
BIOCARTA	m_HBxPathway:Calcium Signaling by HBx of Hepatitis B virus	6	0.683371298	7.E-03 20779, 14784, 20662, 15461, 20416, 1291	188	9	1171	4.E+00	8.E-01	6.E-02	9.E+00
BIOCARTA	m_nkcellsPathway:Ras-Independent pathway in NK cell-mediated	8	0.911161731	8.E-03 18708, 15170, 22324, 26395, 16412, 1847	188	16	1171	3.E+00	8.E-01	6.E-02	9.E+00
BIOCARTA	m_spryPathway:Sprouty regulation of tyrosine kinase signals	8	0.911161731	8.E-03 13649, 20779, 24064, 14784, 20662, 2639	188	16	1171	3.E+00	8.E-01	6.E-02	9.E+00
BIOCARTA	m_biopeptidesPathway:Bioactive Peptide Induced Signaling Pathwa	12	1.366742597	8.E-03 20416, 18751, 18803, 14784, 12315, 2641	188	32	1171	2.E+00	8.E-01	6.E-02	9.E+00
BIOCARTA	m_At1rPathway:Angiotensin II mediated activation of JNK Pathway	11	1.25284738	8.E-03 13649, 18479, 20416, 18751, 20779, 1478	188	28	1171	2.E+00	8.E-01	6.E-02	1.E+01
BIOCARTA	m_eif4Pathway:Regulation of eIF4e and p70 S6 Kinase	9	1.025056948	8.E-03 13684, 18751, 18708, 56717, 13685, 1636	188	20	1171	3.E+00	8.E-01	6.E-02	1.E+01
BIOCARTA	m_rasPathway:Ras Signaling Pathway	9	1.025056948	8.E-03 18708, 12015, 12048, 26395, 15461, 1165	188	20	1171	3.E+00	8.E-01	6.E-02	1.E+01
BIOCARTA	m_integrinPathway:Integrin Signaling Pathway	11	1.25284738	1.E-02 20779, 14784, 20662, 26395, 15461, 1436	188	29	1171	2.E+00	9.E-01	7.E-02	1.E+01
BIOCARTA	m_crebPathway:Transcription factor CREB and its extracellular sigr	9	1.025056948	1.E-02 18751, 18708, 18747, 14784, 20662, 2641	188	21	1171	3.E+00	9.E-01	8.E-02	1.E+01
BIOCARTA	m_cdc25Pathway:cdc25 and chk1 Regulatory Pathway in response	5	0.569476082	1.E-02 22390, 11920, 12649, 12532, 12534	188	7	1171	4.E+00	1.E+00	1.E-01	2.E+01
BIOCARTA	m_eifPathway:Eukaryotic protein translation	5	0.569476082	1.E-02 13669, 217869, 13664, 13629, 67204, 100	188	7	1171	4.E+00	1.E+00	1.E-01	2.E+01
BIOCARTA	m_srcRPTTPPathway:Activation of Src by Protein-tyrosine phosphat	5	0.569476082	1.E-02 18751, 20779, 14784, 12532, 12534	188	7	1171	4.E+00	1.E+00	1.E-01	2.E+01
BIOCARTA	m_erk5Pathway:Role of Erk5 in Neuronal Survival	7	0.797266515	2.E-02 18708, 18803, 14784, 15461, 11651, 2041	188	14	1171	3.E+00	1.E+00	1.E-01	2.E+01
BIOCARTA	m_mTORPathway:mTOR Signaling Pathway	9	1.025056948	2.E-02 13684, 18708, 56717, 19744, 13685, 7570	188	22	1171	3.E+00	1.E+00	1.E-01	2.E+01
BIOCARTA	m_insulinPathway:Insulin Signaling Pathway	9	1.025056948	2.E-02 18708, 16367, 16334, 14784, 20662, 2639	188	22	1171	3.E+00	1.E+00	1.E-01	2.E+01
BIOCARTA	m_erkPathway:Erk1/Erk2 Mapk Signaling pathway	11	1.25284738	2.E-02 18048, 13649, 20779, 14784, 20662, 2639	188	31	1171	2.E+00	1.E+00	1.E-01	2.E+01
BIOCARTA	m_longevityPathway:The IGF-1 Receptor and Longevity	6	0.683371298	2.E-02 18708, 15461, 11651, 16001, 20416, 1600	188	11	1171	3.E+00	1.E+00	1.E-01	2.E+01
BIOCARTA	m_g2Pathway:Cell Cycle: G2/M Checkpoint	9	1.025056948	2.E-02 22390, 18817, 245000, 11920, 12649, 131	188	23	1171	2.E+00	1.E+00	1.E-01	2.E+01
BIOCARTA	m_hdacPathway:Control of skeletal myogenesis by HDAC & calci	8	0.911161731	2.E-02 18019, 18708, 16334, 12315, 12314, 2641	188	19	1171	3.E+00	1.E+00	1.E-01	2.E+01
BIOCARTA	m_egfPathway:EGF Signaling Pathway	10	1.138952164	2.E-02 18751, 18708, 13649, 18803, 14784, 2066	188	28	1171	2.E+00	1.E+00	1.E-01	3.E+01
BIOCARTA	m_fibrinolysisPathway:Fibrinolysis Pathway	5	0.569476082	3.E-02 18787, 18815, 74145, 18792, 18788	188	8	1171	4.E+00	1.E+00	1.E-01	3.E+01
BIOCARTA	m_gsk3Pathway:Inactivation of Gsk3 by AKT causes accumulation	9	1.025056948	3.E-02 18708, 17874, 12475, 16179, 17087, 1244	188	25	1171	2.E+00	1.E+00	2.E-01	4.E+01
BIOCARTA	m_gpcrPathway:Signaling Pathway from G-Protein Families	9	1.025056948	3.E-02 18751, 18747, 18803, 12315, 12314, 2639	188	25	1171	2.E+00	1.E+00	2.E-01	4.E+01
BIOCARTA	m_mitochondriaPathway:Role of Mitochondria in Apoptotic Signa	8	0.911161731	4.E-02 672195, 66593, 12048, 12028, 12122, 120	188	21	1171	2.E+00	1.E+00	2.E-01	4.E+01
BIOCARTA	m_cardiacegfPathway:Role of EGF Receptor Transactivation by GP	7	0.797266515	4.E-02 18751, 13649, 18803, 15461, 17869, 1428	188	17	1171	3.E+00	1.E+00	2.E-01	4.E+01
BIOCARTA	m_fbw7Pathway:Cyclin E Destruction Pathway	5	0.569476082	4.E-02 13555, 19645, 12447, 26965, 12566	188	9	1171	3.E+00	1.E+00	2.E-01	4.E+01
BIOCARTA	m_ceramidePathway:Ceramide Signaling Pathway	8	0.911161731	5.E-02 672195, 12015, 12028, 26395, 12043, 130	188	22	1171	2.E+00	1.E+00	2.E-01	5.E+01
BIOCARTA	m_her2Pathway:Role of ERBB2 in Signal Transduction and Oncolo	8	0.911161731	5.E-02 18708, 16195, 13649, 14784, 20662, 2639	188	22	1171	2.E+00	1.E+00	2.E-01	5.E+01
BIOCARTA	m_akap13Pathway:Rho-Selective Guanine Exchange Factor AKAP1	4	0.455580866	6.E-02 18747, 19088, 14673, 11848	188	6	1171	4.E+00	1.E+00	2.E-01	5.E+01



Biocarta	m_metPathway:Signaling of Hepatocyte Growth Factor Receptor	10	1.138952164	6.E-02 18708, 20779, 14784, 20662, 26395, 1546	188	32	1171	2.E+00	1.E+00	2.E-01	5.E+01
Biocarta	m_hcmvPathway:Human Cytomegalovirus and Map Kinase Pathwa	6	0.683371298	6.E-02 18708, 19645, 26416, 26395, 11651, 1291	188	14	1171	3.E+00	1.E+00	2.E-01	5.E+01
Biocarta	m_cdMacPathway:Cadmium induces DNA synthesis and proliferat	6	0.683371298	6.E-02 18751, 26395, 15461, 17869, 14281, 1879	188	14	1171	3.E+00	1.E+00	2.E-01	5.E+01
Biocarta	m_GATA3pathway:GATA3 participate in activating the Th2 cytokin	5	0.569476082	6.E-02 18019, 18747, 26416, 14462, 16477	188	10	1171	3.E+00	1.E+00	2.E-01	5.E+01
Biocarta	m_skp2e2fPathway:E2F1 Destruction Pathway	5	0.569476082	6.E-02 13555, 19645, 12447, 26965, 12566	188	10	1171	3.E+00	1.E+00	2.E-01	5.E+01
Biocarta	m_pdgfPathway:PDGF Signaling Pathway	9	1.025056948	6.E-02 18751, 18708, 18803, 14784, 20662, 2639	188	28	1171	2.E+00	1.E+00	3.E-01	6.E+01
Biocarta	m_rhoPathway:Rho cell motility signaling pathway	7	0.797266515	7.E-02 20779, 94190, 11856, 11855, 171207, 168	188	19	1171	2.E+00	1.E+00	3.E-01	6.E+01
Biocarta	m_il2Pathway:IL 2 signaling pathway	8	0.911161731	7.E-02 16818, 14784, 20662, 26395, 15461, 1428	188	24	1171	2.E+00	1.E+00	3.E-01	6.E+01
Biocarta	m_d4gdPathway:D4-GDI Signaling Pathway	5	0.569476082	8.E-02 672195, 14939, 11855, 11857, 13063, 123	188	11	1171	3.E+00	1.E+00	3.E-01	7.E+01
Biocarta	m_ptenPathway:PTEN dependent cell cycle arrest and apoptosis	7	0.797266515	8.E-02 18708, 14784, 20662, 11651, 16412, 2041	188	20	1171	2.E+00	1.E+00	3.E-01	7.E+01
Biocarta	m_nos1Pathway:Nitric Oxide Signaling Pathway	4	0.455580866	9.E-02 18751, 18747, 12315, 12314, 12313, 1338	188	7	1171	4.E+00	1.E+00	3.E-01	7.E+01
Biocarta	m_il7Pathway:IL-7 Signal Transduction	6	0.683371298	1.E-01 18708, 16818, 16197, 12043, 14360, 1291	188	16	1171	2.E+00	1.E+00	3.E-01	7.E+01
Biocarta	m_Ccr5Pathway:Pertussis toxin-insensitive CCR5 Signaling in Macr	6	0.683371298	1.E-01 18751, 18803, 12315, 12314, 26416, 1231	188	16	1171	2.E+00	1.E+00	3.E-01	7.E+01
Biocarta	m_vipPathway:Neuropeptides VIP and PACAP inhibit the apoptosi	6	0.683371298	1.E-01 18019, 18747, 18803, 12315, 12314, 1231	188	16	1171	2.E+00	1.E+00	3.E-01	7.E+01
KEGG_PATHWAY	mmu03010:Ribosome	64	7.28929385	1.E-43 666899, 100048462, 20103, 100044516, 1	580	89	5738	7.E+00	2.E-41	2.E-41	2.E-40
KEGG_PATHWAY	mmu04110:Cell cycle	72	8.200455581	2.E-38 50793, 59008, 56150, 12914, 17218, 1721	580	128	5738	6.E+00	3.E-36	1.E-36	2.E-35
KEGG_PATHWAY	mmu04914:Progesterone-mediated oocyte maturation	40	4.555808656	1.E-17 18747, 11651, 59008, 56150, 18709, 1870	580	85	5738	5.E+00	2.E-15	6.E-16	1.E-14
KEGG_PATHWAY	mmu05012:Parkinson's disease	49	5.580865604	2.E-16 70316, 672195, 226646, 100041273, 6637	580	133	5738	4.E+00	4.E-14	9.E-15	3.E-13
KEGG_PATHWAY	mmu00010:Glycolysis / Gluconeogenesis	34	3.872437358	6.E-16 18746, 68263, 100042746, 15275, 15277,	580	68	5738	5.E+00	9.E-14	2.E-14	7.E-13
KEGG_PATHWAY	mmu05010:Alzheimer's disease	58	6.605922551	7.E-16 70316, 672195, 226646, 100041273, 6637	580	182	5738	3.E+00	1.E-13	2.E-14	8.E-13
KEGG_PATHWAY	mmu00190:Oxidative phosphorylation	46	5.239179954	2.E-14 70316, 226646, 100041273, 66377, 59513	580	130	5738	4.E+00	3.E-12	4.E-13	2.E-11
KEGG_PATHWAY	mmu05016:Huntington's disease	56	6.378132118	2.E-14 70316, 672195, 226646, 100041273, 6637	580	183	5738	3.E+00	3.E-12	3.E-13	2.E-11
KEGG_PATHWAY	mmu04114:Oocyte meiosis	42	4.783599089	8.E-14 18747, 26965, 59008, 56150, 103583, 671	580	115	5738	4.E+00	1.E-11	1.E-12	9.E-11
KEGG_PATHWAY	mmu04910:Insulin signaling pathway	42	4.783599089	7.E-11 13684, 19744, 18747, 13685, 11651, 1527	580	138	5738	3.E+00	1.E-08	1.E-09	8.E-08
KEGG_PATHWAY	mmu05214:Glioma	27	3.075170843	1.E-10 13649, 11651, 20416, 18709, 56717, 1880	580	64	5738	4.E+00	2.E-08	2.E-09	1.E-07
KEGG_PATHWAY	mmu05215:Prostate cancer	32	3.644646925	3.E-10 13649, 11651, 12912, 12914, 18709, 5671	580	90	5738	4.E+00	4.E-08	3.E-09	3.E-07
KEGG_PATHWAY	mmu04650:Natural killer cell mediated cytotoxicity	38	4.328018223	3.E-10 14972, 22324, 14939, 20416, 170758, 187	580	122	5738	3.E+00	5.E-08	4.E-09	4.E-07
KEGG_PATHWAY	mmu04115:p53 signaling pathway	27	3.075170843	8.E-10 672195, 245000, 12649, 12445, 12448, 12	580	69	5738	4.E+00	1.E-07	9.E-09	1.E-06
KEGG_PATHWAY	mmu05223:Non-small cell lung cancer	22	2.505694761	2.E-08 13649, 320207, 54354, 11651, 18709, 187	580	54	5738	4.E+00	3.E-06	2.E-07	2.E-05
KEGG_PATHWAY	mmu05200:Pathways in cancer	64	7.28929385	1.E-07 12190, 672195, 14178, 19206, 54354, 170	580	323	5738	2.E+00	2.E-05	1.E-06	1.E-04
KEGG_PATHWAY	mmu04662:B cell receptor signaling pathway	26	2.961275626	1.E-07 22324, 11651, 170758, 18019, 18709, 187	580	80	5738	3.E+00	2.E-05	1.E-06	2.E-04
KEGG_PATHWAY	mmu04664:Fc epsilon RI signaling pathway	26	2.961275626	2.E-07 22324, 11651, 170758, 18709, 18803, 187	580	82	5738	3.E+00	4.E-05	2.E-06	3.E-04
KEGG_PATHWAY	mmu05222:Small cell lung cancer	26	2.961275626	5.E-07 22029, 672195, 17869, 11651, 18709, 187	580	85	5738	3.E+00	8.E-05	4.E-06	6.E-04
KEGG_PATHWAY	mmu04930:Type II diabetes mellitus	19	2.164009112	5.E-07 18746, 320207, 15275, 15277, 384783, 10	580	49	5738	4.E+00	8.E-05	4.E-06	6.E-04
KEGG_PATHWAY	mmu05220:Chronic myeloid leukemia	24	2.733485194	8.E-07 11350, 320207, 433759, 11651, 17869, 20	580	76	5738	3.E+00	1.E-04	6.E-06	1.E-03
KEGG_PATHWAY	mmu04670:Leukocyte transendothelial migration	31	3.530751708	1.E-06 22323, 22324, 69524, 232906, 54354, 118	580	119	5738	3.E+00	2.E-04	1.E-05	2.E-03
KEGG_PATHWAY	mmu04012:ErbB signaling pathway	25	2.84738041	3.E-06 13649, 13685, 17869, 11651, 20416, 1870	580	87	5738	3.E+00	5.E-04	2.E-05	4.E-03
KEGG_PATHWAY	mmu04210:Apoptosis	25	2.84738041	3.E-06 672195, 18747, 11651, 21937, 18709, 187	580	87	5738	3.E+00	5.E-04	2.E-05	4.E-03
KEGG_PATHWAY	mmu04510:Focal adhesion	42	4.783599089	4.E-06 22323, 12831, 22324, 13649, 232906, 227	580	198	5738	2.E+00	7.E-04	3.E-05	5.E-03
KEGG_PATHWAY	mmu04722:Neurotrophin signaling pathway	31	3.530751708	1.E-05 192662, 11651, 11857, 20416, 18709, 188	580	130	5738	2.E+00	2.E-03	6.E-05	1.E-02
KEGG_PATHWAY	mmu04660:T cell receptor signaling pathway	29	3.302961276	1.E-05 22324, 11651, 18019, 18709, 18803, 1870	580	118	5738	2.E+00	2.E-03	7.E-05	1.E-02
KEGG_PATHWAY	mmu04370:VEGF signaling pathway	22	2.505694761	1.E-05 320207, 11651, 170758, 18709, 18751, 18	580	76	5738	3.E+00	2.E-03	7.E-05	1.E-02
KEGG_PATHWAY	mmu05218:Melanoma	21	2.391799544	1.E-05 13649, 14178, 320207, 11651, 14180, 187	580	71	5738	3.E+00	2.E-03	8.E-05	2.E-02
KEGG_PATHWAY	mmu05212:Pancreatic cancer	21	2.391799544	2.E-05 12190, 13649, 320207, 11651, 170758, 18	580	72	5738	3.E+00	3.E-03	1.E-04	2.E-02
KEGG_PATHWAY	mmu04810:Regulation of actin cytoskeleton	43	4.897494305	2.E-05 12475, 227753, 22324, 13649, 14178, 170	580	217	5738	2.E+00	3.E-03	1.E-04	2.E-02
KEGG_PATHWAY	mmu04666:Fc gamma R-mediated phagocytosis	25	2.84738041	3.E-05 22323, 22324, 227753, 13430, 11651, 223	580	98	5738	3.E+00	4.E-03	1.E-04	3.E-02
KEGG_PATHWAY	mmu05210:Colorectal cancer	23	2.619589977	3.E-05 13649, 672195, 320207, 11651, 17869, 12	580	86	5738	3.E+00	4.E-03	1.E-04	3.E-02
KEGG_PATHWAY	mmu04062:Chemokine signaling pathway	37	4.214123007	5.E-05 12765, 22324, 18747, 11651, 20416, 2184	580	182	5738	2.E+00	8.E-03	2.E-04	6.E-02
KEGG_PATHWAY	mmu05221:Acute myeloid leukemia	17	1.936218679	1.E-04 13685, 320207, 17869, 20375, 11651, 187	580	57	5738	3.E+00	2.E-02	5.E-04	1.E-01
KEGG_PATHWAY	mmu00620:Pyruvate metabolism	14	1.59453303	1.E-04 18746, 68263, 18534, 13382, 74551, 1682	580	41	5738	3.E+00	2.E-02	5.E-04	1.E-01
KEGG_PATHWAY	mmu00030:Ribosome	11	1.25284738	1.E-04 56421, 14751, 21351, 230163, 72157, 116	580	26	5738	4.E+00	2.E-02	5.E-04	1.E-01
KEGG_PATHWAY	mmu04120:Ubiquitin mediated proteolysis	29	3.302961276	2.E-04 56550, 218793, 26965, 246710, 22209, 59	580	136	5738	2.E+00	3.E-02	7.E-04	2.E-01
KEGG_PATHWAY	mmu04150:mTOR signaling pathway	16	1.822323462	2.E-04 13684, 19744, 13685, 320207, 11651, 187	580	54	5738	3.E+00	3.E-02	8.E-04	2.E-01
KEGG_PATHWAY	mmu05213:Endometrial cancer	15	1.708428246	5.E-04 13649, 320207, 17869, 11651, 18709, 187	580	52	5738	3.E+00	7.E-02	2.E-03	5.E-01
KEGG_PATHWAY	mmu04620:Toll-like receptor signaling pathway	22	2.505694761	7.E-04 12475, 320207, 27056, 21899, 21898, 116	580	99	5738	1.E-01	3.E-03	8.E-01	
KEGG_PATHWAY	mmu04630:Jak-STAT signaling pathway	28	3.189066059	2.E-03 18414, 17869, 11651, 12914, 18709, 1870	580	152	5738	2.E+00	3.E-01	9.E-03	3.E+00
KEGG_PATHWAY	mmu05213:Renal cell carcinoma	16	1.822323462	4.E-03 20525, 320207, 11651, 18479, 12914, 187	580	70	5738	2.E+00	4.E-01	1.E-02	4.E+00
KEGG_PATHWAY	mmu03030:DNA replication	10	1.138952164	7.E-03 17218, 19891, 17217, 17220, 17216, 1721	580	35	5738	3.E+00	6.E-01	2.E-02	8.E+00
KEGG_PATHWAY	mmu04960:Aldosterone-regulated sodium reabsorption	11	1.25284738	8.E-03 18709, 18751, 18708, 16367, 16333, 1633	580	42	5738	3.E+00	7.E-01	3.E-02	9.E+00
KEGG_PATHWAY	mmu04010:MAPK signaling pathway	40	4.555808656	9.E-03 12475, 13649, 18747, 14178, 11651, 1786	580	265	5738	1.E+00	8.E-01	3.E-02	1.E+01
KEGG_PATHWAY	mmu00020:Citrate cycle (TCA cycle)	9	1.025056948	1.E-02 68263, 235339, 18597, 18598, 18534, 185	580	31	5738	3.E+00	8.E-01	3.E-02	1.E+01
KEGG_PATHWAY	mmu04540:Gap junction	17	1.936218679	1.E-02 22142, 18747, 13649, 14678, 18797, 1879	580	86	5738	2.E+00	8.E-01	4.E-02	1.E+01
KEGG_PATHWAY	mmu00280:Valine, leucine and isoleucine degradation	11	1.25284738	1.E-02 12039, 66885, 15107, 11409, 74147, 1000	580	46	5738	2.E+00	9.E-01	5.E-02	2.E+01
KEGG_PATHWAY	mmu04720:Long-term potentiation	14	1.59453303	2.E-02 18747, 18797, 12914, 18795, 18751, 1151	580	70	5738	2.E+00	1.E+00	7.E-02	2.E+01
KEGG_PATHWAY	mmu05219:Bladder cancer	10	1.138952164	2.E-02 13649, 13555, 19645, 242705, 12443, 263	580	42	5738	2.E+00	1.E+00	7.E-02	2.E+01



KEGG_PATHWAY	mmu05416:Viral myocarditis	17	1.936218679	2.E-02	15007, 14972, 11350, 672195, 15018, 121	580	94	5738	2.E+00	1.E+00	7.E-02	3.E+01
KEGG_PATHWAY	mmu03420:Nucleotide excision repair	10	1.138952164	3.E-02	13872, 19891, 19358, 68240, 17420, 1488	580	43	5738	2.E+00	1.E+00	7.E-02	3.E+01
KEGG_PATHWAY	mmu04730:Long-term depression	14	1.59453303	3.E-02	14674, 14678, 18797, 18795, 18751, 1878	580	72	5738	2.E+00	1.E+00	8.E-02	3.E+01
KEGG_PATHWAY	mmu00640:Propanoate metabolism	8	0.911161731	3.E-02	16828, 74147, 93747, 68738, 16833, 1683	580	30	5738	3.E+00	1.E+00	8.E-02	3.E+01
KEGG_PATHWAY	mmu04912:GnRH signaling pathway	17	1.936218679	3.E-02	18747, 13649, 18797, 18795, 18751, 1878	580	97	5738	2.E+00	1.E+00	9.E-02	3.E+01
KEGG_PATHWAY	mmu04920:Adipocytokine signaling pathway	13	1.480637813	3.E-02	20525, 18534, 11651, 384783, 74551, 219	580	67	5738	2.E+00	1.E+00	9.E-02	3.E+01
KEGG_PATHWAY	mmu00563:Glycosylphosphatidylinositol(GPI)-anchor biosynthesis	7	0.797266515	3.E-02	14731, 56703, 276846, 329777, 18701, 22	580	25	5738	3.E+00	1.E+00	9.E-02	3.E+01
KEGG_PATHWAY	mmu05014:Amyotrophic lateral sclerosis (ALS)	11	1.25284738	6.E-02	672195, 12015, 12048, 12028, 12122, 264	580	57	5738	2.E+00	1.E+00	1.E-01	5.E+01
KEGG_PATHWAY	mmu00500:Starch and sucrose metabolism	8	0.911161731	6.E-02	110095, 14751, 15275, 72157, 15277, 103	580	36	5738	2.E+00	1.E+00	2.E-01	6.E+01
KEGG_PATHWAY	mmu04360:Axon guidance	20	2.277904328	7.E-02	117600, 11350, 11854, 14678, 14270, 184	580	131	5738	2.E+00	1.E+00	2.E-01	6.E+01
KEGG_PATHWAY	mmu00051:Fructose and mannose metabolism	8	0.911161731	7.E-02	56421, 15275, 21991, 230163, 15277, 116	580	37	5738	2.E+00	1.E+00	2.E-01	6.E+01
KEGG_PATHWAY	mmu00071:Fatty acid metabolism	9	1.025056948	8.E-02	11370, 66885, 15107, 11409, 74147, 9374	580	45	5738	2.E+00	1.E+00	2.E-01	6.E+01
KEGG_PATHWAY	mmu00561:Glycerolipid metabolism	9	1.025056948	1.E-01	55979, 28169, 68262, 14732, 669888, 675	580	47	5738	2.E+00	1.E+00	2.E-01	7.E+01

Annotation Cluster 1	Enrichment Score: 32.8837722323287644											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
KEGG_PATHWAY	mmu03010:Ribosome	64	7.28929385	1.E-43	666899, 100048462, 20103, 100044516, 1	580	89	5738	7.E+00	2.E-41	2.E-41	2.E-40
GOTERM_BP_FAT	GO:0006412--translation	96	10.93394077	9.E-42	666899, 100048462, 13669, 100044516, 2	809	319	13588	5.E+00	3.E-38	1.E-38	2.E-38
SP_PIR_KEYWORDS	ribosomal protein	66	7.517084282	5.E-40	666899, 100048462, 20103, 100044516, 1	869	177	17854	8.E+00	2.E-37	5.E-38	7.E-37
GOTERM_MF_FAT	GO:0003735~structural constituent of ribosome	64	7.28929385	5.E-39	666899, 100048462, 20103, 100044516, 1	754	151	13288	7.E+00	4.E-36	4.E-36	7.E-36
GOTERM_CC_FAT	GO:0005840~ribosome	68	7.744874715	9.E-39	666899, 100048462, 20103, 100044516, 1	636	192	12504	7.E+00	4.E-36	2.E-36	1.E-35
SP_PIR_KEYWORDS	ribonucleoprotein	68	7.744874715	8.E-30	666899, 100048462, 20103, 100044516, 1	869	266	17854	5.E+00	3.E-27	6.E-28	1.E-26
GOTERM_CC_FAT	GO:0030529~ribonucleoprotein complex	76	8.656036446	7.E-20	666899, 100048462, 19744, 20103, 10004	636	462	12504	3.E+00	3.E-17	5.E-18	1.E-16
GOTERM_MF_FAT	GO:0005198~structural molecule activity	73	8.314350797	6.E-16	666899, 100048462, 20103, 100044516, 1	754	450	13288	3.E+00	5.E-13	5.E-14	1.E-12

Annotation Cluster 2	Enrichment Score: 29.99199327635345											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR000198:RhoGAP	47	5.353075171	5.E-45	117600, 94190, 232906, 228482, 243362,	860	67	17763	1.E+01	6.E-42	6.E-42	8.E-42
SMART	SM00324:RhoGAP	47	5.353075171	2.E-43	117600, 94190, 232906, 228482, 243362,	492	67	9131	1.E+01	5.E-41	5.E-41	3.E-40
UP_SEQ_FEATURE	domain:Rho-GAP	42	4.783599089	8.E-40	117600, 228482, 232906, 94190, 243362,	861	57	16021	1.E+01	2.E-36	2.E-36	1.E-36
GOTERM_MF_FAT	GO:0030695~GTPase regulator activity	83	9.453302961	2.E-28	22324, 228482, 94190, 192662, 243362, 1	754	361	13288	4.E+00	1.E-25	6.E-26	2.E-25
GOTERM_MF_FAT	GO:0060589~monoside-triphosphatase regulator activity	83	9.453302961	5.E-28	22324, 228482, 94190, 192662, 243362, 1	754	367	13288	4.E+00	4.E-25	1.E-25	8.E-25
SP_PIR_KEYWORDS	GTPase activation	47	5.353075171	8.E-27	117600, 94190, 232906, 228482, 192662,	869	136	17854	7.E+00	3.E-24	4.E-25	1.E-23
GOTERM_MF_FAT	GO:0005096~GTPase activator activity	48	5.466970387	4.E-18	117600, 94190, 232906, 228482, 192662,	754	192	13288	4.E+00	3.E-15	3.E-16	6.E-15
GOTERM_MF_FAT	GO:0008047~enzyme activator activity	52	5.922551253	5.E-16	94190, 228482, 243362, 192662, 14270, 2	754	249	13288	4.E+00	4.E-13	5.E-14	8.E-13

Annotation Cluster 3	Enrichment Score: 20.990479927449783											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0006006~glucose metabolic process	52	5.922551253	2.E-27	18746, 68263, 18679, 11676, 56012, 1167	809	140	13588	6.E+00	6.E-24	2.E-24	4.E-24
SP_PIR_KEYWORDS	glycolysis	29	3.302961276	3.E-27	18746, 68263, 100042746, 15275, 15277,	869	42	17854	1.E+01	1.E-24	2.E-25	4.E-24
GOTERM_BP_FAT	GO:0019320~hexose catabolic process	32	3.644646925	3.E-25	18746, 68263, 100042746, 15275, 15277,	809	52	13588	1.E+01	1.E-21	2.E-22	6.E-22
GOTERM_BP_FAT	GO:0006007~glucose catabolic process	32	3.644646925	3.E-25	18746, 68263, 100042746, 15275, 15277,	809	52	13588	1.E+01	1.E-21	2.E-22	6.E-22
GOTERM_BP_FAT	GO:0046365~monosaccharide catabolic process	32	3.644646925	2.E-24	18746, 68263, 100042746, 15275, 15277,	809	54	13588	1.E+01	5.E-21	8.E-22	3.E-21
GOTERM_BP_FAT	GO:0006096~glycolysis	29	3.302961276	5.E-24	18746, 68263, 100042746, 15275, 15277,	809	44	13588	1.E+01	1.E-20	2.E-21	9.E-21
GOTERM_BP_FAT	GO:0019318~hexose metabolic process	53	6.036446469	6.E-24	18746, 68263, 18679, 11676, 56012, 1167	809	169	13588	5.E+00	2.E-20	2.E-21	1.E-20
GOTERM_BP_FAT	GO:0044275~cellular carbohydrate catabolic process	32	3.644646925	1.E-22	18746, 68263, 100042746, 15275, 15277,	809	60	13588	9.E+00	4.E-19	4.E-20	2.E-19
GOTERM_BP_FAT	GO:0046164~alcohol catabolic process	33	3.758542141	2.E-22	18746, 68263, 100042746, 15275, 15277,	809	65	13588	9.E+00	5.E-19	5.E-20	3.E-19
GOTERM_BP_FAT	GO:0005996~monosaccharide metabolic process	53	6.036446469	3.E-21	18746, 68263, 18679, 11676, 56012, 1167	809	191	13588	5.E+00	9.E-18	8.E-19	5.E-18
GOTERM_BP_FAT	GO:0016052~carbohydrate catabolic process	32	3.644646925	7.E-18	18746, 68263, 100042746, 15275, 15277,	809	81	13588	7.E+00	2.E-14	2.E-15	1.E-14
KEGG_PATHWAY	mmu00010:Glycolysis / Gluconeogenesis	34	3.872437358	6.E-16	18746, 68263, 100042746, 15275, 15277,	580	68	5738	5.E+00	9.E-14	2.E-14	7.E-13
UP_SEQ_FEATURE	binding site:Substrate	31	3.530751708	2.E-04	18746, 66885, 22245, 11676, 11674, 1039	861	275	16021	2.E+00	3.E-01	2.E-02	3.E-01

Annotation Cluster 4	Enrichment Score: 20.148903113208302											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	respiratory chain	49	5.580865604	4.E-51	70316, 672195, 226646, 100041273, 6637	869	62	17854	2.E+01	2.E-48	6.E-49	6.E-48
GOTERM_BP_FAT	GO:0006091~generation of precursor metabolites and energy	96	10.93394077	2.E-50	18746, 226646, 66377, 11676, 56012, 116	809	261	13588	6.E+00	6.E-47	6.E-47	4.E-47



GOTERM_CC_FAT	GO:0070469--respiratory chain	49	5.580865604	1.E-48	70316	672195	226646	100041273	6637	636	65	12504	1.E+01	4.E-46	4.E-46	2.E-45
SP_PIR_KEYWORDS	electron transport	53	6.036446469	1.E-41	70316	672195	226646	100041273	6637	869	100	17854	1.E+01	5.E-39	1.E-39	2.E-38
GOTERM_BP_FAT	GO:0022900--electron transport chain	54	6.150341686	2.E-35	70316	672195	226646	100041273	6637	809	112	13588	8.E+00	7.E-32	2.E-32	4.E-32
GOTERM_MF_FAT	GO:0003954--NADH dehydrogenase activity	22	2.505694761	9.E-24	226646	100041273	66416	67184	17721	754	24	13288	2.E+01	6.E-21	2.E-21	1.E-20
GOTERM_MF_FAT	GO:0050136--NADH dehydrogenase (quinone) activity	22	2.505694761	9.E-24	226646	100041273	66416	67184	17721	754	24	13288	2.E+01	6.E-21	2.E-21	1.E-20
GOTERM_MF_FAT	GO:0008137--NADH dehydrogenase (ubiquinone) activity	22	2.505694761	9.E-24	226646	100041273	66416	67184	17721	754	24	13288	2.E+01	6.E-21	2.E-21	1.E-20
GOTERM_CC_FAT	GO:0044429--mitochondrial part	88	10.02277904	1.E-23	226646	66885	672195	100041273	6826	636	524	12504	3.E+00	5.E-21	2.E-21	2.E-20
GOTERM_MF_FAT	GO:0016651--oxidoreductase activity, acting on NADH or NADPH	29	3.302961276	4.E-22	226646	100041273	66416	67184	14782	754	51	13288	1.E+01	3.E-19	6.E-20	6.E-19
GOTERM_MF_FAT	GO:0016655--oxidoreductase activity, acting on NADH or NADPH,	22	2.505694761	1.E-21	226646	100041273	66416	67184	17721	754	27	13288	1.E+01	8.E-19	1.E-19	2.E-18
SP_PIR_KEYWORDS	mitochondrion	106	12.07289294	1.E-21	66885	226646	66377	18416	243362	14	869	790	17854	3.E+00	6.E-19	6.E-20
GOTERM_CC_FAT	GO:0031966--mitochondrial membrane	68	7.744874715	1.E-20	226646	100041273	66377	18416	59513	636	368	12504	4.E+00	6.E-18	1.E-18	2.E-17
GOTERM_CC_FAT	GO:0005740--mitochondrial envelope	70	7.972665148	2.E-20	226646	100041273	66377	18416	59513	636	391	12504	4.E+00	9.E-18	2.E-18	3.E-17
SP_PIR_KEYWORDS	mitochondrion inner membrane	46	5.239179954	6.E-20	226646	100041273	66377	595136	2227	869	183	17854	5.E+00	2.E-17	2.E-18	8.E-17
GOTERM_CC_FAT	GO:0005743--mitochondrial inner membrane	59	6.719817768	2.E-19	226646	100041273	66377	18416	59513	636	296	12504	4.E+00	7.E-17	1.E-17	2.E-16
SP_PIR_KEYWORDS	ubiquinone	19	2.164009112	2.E-19	70316	226646	17718	17719	68349	662	869	24	17854	2.E+01	9.E-17	6.E-18
GOTERM_CC_FAT	GO:0019866--organelle inner membrane	60	6.833712984	5.E-19	226646	100041273	66377	18416	59513	636	312	12504	4.E+00	2.E-16	2.E-17	7.E-16
GOTERM_CC_FAT	GO:0031967--organelle envelope	81	9.225512528	1.E-18	226646	100041273	66377	18416	59513	636	540	12504	3.E+00	5.E-16	5.E-17	2.E-15
GOTERM_CC_FAT	GO:0031975--envelope	81	9.225512528	1.E-18	226646	100041273	66377	18416	59513	636	542	12504	3.E+00	6.E-16	6.E-17	2.E-15
KEGG_PATHWAY	mmu05012Parkinson's disease	49	5.580865604	2.E-16	70316	672195	226646	100041273	6637	580	133	5738	4.E+00	4.E-14	9.E-15	3.E-13
GOTERM_CC_FAT	GO:0005739--mitochondrion	136	15.48974943	5.E-16	18746	18747	226646	66885	66377	100	636	1322	12504	2.E+00	2.E-13	1.E-14
KEGG_PATHWAY	mmu05010Alzheimer's disease	58	6.605922551	7.E-16	70316	672195	226646	100041273	6637	580	182	5738	3.E+00	1.E-13	2.E-14	8.E-13
KEGG_PATHWAY	mmu00190Oxidative phosphorylation	46	5.239179954	2.E-14	70316	226646	100041273	66377	59513	580	130	5738	4.E+00	3.E-12	4.E-13	2.E-11
KEGG_PATHWAY	mmu05016Huntington's disease	56	6.378132118	2.E-14	70316	672195	226646	100041273	6637	580	183	5738	3.E+00	3.E-12	3.E-13	2.E-11
GOTERM_BP_FAT	GO:0055114--oxidation reduction	90	10.25056948	4.E-13	66885	226646	66377	14782	22273	698	809	672	13588	2.E+00	1.E-09	7.E-11
SP_PIR_KEYWORDS	transit peptide	59	6.719817768	2.E-11	70316	66885	226646	68263	66377	184	869	457	17854	3.E+00	9.E-09	4.E-10
GOTERM_CC_FAT	GO:0031090--organelle membrane	87	9.908883827	3.E-11	226646	100041273	66377	18416	59513	636	809	12504	2.E+00	1.E-08	7.E-10	4.E-08
UP_SEQ_FEATURE	transit peptide:Mitochondrion	59	6.719817768	4.E-10	70316	66885	226646	68263	66377	184	861	449	16021	2.E+00	9.E-07	2.E-07
GOTERM_CC_FAT	GO:0031980--mitochondrial lumen	26	2.961275626	7.E-07	66885	672195	68263	18416	231086	11	636	163	12504	3.E+00	3.E-04	1.E-05
GOTERM_CC_FAT	GO:0005759--mitochondrial matrix	26	2.961275626	7.E-07	66885	672195	68263	18416	231086	11	636	163	12504	3.E+00	3.E-04	1.E-05
SP_PIR_KEYWORDS	nad	25	2.84738041	2.E-06	226646	100042746	56847	17721	17722	869	169	17854	3.E+00	1.E-03	3.E-05	3.E-03
SP_PIR_KEYWORDS	transport	89	10.13667426	9.E-02	70316	226646	672195	100041273	6637	869	1571	17854	1.E+00	1.E+00	3.E-01	7.E+01

Annotation Cluster 5		Enrichment Score: 15.25213542428149															
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR					
SP_PIR_KEYWORDS	protein biosynthesis	50	5.69476082	2.E-29	666899	100048462	66235	13669	56347	869	139	17854	7.E+00	8.E-27	1.E-27	3.E-26	
SP_PIR_KEYWORDS	Initiation factor	24	2.733485194	2.E-16	13684	66235	13669	53356	56347	2690	869	55	17854	9.E+00	1.E-13	6.E-15	3.E-13
GOTERM_MF_FAT	GO:0008135~translation factor activity, nucleic acid binding	31	3.530751708	8.E-15	13684	66235	13669	56347	53356	2690	754	98	13288	6.E+00	6.E-12	6.E-13	1.E-11
GOTERM_MF_FAT	GO:0003743~translation initiation factor activity	24	2.733485194	1.E-13	13684	66235	13669	53356	56347	2690	754	62	13288	7.E+00	8.E-11	6.E-12	2.E-10
GOTERM_CC_FAT	GO:0005852~eukaryotic translation initiation factor 3 complex	11	1.25284738	6.E-12	27979	66085	13669	16341	53356	5634	636	12	12504	2.E+01	3.E-09	2.E-10	9.E-09
GOTERM_BP_FAT	GO:0006413~translational initiation	16	1.822323462	2.E-09	13684	66235	13669	56347	53356	2690	809	38	13588	7.E+00	5.E-06	1.E-07	3.E-06

Annotation Cluster 6		Enrichment Score: 14.90386668789734														
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR				
KEGG_PATHWAY	mmu04110:Cell cycle	72	8.200455581	2.E-38	50793, 59008, 56150, 12914, 17218, 1721	580	128	5738	6.E+00	3.E-36	1.E-36	2.E-35				
SP_PIR_KEYWORDS	cell cycle	81	9.225512528	1.E-24	243362, 59008, 16800, 56150, 18221, 172	869	447	17854	4.E+00	4.E-22	4.E-23	1.E-21				
GOTERM_BP_FAT	GO:0007049~cell cycle	97	11.04783599	4.E-19	12190, 16952, 243362, 59008, 16800, 182	809	611	13588	3.E+00	1.E-15	1.E-16	7.E-16				
SP_PIR_KEYWORDS	cell division	53	6.036446469	6.E-19	16800, 59008, 56150, 17218, 18221, 1300	869	256	17854	4.E+00	3.E-16	2.E-17	9.E-16				
KEGG_PATHWAY	mmu04914:Progesterone-mediated oocyte maturation	40	4.555808656	1.E-17	18747, 11651, 59008, 56150, 18709, 1870	580	85	5738	5.E+00	2.E-15	6.E-16	1.E-14				
GOTERM_BP_FAT	GO:0051301~cell division	57	6.492027335	6.E-16	12190, 59008, 16800, 56150, 18221, 1721	809	281	13588	3.E+00	2.E-12	1.E-13	1.E-12				
GOTERM_BP_FAT	GO:0000278~mitotic cell cycle	51	5.808656036	7.E-15	16800, 59008, 56150, 18221, 13006, 5256	809	244	13588	4.E+00	2.E-11	1.E-12	1.E-11				
KEGG_PATHWAY	mmu04114:Oocyte meiosis	42	4.783599089	8.E-14	18747, 26965, 59008, 56150, 103583, 671	580	115	5738	4.E+00	1.E-11	1.E-12	9.E-11				
SP_PIR_KEYWORDS	mitosis	36	4.10022779	1.E-12	12454, 12236, 59008, 16800, 56150, 2383	869	179	17854	4.E+00	6.E-10	3.E-11	2.E-09				
GOTERM_BP_FAT	GO:0022402~cell cycle process	61	6.9476082	1.E-11	12190, 59008, 16800, 56150, 18221, 1300	809	393	13588	3.E+00	3.E-08	2.E-09	2.E-08				
GOTERM_BP_FAT	GO:0022403~cell cycle phase	54	6.150341686	2.E-11	12190, 16800, 59008, 56150, 18221, 1300	809	328	13588	3.E+00	6.E-08	3.E-09	4.E-08				
GOTERM_BP_FAT	GO:0000087~M phase of mitotic cell cycle	39	4.44191344	5.E-11	12454, 12236, 16800, 59008, 56150, 2383	809	194	13588	3.E+00	2.E-07	7.E-09	1.E-07				
GOTERM_BP_FAT	GO:0007067~mitosis	38	4.328018223	1.E-10	12454, 12236, 16800, 59008, 56150, 2383	809	190	13588	3.E+00	3.E-07	1.E-08	2.E-07				
GOTERM_BP_FAT	GO:0000280~nuclear division	38	4.328018223	1.E-10	12454, 12236, 16800, 59008, 56150, 2383	809	190	13588	3.E+00	3.E-07	1.E-08	2.E-07				
GOTERM_BP_FAT	GO:0048285~organelle fission	38	4.328018223	3.E-10	12454, 12236, 16800, 59008, 56150, 2383	809	197	13588	3.E+00	1.E-06	4.E-08	6.E-07				
GOTERM_BP_FAT	GO:0000279~M phase	43	4.897494305	3.E-08	12190, 12454, 12236, 16800, 59008, 5615	809	283	13588	3.E+00	1.E-04	2.E-06	6.E-05				

Annotation Cluster 7		Enrichment Score: 13.118074445420174															
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR					
GOTERM_CC_FAT	GO:0043232~intracellular non-membrane-bounded organelle	182	20.72892938	2.E-18	666899	22130	94190	100039355	16800	636	1919	12504	2.E+00	6.E-16	6.E-17	2.E-15	
GOTERM_CC_FAT	GO:0043228~non-membrane-bounded organelle	182	20.72892938	2.E-18	666899	22130	94190	100039355	16800	636	1919	12504	2.E+00	6.E-16	6.E-17	2.E-15	
GOTERM_CC_FAT	GO:0005856~cytoskeleton	85	9.681093394	2.E-04	22323	13669	94190	54519	54354	7181	636	1122	12504	1.E+00	7.E-02	2.E-03	2.E-01







GOTERM_MF_FAT	GO:0001882~nucleoside binding	136	15.48974943	2.E-07	18746, 18747, 66885, 71819, 14782, 1721	754	1558	13288	2.E+00	1.E-04	6.E-06	3.E-04
GOTERM_MF_FAT	GO:0001883~purine nucleoside binding	135	15.37585421	2.E-07	18746, 18747, 66885, 71819, 14782, 1721	754	1548	13288	2.E+00	2.E-04	7.E-06	3.E-04
GOTERM_MF_FAT	GO:0030554~adenyl nucleotide binding	134	15.261959	2.E-07	18746, 18747, 66885, 71819, 14782, 1721	754	1535	13288	2.E+00	2.E-04	7.E-06	3.E-04
UP_SEQ_FEATURE	domain:SH3	27	3.075170843	6.E-07	117600, 14270, 75415, 53972, 20491, 151	861	163	16021	3.E+00	1.E-03	1.E-04	1.E-03
UP_SEQ_FEATURE	nucleotide phosphate-binding region:ATP	85	9.681093394	6.E-07	18747, 17218, 23920, 17217, 16818, 1721	861	907	16021	2.E+00	1.E-03	1.E-04	1.E-03
SP_PIR_KEYWORDS	tyrosine-protein kinase	21	2.391799544	7.E-07	11350, 13649, 12229, 23920, 16818, 1859	869	116	17854	4.E+00	3.E-04	9.E-06	1.E-03
GOTERM_BP_FAT	GO:0006468~protein amino acid phosphorylation	70	7.972665148	1.E-06	18747, 13665, 12912, 16543, 23920, 1681	809	640	13588	2.E+00	3.E-03	5.E-05	2.E-03
UP_SEQ_FEATURE	domain:SH2	19	2.164009112	1.E-06	11350, 22324, 12229, 57257, 20416, 2049	861	90	16021	4.E+00	2.E-03	2.E-04	2.E-03
GOTERM_MF_FAT	GO:0004715~non-membrane spanning protein tyrosine kinase ac	13	1.480637813	1.E-06	11350, 12229, 16818, 14191, 22390, 2077	754	40	13288	6.E+00	1.E-03	4.E-05	2.E-03
INTERPRO	IPR008266:Tyrosine protein kinase, active site	19	2.164009112	1.E-06	11350, 13649, 12229, 23920, 16818, 1859	860	101	17763	4.E+00	2.E-03	1.E-04	2.E-03
SP_PIR_KEYWORDS	transferase	107	12.18678815	2.E-06	18746, 18747, 18416, 22271, 12914, 2392	869	1385	17854	2.E+00	7.E-04	2.E-05	2.E-03
INTERPRO	IPR017441:Protein kinase, ATP binding site	47	5.353075171	4.E-06	18747, 107951, 13649, 12649, 11651, 122	860	467	17763	2.E+00	5.E-03	3.E-04	6.E-03
UP_SEQ_FEATURE	binding site:ATP	56	6.378132118	5.E-06	18747, 16818, 23920, 20779, 12567, 1256	861	545	16021	2.E+00	1.E-02	7.E-04	8.E-03
INTERPRO	IPR001245:Tyrosine protein kinase	20	2.277904328	8.E-06	11350, 13649, 12229, 23920, 16818, 1859	860	124	17763	3.E+00	1.E-02	5.E-04	1.E-02
GOTERM_MF_FAT	GO:0032559~adenyl ribonucleotide binding	122	13.8952164	8.E-06	18746, 18747, 71819, 17218, 23920, 1721	754	1460	13288	1.E+00	6.E-03	2.E-04	1.E-02
GOTERM_MF_FAT	GO:0004672~protein kinase activity	59	6.719817768	2.E-05	18747, 16818, 23920, 20779, 14884, 1256	754	583	13288	2.E+00	1.E-02	4.E-04	3.E-02
GOTERM_MF_FAT	GO:0005524~ATP binding	119	13.55353075	2.E-05	18746, 18747, 71819, 17218, 23920, 1721	754	1443	13288	1.E+00	2.E-02	5.E-04	3.E-02
INTERPRO	IPR000719:Protein kinase, core	46	5.239179954	3.E-05	18747, 107951, 13649, 12649, 11651, 122	860	491	17763	2.E+00	4.E-02	2.E-03	5.E-02
SMART	SM00219:TyrKc	20	2.277904328	3.E-05	11350, 13649, 12229, 23920, 16818, 1859	492	124	9131	3.E+00	7.E-03	8.E-04	4.E-02
UP_SEQ_FEATURE	domain:Protein kinase	45	5.125284738	3.E-04	18747, 107951, 13649, 12649, 11651, 122	861	476	16021	2.E+00	5.E-01	3.E-02	5.E-01
SP_PIR_KEYWORDS	tyrosine-specific protein kinase	9	1.025056948	3.E-04	18596, 14191, 20779, 19713, 14302, 1436	869	37	17854	5.E+00	1.E-01	3.E-03	5.E-01
GOTERM_MF_FAT	GO:0004713~protein tyrosine kinase activity	22	2.505694761	4.E-04	11350, 13649, 12229, 23920, 16818, 1859	754	164	13288	2.E+00	2.E+00	6.E-03	6.E-01
GOTERM_BP_FAT	GO:0018212~peptidyl-tyrosine modification	9	1.025056948	1.E-03	11350, 16818, 12229, 20779, 18413, 1436	809	37	13588	4.E+00	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0018108~peptidyl-tyrosine phosphorylation	9	1.025056948	1.E-03	11350, 16818, 12229, 20779, 18413, 1436	809	37	13588	4.E+00	1.E+00	2.E-02	2.E+00
GOTERM_MF_FAT	GO:0004674~protein serine/threonine kinase activity	38	4.328018223	5.E-03	107951, 18747, 245000, 12649, 11651, 12	754	421	13288	2.E+00	1.E+00	6.E-02	8.E+00
INTERPRO	IPR008271:Serine/threonine protein kinase, active site	28	3.189066059	2.E-02	107951, 18747, 12649, 11651, 12236, 545	860	360	17763	2.E+00	1.E+00	3.E-01	2.E+01
INTERPRO	IPR002290:Serine/threonine protein kinase	22	2.505694761	2.E-02	107951, 18747, 270672, 12649, 20871, 18	860	265	17763	2.E+00	1.E+00	4.E-01	3.E+01
SP_PIR_KEYWORDS	serine/threonine-protein kinase	29	3.302961276	2.E-02	107951, 18747, 245000, 12649, 11651, 12	869	384	17854	2.E+00	1.E+00	1.E-01	3.E+01
INTERPRO	IPR017442:Serine/threonine protein kinase-related	27	3.075170843	4.E-02	107951, 18747, 12649, 11651, 545156, 22	860	374	17763	1.E+00	1.E+00	6.E-01	5.E+01
SMART	SM00220:S_TKc	22	2.505694761	5.E-02	107951, 18747, 270672, 12649, 20871, 18	492	265	9131	2.E+00	1.E+00	4.E-01	5.E+01

Annotation Cluster 13	Enrichment Score: 6.737200438197317											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0030029~actin filament-based process	37	4.214123007	5.E-11	22323, 215280, 227753, 94190, 11856, 16	809	176	13588	4.E+00	1.E-07	6.E-09	9.E-08
GOTERM_BP_FAT	GO:0030036~actin cytoskeleton organization	33	3.758542141	2.E-09	22323, 227753, 94190, 11856, 16800, 204	809	165	13588	3.E+00	7.E-06	2.E-07	4.E-06
GOTERM_BP_FAT	GO:0007015~actin filament organization	13	1.480637813	9.E-05	227753, 13800, 12043, 11856, 16800, 140	809	56	13588	4.E+00	2.E-01	3.E-03	2.E-01
GOTERM_BP_FAT	GO:0007010~cytoskeleton organization	38	4.328018223	1.E-04	22323, 227753, 94190, 11856, 16800, 204	809	326	13588	2.E+00	3.E-01	4.E-03	2.E-01

Annotation Cluster 14	Enrichment Score: 6.664853543560962											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	ubli conjugation	60	6.833712984	2.E-09	100048462, 665032, 14815, 319191, 5601	869	524	17854	2.E+00	7.E-07	2.E-08	2.E-06
SP_PIR_KEYWORDS	isopeptide bond	34	3.872437358	2.E-06	100048462, 13649, 665032, 16952, 12649	869	277	17854	3.E+00	9.E-04	2.E-05	3.E-03
UP_SEQ_FEATURE	cross-link:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter	26	2.961275626	3.E-06	100048462, 13649, 665032, 12649, 26965	861	168	16021	3.E+00	7.E-03	5.E-04	6.E-03

Annotation Cluster 15	Enrichment Score: 6.477689571187648											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	cyclin	16	1.822323462	4.E-09	107951, 12454, 12445, 12448, 12447, 124	869	48	17854	7.E+00	2.E-06	6.E-08	6.E-06
SP_PIR_KEYWORDS	cell cycle control	11	1.25284738	8.E-09	12445, 12447, 26416, 12443, 12567, 1253	869	20	17854	1.E+01	4.E-06	1.E-07	1.E-05
INTERPRO	IPR004367:Cyclin, C-terminal	9	1.025056948	1.E-07	12445, 12448, 12447, 12442, 209091, 124	860	15	17763	1.E+01	2.E-04	2.E-05	2.E-04
INTERPRO	IPR006670:Cyclin	12	1.366742597	2.E-07	12445, 19645, 12448, 12447, 12442, 2090	860	33	17763	8.E+00	3.E-04	3.E-05	4.E-04
INTERPRO	IPR013763:Cyclin-related	12	1.366742597	2.E-07	12445, 19645, 12448, 12447, 12442, 2090	860	33	17763	8.E+00	3.E-04	3.E-05	4.E-04
INTERPRO	IPR006671:Cyclin, N-terminal	11	1.25284738	3.E-07	12445, 12448, 12447, 12442, 209091, 124	860	27	17763	8.E+00	4.E-04	3.E-05	4.E-04
SMART	SM00385:CYCLIN	12	1.366742597	6.E-07	12445, 19645, 12448, 12447, 12442, 2090	492	33	9131	7.E+00	1.E-04	2.E-05	8.E-04
INTERPRO	IPR014400:Cyclin, A/B/D/E	7	0.797266515	2.E-06	12445, 12448, 12447, 12442, 12443, 1242	860	10	17763	1.E+01	3.E-03	2.E-04	4.E-03
PIR_SUPERFAMILY	PIRSF001771:cyclin, A/B/D/E types	7	0.797266515	8.E-06	12445, 12448, 12447, 12442, 12443, 1242	576	9	8136	1.E+01	5.E-03	2.E-03	1.E-02
PIR_SUPERFAMILY	PIRSF001771:Cyclin_A_B_D_E	7	0.797266515	2.E-05	12445, 12448, 12447, 12442, 12443, 1242	576	10	8136	1.E+01	1.E-02	4.E-03	3.E-02

Annotation Cluster 16	Enrichment Score: 6.07988443658806											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR003578:Ras small GTPase, Rho type	15	1.708428246	3.E-14	228543, 11852, 69288, 246710, 11854, 11	860	21	17763	1.E+01	4.E-11	1.E-11	5.E-11
SMART	SM00174:RHO	15	1.708428246	1.E-13	228543, 11852, 69288, 246710, 11854, 11	492	21	9131	1.E+01	2.E-11	8.E-12	1.E-10
SP_PIR_KEYWORDS	methylation	36	4.10022779	6.E-10	19744, 100042746, 27041, 12955, 11852,	869	221	17854	3.E+00	3.E-07	9.E-09	9.E-07
GOTERM_BP_FAT	GO:0007264~small GTPase mediated signal transduction	42	4.783599089	7.E-09	117600, 228543, 19744, 232906, 11852, 1	809	258	13588	3.E+00	2.E-05	5.E-07	1.E-05
PIR_SUPERFAMILY	PIRSF037169:small GTPase, Rho type	11	1.25284738	2.E-08	80837, 228543, 11852, 11854, 104215, 11	576	16	8136	1.E+01	9.E-06	9.E-06	2.E-05
SP_PIR_KEYWORDS	gtp-binding	39	4.44191344	2.E-07	228543, 19744, 11852, 26905, 13627, 136	869	313	17854	3.E+00	9.E-05	2.E-06	3.E-04



INTERPRO	IPR001806:Ras GTPase	23	2.619589977	3.E-07	228543, 19744, 69288, 11852, 232906, 24	860	130	17763	4.E+00	4.E-04	3.E-05	4.E-04
INTERPRO	IPR013753:Ras	21	2.391799544	1.E-06	228543, 19744, 69288, 11852, 232906, 24	860	121	17763	4.E+00	2.E-03	1.E-04	2.E-03
UP_SEQ_FEATURE	nucleotide phosphate-binding region:GTP	36	4.10022779	2.E-06	228543, 19744, 11852, 26905, 13627, 136	861	274	16021	2.E+00	3.E-03	3.E-04	3.E-03
GOTERM_MF_FAT	GO:0003924--GTPase activity	23	2.619589977	3.E-06	22142, 14674, 14675, 26905, 13627, 1467	754	128	13288	3.E+00	2.E-03	7.E-05	4.E-03
INTERPRO	IPR005225:Small GTP-binding protein	23	2.619589977	1.E-05	228543, 19744, 69288, 11852, 246710, 11	860	164	17763	3.E+00	2.E-02	9.E-04	2.E-02
GOTERM_MF_FAT	GO:0005525--GTP binding	41	4.669703872	2.E-05	228543, 19744, 232906, 11852, 26905, 13	754	354	13288	2.E+00	2.E-02	5.E-04	4.E-02
GOTERM_MF_FAT	GO:0032561--guanyl ribonucleotide binding	41	4.669703872	4.E-05	228543, 19744, 232906, 11852, 26905, 13	754	363	13288	2.E+00	3.E-02	8.E-04	6.E-02
GOTERM_MF_FAT	GO:0019001--guanyl nucleotide binding	41	4.669703872	4.E-05	228543, 19744, 232906, 11852, 26905, 13	754	363	13288	2.E+00	3.E-02	8.E-04	6.E-02
UP_SEQ_FEATURE	short sequence motif:Effector region	15	1.708428246	4.E-04	19744, 11852, 11854, 11853, 74734, 1707	861	92	16021	3.E+00	5.E-01	3.E-02	6.E-01
SP_PIR_KEYWORDS	prenylation	18	2.050113895	7.E-04	19744, 11852, 11854, 102093, 11853, 747	869	145	17854	3.E+00	3.E-01	5.E-03	1.E+00
UP_SEQ_FEATURE	propeptide:Removed in mature form	19	2.164009112	5.E-02	19370, 19744, 12475, 11852, 11854, 1185	861	220	16021	2.E+00	1.E+00	8.E-01	6.E+01
UP_SEQ_FEATURE	lipid moiety-binding region:S-geranylgeranyl cysteine	10	1.138952164	7.E-02	19354, 11854, 11853, 23912, 74734, 1254	861	95	16021	2.E+00	1.E+00	9.E-01	7.E+01

Annotation Cluster 17	Enrichment Score: 5.9051171367880455											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
KEGG_PATHWAY	mmu05214:Glioma	27	3.075170843	1.E-10	13649, 11651, 20416, 18709, 56717, 1880	580	64	5738	4.E+00	2.E-08	2.E-09	1.E-07
KEGG_PATHWAY	mmu05215:Prostate cancer	32	3.644646925	3.E-10	13649, 11651, 12912, 12914, 18709, 5671	580	90	5738	4.E+00	4.E-08	3.E-09	3.E-07
KEGG_PATHWAY	mmu04650:Natural killer cell mediated cytotoxicity	38	4.328018223	3.E-10	14972, 22324, 14939, 20416, 170758, 187	580	122	5738	3.E+00	5.E-08	4.E-09	4.E-07
KEGG_PATHWAY	mmu05223:Non-small cell lung cancer	22	2.505694761	2.E-08	13649, 320207, 54354, 11651, 18709, 187	580	54	5738	4.E+00	3.E-06	2.E-07	2.E-05
KEGG_PATHWAY	mmu05200:Pathways in cancer	64	7.28929385	1.E-07	12190, 672195, 14178, 19206, 54354, 170	580	323	5738	2.E+00	2.E-05	1.E-06	1.E-04
KEGG_PATHWAY	mmu04662:B cell receptor signaling pathway	26	2.961275626	1.E-07	22324, 11651, 170758, 18019, 18709, 187	580	80	5738	3.E+00	2.E-05	1.E-06	2.E-04
KEGG_PATHWAY	mmu04664:Fc epsilon RI signaling pathway	26	2.961275626	2.E-07	22324, 11651, 170758, 18709, 18803, 187	580	82	5738	3.E+00	4.E-05	2.E-06	3.E-04
KEGG_PATHWAY	mmu05222:Small cell lung cancer	26	2.961275626	5.E-07	22029, 672195, 17869, 11651, 18709, 187	580	85	5738	3.E+00	8.E-05	4.E-06	6.E-04
KEGG_PATHWAY	mmu05220:Chronic myeloid leukemia	24	2.733485194	8.E-07	11350, 320207, 433759, 11651, 17869, 20	580	76	5738	3.E+00	1.E-04	6.E-06	1.E-03
KEGG_PATHWAY	mmu04012:ErbB signaling pathway	25	2.84738041	3.E-06	13649, 13685, 17869, 11651, 20416, 1870	580	87	5738	3.E+00	5.E-04	2.E-05	4.E-03
KEGG_PATHWAY	mmu04510:Focal adhesion	42	4.783599089	4.E-06	22323, 12831, 22324, 13649, 232906, 227	580	198	5738	2.E+00	7.E-04	3.E-05	5.E-03
KEGG_PATHWAY	mmu04722:Neurotrophin signaling pathway	31	3.530751708	1.E-05	192662, 11651, 11857, 20416, 18709, 188	580	130	5738	2.E+00	2.E-03	6.E-05	1.E-02
KEGG_PATHWAY	mmu04660:T cell receptor signaling pathway	29	3.302961276	1.E-05	22324, 11651, 18019, 18709, 18803, 1870	580	118	5738	2.E+00	2.E-03	7.E-05	1.E-02
KEGG_PATHWAY	mmu04370:VEGF signaling pathway	22	2.505694761	1.E-05	320207, 11651, 170758, 18709, 18751, 18	580	76	5738	3.E+00	2.E-03	7.E-05	1.E-02
KEGG_PATHWAY	mmu05218:Melanoma	21	2.391799544	1.E-05	13649, 14178, 320207, 11651, 14180, 187	580	71	5738	3.E+00	2.E-03	8.E-05	2.E-02
KEGG_PATHWAY	mmu05212:Pancreatic cancer	21	2.391799544	2.E-05	12190, 13649, 320207, 11651, 170758, 18	580	72	5738	3.E+00	3.E-03	1.E-04	2.E-02
KEGG_PATHWAY	mmu04666:Fc gamma R-mediated phagocytosis	25	2.84738041	3.E-05	22323, 22324, 227753, 13430, 11651, 223	580	98	5738	3.E+00	4.E-03	1.E-04	3.E-02
KEGG_PATHWAY	mmu05210:Colorectal cancer	23	2.619589977	3.E-05	13649, 672195, 320207, 11651, 17869, 12	580	86	5738	3.E+00	4.E-03	1.E-04	3.E-02
KEGG_PATHWAY	mmu05221:Acute myeloid leukemia	17	1.936218679	1.E-04	13685, 320207, 17869, 20375, 11651, 187	580	57	5738	3.E+00	2.E-02	5.E-04	1.E-01
KEGG_PATHWAY	mmu05213:Endometrial cancer	15	1.708428246	5.E-04	13649, 320207, 17869, 11651, 18709, 187	580	52	5738	3.E+00	7.E-02	2.E-03	5.E-01
KEGG_PATHWAY	mmu05211:Renal cell carcinoma	16	1.822323462	4.E-03	20525, 320207, 11651, 18479, 12914, 187	580	70	5738	2.E+00	4.E-01	1.E-02	4.E+00

Annotation Cluster 18	Enrichment Score: 5.475288080522823											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0001775--cell activation	43	4.897494305	5.E-10	22324, 19934, 16803, 14026, 22376, 5824	809	246	13588	3.E+00	1.E-06	5.E-08	9.E-07
GOTERM_BP_FAT	GO:0045321--leukocyte activation	39	4.44191344	2.E-09	22324, 19934, 16803, 22376, 58240, 1205	809	219	13588	3.E+00	6.E-06	2.E-07	4.E-06
GOTERM_BP_FAT	GO:0042110--T cell activation	26	2.961275626	1.E-08	22324, 19934, 22376, 58240, 16408, 1205	809	116	13588	4.E+00	4.E-05	1.E-06	3.E-05
GOTERM_BP_FAT	GO:0046649--lymphocyte activation	33	3.758542141	9.E-08	22324, 19934, 22376, 58240, 12051, 1640	809	191	13588	3.E+00	3.E-04	6.E-06	2.E-04
GOTERM_BP_FAT	GO:0048534--hemopoietic or lymphoid organ development	41	4.669703872	2.E-07	12190, 22324, 14151, 19934, 21934, 5824	809	281	13588	2.E+00	7.E-04	1.E-05	4.E-04
GOTERM_BP_FAT	GO:0030097--hemopoiesis	38	4.328018223	3.E-07	12190, 22324, 14151, 19934, 15163, 1590	809	251	13588	3.E+00	8.E-04	2.E-05	5.E-04
GOTERM_BP_FAT	GO:0002520--immune system development	41	4.669703872	8.E-07	12190, 22324, 14151, 19934, 21934, 5824	809	295	13588	2.E+00	3.E-03	5.E-05	2.E-03
GOTERM_BP_FAT	GO:0048872--homeostasis of number of cells	20	2.277904328	3.E-05	14151, 11651, 12043, 20375, 12183, 6827	809	113	13588	3.E+00	1.E-01	1.E-03	6.E-02
GOTERM_BP_FAT	GO:0030098--lymphocyte differentiation	19	2.164009112	1.E-04	22324, 19934, 12043, 20375, 74734, 1081	809	114	13588	3.E+00	3.E-01	4.E-03	2.E-01
GOTERM_BP_FAT	GO:0002521--leukocyte differentiation	21	2.391799544	3.E-04	22324, 19934, 12043, 20375, 74734, 1081	809	142	13588	2.E+00	6.E-01	8.E-03	5.E-01
GOTERM_BP_FAT	GO:0030218--erythrocyte differentiation	11	1.25284738	4.E-04	14151, 19645, 18771, 21349, 20085, 2037	809	48	13588	4.E+00	7.E-01	1.E-02	8.E-01
GOTERM_BP_FAT	GO:0030099--myeloid cell differentiation	16	1.822323462	5.E-04	14151, 20375, 12183, 15902, 15163, 2134	809	96	13588	3.E+00	8.E-01	1.E-02	9.E-01
GOTERM_BP_FAT	GO:0034101--erythrocyte homeostasis	11	1.25284738	7.E-04	14151, 19645, 18771, 21349, 20085, 2037	809	51	13588	4.E+00	9.E-01	2.E-02	1.E+00
GOTERM_BP_FAT	GO:0030217--T cell differentiation	13	1.480637813	2.E-03	22324, 19934, 12043, 74734, 108138, 100	809	76	13588	3.E+00	1.E+00	3.E-02	3.E+00

Annotation Cluster 19	Enrichment Score: 4.784801505165352											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0005747--mitochondrial respiratory chain complex I	6	0.683371298	2.E-06	226646, 67264, 68349, 227197, 17993, 17	636	6	12504	2.E+01	8.E-04	3.E-05	3.E-03
GOTERM_CC_FAT	GO:0045271--respiratory chain complex I	6	0.683371298	2.E-06	226646, 67264, 68349, 227197, 17993, 17	636	6	12504	2.E+01	8.E-04	3.E-05	3.E-03
GOTERM_CC_FAT	GO:0030964--NADH dehydrogenase complex	6	0.683371298	2.E-06	226646, 67264, 68349, 227197, 17993, 17	636	6	12504	2.E+01	8.E-04	3.E-05	3.E-03
GOTERM_CC_FAT	GO:0005746--mitochondrial respiratory chain	7	0.797266515	6.E-05	226646, 67184, 67264, 68349, 227197, 17	636	15	12504	9.E+00	2.E-02	7.E-04	8.E-02
GOTERM_CC_FAT	GO:0044455--mitochondrial membrane part	9	1.025056948	3.E-03	226646, 67184, 67264, 68349, 227197, 17	636	49	12504	4.E+00	7.E-01	3.E-02	4.E+00

Annotation Cluster 20	Enrichment Score: 4.622895155061082											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0030027--lamellipodium	17	1.936218679	6.E-08	22323, 14163, 227753, 13800, 54519, 116	636	63	12504	5.E+00	3.E-05	1.E-06	9.E-05



GOTERM_CC_FAT	GO:0031252~cell leading edge	20	2.277904328	3.E-06	22323	14163	227753	13800	54519	228	636	112	12504	4.E+00	1.E-03	5.E-05	5.E-03
GOTERM_CC_FAT	GO:0042995~cell projection	49	5.580865604	5.E-04	22323	18746	94190	16952	54519	1680	636	575	12504	2.E+00	2.E-01	5.E-03	7.E-01
SP_PIR_KEYWORDS	cell projection	20	2.277904328	3.E-03	22323	14163	73750	13800	94190	1695	869	196	17854	2.E+00	8.E-01	2.E-02	5.E+00

Annotation Cluster 21	Enrichment Score: 4.3168278617499																
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR					
GOTERM_BP_FAT	GO:0042325~regulation of phosphorylation	47	5.353075171	9.E-10	13649	14151	20416	16543	15163	1870	809	290	13588	3.E+00	3.E-06	8.E-08	2.E-06
GOTERM_BP_FAT	GO:0019220~regulation of phosphate metabolic process	47	5.353075171	3.E-09	13649	14151	20416	16543	15163	1870	809	301	13588	3.E+00	9.E-06	2.E-07	5.E-06
GOTERM_BP_FAT	GO:0051174~regulation of phosphorus metabolic process	47	5.353075171	3.E-09	13649	14151	20416	16543	15163	1870	809	301	13588	3.E+00	9.E-06	2.E-07	5.E-06
GOTERM_BP_FAT	GO:0001932~regulation of protein amino acid phosphorylation	27	3.0751170843	8.E-09	13649	14151	16543	15163	56717	1859	809	121	13588	4.E+00	2.E-05	6.E-07	1.E-05
GOTERM_BP_FAT	GO:0031399~regulation of protein modification process	31	3.530751708	3.E-08	13649	14151	67141	16543	15163	5671	809	165	13588	3.E+00	1.E-04	2.E-06	6.E-05
GOTERM_BP_FAT	GO:0044093~positive regulation of molecular function	44	5.011389522	1.E-07	672195	66593	11856	17869	14852	204	809	306	13588	2.E+00	4.E-04	8.E-06	2.E-04
GOTERM_BP_FAT	GO:0032268~regulation of cellular protein metabolic process	40	4.555808656	6.E-07	13684	13649	13685	14151	13665	1165	809	280	13588	2.E+00	2.E-03	3.E-05	1.E-03
GOTERM_BP_FAT	GO:0043085~positive regulation of catalytic activity	37	4.214123007	2.E-06	672195	66593	11856	17869	14852	204	809	261	13588	2.E+00	6.E-03	1.E-04	4.E-03
GOTERM_BP_FAT	GO:0051338~regulation of transferase activity	29	3.302961276	2.E-05	20416	16543	56717	16367	19164	1254	809	199	13588	2.E+00	5.E-02	8.E-04	3.E-02
GOTERM_BP_FAT	GO:0043549~regulation of kinase activity	28	3.189066059	3.E-05	20416	16543	56717	16367	19164	1254	809	192	13588	2.E+00	8.E-02	1.E-03	5.E-02
GOTERM_BP_FAT	GO:0051347~positive regulation of transferase activity	22	2.505694761	5.E-05	11806	14678	21899	21898	57257	2041	809	135	13588	3.E+00	1.E-01	2.E-03	8.E-02
GOTERM_BP_FAT	GO:0007243~protein kinase cascade	31	3.530751708	7.E-05	11651	20416	16543	55979	12703	1636	809	236	13588	2.E+00	2.E-01	2.E-03	1.E-01
GOTERM_BP_FAT	GO:0033674~positive regulation of kinase activity	21	2.391799544	8.E-05	14678	21899	21898	57257	20416	1338	809	130	13588	3.E+00	2.E-01	3.E-03	1.E-01
GOTERM_BP_FAT	GO:0043507~positive regulation of JUN kinase activity	7	0.797266515	2.E-04	16179	16334	21899	117149	20963	165	809	16	13588	7.E+00	5.E-01	6.E-03	4.E-01
GOTERM_BP_FAT	GO:0043408~regulation of MAPKKK cascade	16	1.822323462	4.E-04	15170	21899	21898	14180	224014	165	809	93	13588	3.E+00	7.E-01	1.E-02	7.E-01
GOTERM_BP_FAT	GO:0045859~regulation of protein kinase activity	24	2.733485194	7.E-04	15170	21899	14678	21898	20416	1338	809	186	13588	2.E+00	9.E-01	1.E-02	1.E+00
GOTERM_BP_FAT	GO:0043506~regulation of JUN kinase activity	7	0.797266515	1.E-03	16179	16334	21899	117149	20963	165	809	21	13588	6.E+00	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0046328~regulation of JNK cascade	10	1.138952164	1.E-03	17874	16179	16334	21899	21898	1171	809	45	13588	4.E+00	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0070302~regulation of stress-activated protein kinase signalin	10	1.138952164	1.E-03	17874	16179	16334	21899	21898	1171	809	46	13588	4.E+00	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0080135~regulation of cellular response to stress	13	1.480637813	1.E-03	14151	21899	21898	224014	16543	117	809	75	13588	3.E+00	1.E+00	3.E-02	3.E+00
GOTERM_BP_FAT	GO:0045860~positive regulation of protein kinase activity	17	1.936218679	3.E-03	14678	21899	21898	20416	13383	2240	809	124	13588	2.E+00	1.E+00	4.E-02	5.E+00
GOTERM_BP_FAT	GO:0031098~stress-activated protein kinase signaling pathway	8	0.911161731	4.E-03	17874	57874	16334	74155	117149	209	809	35	13588	4.E+00	1.E+00	6.E-02	7.E+00
GOTERM_BP_FAT	GO:0007257~activation of JUN kinase activity	5	0.569476082	6.E-03	16334	117149	20963	16543	224014		809	13	13588	6.E+00	1.E+00	8.E-02	1.E+01
GOTERM_BP_FAT	GO:0000165~MAPKKK cascade	15	1.708428246	8.E-03	14678	20416	224014	16543	17873	178	809	114	13588	2.E+00	1.E+00	1.E-01	1.E+01
GOTERM_BP_FAT	GO:0043406~positive regulation of MAP kinase activity	10	1.138952164	8.E-03	16179	16334	21899	26395	19164	2041	809	59	13588	3.E+00	1.E+00	1.E-01	1.E+01
GOTERM_BP_FAT	GO:0007254~JNK cascade	7	0.797266515	1.E-02	17874	57874	16334	117149	20963	165	809	32	13588	4.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0043405~regulation of MAP kinase activity	12	1.366742597	1.E-02	15170	24064	16179	16334	21899	2639	809	84	13588	2.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0000187~activation of MAPK activity	7	0.797266515	7.E-02	16334	26395	20416	117149	20963	165	809	50	13588	2.E+00	1.E+00	5.E-01	8.E+01

Annotation Cluster 22	Enrichment Score: 4.279056102878084																
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR					
BIOCARTA	m_p53Pathwayp53 Signaling Pathway	12	1.366742597	3.E-06	13555	19645	12447	11920	12028	1244	188	16	1171	5.E+00	6.E-04	6.E-04	4.E-03
GOTERM_CC_FAT	GO:0000307~cyclin-dependent protein kinase holoenzyme compl	6	0.683371298	4.E-05	12447	12443	12567	12566	18538	1257	636	9	12504	1.E+01	1.E-02	5.E-04	5.E-02
BIOCARTA	m_RacCycDPATHwayInfluence of Ras and Rho proteins on G1 to S	13	1.480637813	9.E-05	11651	18479	11848	18708	13555	1964	188	24	1171	3.E+00	2.E-02	5.E-03	1.E-01
BIOCARTA	m_g1PathwayCell Cycle: G1/S Check Point	13	1.480637813	2.E-04	11350	245000	13555	19645	12447	119	188	25	1171	3.E+00	3.E-02	7.E-03	2.E-01
BIOCARTA	m_cellcyclePathwayCyclins and Cell Cycle Regulation	12	1.366742597	3.E-04	12445	13555	19645	12447	12443	1256	188	23	1171	3.E+00	7.E-02	8.E-03	4.E-01

Annotation Cluster 23	Enrichment Score: 4.071354464138146																
Category	Term: Rho/Rac/Ras GTPase actiator activity	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR					
GOTERM_MF_FAT	GO:0005100~Rho GTPase activator activity	10	1.138952164	2.E-07	117600	71709	17925	50768	228359	76	754	18	13288	1.E+01	1.E-04	6.E-06	3.E-04
GOTERM_MF_FAT	GO:0030675~Rac GTPase activator activity	5	0.569476082	1.E-03	228359	76117	19765	233071	106952		754	9	13288	1.E+01	5.E-01	1.E-02	2.E+00
GOTERM_MF_FAT	GO:0005099~Ras GTPase activator activity	11	1.25284738	3.E-03	117600	71709	17925	50768	228359	76	754	65	13288	3.E+00	9.E-01	4.E-02	5.E+00

Annotation Cluster 24	Enrichment Score: 3.8861385584405066																
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR					
GOTERM_MF_FAT	GO:0019207~kinase regulator activity	15	1.708428246	5.E-05	66214	19085	19088	100039474	66197		754	73	13288	4.E+00	4.E-02	1.E-03	8.E-02
GOTERM_MF_FAT	GO:0016538~cyclin-dependent protein kinase regulator activity	7	0.797266515	1.E-04	12448	12447	12443	100044764	54124		754	15	13288	8.E+00	7.E-02	2.E-03	2.E-01
GOTERM_MF_FAT	GO:0019887~protein kinase regulator activity	12	1.366742597	4.E-04	66214	19085	19088	100039474	66197		754	59	13288	4.E+00	3.E-01	7.E-03	6.E-01

Annotation Cluster 25	Enrichment Score: 3.82464515764741																
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR					
INTERPRO	IPR010911:Rab-binding domain	10	1.138952164	3.E-10	245049	269589	19894	320051	380714		860	12	17763	2.E+01	4.E-07	4.E-08	4.E-07
UP_SEQ_FEATURE	domain:RabBD	10	1.138952164	7.E-10	245049	269589	19894	320051	380714		861	12	16021	2.E+01	1.E-06	2.E-07	1.E-06
GOTERM_MF_FAT	GO:0017016~Ras GTPase binding	17	1.936218679	6.E-08	117600	269589	19894	17970	380714	1	754	57	13288	5.E+00	5.E-05	2.E-06	1.E-04
GOTERM_MF_FAT	GO:0031267~small GTPase binding	17	1.936218679	1.E-07	117600	269589	19894	17970	380714	1	754	59	13288	5.E+00	8.E-05	4.E-06	2.E-04
GOTERM_MF_FAT	GO:0051020~GTPase binding	17	1.936218679	2.E-07	117600	269589	19894	17970	380714	1	754	62	13288	5.E+00	2.E-04	7.E-06	3.E-04
GOTERM_MF_FAT	GO:0017137~Rab GTPase binding	10	1.138952164	3.E-07	245049	269589	19894	320051	380714		754	19	13288	9.E+00	2.E-04	9.E-06	5.E-04
GOTERM_MF_FAT	GO:0019899~enzyme binding	32	3.644646925	6.E-06	117600	269589	26965	12649	13605	16	754	229	13288	2.E+00	4.E-03	1.E-04	9.E-03
INTERPRO	IPR003315:Rabphilin-3A effector; zinc-binding	5	0.569476082	8.E-05	19894	380714	27359	236643	83672		860	6	17763	2.E+01	1.E-01	4.E-03	1.E-01



GOTERM_MF_FAT	GO:0042043~neurexin binding	5	0.569476082	3.E-04	269589, 27359, 83671, 13385, 83672	754	7	13288	1.E+01	2.E-01	5.E-03	5.E-01
GOTERM_BP_FAT	GO:0034613~cellular protein localization	25	2.84738041	8.E-02	269589, 171531, 236643, 320051, 231103	809	299	13588	1.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0070727~cellular macromolecule localization	25	2.84738041	9.E-02	269589, 171531, 236643, 320051, 231103	809	301	13588	1.E+00	1.E+00	5.E-01	8.E+01
UP_SEQ_FEATURE	domain:C2 2	6	0.683371298	2.E-01	269589, 19894, 27359, 83671, 236643, 83	861	57	16021	2.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	domain:C2 1	6	0.683371298	2.E-01	269589, 19894, 27359, 83671, 236643, 83	861	57	16021	2.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0006887~exocytosis	10	1.138952164	2.E-01	269589, 19894, 77579, 380714, 19164, 27	809	110	13588	2.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0006886~intracellular protein transport	21	2.391799544	2.E-01	269589, 19894, 56338, 54401, 380714, 12	809	276	13588	1.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0032940~secretion by cell	15	1.708428246	2.E-01	269589, 19894, 380714, 14226, 236643, 1	809	186	13588	1.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0046903~secretion	16	1.822323462	3.E-01	269589, 19894, 380714, 14226, 16952, 23	809	221	13588	1.E+00	1.E+00	9.E-01	1.E+02

Annotation Cluster 26	Enrichment Score: 3.8007352255404787											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0043009~chordate embryonic development		50	5.69476082	5.E-06 12190, 22323, 19206, 238055, 18803, 114	809	421	13588	2.E+00	1.E-02	2.E-04	9.E-03
GOTERM_BP_FAT	GO:0009792~embryonic development ending in birth or egg hatch		50	5.69476082	6.E-06 12190, 22323, 19206, 238055, 18803, 114	809	425	13588	2.E+00	2.E-02	3.E-04	1.E-02
GOTERM_BP_FAT	GO:0001701~in utero embryonic development		29	3.302961276	3.E-03 12190, 13649, 18107, 22209, 11651, 2380	809	267	13588	2.E+00	1.E+00	4.E-02	4.E+00
GOTERM_BP_FAT	GO:0048598~embryonic morphogenesis		34	3.872437358	9.E-03 22323, 18747, 232906, 19206, 15376, 178	809	359	13588	2.E+00	1.E+00	1.E-01	1.E+01

Annotation Cluster 27	Enrichment Score: 3.6895827127215632												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_BP_FAT	GO:0006259~DNA metabolic process		54	6.150341686	2.E-07 12190, 50793, 17218, 17217, 17216, 1300	809	809	421	13588	2.E+00	5.E-04	1.E-05	3.E-04
GOTERM_BP_FAT	GO:0033554~cellular response to stress		44	5.011389522	1.E-04 12190, 80905, 245000, 12649, 22209, 136	809	809	404	13588	2.E+00	4.E-01	4.E-03	3.E-01
GOTERM_BP_FAT	GO:0006974~response to DNA damage stimulus		33	3.758542141	5.E-04 12190, 80905, 245000, 12649, 22209, 120	809	809	287	13588	2.E+00	7.E-01	1.E-02	8.E-01
SP_PIR_KEYWORDS	DNA damage		22	2.505694761	5.E-04 382985, 12190, 80905, 245000, 12649, 53	869	869	194	17854	2.E+00	2.E-01	4.E-03	7.E-01
SP_PIR_KEYWORDS	dna repair		19	2.164009112	2.E-03 382985, 80905, 12190, 245000, 53610, 12	869	869	173	17854	2.E+00	6.E-01	1.E-02	3.E+00
GOTERM_BP_FAT	GO:0006281~DNA repair		24	2.733485194	7.E-03 382985, 12190, 80905, 11546, 245000, 12	809	809	222	13588	2.E+00	1.E+00	9.E-02	1.E+01

Annotation Cluster 28	Enrichment Score: 3.6396682224025336											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0008219~cell death		54	6.150341686	4.E-05 12765, 672195, 54354, 14852, 100046871	809	507	13588	2.E+00	1.E-01	2.E-03	8.E-02
GOTERM_BP_FAT	GO:0016265~death		54	6.150341686	8.E-05 12765, 672195, 54354, 14852, 100046871	809	519	13588	2.E+00	2.E-01	3.E-03	1.E-01
GOTERM_BP_FAT	GO:0006915~apoptosis		49	5.580865604	1.E-04 672195, 12765, 54354, 14852, 100046871	809	465	13588	2.E+00	3.E-01	4.E-03	2.E-01
GOTERM_BP_FAT	GO:0012501~programmed cell death		49	5.580865604	2.E-04 672195, 12765, 54354, 14852, 100046871	809	473	13588	2.E+00	4.E-01	6.E-03	3.E-01
SP_PIR_KEYWORDS	Apoptosis		28	3.189066059	8.E-03 22029, 66593, 67184, 11852, 14939, 1165	869	337	17854	2.E+00	1.E+00	4.E-02	1.E+01

Annotation Cluster 29	Enrichment Score: 3.5641212147851236											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	blocked amino end	11	1.25284738	1.E-06	18747, 14191, 20779, 14751, 14678, 1430	869	31	17854	7.E+00	5.E-04	1.E-05	2.E-03
SP_PIR_KEYWORDS	tyrosine-specific protein kinase	9	1.025056948	3.E-04	18596, 14191, 20779, 19713, 14302, 1436	869	37	17854	5.E+00	1.E-01	3.E-03	5.E-01
SP_PIR_KEYWORDS	myristylation	7	0.797266515	6.E-04	18747, 14191, 20779, 14678, 14302, 1436	869	23	17854	6.E+00	3.E-01	5.E-03	9.E-01
SP_PIR_KEYWORDS	autophosphorylation	8	0.911161731	1.E-03	18751, 18596, 14191, 20779, 14360, 1297	869	34	17854	5.E+00	4.E-01	7.E-03	1.E+00
PIRSF_SUPERFAMILY	PIRSF000601:tyrosine-protein kinase, proto-oncogene SRC type	5	0.569476082	5.E-03	14191, 20779, 22612, 14302, 17096	576	11	8136	6.E+00	1.E+00	4.E-01	8.E+00

Annotation Cluster 30	Enrichment Score: 3.531668807969763											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0002757~immune response-activating signal transduction		13	1.480637813	2.E-05 15170, 27007, 16818, 17874, 18803, 1412	809	48	13588	5.E+00	5.E-02	8.E-04	3.E-02
GOTERM_BP_FAT	GO:0002684~positive regulation of immune system process		29	3.302961276	4.E-05 14972, 15018, 16396, 16803, 12010, 1640	809	206	13588	2.E+00	1.E-01	1.E-03	6.E-02
GOTERM_BP_FAT	GO:0002764~immune response-regulating signal transduction		13	1.480637813	4.E-05 15170, 27007, 16818, 17874, 18803, 1412	809	52	13588	4.E+00	1.E-01	2.E-03	7.E-02
UP_SEQ_FEATURE	domain:SH2 2	6	0.683371298	5.E-05 18709, 18708, 15170, 18803, 234779, 209	861	9	16021	1.E+01	9.E-02	5.E-03	8.E-02	
UP_SEQ_FEATURE	domain:SH2 1	6	0.683371298	5.E-05 18709, 18708, 15170, 18803, 234779, 209	861	9	16021	1.E+01	9.E-02	5.E-03	8.E-02	
GOTERM_BP_FAT	GO:0050778~positive regulation of immune response		22	2.505694761	5.E-05 19370, 14972, 15170, 15018, 27007, 2189	809	136	13588	3.E+00	1.E-01	2.E-03	9.E-02
GOTERM_BP_FAT	GO:0048584~positive regulation of response to stimulus		26	2.961275626	1.E-04 14972, 15018, 16803, 12010, 21937, 1880	809	186	13588	2.E+00	3.E-01	4.E-03	2.E-01
GOTERM_BP_FAT	GO:0002253~activation of immune response		16	1.822323462	1.E-04 15170, 27007, 21898, 16818, 17874, 1880	809	86	13588	3.E+00	4.E-01	4.E-03	3.E-01
GOTERM_BP_FAT	GO:0002429~immune response-activating cell surface receptor signaling		10	1.138952164	6.E-04 14127, 15170, 18803, 16818, 234779, 270	809	41	13588	4.E+00	8.E-01	1.E-02	1.E+00
GOTERM_BP_FAT	GO:0002768~immune response-regulating cell surface receptor signaling		10	1.138952164	1.E-03 14127, 15170, 18803, 16818, 234779, 270	809	44	13588	4.E+00	9.E-01	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0031349~positive regulation of defense response		10	1.138952164	6.E-03 19370, 14127, 17874, 16179, 21898, 2700	809	57	13588	3.E+00	1.E+00	8.E-02	1.E+01
GOTERM_BP_FAT	GO:0050851~antigen receptor-mediated signaling pathway		7	0.797266515	2.E-02 15170, 18803, 16818, 234779, 19164, 209	809	36	13588	3.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0050853~B cell receptor signaling pathway		4	0.455580866	5.E-02 15170, 16818, 20963, 17096	809	14	13588	5.E+00	1.E+00	3.E-01	6.E+01

Annotation Cluster 31	Enrichment Score: 3.379190611226443											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	oxidative phosphorylation	8	0.911161731	3.E-06	672195, 17718, 17719, 17721, 17716, 177	869	15	17854	1.E+01	1.E-03	3.E-05	4.E-03
SP_PIR_KEYWORDS	membrane-associated complex	5	0.569476082	4.E-03	17718, 17719, 17721, 17716, 17717, 1772	869	14	17854	7.E+00	8.E-01	2.E-02	5.E+00
INTERPRO	IPR001750:NADH:ubiquinone/plastoquinone oxidoreductase	3	0.341685649	7.E-03	17719, 17721, 17717, 17722	860	3	17763	2.E+01	1.E+00	2.E-01	1.E+01

Annotation Cluster 32    Enrichment Score: 3.3579761785240074



Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0005819--spindle	21	2.391799544	5.E-07	26934, 20871, 18005, 11651, 17869, 2087	636	109	12504	4.E+00	2.E-04	1.E-05	7.E-04
GOTERM_CC_FAT	GO:0005856--cytoskeleton	85	9.681093394	2.E-04	22323, 13669, 94190, 54519, 54354, 7181	636	1122	12504	1.E+00	7.E-02	2.E-03	2.E-01
GOTERM_CC_FAT	GO:0015630--microtubule cytoskeleton	35	3.986332574	1.E-02	13669, 66214, 13430, 11651, 17869, 5435	636	450	12504	2.E+00	1.E+00	8.E-02	2.E+01
GOTERM_CC_FAT	GO:0044430--cytoskeletal part	52	5.922551253	3.E-02	13669, 54354, 16800, 71819, 56150, 1707	636	774	12504	1.E+00	1.E+00	2.E-01	4.E+01
Annotation Cluster 33	Enrichment Score: 3.243163061829678											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0006270--DNA replication initiation	9	1.025056948	6.E-09	17218, 17217, 17220, 12448, 17216, 1244	809	10	13588	2.E+01	2.E-05	5.E-07	1.E-05
INTERPRO	IPR012340:Nucleic acid-binding, OB-fold	16	1.822323462	7.E-08	19891, 66235, 26961, 13664, 13665, 6824	860	58	17763	6.E+00	9.E-05	9.E-06	1.E-04
INTERPRO	IPR001208:DNA-dependent ATPase MCM	7	0.797266515	3.E-07	17218, 17217, 66634, 17220, 17216, 1721	860	8	17763	2.E+01	4.E-04	3.E-05	5.E-04
INTERPRO	IPR018525:DNA-dependent ATPase MCM, conserved site	7	0.797266515	3.E-07	17218, 17217, 66634, 17220, 17216, 1721	860	8	17763	2.E+01	4.E-04	3.E-05	5.E-04
SMART	SM00350:MCM	7	0.797266515	6.E-07	17218, 17217, 66634, 17220, 17216, 1721	492	8	9131	2.E+01	1.E-04	2.E-05	8.E-04
UP_SEQ_FEATURE	domain:MCM	7	0.797266515	6.E-07	17218, 17217, 66634, 17220, 17216, 1721	861	8	16021	2.E+01	1.E-03	1.E-04	1.E-03
GOTERM_BP_FAT	GO:0006261--DNA-dependent DNA replication	11	1.25284738	2.E-05	382985, 17218, 12190, 17217, 17220, 124	809	34	13588	5.E+00	5.E-02	8.E-04	3.E-02
KEGG_PATHWAY	mmu03030:DNA replication	10	1.138952164	7.E-03	17218, 19891, 17217, 17220, 17216, 1721	580	35	5738	3.E+00	6.E-01	2.E-02	8.E+00
GOTERM_BP_FAT	GO:0006268--DNA unwinding during replication	4	0.455580866	2.E-02	17217, 17220, 17216, 17219	809	11	13588	6.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0032508--DNA duplex unwinding	4	0.455580866	3.E-02	17217, 17220, 17216, 17219	809	12	13588	6.E+00	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0032392--DNA geometric change	4	0.455580866	4.E-02	17217, 17220, 17216, 17219	809	13	13588	5.E+00	1.E+00	3.E-01	5.E+01
GOTERM_MF_FAT	GO:0003678--DNA helicase activity	4	0.455580866	2.E-01	13872, 17217, 17220, 17219	754	25	13288	3.E+00	1.E+00	7.E-01	9.E+01
GOTERM_MF_FAT	GO:0043566--structure-specific DNA binding	7	0.797266515	3.E-01	12190, 17217, 17220, 17219, 17869, 1428	754	76	13288	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_MF_FAT	GO:0003697--single-stranded DNA binding	4	0.455580866	3.E-01	12190, 17217, 17220, 17219	754	33	13288	2.E+00	1.E+00	9.E-01	1.E+02
INTERPRO	IPR003593:ATPase, AAA+ type, core	9	1.025056948	4.E-01	17217, 66634, 17220, 18392, 17215, 1935	860	138	17763	1.E+00	1.E+00	1.E+00	1.E+02
SMART	SM00382:AAA	9	1.025056948	5.E-01	17217, 66634, 17220, 18392, 17215, 1935	492	138	9131	1.E+00	1.E+00	1.E+00	1.E+02
INTERPRO	IPR003959:ATPase, AAA-type, core	3	0.341685649	7.E-01	18392, 18195, 23834	860	46	17763	1.E+00	1.E+00	1.E+00	1.E+02
Annotation Cluster 34	Enrichment Score: 3.203584865794646											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0010033--response to organic substance	54	6.150341686	4.E-05	12475, 14815, 20191, 16803, 12912, 1464	809	505	13588	2.E+00	1.E-01	1.E-03	7.E-02
GOTERM_BP_FAT	GO:0009725--response to hormone stimulus	24	2.733485194	1.E-04	13685, 12842, 109900, 232087, 11651, 12	809	165	13588	2.E+00	3.E-01	4.E-03	2.E-01
GOTERM_BP_FAT	GO:0043434--response to peptide hormone stimulus	16	1.822323462	5.E-04	13685, 12842, 109900, 12043, 11651, 384	809	95	13588	3.E+00	7.E-01	1.E-02	8.E-01
GOTERM_BP_FAT	GO:0009719--response to endogenous stimulus	24	2.733485194	6.E-04	13685, 12842, 109900, 232087, 11651, 12	809	184	13588	2.E+00	8.E-01	1.E-02	1.E+00
GOTERM_BP_FAT	GO:0032869--cellular response to insulin stimulus	10	1.138952164	8.E-04	18709, 18708, 13685, 16367, 16334, 1042	809	43	13588	4.E+00	9.E-01	2.E-02	1.E+00
GOTERM_BP_FAT	GO:0032870--cellular response to hormone stimulus	11	1.25284738	2.E-03	18709, 18708, 13685, 16367, 16334, 1042	809	58	13588	3.E+00	1.E+00	3.E-02	4.E+00
GOTERM_BP_FAT	GO:0032868--response to insulin stimulus	11	1.25284738	2.E-03	18709, 18708, 56717, 13685, 16367, 1633	809	59	13588	3.E+00	1.E+00	4.E-02	4.E+00
GOTERM_BP_FAT	GO:0008286--insulin receptor signaling pathway	7	0.797266515	5.E-03	18709, 18708, 13685, 16367, 16334, 1165	809	28	13588	4.E+00	1.E+00	7.E-02	9.E+00
Annotation Cluster 35	Enrichment Score: 3.096364920346249											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0031974--membrane-enclosed lumen	92	10.47835991	2.E-05	18747, 66885, 672195, 68263, 22130, 184	636	1174	12504	2.E+00	9.E-03	4.E-04	3.E-02
GOTERM_CC_FAT	GO:0043233--organelle lumen	89	10.13667426	3.E-05	18747, 66885, 672195, 68263, 22130, 184	636	1136	12504	2.E+00	1.E-02	5.E-04	5.E-02
GOTERM_CC_FAT	GO:0070013--intracellular organelle lumen	88	10.02277904	5.E-05	18747, 66885, 672195, 68263, 22130, 184	636	1133	12504	2.E+00	2.E-02	7.E-04	7.E-02
GOTERM_CC_FAT	GO:0005667--transcription factor complex	26	2.961275626	4.E-04	18181, 21869, 12912, 12914, 13872, 1355	636	234	12504	2.E+00	1.E-01	4.E-03	5.E-01
GOTERM_CC_FAT	GO:0005654--nucleoplasm	45	5.125284738	9.E-03	60406, 18747, 18181, 67184, 12649, 4337	636	599	12504	1.E+00	1.E+00	6.E-02	1.E+01
GOTERM_CC_FAT	GO:0031981--nuclear lumen	58	6.605922551	4.E-02	18747, 22130, 101206, 21869, 12912, 129	636	883	12504	1.E+00	1.E+00	2.E-01	4.E+01
GOTERM_CC_FAT	GO:0044451--nucleoplasm part	36	4.10022779	5.E-02	60406, 18181, 433759, 101206, 17869, 21	636	513	12504	1.E+00	1.E+00	2.E-01	5.E+01
Annotation Cluster 36	Enrichment Score: 2.9618315551430765											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0043068--positive regulation of programmed cell death	34	3.872437358	1.E-05	12190, 672195, 66593, 67184, 11816, 149	809	250	13588	2.E+00	4.E-02	6.E-04	2.E-02
GOTERM_BP_FAT	GO:0010942--positive regulation of cell death	34	3.872437358	2.E-05	12190, 672195, 66593, 67184, 11816, 149	809	252	13588	2.E+00	5.E-02	7.E-04	3.E-02
GOTERM_BP_FAT	GO:0043065--positive regulation of apoptosis	33	3.758542141	3.E-05	12190, 672195, 66593, 67184, 11816, 149	809	248	13588	2.E+00	8.E-02	1.E-03	5.E-02
GOTERM_BP_FAT	GO:0043067--regulation of programmed cell death	55	6.264236902	3.E-04	12190, 672195, 13628, 14815, 14852, 120	809	560	13588	2.E+00	6.E-01	8.E-03	5.E-01
GOTERM_BP_FAT	GO:0010941--regulation of cell death	55	6.264236902	3.E-04	12190, 672195, 13628, 14815, 14852, 120	809	563	13588	2.E+00	6.E-01	9.E-03	6.E-01
GOTERM_BP_FAT	GO:0042981--regulation of apoptosis	54	6.150341686	4.E-04	12190, 672195, 13628, 14815, 14852, 120	809	553	13588	2.E+00	7.E-01	1.E-02	7.E-01
GOTERM_BP_FAT	GO:0012502--induction of programmed cell death	22	2.505694761	9.E-04	382985, 12190, 15170, 66593, 67184, 118	809	167	13588	2.E+00	9.E-01	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0006917--induction of apoptosis	22	2.505694761	9.E-04	382985, 12190, 15170, 66593, 67184, 118	809	167	13588	2.E+00	9.E-01	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0043069--negative regulation of programmed cell death	23	2.619589977	3.E-02	13628, 11651, 17869, 12043, 108138, 204	809	244	13588	2.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0060548--negative regulation of cell death	23	2.619589977	4.E-02	13628, 11651, 17869, 12043, 108138, 204	809	245	13588	2.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0043066--negative regulation of apoptosis	22	2.505694761	5.E-02	13628, 11651, 17869, 12043, 108138, 204	809	239	13588	2.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0006916--anti-apoptosis	8	0.911161731	3.E-01	12048, 13628, 11651, 12043, 17869, 2203	809	88	13588	2.E+00	1.E+00	8.E-01	1.E+02
Annotation Cluster 37	Enrichment Score: 2.939622434768651											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
COG_ONTOLOGY	Energy production and conversion	7	0.797266515	5.E-05	12039, 18597, 110842, 18598, 66445, 668	66	23	2040	9.E+00	1.E-03	5.E-04	4.E-02



GOTERM_MF_FAT	GO:0016624~oxidoreductase activity, acting on the aldehyde or c	6	0.683371298	6.E-05	12039, 68263, 18597, 18598, 100048676,	754	9	13288	1.E+01	4.E-02	1.E-03	9.E-02
SP_PIR_KEYWORDS	thiamine pyrophosphate	5	0.569476082	1.E-03	12039, 68263, 18597, 18598, 21881	869	11	17854	9.E+00	5.E-01	9.E-03	2.E+00
PIR_SUPERFAMILY	PIRSF000152:pyruvate dehydrogenase (lipoamide) alpha chain	3	0.341685649	1.E-02	12039, 18597, 18598	576	3	8136	1.E+01	1.E+00	6.E-01	2.E+01
INTERPRO	IPR001017:Dehydrogenase, E1 component	3	0.341685649	3.E-02	12039, 18597, 18598	860	6	17763	1.E+01	1.E+00	5.E-01	4.E+01
Annotation Cluster 38	Enrichment Score: 2.9019665556677188											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0051329~interphase of mitotic cell cycle	11	1.25284738	5.E-04	104394, 19645, 13559, 12649, 12443, 131	809	49	13588	4.E+00	8.E-01	1.E-02	9.E-01
GOTERM_BP_FAT	GO:0051325~interphase	11	1.25284738	7.E-04	104394, 19645, 13559, 12649, 12443, 131	809	51	13588	4.E+00	9.E-01	2.E-02	1.E+00
GOTERM_BP_FAT	GO:0000082~G1/S transition of mitotic cell cycle	7	0.797266515	5.E-03	104394, 19645, 13559, 12443, 12043, 164	809	28	13588	4.E+00	1.E+00	7.E-02	9.E+00
Annotation Cluster 39	Enrichment Score: 2.8803474419997155											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	myristylation	7	0.797266515	6.E-04	18747, 14191, 20779, 14678, 14302, 1436	869	23	17854	6.E+00	3.E-01	5.E-03	9.E-01
SP_PIR_KEYWORDS	myristate	15	1.708428246	8.E-04	11350, 18747, 14678, 70231, 21844, 2049	869	109	17854	3.E+00	3.E-01	6.E-03	1.E+00
UP_SEQ_FEATURE	lipid moiety-binding region:N-myristoyl glycine	14	1.59453303	4.E-03	18747, 14678, 70231, 21844, 20491, 2400	861	106	16021	2.E+00	1.E+00	2.E-01	7.E+00
Annotation Cluster 40	Enrichment Score: 2.8643914798390604											
Category	Term: electron carrier activity/Acyl-CoA dehydrogenase	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0009055~electron carrier activity	28	3.189066059	3.E-05	66885, 672195, 226646, 14782, 66414, 11	754	202	13288	2.E+00	2.E-02	6.E-04	4.E-02
SP_PIR_KEYWORDS	Flavoprotein	17	1.936218679	4.E-05	66885, 229211, 14782, 13382, 99586, 113	869	103	17854	3.E+00	2.E-02	3.E-04	5.E-02
INTERPRO	IPR006089:Acyl-CoA dehydrogenase, conserved site	6	0.683371298	5.E-05	11370, 66885, 11409, 229211, 11364, 113	860	10	17763	1.E+01	7.E-02	3.E-03	9.E-02
INTERPRO	IPR006092:Acyl-CoA dehydrogenase, N-terminal	6	0.683371298	9.E-05	11370, 66885, 11409, 229211, 11364, 113	860	11	17763	1.E+01	1.E-01	5.E-03	2.E-01
GOTERM_MF_FAT	GO:0050662~coenzyme binding	23	2.619589977	1.E-04	226646, 66885, 100042746, 56847, 14782	754	160	13288	3.E+00	7.E-02	2.E-03	2.E-01
INTERPRO	IPR006090:Acyl-CoA oxidase/dehydrogenase, type 1	6	0.683371298	2.E-04	11370, 66885, 11409, 229211, 11364, 113	860	13	17763	1.E+01	3.E-01	1.E-02	4.E-01
SP_PIR_KEYWORDS	FAD	16	1.822323462	3.E-04	66885, 229211, 14782, 13382, 99586, 113	869	109	17854	3.E+00	1.E-01	2.E-03	4.E-01
INTERPRO	IPR013786:Acyl-CoA dehydrogenase/oxidase, N-terminal	6	0.683371298	4.E-04	11370, 66885, 11409, 229211, 11364, 113	860	14	17763	9.E+00	4.E-01	2.E-02	6.E-01
GOTERM_MF_FAT	GO:0048037~cofactor binding	27	3.075170843	5.E-04	70316, 66885, 226646, 100042746, 14782	754	226	13288	2.E+00	3.E-01	7.E-03	7.E-01
INTERPRO	IPR013764:Acyl-CoA oxidase/dehydrogenase, type1/2, C-terminal	6	0.683371298	5.E-04	11370, 66885, 11409, 229211, 11364, 113	860	15	17763	8.E+00	5.E-01	2.E-02	9.E-01
INTERPRO	IPR006091:Acyl-CoA oxidase/dehydrogenase, central region	6	0.683371298	7.E-04	11370, 66885, 11409, 229211, 11364, 113	860	16	17763	8.E+00	6.E-01	3.E-02	1.E+00
UP_SEQ_FEATURE	nucleotide phosphate-binding region:FAD	11	1.25284738	9.E-04	11370, 66885, 18126, 11409, 110842, 264	861	58	16021	4.E+00	9.E-01	7.E-02	2.E+00
GOTERM_MF_FAT	GO:0003995~acyl-CoA dehydrogenase activity	6	0.683371298	1.E-03	11370, 66885, 11409, 229211, 11364, 113	754	16	13288	7.E+00	7.E-01	2.E-02	2.E+00
GOTERM_MF_FAT	GO:0050660~FAD binding	12	1.366742597	2.E-03	11370, 66885, 18126, 11409, 110842, 264	754	71	13288	3.E+00	8.E-01	3.E-02	3.E+00
COG_ONTOLOGY	Lipid metabolism	9	1.025056948	5.E-03	11370, 66885, 18107, 15107, 11409, 2292	66	86	2040	3.E+00	1.E-01	3.E-02	4.E+00
PIR_SUPERFAMILY	PIRSF000182:acyl-CoA dehydrogenase	4	0.455580866	6.E-03	66885, 11409, 11364, 11363	576	6	8136	9.E+00	1.E+00	4.E-01	8.E+00
SP_PIR_KEYWORDS	fatty acid metabolism	9	1.025056948	9.E-03	11370, 66885, 15107, 11409, 74147, 9374	869	61	17854	3.E+00	1.E+00	4.E-02	1.E+01
GOTERM_BP_FAT	GO:0006631~fatty acid metabolic process	19	2.164009112	3.E-02	70316, 66885, 19317, 15107, 11807, 1908	809	184	13588	2.E+00	1.E+00	2.E-01	4.E+01
SP_PIR_KEYWORDS	lipid metabolism	13	1.480637813	3.E-02	66885, 15107, 11806, 20887, 11364, 1136	869	136	17854	2.E+00	1.E+00	1.E-01	4.E+01
UP_SEQ_FEATURE	binding site:Substrate; via carbonyl oxygen	5	0.569476082	5.E-02	11370, 66885, 11409, 11364, 11720	861	26	16021	4.E+00	1.E+00	8.E-01	6.E+01
KEGG_PATHWAY	mmu00071:Fatty acid metabolism	9	1.025056948	8.E-02	11370, 66885, 15107, 11409, 74147, 9374	580	45	5738	2.E+00	1.E+00	2.E-01	6.E+01
KEGG_PATHWAY	mmu00062:Fatty acid elongation in mitochondria	3	0.341685649	2.E-01	15107, 93747, 231086	580	8	5738	4.E+00	1.E+00	4.E-01	9.E+01
Annotation Cluster 41	Enrichment Score: 2.8167058622169336											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0051336~regulation of hydrolase activity	28	3.189066059	4.E-05	22324, 672195, 66593, 17869, 11856, 148	809	196	13588	2.E+00	1.E-01	1.E-03	7.E-02
GOTERM_BP_FAT	GO:0001836~release of cytochrome c from mitochondria	7	0.797266515	2.E-04	12048, 12028, 12122, 12018, 12043, 1786	809	16	13588	7.E+00	5.E-01	6.E-03	4.E-01
GOTERM_BP_FAT	GO:0006919~activation of caspase activity	9	1.025056948	6.E-04	16818, 672195, 66593, 12028, 12018, 178	809	33	13588	5.E+00	8.E-01	1.E-02	1.E+00
GOTERM_BP_FAT	GO:0051345~positive regulation of hydrolase activity	14	1.59453303	9.E-04	672195, 66593, 17869, 11856, 14852, 168	809	81	13588	3.E+00	9.E-01	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0043280~positive regulation of caspase activity	9	1.025056948	1.E-03	16818, 672195, 66593, 12028, 12018, 178	809	36	13588	4.E+00	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0010952~positive regulation of peptidase activity	9	1.025056948	1.E-03	16818, 672195, 66593, 12028, 12018, 178	809	36	13588	4.E+00	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0043281~regulation of caspase activity	10	1.138952164	2.E-03	16818, 672195, 12015, 66593, 12028, 120	809	50	13588	3.E+00	1.E+00	4.E-02	4.E+00
GOTERM_BP_FAT	GO:0052548~regulation of endopeptidase activity	10	1.138952164	2.E-03	16818, 672195, 12015, 66593, 12028, 120	809	50	13588	3.E+00	1.E+00	4.E-02	4.E+00
GOTERM_BP_FAT	GO:0052547~regulation of peptidase activity	10	1.138952164	3.E-03	16818, 672195, 12015, 66593, 12028, 120	809	51	13588	3.E+00	1.E+00	5.E-02	5.E+00
GOTERM_BP_FAT	GO:0008635~activation of caspase activity by cytochrome c	3	0.341685649	3.E-02	672195, 12028, 12018, 13063	809	5	13588	1.E+01	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0001783~B cell apoptosis	3	0.341685649	5.E-02	12028, 12018, 17869	809	6	13588	8.E+00	1.E+00	3.E-01	6.E+01
Annotation Cluster 42	Enrichment Score: 2.796134398880119											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_SEQ_FEATURE	domain:PH 1	11	1.25284738	6.E-06	14163, 18803, 26382, 30938, 19417, 2122	861	33	16021	6.E+00	1.E-02	7.E-04	1.E-02
UP_SEQ_FEATURE	domain:PH 2	10	1.138952164	3.E-05	14163, 26382, 30938, 19417, 212285, 218	861	32	16021	6.E+00	6.E-02	4.E-03	6.E-02
UP_SEQ_FEATURE	zinc finger region:FYVE-type	10	1.138952164	1.E-04	14163, 245049, 19894, 26382, 380714, 30	861	37	16021	5.E+00	2.E-01	1.E-02	2.E-01
PIR_SUPERFAMILY	PIRSF037335:FYVE, RhoGEF and PH domain containing protein(1-	4	0.455580866	1.E-03	14163, 26382, 30938, 224014	576	4	8136	1.E+01	5.E-01	1.E-01	2.E+00
INTERPRO	IPR017455:Zinc finger, FYVE-related	6	0.683371298	3.E-02	14163, 19894, 26382, 380714, 30938, 224	860	35	17763	4.E+00	1.E+00	4.E-01	3.E+01
INTERPRO	IPR000306:Zinc finger, FYVE-type	4	0.455580866	2.E-01	14163, 26382, 30938, 224014	860	30	17763	3.E+00	1.E+00	9.E-01	1.E+02
SMART	SM00064:FYVE	4	0.455580866	2.E-01	14163, 26382, 30938, 224014	492	30	9131	2.E+00	1.E+00	8.E-01	1.E+02



Annotation Cluster 43		Enrichment Score: 2.765791703456401										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0030427~site of polarized growth	11	1.25284738	2.E-04	11785, 73750, 77579, 19164, 18479, 1256	636	51	12504	4.E+00	8.E-02	2.E-03	3.E-01
GOTERM_CC_FAT	GO:0030426~growth cone	11	1.25284738	2.E-04	11785, 73750, 77579, 19164, 18479, 1256	636	51	12504	4.E+00	8.E-02	2.E-03	3.E-01
GOTERM_CC_FAT	GO:0043005~neuron projection	18	2.050113895	1.E-01	11658, 73750, 94190, 17869, 16800, 1847	636	245	12504	1.E+00	1.E+00	4.E-01	8.E+01
Annotation Cluster 44		Enrichment Score: 2.735091028823163										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	gluconeogenesis	10	1.138952164	2.E-08	100042746, 18534, 11676, 11674, 100041	869	17	17854	1.E+01	1.E-05	3.E-07	4.E-05
GOTERM_BP_FAT	GO:0034637~cellular carbohydrate biosynthetic process	12	1.366742597	4.E-04	18682, 14751, 234779, 18534, 11651, 219	809	56	13588	4.E+00	7.E-01	1.E-02	7.E-01
GOTERM_BP_FAT	GO:0006090~pyruvate metabolic process	7	0.797266515	3.E-03	14751, 235339, 18534, 21991, 230163, 18	809	25	13588	5.E+00	1.E+00	5.E-02	5.E+00
GOTERM_BP_FAT	GO:0006094~gluconeogenesis	6	0.683371298	5.E-03	14751, 18534, 21991, 230163, 18563, 745	809	20	13588	5.E+00	1.E+00	8.E-02	9.E+00
GOTERM_BP_FAT	GO:0046165~alcohol biosynthetic process	8	0.911161731	6.E-03	14751, 234779, 18534, 21991, 230163, 18	809	37	13588	4.E+00	1.E+00	8.E-02	9.E+00
GOTERM_BP_FAT	GO:0046364~monosaccharide biosynthetic process	7	0.797266515	9.E-03	14751, 18534, 21991, 230163, 18563, 143	809	31	13588	4.E+00	1.E+00	1.E-01	1.E+01
GOTERM_BP_FAT	GO:0016051~carbohydrate biosynthetic process	12	1.366742597	1.E-02	18682, 14751, 234779, 18534, 11651, 219	809	83	13588	2.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0019319~hexose biosynthetic process	6	0.683371298	1.E-02	14751, 18534, 21991, 230163, 18563, 745	809	25	13588	4.E+00	1.E+00	2.E-01	2.E+01
UP_SEQ_FEATURE	metal ion-binding site:Manganese	4	0.455580866	2.E-01	19053, 18534, 18563, 74551	861	31	16021	2.E+00	1.E+00	1.E+00	1.E+02
Annotation Cluster 45		Enrichment Score: 2.6864735055409783										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0015980~energy derivation by oxidation of organic compound	26	2.961275626	3.E-10	66416, 11651, 17721, 17722, 18679, 2227	809	98	13588	4.E+00	1.E-06	4.E-08	6.E-07
GOTERM_BP_FAT	GO:0006073~cellular glucan metabolic process	9	1.025056948	6.E-04	18682, 110095, 16195, 102093, 110094, 1	809	33	13588	5.E+00	8.E-01	1.E-02	1.E+00
GOTERM_BP_FAT	GO:0040402~glucan metabolic process	9	1.025056948	6.E-04	18682, 110095, 16195, 102093, 110094, 1	809	33	13588	5.E+00	8.E-01	1.E-02	1.E+00
GOTERM_BP_FAT	GO:0005977~glycogen metabolic process	9	1.025056948	6.E-04	18682, 110095, 16195, 102093, 110094, 1	809	33	13588	5.E+00	8.E-01	1.E-02	1.E+00
GOTERM_BP_FAT	GO:0006112~energy reserve metabolic process	9	1.025056948	1.E-03	18682, 110095, 16195, 102093, 110094, 1	809	37	13588	4.E+00	1.E+00	2.E-02	2.E+00
SP_PIR_KEYWORDS	glycogen metabolism	6	0.683371298	2.E-03	18682, 110095, 102093, 110094, 11651, 1	869	19	17854	6.E+00	5.E-01	1.E-02	2.E+00
SP_PIR_KEYWORDS	carbohydrate metabolism	11	1.25284738	3.E-03	18682, 110095, 16333, 16334, 102093, 11	869	73	17854	3.E+00	7.E-01	2.E-02	4.E+00
GOTERM_BP_FAT	GO:004264~cellular polysaccharide metabolic process	9	1.025056948	3.E-03	18682, 110095, 16195, 102093, 110094, 1	809	43	13588	4.E+00	1.E+00	5.E-02	6.E+00
INTERPRO	IPR008734:Phosphorylase kinase alphabeta	3	0.341685649	7.E-03	102093, 110094, 18679	860	3	17763	2.E+01	1.E+00	2.E-01	1.E+01
GOTERM_BP_FAT	GO:0009250~glucan biosynthetic process	4	0.455580866	2.E-02	18682, 11651, 27357, 77559	809	11	13588	6.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0005978~glycogen biosynthetic process	4	0.455580866	2.E-02	18682, 11651, 27357, 77559	809	11	13588	6.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0033692~cellular polysaccharide biosynthetic process	4	0.455580866	1.E-01	18682, 11651, 27357, 77559	809	20	13588	3.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0005976~polysaccharide metabolic process	9	1.025056948	2.E-01	18682, 110095, 16195, 102093, 110094, 1	809	92	13588	2.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0000271~polysaccharide biosynthetic process	4	0.455580866	3.E-01	18682, 11651, 27357, 77559	809	30	13588	2.E+00	1.E+00	8.E-01	1.E+02
Annotation Cluster 46		Enrichment Score: 2.6779125184016004										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0010627~regulation of protein kinase cascade	27	3.075170843	1.E-06	12234, 16543, 15163, 16994, 12703, 1478	809	155	13588	3.E+00	4.E-03	7.E-05	3.E-03
UP_SEQ_FEATURE	domain:TLR	8	0.911161731	3.E-04	17874, 239081, 21899, 21898, 117149, 24	861	25	16021	6.E+00	4.E-01	2.E-02	4.E-01
GOTERM_BP_FAT	GO:0043122~regulation of I-kappaB kinase/NF-kappaB cascade	10	1.138952164	5.E-04	16994, 17874, 21899, 21898, 56722, 1921	809	40	13588	4.E+00	7.E-01	1.E-02	8.E-01
GOTERM_BP_FAT	GO:0010740~positive regulation of protein kinase cascade	14	1.59453303	2.E-03	21899, 21898, 14180, 11848, 15163, 1699	809	88	13588	3.E+00	1.E+00	3.E-02	4.E+00
GOTERM_BP_FAT	GO:0043123~positive regulation of I-kappaB kinase/NF-kappaB cascade	8	0.911161731	3.E-03	16994, 17874, 21899, 21898, 56722, 1921	809	33	13588	4.E+00	1.E+00	5.E-02	5.E+00
GOTERM_BP_FAT	GO:0009967~positive regulation of signal transduction	20	2.277904328	7.E-03	21899, 21898, 14180, 56847, 15163, 1184	809	172	13588	2.E+00	1.E+00	9.E-02	1.E+01
GOTERM_BP_FAT	GO:0042108~positive regulation of cytokine biosynthetic process	8	0.911161731	1.E-02	12051, 16994, 17874, 11807, 21899, 2189	809	42	13588	3.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0010647~positive regulation of cell communication	20	2.277904328	2.E-02	21899, 21898, 14180, 56847, 15163, 1184	809	189	13588	2.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0042035~regulation of cytokine biosynthetic process	9	1.025056948	4.E-02	12051, 16994, 17874, 11807, 21899, 2189	809	64	13588	2.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0032675~regulation of interleukin-6 production	6	0.683371298	4.E-02	14127, 17874, 21899, 21898, 24088, 1067	809	32	13588	3.E+00	1.E+00	3.E-01	5.E+01
Annotation Cluster 47		Enrichment Score: 2.620764449707421										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0001568~blood vessel development	31	3.530751708	1.E-04	12831, 11852, 11816, 11651, 238055, 204	809	244	13588	2.E+00	3.E-01	4.E-03	2.E-01
GOTERM_BP_FAT	GO:0001944~vasculature development	31	3.530751708	2.E-04	12831, 11852, 11816, 11651, 238055, 204	809	250	13588	2.E+00	4.E-01	5.E-03	3.E-01
GOTERM_BP_FAT	GO:0048514~blood vessel morphogenesis	21	2.391799544	1.E-02	19317, 14674, 11852, 11816, 238055, 141	809	198	13588	2.E+00	1.E+00	2.E-01	2.E+01
GOTERM_BP_FAT	GO:0001525~angiogenesis	13	1.480637813	1.E-01	14674, 11852, 14180, 20416, 18771, 1475	809	133	13588	2.E+00	1.E+00	5.E-01	8.E+01
Annotation Cluster 48		Enrichment Score: 2.5859330346468146										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	pyruvate	8	0.911161731	1.E-05	18746, 18770, 68263, 27402, 18597, 1859	869	18	17854	9.E+00	6.E-03	1.E-04	2.E-02
GOTERM_MF_FAT	GO:0016624~oxidoreductase activity, acting on the aldehyde or carbon-oxygen bond	6	0.683371298	6.E-05	12039, 68263, 18597, 18598, 100048676, 6	754	9	13288	1.E+01	4.E-02	1.E-03	9.E-02
KEGG_PATHWAY	mmu00620:Pyruvate metabolism	14	1.59453303	1.E-04	18746, 68263, 18534, 13382, 74551, 1682	580	41	5738	3.E+00	2.E-02	5.E-04	1.E-01
SP_PIR_KEYWORDS	thiamine pyrophosphate	5	0.569476082	1.E-03	12039, 68263, 18597, 18598, 21881	869	11	17854	9.E+00	5.E-01	9.E-03	2.E+00
GOTERM_MF_FAT	GO:0004738~pyruvate dehydrogenase activity	3	0.341685649	9.E-03	68263, 18597, 18598	754	3	13288	2.E+01	1.E+00	1.E-01	1.E+01
GOTERM_MF_FAT	GO:0004739~pyruvate dehydrogenase (acetyl-transferring) activity	3	0.341685649	9.E-03	68263, 18597, 18598	754	3	13288	2.E+01	1.E+00	1.E-01	1.E+01
KEGG_PATHWAY	mmu00020:Citrate cycle (TCA cycle)	9	1.025056948	1.E-02	68263, 235339, 18597, 18598, 18534, 185	580	31	5738	3.E+00	8.E-01	3.E-02	1.E+01



KEGG_PATHWAY	mmu00650:Butanoate metabolism	7	0.797266515	2.E-01	68263, 15107, 11409, 74147, 18597, 1859	580	37	5738	2.E+00	1.E+00	3.E-01	9.E+01
KEGG_PATHWAY	mmu00290:Valine, leucine and isoleucine biosynthesis	3	0.341685649	3.E-01	68263, 18597, 18598	580	11	5738	3.E+00	1.E+00	5.E-01	1.E+02
Annotation Cluster 49	Enrichment Score: 2.57787029200432											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0019992~diacylglycerol binding	12	1.366742597	4.E-04	18751, 22324, 26934, 78816, 13350, 1792	754	59	13288	4.E+00	3.E-01	7.E-03	6.E-01
UP_SEQ_FEATURE	zinc finger region:Phorbol-ester/DAG-type	9	1.025056948	8.E-04	22324, 26934, 78816, 17925, 70719, 5435	861	38	16021	4.E+00	8.E-01	6.E-02	1.E+00
INTERPRO	IPR002219:Protein kinase C-like, phorbol ester/diacylglycerol bind	11	1.25284738	1.E-03	18751, 22324, 26934, 78816, 17925, 7071	860	66	17763	3.E+00	8.E-01	4.E-02	2.E+00
SMART	SM00109:C1	11	1.25284738	3.E-03	18751, 22324, 26934, 78816, 17925, 7071	492	66	9131	3.E+00	4.E-01	5.E-02	3.E+00
INTERPRO	IPR002219:Protein kinase C, phorbol ester/diacylglycerol binding	8	0.911161731	1.E-02	22324, 78816, 17925, 70719, 270163, 543	860	52	17763	3.E+00	1.E+00	3.E-01	2.E+01
GOTERM_MF_FAT	GO:0030676~Rac guanyl-nucleotide exchange factor activity	3	0.341685649	3.E-02	22324, 57257, 16800	754	5	13288	1.E+01	1.E+00	3.E-01	4.E+01
Annotation Cluster 50	Enrichment Score: 2.44869404502878											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0017124~SH3 domain binding	14	1.59453303	5.E-04	22323, 20401, 15170, 19317, 13800, 2283	754	79	13288	3.E+00	3.E-01	7.E-03	7.E-01
GOTERM_MF_FAT	GO:0019904~protein domain specific binding	24	2.733485194	5.E-04	22323, 11350, 15170, 20401, 19317, 1380	754	192	13288	2.E+00	3.E-01	8.E-03	8.E-01
SP_PIR_KEYWORDS	sh3-binding	9	1.025056948	6.E-03	22323, 20401, 19317, 13800, 80987, 3093	869	57	17854	3.E+00	9.E-01	3.E-02	8.E+00
UP_SEQ_FEATURE	short sequence motif:SH3-binding	6	0.683371298	1.E-01	14163, 20401, 19317, 30939, 228359, 118	861	47	16021	2.E+00	1.E+00	1.E+00	9.E+01
Annotation Cluster 51	Enrichment Score: 2.440992102288333											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0005092~GDP-dissociation inhibitor activity	5	0.569476082	5.E-05	14570, 192662, 14567, 11857, 14569	754	5	13288	2.E+01	4.E-02	1.E-03	7.E-02
INTERPRO	IPR000406:RHO protein GDP dissociation inhibitor	3	0.341685649	7.E-03	14570, 192662, 11857	860	3	17763	2.E+01	1.E+00	2.E-01	1.E+01
GOTERM_MF_FAT	GO:0005094~Rho GDP-dissociation inhibitor activity	3	0.341685649	9.E-03	14570, 192662, 11857	754	3	13288	2.E+01	1.E+00	1.E-01	1.E+01
PIR_SUPERFAMILY	PIRSF015597:rho GDP dissociation inhibitor	3	0.341685649	1.E-02	14570, 192662, 11857	576	3	8136	1.E+01	1.E+00	6.E-01	2.E+01
PIR_SUPERFAMILY	PIRSF500829:animal rho GDP dissociation inhibitor	3	0.341685649	1.E-02	14570, 192662, 11857	576	3	8136	1.E+01	1.E+00	6.E-01	2.E+01
Annotation Cluster 52	Enrichment Score: 2.353117343838236											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0002263~cell activation during immune response	9	1.025056948	3.E-04	12051, 11486, 18826, 234779, 19164, 118	809	31	13588	5.E+00	6.E-01	9.E-03	6.E-01
GOTERM_BP_FAT	GO:0002366~leukocyte activation during immune response	9	1.025056948	3.E-04	12051, 11486, 18826, 234779, 19164, 118	809	31	13588	5.E+00	6.E-01	9.E-03	6.E-01
GOTERM_BP_FAT	GO:0002285~lymphocyte activation during immune response	7	0.797266515	6.E-04	12051, 11486, 18826, 234779, 19164, 118	809	19	13588	6.E+00	8.E-01	1.E-02	1.E+00
GOTERM_BP_FAT	GO:0002286~T cell activation during immune response	5	0.569476082	8.E-03	12051, 18826, 19164, 11891, 23882	809	14	13588	6.E+00	1.E+00	1.E-01	1.E+01
GOTERM_BP_FAT	GO:0002313~mature B cell differentiation during immune response	3	0.341685649	3.E-02	12051, 11486, 234779	809	5	13588	1.E+01	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0002312~B cell activation during immune response	3	0.341685649	3.E-02	12051, 11486, 234779	809	5	13588	1.E+01	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0002335~mature B cell differentiation	3	0.341685649	6.E-02	12051, 11486, 234779	809	7	13588	7.E+00	1.E+00	4.E-01	7.E+01
Annotation Cluster 53	Enrichment Score: 2.2583213225119296											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0009611~response to wounding	38	4.328018223	4.E-04	12475, 11651, 18793, 16803, 14026, 2193	809	347	13588	2.E+00	7.E-01	1.E-02	7.E-01
GOTERM_BP_FAT	GO:0009617~response to bacterium	21	2.391799544	1.E-03	14972, 12475, 239081, 21898, 13035, 168	809	157	13588	2.E+00	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0045087~innate immune response	15	1.708428246	4.E-03	15170, 239081, 21899, 21898, 16803, 178	809	107	13588	2.E+00	1.E+00	6.E-02	8.E+00
SP_PIR_KEYWORDS	inflammatory response	11	1.25284738	4.E-03	20310, 17874, 12475, 239081, 246779, 17	869	78	17854	3.E+00	9.E-01	2.E-02	6.E+00
GOTERM_BP_FAT	GO:0006955~immune response	43	4.897494305	6.E-03	14972, 12475, 22324, 15018, 16803, 1201	809	471	13588	2.E+00	1.E+00	8.E-02	1.E+01
SP_PIR_KEYWORDS	immune response	18	2.050113895	8.E-03	15007, 14972, 12475, 15018, 239081, 218	869	184	17854	2.E+00	1.E+00	4.E-02	1.E+01
GOTERM_BP_FAT	GO:0006954~inflammatory response	22	2.505694761	3.E-02	12475, 239081, 21899, 21898, 11651, 164	809	225	13588	2.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0006952~defense response	35	3.986332574	8.E-02	14972, 12475, 15018, 11651, 16803, 1201	809	448	13588	1.E+00	1.E+00	5.E-01	8.E+01
Annotation Cluster 54	Enrichment Score: 2.2068705060030114											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
BIOCARTA	m_igf1Intorpathway:Skeletal muscle hypertrophy is regulated via	10	1.138952164	2.E-03	13684, 18708, 56717, 13685, 26905, 1366	188	20	1171	3.E+00	3.E-01	3.E-02	2.E+00
BIOCARTA	m_eif4Pathway:Regulation of eIF4e and p70 S6 Kinase	9	1.025056948	8.E-03	13684, 18751, 18708, 56717, 13685, 1636	188	20	1171	3.E+00	8.E-01	6.E-02	1.E+01
BIOCARTA	m_mTORPathway:mTOR Signaling Pathway	9	1.025056948	2.E-02	13684, 18708, 56717, 19744, 13685, 7570	188	22	1171	3.E+00	1.E+00	1.E-01	2.E+01
Annotation Cluster 55	Enrichment Score: 2.1613895144814546											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
BIOCARTA	m_igf1rPathway:Multiple antiapoptotic pathways from IGF-1R sig	11	1.25284738	2.E-04	18708, 18747, 12015, 16367, 14784, 2066	188	19	1171	4.E+00	5.E-02	7.E-03	3.E-01
GOTERM_BP_FAT	GO:0048009~insulin-like growth factor receptor signaling pathwa	5	0.569476082	1.E-03	18708, 16367, 11651, 16001, 16000	809	9	13588	9.E+00	1.E+00	2.E-02	2.E+00
BIOCARTA	m_longevityPathway:The IGF-1 Receptor and Longevity	6	0.683371298	2.E-02	18708, 15461, 11651, 16001, 20416, 1600	188	11	1171	3.E+00	1.E+00	1.E-01	2.E+01
BIOCARTA	m_hdacPathway:Control of skeletal myogenesis by HDAC & calcu	8	0.911161731	2.E-02	18019, 18708, 16334, 12315, 12314, 2641	188	19	1171	3.E+00	1.E+00	1.E-01	2.E+01
BIOCARTA	m_nfaiPathway:NFAT and Hypertrophy of the heart (Transcription	10	1.138952164	1.E-01	18708, 18747, 12315, 12314, 26416, 2639	188	38	1171	2.E+00	1.E+00	4.E-01	8.E+01
Annotation Cluster 56	Enrichment Score: 2.158514641149785											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0035295~tube development	31	3.530751708	5.E-04	22323, 14178, 19206, 232906, 15376, 148	809	264	13588	2.E+00	8.E-01	1.E-02	9.E-01



GOTERM_BP_FAT	GO:0002009~morphogenesis of an epithelium	23	2.619589977	6.E-04	22323	13649	13800	19206	232906	169	809	173	13588	2.E+00	8.E-01	1.E-02	1.E+00
GOTERM_BP_FAT	GO:0060562~epithelial tube morphogenesis	17	1.936218679	8.E-04	22323	13800	19206	232906	16911	148	809	111	13588	3.E+00	9.E-01	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0048729~tissue morphogenesis	28	3.189066059	9.E-04	22323	13649	18747	14178	19206	2329	809	238	13588	2.E+00	9.E-01	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0035239~tube morphogenesis	22	2.505694761	1.E-03	22323	14674	13800	19206	232906	169	809	171	13588	2.E+00	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0060429~epithelium development	30	3.416856492	2.E-03	22323	13649	19206	232906	15376	148	809	271	13588	2.E+00	1.E+00	3.E-02	3.E+00
GOTERM_BP_FAT	GO:0016331~morphogenesis of embryonic epithelium	12	1.366742597	6.E-03	22323	13800	16911	232906	19206	197	809	78	13588	3.E+00	1.E+00	8.E-02	1.E+01
GOTERM_BP_FAT	GO:0001838~embryonic epithelial tube formation	9	1.025056948	1.E-02	22323	13800	16911	232906	19206	197	809	54	13588	3.E+00	1.E+00	2.E-01	2.E+01
GOTERM_BP_FAT	GO:0035148~tube lumen formation	9	1.025056948	2.E-02	22323	13800	16911	232906	19206	197	809	59	13588	3.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0021915~neural tube development	11	1.25284738	2.E-02	22323	13836	13800	16911	232906	192	809	83	13588	2.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0060606~tube closure	7	0.797266515	3.E-02	22323	13800	16911	232906	19206	507	809	39	13588	3.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0001843~neural tube closure	7	0.797266515	3.E-02	22323	13800	16911	232906	19206	507	809	39	13588	3.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0001841~neural tube formation	8	0.911161731	3.E-02	22323	13800	16911	232906	19206	507	809	51	13588	3.E+00	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0001763~morphogenesis of a branching structure	14	1.59453303	3.E-02	14674	14178	15376	12043	13383	1223	809	125	13588	2.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0014020~primary neural tube formation	7	0.797266515	4.E-02	22323	13800	16911	232906	19206	507	809	42	13588	3.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0048754~branching morphogenesis of a tube	11	1.25284738	5.E-02	15402	14674	20779	24064	15376	1204	809	93	13588	2.E+00	1.E+00	4.E-01	6.E+01

Annotation Cluster 57	Enrichment Score: 2.117325351723703																
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR					
GOTERM_MF_FAT	GO:0016411~acylglycerol O-acyltransferase activity	6	0.683371298	2.E-04	55979	28169	68262	67512	13350	5212	754	11	13288	1.E+01	1.E-01	3.E-03	3.E-01
GOTERM_MF_FAT	GO:0003841~1-acylglycerol-3-phosphate O-acyltransferase activit	5	0.569476082	3.E-04	55979	28169	68262	67512	52123		754	7	13288	1.E+01	2.E-01	5.E-03	5.E-01
GOTERM_BP_FAT	GO:0008654~phospholipid biosynthetic process	14	1.59453303	1.E-03	14178	68262	276846	329777	52123	10	809	83	13588	3.E+00	1.E+00	2.E-02	2.E+00
UP_SEQ_FEATURE	short sequence motif:HXXXD motif	6	0.683371298	2.E-03	55979	28169	68262	14732	67512	5212	861	17	16021	7.E+00	1.E+00	1.E-01	3.E+00
INTERPRO	IPR002123:Phospholipid/glycerol acyltransferase	6	0.683371298	2.E-03	55979	28169	68262	14732	67512	5212	860	19	17763	7.E+00	9.E-01	6.E-02	3.E+00
SMART	SM00563:PlsC	6	0.683371298	3.E-03	55979	28169	68262	14732	67512	5212	492	19	9131	6.E+00	4.E-01	4.E-02	3.E+00
SP_PIR_KEYWORDS	Acyltransferase	16	1.822323462	9.E-03	18108	18107	68262	52123	231086	559	869	155	17854	2.E+00	1.E+00	4.E-02	1.E+01
GOTERM_MF_FAT	GO:0008374~O-acyltransferase activity	7	0.797266515	1.E-02	55979	28169	68262	14732	67512	1335	754	35	13288	4.E+00	1.E+00	1.E-01	2.E+01
PIR_SUPERFAMILY	PIRSF005233:1-acyl-sn-glycerol-3-phosphate acyltransferase	3	0.341685649	1.E-02	28169	68262	52123				576	3	8136	1.E+01	1.E+00	6.E-01	2.E+01
SP_PIR_KEYWORDS	phospholipid biosynthesis	6	0.683371298	5.E-02	55979	28169	68262	14732	67512	5212	869	42	17854	3.E+00	1.E+00	2.E-01	5.E+01
KEGG_PATHWAY	mmu00561:Glycerolipid metabolism	9	1.025056948	1.E-01	55979	28169	68262	14732	669888	675	580	47	5738	2.E+00	1.E+00	2.E-01	7.E+01
KEGG_PATHWAY	mmu00565:Ether lipid metabolism	7	0.797266515	1.E-01	18783	55979	28169	68262	67512	1901	580	35	5738	2.E+00	1.E+00	3.E-01	8.E+01
KEGG_PATHWAY	mmu00564:Glycerophospholipid metabolism	8	0.911161731	5.E-01	18783	55979	28169	68262	14732	6751	580	67	5738	1.E+00	1.E+00	7.E-01	1.E+02

Annotation Cluster 58	Enrichment Score: 2.1136718074421066																
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR					
GOTERM_BP_FAT	GO:0043550~regulation of lipid kinase activity	5	0.569476082	7.E-04	18048	19645	16367	57257	12540		809	8	13588	1.E+01	9.E-01	2.E-02	1.E+00
GOTERM_BP_FAT	GO:0043551~regulation of phosphoinositide 3-kinase activity	4	0.455580866	4.E-03	18048	16367	57257	12540			809	6	13588	1.E+01	1.E+00	6.E-02	6.E+00
GOTERM_BP_FAT	GO:0043552~positive regulation of phosphoinositide 3-kinase act	4	0.455580866	4.E-03	18048	16367	57257	12540			809	6	13588	1.E+01	1.E+00	6.E-02	6.E+00
GOTERM_BP_FAT	GO:0045834~positive regulation of lipid metabolic process	5	0.569476082	5.E-02	18048	16367	11816	57257	12540		809	24	13588	3.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0019216~regulation of lipid metabolic process	8	0.911161731	6.E-02	18048	19645	16367	11816	57257	2380	809	58	13588	2.E+00	1.E+00	4.E-01	6.E+01

Annotation Cluster 59	Enrichment Score: 2.1055078035446986																
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR					
GOTERM_BP_FAT	GO:0051240~positive regulation of multicellular organismal proce	24	2.733485194	1.E-04	12475	15018	16803	12912	12051	1699	809	163	13588	2.E+00	3.E-01	3.E-03	2.E-01
GOTERM_BP_FAT	GO:0032760~positive regulation of tumor necrosis factor product	7	0.797266515	1.E-04	14127	17874	12475	21898	24088	1680	809	15	13588	8.E+00	3.E-01	4.E-03	2.E-01
UP_SEQ_FEATURE	domain:TIR	8	0.911161731	3.E-04	17874	239081	21899	21898	117149	24	861	25	16021	6.E+00	4.E-01	2.E-02	4.E-01
GOTERM_BP_FAT	GO:0002237~response to molecule of bacterial origin	11	1.25284738	5.E-04	17874	12475	16179	17087	234779	264	809	49	13588	4.E+00	8.E-01	1.E-02	9.E-01
GOTERM_BP_FAT	GO:0045428~regulation of nitric oxide biosynthetic process	7	0.797266515	6.E-04	19370	21898	27007	11847	16414	3790	809	19	13588	6.E+00	8.E-01	1.E-02	1.E+00
KEGG_PATHWAY	mmu04620:Toll-like receptor signaling pathway	22	2.505694761	7.E-04	12475	320207	27056	21899	21898	116	580	99	5738	2.E+00	1.E-01	3.E-03	8.E-01
GOTERM_BP_FAT	GO:0032680~regulation of tumor necrosis factor production	8	0.911161731	8.E-04	12051	14127	17874	12475	21898	2408	809	27	13588	5.E+00	9.E-01	2.E-02	1.E+00
GOTERM_BP_FAT	GO:0002218~activation of innate immune response	6	0.683371298	9.E-04	17874	16179	21898	27007	24088	1067	809	14	13588	7.E+00	9.E-01	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0001819~positive regulation of cytokine production	12	1.366742597	1.E-03	19370	12475	15018	27007	21898	1446	809	62	13588	3.E+00	9.E-01	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0009617~response to bacterium	21	2.391799544	1.E-03	14972	12475	239081	21898	13035	168	809	157	13588	2.E+00	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0045429~positive regulation of nitric oxide biosynthetic proce	6	0.683371298	1.E-03	19370	21898	27007	16414	379043	240	809	15	13588	7.E+00	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0032496~response to lipopolysaccharide	9	1.025056948	1.E-03	17874	12475	16179	17087	234779	264	809	38	13588	4.E+00	1.E+00	3.E-02	3.E+00
GOTERM_BP_FAT	GO:0070391~response to lipoteichoic acid	4	0.455580866	2.E-03	12475	21898	24088	16803			809	5	13588	1.E+01	1.E+00	3.E-02	3.E+00
GOTERM_BP_FAT	GO:0002274~myeloid leukocyte activation	8	0.911161731	4.E-03	23880	14127	21898	20375	74734	1682	809	35	13588	4.E+00	1.E+00	6.E-02	7.E+00
GOTERM_BP_FAT	GO:0002758~innate immune response-activating signal transduct	5	0.569476082	4.E-03	17874	16179	27007	24088	106759		809	12	13588	7.E+00	1.E+00	6.E-02	7.E+00
GOTERM_BP_FAT	GO:0045089~positive regulation of innate immune response	8	0.911161731	5.E-03	19370	17874	16179	21898	27007	3790	809	36	13588	4.E+00	1.E+00	7.E-02	8.E+00
GOTERM_BP_FAT	GO:0031349~positive regulation of defense response	10	1.138952164	6.E-03	19370	14127	17874	16179	21898	2700	809	57	13588	3.E+00	1.E+00	8.E-02	1.E+01
GOTERM_BP_FAT	GO:0002224~toll-like receptor signaling pathway	4	0.455580866	6.E-03	17874	16179	24088	106759			809	7	13588	1.E+01	1.E+00	8.E-02	1.E+01
GOTERM_BP_FAT	GO:0051098~regulation of binding	13	1.480637813	7.E-03	245000	21898	17869	16414	12914	178	809	90	13588	2.E+00	1.E+00	9.E-02	1.E+01
GOTERM_MF_FAT	GO:0001530~lipopolysaccharide binding	4	0.455580866	8.E-03	12475	17087	21898	16803			754	8	13288	9.E+00	1.E+00	9.E-02	1.E+01
GOTERM_BP_FAT	GO:0043388~positive regulation of DNA binding	8	0.911161731	1.E-02	17874	16179	12315	12314	12313	2189	809	42	13588	3.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0051091~positive regulation of transcription factor activity	7	0.797266515	1.E-02	17874	16179	21898	16414	24088	1067	809	34	13588	3.E+00	1.E+00	2.E-01	2.E+01
GOTERM_BP_FAT	GO:0051092~positive regulation of NF-kappaB transcription facto	6	0.683371298	1.E-02	17874	16179	21898	16414	24088	1067	809	25	13588	4.E+00	1.E+00	2.E-01	2.E+01



GOTERM_BP_FAT	GO:0051099~positive regulation of binding	8	0.911161731	2.E-02	17874, 16179, 12315, 12314, 12313, 2189	809	45	13588	3.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0045088~regulation of innate immune response	8	0.911161731	2.E-02	19370, 17874, 16179, 21898, 27007, 3790	809	46	13588	3.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0001817~regulation of cytokine production	16	1.822323462	2.E-02	19370, 12475, 15018, 11807, 21899, 2700	809	139	13588	2.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0002221~pattern recognition receptor signaling pathway	4	0.455580866	2.E-02	17874, 16179, 24088, 106759	809	10	13588	7.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0032755~positive regulation of interleukin-6 production	5	0.569476082	2.E-02	14127, 17874, 21898, 24088, 106759	809	18	13588	5.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0032494~response to peptidoglycan	4	0.455580866	2.E-02	17874, 16179, 26416, 24088	809	11	13588	6.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0031663~lipopolysaccharide-mediated signaling pathway	4	0.455580866	3.E-02	17874, 16179, 26416, 106759	809	12	13588	6.E+00	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0051101~regulation of DNA binding	10	1.138952164	3.E-02	17874, 16179, 12315, 12314, 12313, 2189	809	74	13588	2.E+00	1.E+00	3.E-01	4.E+01
BIOCARTA	m_gsk3Pathway:Inactivation of Gsk3 by AKT causes accumulation	9	1.025056948	3.E-02	18708, 17874, 12475, 16179, 17087, 1244	188	25	1171	2.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0032675~regulation of interleukin-6 production	6	0.683371298	4.E-02	14127, 17874, 21899, 21898, 24088, 1067	809	32	13588	3.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0042742~defense response to bacterium	12	1.366742597	6.E-02	12051, 14972, 14127, 17874, 18126, 1419	809	108	13588	2.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0051090~regulation of transcription factor activity	8	0.911161731	6.E-02	17874, 16179, 21898, 16414, 192176, 240	809	59	13588	2.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0006952~defense response	35	3.986332574	8.E-02	14972, 12475, 15018, 11651, 16803, 1201	809	448	13588	1.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0042116~macrophage activation	3	0.341685649	1.E-01	21898, 16803, 106759	809	10	13588	5.E+00	1.E+00	6.E-01	9.E+01
BIOCARTA	m_nth1Pathway:NfKb activation by Nontypeable Hemophilus influ	5	0.569476082	5.E-01	17874, 26416, 14815, 24088, 12914	188	23	1171	1.E+00	1.E+00	8.E-01	1.E+02
BIOCARTA	m_nfkBPathway:NF-kB Signaling Pathway	3	0.341685649	9.E-01	17874, 16179, 21898	188	21	1171	9.E-01	1.E+00	1.E+00	1.E+02
BIOCARTA	m_il1rPathway:Signal transduction through IL1R	3	0.341685649	9.E-01	17874, 16179, 26416	188	25	1171	7.E-01	1.E+00	1.E+00	1.E+02
Annotation Cluster 60	Enrichment Score: 2.0961390265357536											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
BIOCARTA	m_rbPathway:RB Tumor Suppressor/Checkpoint Signaling in resp	8	0.911161731	4.E-04	19645, 22390, 11920, 12649, 12567, 1253	188	11	1171	5.E+00	1.E-01	1.E-02	6.E-01
BIOCARTA	m_cdc25Pathway:cdc25 and chk1 Regulatory Pathway in response	5	0.569476082	1.E-02	22390, 11920, 12649, 12532, 12534	188	7	1171	4.E+00	1.E+00	1.E-01	2.E+01
BIOCARTA	m_g2Pathway:Cell Cycle: G2/M Checkpoint	9	1.025056948	2.E-02	22390, 18817, 245000, 11920, 12649, 131	188	23	1171	2.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0000077~DNA damage checkpoint	6	0.683371298	3.E-02	245000, 11920, 26416, 12649, 12443, 125	809	30	13588	3.E+00	1.E+00	3.E-01	4.E+01
Annotation Cluster 61	Enrichment Score: 2.0876060443312436											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0048770~pigment granule	14	1.59453303	3.E-04	269589, 14674, 18453, 20525, 54401, 148	636	85	12504	3.E+00	1.E-01	4.E-03	5.E-01
GOTERM_CC_FAT	GO:0042470~melanosome	14	1.59453303	3.E-04	269589, 14674, 18453, 20525, 54401, 148	636	85	12504	3.E+00	1.E-01	4.E-03	5.E-01
GOTERM_CC_FAT	GO:0031988~membrane-bounded vesicle	32	3.644646925	2.E-02	215280, 13649, 269589, 100046871, 1167	636	420	12504	1.E+00	1.E+00	1.E-01	3.E+01
GOTERM_CC_FAT	GO:0031982~vesicle	37	4.214123007	4.E-02	215280, 13649, 269589, 16396, 10004687	636	519	12504	1.E+00	1.E+00	2.E-01	4.E+01
GOTERM_CC_FAT	GO:0016023~cytoplasmic membrane-bounded vesicle	30	3.416856492	5.E-02	13649, 215280, 269589, 100046871, 1715	636	414	12504	1.E+00	1.E+00	2.E-01	5.E+01
GOTERM_CC_FAT	GO:0031410~cytoplasmic vesicle	35	3.986332574	6.E-02	215280, 13649, 269589, 16396, 10004687	636	508	12504	1.E+00	1.E+00	2.E-01	6.E+01
Annotation Cluster 62	Enrichment Score: 2.085880011331479											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	Redox-active center	10	1.138952164	8.E-05	18453, 12304, 93692, 26462, 50493, 1482	869	39	17854	5.E+00	4.E-02	7.E-04	1.E-01
UP_SEQ_FEATURE	nucleotide phosphate-binding region:FAD	11	1.25284738	9.E-04	11370, 66885, 18126, 11409, 110842, 264	861	58	16021	4.E+00	9.E-01	7.E-02	2.E+00
INTERPRO	IPR012999:Pyridine nucleotide-disulphide oxidoreductase, class I	4	0.455580866	1.E-03	26462, 50493, 14782, 13382	860	5	17763	2.E+01	8.E-01	4.E-02	2.E+00
INTERPRO	IPR013027:FAD-dependent pyridine nucleotide-disulphide oxidore	6	0.683371298	2.E-03	26462, 50493, 14782, 13382, 66841, 9958	860	19	17763	7.E+00	9.E-01	6.E-02	3.E+00
GOTERM_MF_FAT	GO:0050660~FAD binding	12	1.366742597	2.E-03	11370, 66885, 18126, 11409, 110842, 264	754	71	13288	3.E+00	8.E-01	3.E-02	3.E+00
GOTERM_MF_FAT	GO:0016668~oxidoreductase activity, acting on sulfur group of di	4	0.455580866	3.E-03	26462, 50493, 14782, 13382	754	6	13288	1.E+01	9.E-01	4.E-02	5.E+00
INTERPRO	IPR004099:Pyridine nucleotide-disulphide oxidoreductase, dimeric	4	0.455580866	3.E-03	26462, 50493, 14782, 13382	860	7	17763	1.E+01	1.E+00	1.E-01	5.E+00
INTERPRO	IPR001327:Pyridine nucleotide-disulphide oxidoreductase, NAD-bi	4	0.455580866	5.E-03	26462, 50493, 14782, 13382	860	8	17763	1.E+01	1.E+00	2.E-01	8.E+00
GOTERM_BP_FAT	GO:0045454~cell redox homeostasis	10	1.138952164	1.E-02	18453, 12304, 93692, 26462, 50493, 1482	809	62	13588	3.E+00	1.E+00	1.E-01	2.E+01
INTERPRO	IPR000815:Mercuric reductase	3	0.341685649	1.E-02	50493, 14782, 13382	860	4	17763	2.E+01	1.E+00	3.E-01	2.E+01
GOTERM_MF_FAT	GO:0050661~NADP or NADPH binding	4	0.455580866	1.E-01	18126, 26462, 50493, 14782	754	21	13288	3.E+00	1.E+00	6.E-01	8.E+01
GOTERM_MF_FAT	GO:0016667~oxidoreductase activity, acting on sulfur group of di	5	0.569476082	1.E-01	93692, 26462, 50493, 14782, 13382	754	33	13288	3.E+00	1.E+00	6.E-01	8.E+01
GOTERM_MF_FAT	GO:0016209~antioxidant activity	4	0.455580866	4.E-01	26462, 50493, 54683, 14782	754	40	13288	2.E+00	1.E+00	9.E-01	1.E+02
SP_PIR_KEYWORDS	nadp	8	0.911161731	5.E-01	18126, 14661, 26462, 50493, 14782, 1438	869	142	17854	1.E+00	1.E+00	9.E-01	1.E+02
Annotation Cluster 63	Enrichment Score: 2.0725281230015717											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0007346~regulation of mitotic cell cycle	17	1.936218679	2.E-04	12190, 17869, 12043, 56150, 67141, 1338	809	96	13588	3.E+00	4.E-01	5.E-03	3.E-01
GOTERM_BP_FAT	GO:0010564~regulation of cell cycle process	13	1.480637813	1.E-03	12190, 56150, 67141, 11785, 16994, 5256	809	73	13588	3.E+00	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0051783~regulation of nuclear division	6	0.683371298	6.E-02	16994, 11920, 52563, 12540, 56150, 6899	809	36	13588	3.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0007088~regulation of mitosis	6	0.683371298	6.E-02	16994, 11920, 52563, 12540, 56150, 6899	809	36	13588	3.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0030071~regulation of mitotic metaphase/anaphase transitor	4	0.455580866	7.E-02	11920, 52563, 56150, 68999	809	16	13588	4.E+00	1.E+00	4.E-01	7.E+01
Annotation Cluster 64	Enrichment Score: 2.0672739917474527											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0007169~transmembrane receptor protein tyrosine kinase sig	26	2.961275626	2.E-04	13649, 13685, 14178, 11651, 21844, 1870	809	192	13588	2.E+00	4.E-01	5.E-03	3.E-01
GOTERM_BP_FAT	GO:0007167~enzyme linked receptor protein signaling pathway	29	3.302961276	3.E-03	13649, 13685, 14178, 11651, 21844, 1870	809	273	13588	2.E+00	1.E+00	5.E-02	6.E+00
GOTERM_BP_FAT	GO:0007166~cell surface receptor linked signal transduction	71	8.086560364	1.E+00	12765, 22324, 14178, 19206, 18414, 2193	809	2495	13588	5.E-01	1.E+00	1.E+00	1.E+02



Annotation Cluster 65		Enrichment Score: 2.064460303559783										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0006739~NADP metabolic process		7	0.797266515	9.E-05 17970, 21991, 21351, 17969, 66171, 1039	809	14	13588	8.E+00	2.E-01	3.E-03	2.E-01
GOTERM_BP_FAT	GO:0043603~cellular amide metabolic process		10	1.138952164	4.E-04 18416, 17970, 109900, 11847, 21991, 213	809	39	13588	4.E+00	7.E-01	1.E-02	7.E-01
GOTERM_BP_FAT	GO:0046496~nicotinamide nucleotide metabolic process		7	0.797266515	2.E-03 17970, 21991, 21351, 17969, 66171, 1039	809	24	13588	5.E+00	1.E+00	4.E-02	4.E+00
GOTERM_BP_FAT	GO:0006769~nicotinamide metabolic process		7	0.797266515	2.E-03 17970, 21991, 21351, 17969, 66171, 1039	809	24	13588	5.E+00	1.E+00	4.E-02	4.E+00
GOTERM_BP_FAT	GO:0009820~alkaloid metabolic process		7	0.797266515	2.E-03 17970, 21991, 21351, 17969, 66171, 1039	809	24	13588	5.E+00	1.E+00	4.E-02	4.E+00
GOTERM_BP_FAT	GO:0019362~pyridine nucleotide metabolic process		7	0.797266515	5.E-03 17970, 21991, 21351, 17969, 66171, 1039	809	28	13588	4.E+00	1.E+00	7.E-02	9.E+00
GOTERM_BP_FAT	GO:0019748~secondary metabolic process		11	1.25284738	7.E-03 17970, 19378, 12043, 21991, 21351, 5684	809	69	13588	3.E+00	1.E+00	9.E-02	1.E+01
GOTERM_BP_FAT	GO:0006733~oxidoreduction coenzyme metabolic process		7	0.797266515	2.E-02 17970, 21991, 21351, 17969, 66171, 1039	809	38	13588	3.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0006098~pentose-phosphate shunt		3	0.341685649	8.E-02 21991, 21351, 66171	809	8	13588	6.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0051186~cofactor metabolic process		16	1.822323462	1.E-01 14151, 17970, 14782, 66171, 103988, 209	809	182	13588	1.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0006732~coenzyme metabolic process		13	1.480637813	1.E-01 17970, 14782, 103988, 66171, 20916, 741	809	143	13588	2.E+00	1.E+00	7.E-01	9.E+01
GOTERM_BP_FAT	GO:0006767~water-soluble vitamin metabolic process		4	0.455580866	3.E-01 17970, 17969, 11364, 14381	809	34	13588	2.E+00	1.E+00	9.E-01	1.E+02

Annotation Cluster 66		Enrichment Score: 2.058018394276523										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0043086~negative regulation of catalytic activity	16	1.822323462	9.E-04	15170, 11806, 11807, 14678, 11847, 6714	809	101	13588	3.E+00	9.E-01	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0044092~negative regulation of molecular function	18	2.050113895	2.E-03	15170, 11806, 11807, 14678, 17869, 1184	809	132	13588	2.E+00	1.E+00	4.E-02	4.E+00
GOTERM_BP_FAT	GO:0006469~negative regulation of protein kinase activity	9	1.025056948	1.E-02	17873, 15170, 19645, 24064, 13197, 1916	809	51	13588	3.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0033673~negative regulation of kinase activity	9	1.025056948	1.E-02	17873, 15170, 19645, 24064, 13197, 1916	809	51	13588	3.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0051348~negative regulation of transferase activity	9	1.025056948	1.E-02	17873, 15170, 19645, 24064, 13197, 1916	809	53	13588	3.E+00	1.E+00	1.E-01	2.E+01
PIR_SUPERFAMILY	PIRSF010369:growth arrest and DNA-damage-inducible protein G	3	0.341685649	1.E-02	17873, 13197, 23882	576	3	8136	1.E+01	1.E+00	6.E-01	2.E+01
GOTERM_BP_FAT	GO:0007050~cell cycle arrest	7	0.797266515	1.E-01	11785, 19645, 14208, 13197, 11636, 1257	809	57	13588	2.E+00	1.E+00	6.E-01	9.E+01

Annotation Cluster 67	Enrichment Score: 2.0478335485903436											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
BIOCARTA	m_fcer1Pathway:Fc Epsilon Receptor I Signaling in Mast Cells	16	1.822323462	3.E-05	22324, 12229, 14281, 20416, 18751, 1412	188	32	1171	3.E+00	7.E-03	3.E-03	4.E-02
BIOCARTA	m_il2rbPathway:IL-2 Receptor Beta Chain in T Cell Activation	17	1.936218679	4.E-05	15170, 11651, 17869, 12043, 14281, 2041	188	36	1171	3.E+00	8.E-03	3.E-03	5.E-02
BIOCARTA	m_ghPathway:Growth Hormone Signaling Pathway	13	1.480637813	2.E-04	15170, 20416, 18751, 18708, 18803, 1270	188	25	1171	3.E+00	3.E-02	7.E-03	2.E-01
BIOCARTA	m_bcrPathway:BCR Signaling Pathway	14	1.59453303	2.E-04	22324, 12229, 14281, 20416, 18751, 1880	188	29	1171	3.E+00	4.E-02	7.E-03	2.E-01
BIOCARTA	m_lgf1rPathway:Multiple antiapoptotic pathways from IGF-1R sigr	11	1.25284738	2.E-04	18708, 18747, 12015, 16367, 14784, 2066	188	19	1171	4.E+00	5.E-02	7.E-03	3.E-01
BIOCARTA	m_trkaPathway:Trka Receptor Signaling Pathway	9	1.025056948	2.E-04	18048, 18751, 18708, 18803, 14784, 2066	188	13	1171	4.E+00	5.E-02	6.E-03	3.E-01
BIOCARTA	m_tffPathway:Trefoil Factors Initiate Mucosal Healing	11	1.25284738	1.E-03	18708, 13649, 672195, 12015, 14784, 206	188	23	1171	3.E+00	3.E-01	3.E-02	2.E+00
BIOCARTA	m_il3Pathway:IL 3 signaling pathway	9	1.025056948	1.E-03	15170, 12983, 14784, 20662, 26395, 1546	188	16	1171	4.E+00	3.E-01	3.E-02	2.E+00
BIOCARTA	m_plcPathway:Phospholipase C Signaling Pathway	6	0.683371298	2.E-03	18751, 18708, 22324, 18803, 11651, 1879	188	7	1171	5.E+00	3.E-01	3.E-02	2.E+00
BIOCARTA	m_pyk2Pathway:Links between Pyk2 and Map Kinases	12	1.366742597	2.E-03	18479, 20416, 18751, 18803, 20779, 1478	188	27	1171	3.E+00	3.E-01	3.E-02	2.E+00
BIOCARTA	m_lgf1Pathway:IGF-1 Signaling Pathway	10	1.138952164	3.E-03	18708, 16367, 14784, 20662, 26395, 1546	188	21	1171	3.E+00	5.E-01	4.E-02	4.E+00
BIOCARTA	m_epoPathway:EPO Signaling Pathway	10	1.138952164	3.E-03	15170, 18803, 13857, 14784, 20662, 2639	188	21	1171	3.E+00	5.E-01	4.E-02	4.E+00
BIOCARTA	m_gleevecPathway:Inhibition of Cellular Proliferation by Gleevec	10	1.138952164	4.E-03	18708, 12015, 14784, 20662, 26395, 1546	188	22	1171	3.E+00	6.E-01	4.E-02	5.E+00
BIOCARTA	m_nrgfPathway:Nerve growth factor pathway (NGF)	9	1.025056948	6.E-03	18048, 18708, 18803, 14784, 20662, 2639	188	19	1171	3.E+00	7.E-01	6.E-02	7.E+00
BIOCARTA	m_ecmPathway:Erk and PI-3 Kinase Are Necessary for Collagen Bi	9	1.025056948	6.E-03	18708, 20779, 26395, 15461, 11855, 1436	188	19	1171	3.E+00	7.E-01	6.E-02	7.E+00
BIOCARTA	m_TPOPathway:TPO Signaling Pathway	10	1.138952164	6.E-03	18751, 18708, 18803, 14784, 20662, 2639	188	23	1171	3.E+00	7.E-01	6.E-02	7.E+00
BIOCARTA	m_tcrPathway:T Cell Receptor Signaling Pathway	13	1.480637813	7.E-03	22324, 14281, 20416, 18751, 16818, 1870	188	36	1171	2.E+00	8.E-01	6.E-02	9.E+00
BIOCARTA	m_HBxPathway:Calcium Signaling by HBx of Hepatitis B virus	6	0.683371298	7.E-03	20779, 14784, 20662, 15461, 20416, 1291	188	9	1171	4.E+00	8.E-01	6.E-02	9.E+00
BIOCARTA	m_spryPathway:Sprouty regulation of tyrosine kinase signals	8	0.911161731	8.E-03	13649, 20779, 24064, 14784, 20662, 2639	188	16	1171	3.E+00	8.E-01	6.E-02	9.E+00
BIOCARTA	m_biopепptidesPathway:Bioactive Peptide Induced Signaling Pathw	12	1.366742597	8.E-03	20416, 18751, 18803, 14784, 12315, 2641	188	32	1171	2.E+00	8.E-01	6.E-02	9.E+00
BIOCARTA	m_At1rPathway:Angiotensin II mediated activation of JNK Pathwa	11	1.25284738	8.E-03	13649, 18479, 20416, 18751, 20779, 1478	188	28	1171	2.E+00	8.E-01	6.E-02	1.E+01
BIOCARTA	m_integrinPathway:Integrin Signaling Pathway	11	1.25284738	1.E-02	20779, 14784, 20662, 26395, 15461, 1436	188	29	1171	2.E+00	9.E-01	7.E-02	1.E+01
BIOCARTA	m_crebPathway:Transcription factor CREB and its extracellular sigr	9	1.025056948	1.E-02	18751, 18708, 18747, 14784, 20662, 2641	188	21	1171	3.E+00	9.E-01	8.E-02	1.E+01
BIOCARTA	m_erk5Pathway:Role of Erk5 in Neuronal Survival	7	0.797266515	2.E-02	18708, 18803, 14784, 15461, 11651, 2041	188	14	1171	3.E+00	1.E+00	1.E-01	2.E+01
BIOCARTA	m_insulinPathway:Insulin Signaling Pathway	9	1.025056948	2.E-02	18708, 16367, 16334, 14784, 20662, 2639	188	22	1171	3.E+00	1.E+00	1.E-01	2.E+01
BIOCARTA	m_erkPathway:Erk1/Erk2 Mapk Signaling pathway	11	1.25284738	2.E-02	18048, 13649, 20779, 14784, 20662, 2639	188	31	1171	2.E+00	1.E+00	1.E-01	2.E+01
BIOCARTA	m_egfPathway:EGF Signaling Pathway	10	1.138952164	2.E-02	18751, 18708, 13649, 18803, 14784, 2066	188	28	1171	2.E+00	1.E+00	1.E-01	3.E+01
BIOCARTA	m_gpcrPathway:Signaling Pathway from G-Protein Families	9	1.025056948	3.E-02	18751, 18747, 18803, 12315, 12314, 2639	188	25	1171	2.E+00	1.E+00	2.E-01	4.E+01
BIOCARTA	m_cardiacegfPathway:Role of EGF Receptor Transactivation by GP	7	0.797266515	4.E-02	18751, 13649, 18803, 15461, 17869, 1428	188	17	1171	3.E+00	1.E+00	2.E-01	4.E+01
BIOCARTA	m_her2Pathway:Role of ERBB2 in Signal Transduction and Oncolo	8	0.911161731	5.E-02	18708, 16195, 13649, 14784, 20662, 2639	188	22	1171	2.E+00	1.E+00	2.E-01	5.E+01
BIOCARTA	m_metPathway:Signaling of Hepatocyte Growth Factor Receptor	10	1.138952164	6.E-02	18708, 20779, 14784, 20662, 26395, 1546	188	32	1171	2.E+00	1.E+00	2.E-01	5.E+01
BIOCARTA	m_cdMacPathway:Cadmium induces DNA synthesis and proliferat	6	0.683371298	6.E-02	18751, 26395, 15461, 17869, 14281, 1879	188	14	1171	3.E+00	1.E+00	2.E-01	5.E+01
BIOCARTA	m_pdgfPathway:PDGF Signaling Pathway	9	1.025056948	6.E-02	18751, 18708, 18803, 14784, 20662, 2639	188	28	1171	2.E+00	1.E+00	3.E-01	6.E+01
BIOCARTA	m_il2Pathway:IL 2 signaling pathway	8	0.911161731	7.E-02	16818, 14784, 20662, 26395, 15461, 1428	188	24	1171	2.E+00	1.E+00	3.E-01	6.E+01
BIOCARTA	m_ptenPathway:PTEN dependent cell cycle arrest and apoptosis	7	0.797266515	8.E-02	18708, 14784, 20662, 11651, 16412, 2041	188	20	1171	2.E+00	1.E+00	3.E-01	7.E+01
BIOCARTA	m_vipPathway:Neuropeptides VIP and PACAP inhibit the apoptosi	6	0.683371298	1.E-01	18019, 18747, 18803, 12315, 12314, 1231	188	16	1171	2.E+00	1.E+00	3.E-01	7.E+01
BIOCARTA	m_Ccr5Pathway:Pertussis toxin-insensitive CCR5 Signaling in Macr	6	0.683371298	1.E-01	18751, 18803, 12315, 12314, 26416, 1231	188	16	1171	2.E+00	1.E+00	3.E-01	7.E+01
BIOCARTA	m_il6Pathway:IL 6 signaling pathway	7	0.797266515	1.E-01	16195, 14784, 20662, 26395, 15461, 1428	188	21	1171	2.E+00	1.E+00	3.E-01	8.E+01



BIOCARTA	m_calcineurinPathway:Effects of calcineurin in Keratinocyte Differ	5	0.569476082	1.E-01 18751, 18803, 12315, 12314, 12313, 1468	188	12	1171	3.E+00	1.E+00	4.E-01	8.E+01
BIOCARTA	m_i4PPathway:IL 4 signaling pathway	5	0.569476082	1.E-01 16367, 14784, 11651, 16190, 20416	188	12	1171	3.E+00	1.E+00	4.E-01	8.E+01
BIOCARTA	m_p38mapkPathway:p38 MAPK Signaling Pathway	9	1.025056948	1.E-01 14784, 26416, 15461, 17869, 12540, 2041	188	32	1171	2.E+00	1.E+00	4.E-01	8.E+01
KEGG_PATHWAY	mmu04320:Dorso-ventral axis formation	5	0.569476082	2.E-01 13649, 14784, 20662, 20663, 26395	580	22	5738	2.E+00	1.E+00	3.E-01	9.E+01
BIOCARTA	m_cxcr4Pathway:CXCR4 Signaling Pathway	6	0.683371298	3.E-01 18751, 18708, 18803, 26395, 15461, 1468	188	22	1171	2.E+00	1.E+00	6.E-01	1.E+02

Annotation Cluster 68		Enrichment Score: 2.0440130104639946										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR015633:E2F Family	4	0.455580866	5.E-03	104394, 13555, 242705, 13559	860	8	17763	1.E+01	1.E+00	2.E-01	8.E+00
UP_SEQ_FEATURE	region of interest:Dimerization	5	0.569476082	7.E-03	104394, 13555, 18181, 242705, 13559	861	15	16021	6.E+00	1.E+00	3.E-01	1.E+01
UP_SEQ_FEATURE	region of interest:Transactivation	4	0.455580866	7.E-03	104394, 13555, 242705, 13559	861	8	16021	9.E+00	1.E+00	3.E-01	1.E+01
UP_SEQ_FEATURE	short sequence motif:DEF box	4	0.455580866	7.E-03	104394, 13555, 242705, 13559	861	8	16021	9.E+00	1.E+00	3.E-01	1.E+01
INTERPRO	IPR003316:Transcription factor E2F/dimerisation partner (TDP)	4	0.455580866	1.E-02	104394, 13555, 242705, 13559	860	10	17763	8.E+00	1.E+00	3.E-01	2.E+01
UP_SEQ_FEATURE	domain:Leucine-zipper	12	1.366742597	3.E-02	104394, 13555, 242705, 13559, 17869, 16	861	107	16021	2.E+00	1.E+00	7.E-01	4.E+01

Annotation Cluster 69	Enrichment Score: 2.009135217899196											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_SEQ_FEATURE	metal ion-binding site:Magnesium	14	1.59453303	3.E-03	18746, 80905, 19744, 232087, 13807, 721	861	103	16021	3.E+00	1.E+00	2.E-01	6.E+00
SP_PIR_KEYWORDS	magnesium	33	3.758542141	5.E-03	228543, 80905, 18746, 19744, 18747, 232	869	403	17854	2.E+00	9.E-01	2.E-02	6.E+00
GOTERM_MF_FAT	GO:0000287~magnesium ion binding	32	3.644646925	6.E-02	228543, 80905, 18746, 19744, 232087, 54	754	409	13288	1.E+00	1.E+00	4.E-01	6.E+01

Annotation Cluster 70	Enrichment Score: 2.0062919393132908											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR001060:Fps/Fes/Fer/CIP4 homology	6	0.683371298	3.E-03	117600, 70719, 14270, 14159, 171207, 19	860	21	17763	6.E+00	1.E+00	9.E-02	4.E+00
SMART	SM00055:FCH	6	0.683371298	4.E-03	117600, 70719, 14270, 14159, 171207, 19	492	21	9131	5.E+00	6.E-01	6.E-02	5.E+00
UP_SEQ_FEATURE	domain:FCH	4	0.455580866	8.E-02	117600, 14270, 14159, 19200	861	19	16021	4.E+00	1.E+00	9.E-01	8.E+01

Annotation Cluster 71		Enrichment Score: 1.9710075153615563											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
COG_ONTOLOGY	Nucleotide transport and metabolism	6	0.683371298	1.E-05	80914, 68556, 22245, 67273, 56749, 9958		66	11	2040	2.E+01	2.E-04	2.E-04	9.E-03
INTERPRO	IPR000764:Uridine kinase	3	0.341685649	1.E-02	80914, 68556, 22245		860	4	17763	2.E+01	1.E+00	3.E-01	2.E+01
INTERPRO	IPR006083:Phosphoribulokinase/uridine kinase	3	0.341685649	1.E-02	80914, 68556, 22245		860	4	17763	2.E+01	1.E+00	3.E-01	2.E+01
GOTERM_MF_FAT	GO:0019205~nucleobase, nucleoside, nucleotide kinase activity	7	0.797266515	1.E-02	80914, 68556, 22245, 14923, 11636, 6658		754	36	13288	3.E+00	1.E+00	1.E-01	2.E+01
GOTERM_MF_FAT	GO:0004849~uridine kinase activity	3	0.341685649	2.E-02	80914, 68556, 22245		754	4	13288	1.E+01	1.E+00	2.E-01	2.E+01
GOTERM_MF_FAT	GO:0019206~nucleoside kinase activity	3	0.341685649	9.E-02	80914, 68556, 22245		754	9	13288	6.E+00	1.E+00	5.E-01	8.E+01
KEGG_PATHWAY	mmu00983:Drug metabolism	7	0.797266515	4.E-01	80914, 68556, 22017, 72269, 22245, 2227		580	48	5738	1.E+00	1.E+00	6.E-01	1.E+02

Annotation Cluster 72	Enrichment Score: 1.9408379979195347											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	pentose phosphate pathway	4	0.455580866	4.E-04	21991, 11676, 11674, 14381	869	4	17854	2.E+01	2.E-01	4.E-03	6.E-01
INTERPRO	IPR013785:Aldolase-type TIM barrel	8	0.911161731	4.E-03	21991, 21351, 56749, 230163, 18563, 116	860	43	17763	4.E+00	1.E+00	1.E-01	7.E+00
UP_SEQ_FEATURE	site:Necessary for preference for fructose 1,6-bisphosphate over f	3	0.341685649	8.E-03	230163, 11676, 11674	861	3	16021	2.E+01	1.E+00	3.E-01	1.E+01
UP_SEQ_FEATURE	active site:Schiff-base intermediate with dihydroxyacetone-P	3	0.341685649	8.E-03	230163, 11676, 11674	861	3	16021	2.E+01	1.E+00	3.E-01	1.E+01
SP_PIR_KEYWORDS	Schiff base	4	0.455580866	1.E-02	80905, 230163, 11676, 11674	869	10	17854	8.E+00	1.E+00	5.E-02	1.E+01
INTERPRO	IPR000741:Fructose-bisphosphate aldolase, class-I	3	0.341685649	2.E-02	230163, 11676, 11674	860	5	17763	1.E+01	1.E+00	4.E-01	3.E+01
GOTERM_MF_FAT	GO:0004332~fructose-bisphosphate aldolase activity	3	0.341685649	3.E-02	230163, 11676, 11674	754	5	13288	1.E+01	1.E+00	3.E-01	4.E+01
GOTERM_MF_FAT	GO:0016832~aldehyde-lyase activity	3	0.341685649	6.E-02	230163, 11676, 11674	754	7	13288	8.E+00	1.E+00	4.E-01	6.E+01
KEGG_PATHWAY	mmu00051:Fructose and mannose metabolism	8	0.911161731	7.E-02	56421, 15275, 21991, 230163, 15277, 116	580	37	5738	2.E+00	1.E+00	2.E-01	6.E+01

Annotation Cluster 73	Enrichment Score: 1.938660724544557											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	sh3-binding	9	1.025056948	6.E-03	22323, 20401, 19317, 13800, 80987, 3093	869	57	17854	3.E+00	9.E-01	3.E-02	8.E+00
INTERPRO	IPR014885:VASP tetramerisation	3	0.341685649	7.E-03	22323, 13800, 14026	860	3	17763	2.E+01	1.E+00	2.E-01	1.E+01
UP_SEQ_FEATURE	region of interest:EVI2 block C	3	0.341685649	8.E-03	22323, 13800, 14026	861	3	16021	2.E+01	1.E+00	3.E-01	1.E+01
UP_SEQ_FEATURE	region of interest:EVI2 block A	3	0.341685649	8.E-03	22323, 13800, 14026	861	3	16021	2.E+01	1.E+00	3.E-01	1.E+01
UP_SEQ_FEATURE	region of interest:EVI2 block B	3	0.341685649	8.E-03	22323, 13800, 14026	861	3	16021	2.E+01	1.E+00	3.E-01	1.E+01
UP_SEQ_FEATURE	region of interest:EVI2	3	0.341685649	8.E-03	22323, 13800, 14026	861	3	16021	2.E+01	1.E+00	3.E-01	1.E+01
UP_SEQ_FEATURE	short sequence motif:KLKR	3	0.341685649	8.E-03	22323, 13800, 14026	861	3	16021	2.E+01	1.E+00	3.E-01	1.E+01
INTERPRO	IPR000697:EVI1	4	0.455580866	1.E-02	22323, 13800, 14026, 22376	860	11	17763	8.E+00	1.E+00	3.E-01	2.E+01
SMART	SM00461:WH1	4	0.455580866	2.E-02	22323, 13800, 14026, 22376	492	11	9131	7.E+00	1.E+00	2.E-01	2.E+01
UP_SEQ_FEATURE	domain:WH1	4	0.455580866	3.E-02	22323, 13800, 14026, 22376	861	13	16021	6.E+00	1.E+00	7.E-01	4.E+01
GOTERM_BP_FAT	GO:0008154~actin polymerization or depolymerization	4	0.455580866	4.E-02	227753, 13800, 14026, 22376	809	13	13588	5.E+00	1.E+00	3.E-01	5.E+01

Annotation Cluster 74		Enrichment Score: 1.9202641119686223										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR



GOTERM_BP_FAT	GO:0030217~T cell differentiation	13	1.480637813	2.E-03	22324, 19934, 12043, 74734, 108138, 100	809	76	13588	3.E+00	1.E+00	3.E-02	3.E+00
GOTERM_BP_FAT	GO:0046632~alpha-beta T cell differentiation	5	0.569476082	2.E-02	12051, 19934, 12043, 20963, 100047372,	809	19	13588	4.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0046631~alpha-beta T cell activation	5	0.569476082	4.E-02	12051, 19934, 12043, 20963, 100047372,	809	23	13588	4.E+00	1.E+00	3.E-01	6.E+01

Annotation Cluster 75	Enrichment Score: 1.9155932443283457											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0042157~lipoprotein metabolic process	19	2.164009112	3.E-07	18108, 18107, 11814, 11806, 276846, 118	809	76	13588	4.E+00	1.E-03	2.E-05	6.E-04
GOTERM_BP_FAT	GO:0019637~organophosphate metabolic process	28	3.189066059	5.E-06	68262, 14178, 276846, 329777, 52123, 21	809	176	13588	3.E+00	2.E-02	3.E-04	9.E-03
GOTERM_BP_FAT	GO:0042158~lipoprotein biosynthetic process	14	1.59453303	1.E-05	18108, 18107, 276846, 11806, 11816, 329	809	55	13588	4.E+00	4.E-02	7.E-04	3.E-02
GOTERM_BP_FAT	GO:0006644~phospholipid metabolic process	25	2.84738041	3.E-05	68262, 14178, 276846, 329777, 52123, 21	809	163	13588	3.E+00	1.E-01	1.E-03	6.E-02
GOTERM_CC_FAT	GO:0042765~GPI-anchor transamidase complex	4	0.455580866	5.E-04	14731, 329777, 228812, 100046871, 7892	636	4	12504	2.E+01	2.E-01	5.E-03	7.E-01
GOTERM_BP_FAT	GO:0006497~protein amino acid lipidation	11	1.25284738	6.E-04	18108, 18107, 14731, 56703, 108672, 177	809	50	13588	4.E+00	8.E-01	1.E-02	1.E+00
GOTERM_MF_FAT	GO:0003923~GPI-anchor transamidase activity	4	0.455580866	7.E-04	14731, 276846, 329777, 100046871, 7892	754	4	13288	2.E+01	4.E-01	1.E-02	1.E+00
SP_PIR_KEYWORDS	gpi-anchor biosynthesis	7	0.797266515	8.E-04	14731, 56703, 276846, 329777, 18701, 22	869	24	17854	6.E+00	3.E-01	6.E-03	1.E+00
GOTERM_BP_FAT	GO:0008654~phospholipid biosynthetic process	14	1.59453303	1.E-03	14178, 68262, 276846, 329777, 52123, 10	809	83	13588	3.E+00	1.E+00	2.E-02	2.E+00
GOTERM_BP_FAT	GO:0046486~glycerolipid metabolic process	17	1.936218679	4.E-03	11814, 276846, 329777, 18534, 238055, 1	809	129	13588	2.E+00	1.E+00	6.E-02	7.E+00
GOTERM_BP_FAT	GO:0045017~glycerolipid biosynthetic process	10	1.138952164	7.E-03	14731, 56703, 276846, 13350, 19012, 329	809	58	13588	3.E+00	1.E+00	9.E-02	1.E+01
GOTERM_BP_FAT	GO:0006506~GPI anchor biosynthetic process	7	0.797266515	8.E-03	14731, 56703, 276846, 329777, 18701, 22	809	30	13588	4.E+00	1.E+00	1.E-01	1.E+01
GOTERM_BP_FAT	GO:0046489~phosphoinositide biosynthetic process	7	0.797266515	9.E-03	14731, 56703, 276846, 329777, 18701, 22	809	31	13588	4.E+00	1.E+00	1.E-01	1.E+01
GOTERM_BP_FAT	GO:0006505~GPI anchor metabolic process	7	0.797266515	1.E-02	14731, 56703, 276846, 329777, 18701, 22	809	32	13588	4.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0030384~phosphoinositide metabolic process	10	1.138952164	1.E-02	18708, 14731, 56703, 276846, 329777, 30	809	63	13588	3.E+00	1.E+00	1.E-01	2.E+01
KEGG_PATHWAY	mmu00563:Glycosylphosphatidylinositol(GPI)-anchor biosynthesis	7	0.797266515	3.E-02	14731, 56703, 276846, 329777, 18701, 22	580	25	5738	3.E+00	1.E+00	9.E-02	3.E+01
GOTERM_BP_FAT	GO:0046474~glycerophospholipid biosynthetic process	7	0.797266515	5.E-02	14731, 56703, 276846, 329777, 18701, 22	809	46	13588	3.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0008610~lipid biosynthetic process	25	2.84738041	5.E-02	70316, 14178, 68262, 276846, 329777, 52	809	285	13588	1.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0006650~glycerophospholipid metabolic process	10	1.138952164	8.E-02	18708, 14731, 56703, 276846, 329777, 30	809	88	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_CC_FAT	GO:0030176~integral to endoplasmic reticulum membrane	4	0.455580866	2.E-01	14731, 329777, 228812, 100046871, 7892	636	33	12504	2.E+00	1.E+00	6.E-01	1.E+02
GOTERM_CC_FAT	GO:0042175~nuclear envelope-endoplasmic reticulum network	11	1.25284738	3.E-01	14731, 56703, 14226, 329777, 18701, 191	636	160	12504	1.E+00	1.E+00	7.E-01	1.E+02
GOTERM_CC_FAT	GO:0005789~endoplasmic reticulum membrane	10	1.138952164	4.E-01	14731, 56703, 14226, 329777, 18701, 120	636	152	12504	1.E+00	1.E+00	8.E-01	1.E+02
GOTERM_CC_FAT	GO:0044432~endoplasmic reticulum part	14	1.59453303	4.E-01	18453, 14226, 329777, 12043, 14827, 201	636	231	12504	1.E+00	1.E+00	8.E-01	1.E+02
GOTERM_CC_FAT	GO:0031301~integral to organelle membrane	6	0.683371298	5.E-01	14731, 329777, 228812, 100046871, 5904	636	89	12504	1.E+00	1.E+00	9.E-01	1.E+02
GOTERM_CC_FAT	GO:0031227~intrinsic to endoplasmic reticulum membrane	4	0.455580866	5.E-01	14731, 329777, 228812, 100046871, 7892	636	52	12504	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_CC_FAT	GO:0031300~intrinsic to organelle membrane	6	0.683371298	7.E-01	14731, 329777, 228812, 100046871, 5904	636	112	12504	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_CC_FAT	GO:0012505~endomembrane system	26	2.961275626	7.E-01	19720, 329777, 20191, 170758, 10004687	636	535	12504	1.E+00	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	endoplasmic reticulum	24	2.733485194	1.E+00	276846, 329777, 100046871, 56717, 1473	869	678	17854	7.E-01	1.E+00	1.E+00	1.E+02
GOTERM_CC_FAT	GO:0005783~endoplasmic reticulum	32	3.644646925	1.E+00	276846, 329777, 238055, 20191, 1000468	636	838	12504	8.E-01	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	topological domain:Luminal	8	0.911161731	1.E+00	14731, 276846, 329777, 19164, 98238, 67	861	414	16021	4.E-01	1.E+00	1.E+00	1.E+02

Annotation Cluster 76	Enrichment Score: 1.9152551714672388											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0000267~cell fraction	46	5.239179954	5.E-03	672195, 12955, 665032, 238055, 21869, 1	636	596	12504	2.E+00	9.E-01	4.E-02	7.E+00
GOTERM_CC_FAT	GO:0005626~insoluble fraction	40	4.555808656	1.E-02	269589, 11852, 12955, 665032, 238055, 1	636	528	12504	1.E+00	1.E+00	7.E-02	2.E+01
GOTERM_CC_FAT	GO:0005624~membrane fraction	37	4.214123007	3.E-02	269589, 11852, 665032, 238055, 16396, 1	636	510	12504	1.E+00	1.E+00	1.E-01	3.E+01

Annotation Cluster 77	Enrichment Score: 1.9031851569163833											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR018029:C2 membrane targeting protein	15	1.708428246	6.E-04	269589, 19894, 17999, 16396, 18797, 109	860	106	17763	3.E+00	5.E-01	3.E-02	9.E-01
INTERPRO	IPR000008:C2 calcium-dependent membrane targeting	16	1.822323462	2.E-03	269589, 19894, 17999, 16396, 18797, 109	860	130	17763	3.E+00	9.E-01	5.E-02	3.E+00
SMART	SM00239:C2	16	1.822323462	4.E-03	269589, 19894, 17999, 16396, 18797, 109	492	130	9131	2.E+00	6.E-01	6.E-02	5.E+00
UP_SEQ_FEATURE	domain:C2	9	1.025056948	3.E-02	18751, 18783, 18803, 17999, 234779, 163	861	68	16021	2.E+00	1.E+00	7.E-01	4.E+01
UP_SEQ_FEATURE	domain:C2 2	6	0.683371298	2.E-01	269589, 19894, 27359, 83671, 236643, 83	861	57	16021	2.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	domain:C2 1	6	0.683371298	2.E-01	269589, 19894, 27359, 83671, 236643, 83	861	57	16021	2.E+00	1.E+00	1.E+00	1.E+02

Annotation Cluster 78	Enrichment Score: 1.8648049742314605											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0008156~negative regulation of DNA replication	5	0.569476082	3.E-03	12190, 57441, 22130, 67177, 269582	809	11	13588	8.E+00	1.E+00	5.E-02	5.E+00
GOTERM_BP_FAT	GO:0006275~regulation of DNA replication	6	0.683371298	3.E-03	12190, 57441, 22130, 67177, 18538, 2695	809	18	13588	6.E+00	1.E+00	5.E-02	6.E+00
GOTERM_BP_FAT	GO:0051053~negative regulation of DNA metabolic process	5	0.569476082	3.E-02	12190, 57441, 22130, 67177, 269582	809	20	13588	4.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0051052~regulation of DNA metabolic process	7	0.797266515	1.E-01	11785, 12190, 57441, 22130, 67177, 1853	809	58	13588	2.E+00	1.E+00	6.E-01	9.E+01

Annotation Cluster 79	Enrichment Score: 1.8427620609264395											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR004167:E3 binding	3	0.341685649	7.E-03	235339, 27402, 13171	860	3	17763	2.E+01	1.E+00	2.E-01	1.E+01
INTERPRO	IPR000089:Biotin/lipoyl attachment	4	0.455580866	8.E-03	235339, 27402, 18563, 13171	860	9	17763	9.E+00	1.E+00	2.E-01	1.E+01
INTERPRO	IPR001078:2-oxoacid dehydrogenase acyltransferase, catalytic dor	3	0.341685649	1.E-02	235339, 27402, 13171	860	4	17763	2.E+01	1.E+00	3.E-01	2.E+01
INTERPRO	IPR003016:2-oxo acid dehydrogenase, lipoyl-binding site	3	0.341685649	2.E-02	235339, 27402, 13171	860	5	17763	1.E+01	1.E+00	4.E-01	3.E+01



SP_PIR_KEYWORDS	lipoyl	3	0.341685649	2.E-02	235339, 27402, 13171	869	5	17854	1.E+01	1.E+00	1.E-01	3.E+01
GOTERM_MF_FAT	GO:0031405~liponic acid binding	3	0.341685649	3.E-02	235339, 27402, 13171	754	5	13288	1.E+01	1.E+00	3.E-01	4.E+01
Annotation Cluster 80	Enrichment Score: 1.8357214574277725											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	allosteric enzyme	9	1.025056948	3.E-04	18746, 110095, 18770, 56421, 20133, 152	869	36	17854	5.E+00	1.E-01	2.E-03	4.E-01
INTERPRO	IPR019807:Hexokinase, conserved site	4	0.455580866	1.E-03	15275, 15277, 103988, 212032	860	5	17763	2.E+01	8.E-01	4.E-02	2.E+00
INTERPRO	IPR001312:Hexokinase	4	0.455580866	2.E-03	15275, 15277, 103988, 212032	860	6	17763	1.E+01	9.E-01	7.E-02	3.E+00
GOTERM_MF_FAT	GO:0004396~hexokinase activity	4	0.455580866	3.E-03	15275, 15277, 103988, 212032	754	6	13288	1.E+01	9.E-01	4.E-02	5.E+00
UP_SEQ_FEATURE	region of interest:Regulatory	3	0.341685649	2.E-02	15275, 15277, 212032	861	4	16021	1.E+01	1.E+00	5.E-01	2.E+01
COG_ONTOLOGY	Carbohydrate transport and metabolism	5	0.569476082	2.E-02	15275, 15277, 103988, 23971, 212032	66	32	2040	5.E+00	3.E-01	8.E-02	1.E+01
GOTERM_MF_FAT	GO:0019200~carbohydrate kinase activity	5	0.569476082	2.E-02	56421, 15275, 15277, 103988, 212032	754	20	13288	4.E+00	1.E+00	2.E-01	3.E+01
PIR_SUPERFAMILY	PIRSF000527:hexokinase I	3	0.341685649	3.E-02	15275, 15277, 212032	576	4	8136	1.E+01	1.E+00	8.E-01	3.E+01
KEGG_PATHWAY	mmu00500:Starch and sucrose metabolism	8	0.911161731	6.E-02	110095, 14751, 15275, 72157, 15277, 103	580	36	5738	2.E+00	1.E+00	2.E-01	6.E+01
KEGG_PATHWAY	mmu00051:Fructose and mannose metabolism	8	0.911161731	7.E-02	56421, 15275, 21991, 230163, 15277, 116	580	37	5738	2.E+00	1.E+00	2.E-01	6.E+01
KEGG_PATHWAY	mmu00052:Galactose metabolism	6	0.683371298	1.E-01	56421, 15275, 72157, 15277, 103988, 212	580	27	5738	2.E+00	1.E+00	3.E-01	8.E+01
KEGG_PATHWAY	mmu00520:Amino sugar and nucleotide sugar metabolism	6	0.683371298	5.E-01	14751, 15275, 72157, 15277, 103988, 212	580	44	5738	1.E+00	1.E+00	7.E-01	1.E+02
Annotation Cluster 81	Enrichment Score: 1.815283608208076											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	iron-sulfur	10	1.138952164	4.E-04	66694, 226646, 14151, 17995, 227197, 22	869	47	17854	4.E+00	2.E-01	3.E-03	5.E-01
SP_PIR_KEYWORDS	4Fe-4s	7	0.797266515	6.E-04	226646, 17995, 227197, 225887, 66841, 7	869	23	17854	6.E+00	3.E-01	5.E-03	9.E-01
GOTERM_MF_FAT	GO:0051539~4 iron, 4 sulfur cluster binding	7	0.797266515	1.E-03	226646, 17995, 227197, 225887, 66841, 7	754	23	13288	5.E+00	7.E-01	2.E-02	2.E+00
GOTERM_MF_FAT	GO:0051536~iron-sulfur cluster binding	10	1.138952164	2.E-03	66694, 226646, 14151, 17995, 227197, 22	754	50	13288	4.E+00	7.E-01	2.E-02	3.E+00
GOTERM_MF_FAT	GO:0051540~metal cluster binding	10	1.138952164	2.E-03	66694, 226646, 14151, 17995, 227197, 22	754	50	13288	4.E+00	7.E-01	2.E-02	3.E+00
INTERPRO	IPR017896:4Fe-4S ferredoxin, iron-sulphur binding domain	3	0.341685649	3.E-02	225887, 66841, 99586	860	6	17763	1.E+01	1.E+00	5.E-01	4.E+01
UP_SEQ_FEATURE	metal ion-binding siteIron-sulfur 2 (4Fe-4S)	3	0.341685649	4.E-02	227197, 225887, 99586	861	6	16021	9.E+00	1.E+00	7.E-01	5.E+01
UP_SEQ_FEATURE	metal ion-binding siteIron-sulfur (4Fe-4S)	4	0.455580866	4.E-02	226646, 17995, 66841, 75406	861	15	16021	5.E+00	1.E+00	8.E-01	5.E+01
SP_PIR_KEYWORDS	2Fe-2S	4	0.455580866	6.E-02	66694, 14151, 227197, 72900	869	19	17854	4.E+00	1.E+00	2.E-01	6.E+01
GOTERM_MF_FAT	GO:0051537~2 iron, 2 sulfur cluster binding	4	0.455580866	9.E-02	66694, 14151, 227197, 72900	754	19	13288	4.E+00	1.E+00	5.E-01	8.E+01
UP_SEQ_FEATURE	metal ion-binding siteIron-sulfur (2Fe-2S)	3	0.341685649	1.E-01	66694, 14151, 72900	861	11	16021	5.E+00	1.E+00	1.E+00	9.E+01
SP_PIR_KEYWORDS	iron	21	2.391799544	2.E-01	382985, 66694, 672195, 226646, 14151, 6	869	321	17854	1.E+00	1.E+00	4.E-01	9.E+01
GOTERM_MF_FAT	GO:0005506~iron ion binding	21	2.391799544	5.E-01	382985, 66694, 672195, 226646, 14151, 6	754	343	13288	1.E+00	1.E+00	1.E+00	1.E+02
Annotation Cluster 82	Enrichment Score: 1.8075196860927323											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0031960~response to corticosteroid stimulus	8	0.911161731	3.E-04	12039, 20779, 12842, 11409, 109900, 263	809	23	13588	6.E+00	6.E-01	8.E-03	5.E-01
GOTERM_BP_FAT	GO:0051384~response to glucocorticoid stimulus	6	0.683371298	4.E-03	12039, 11409, 109900, 26395, 12043, 230	809	19	13588	5.E+00	1.E+00	6.E-02	7.E+00
GOTERM_BP_FAT	GO:0051591~response to cAMP	4	0.455580866	2.E-02	12039, 12842, 109900, 232087	809	11	13588	6.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0048545~response to steroid hormone stimulus	9	1.025056948	2.E-02	12039, 20779, 12842, 11409, 109900, 263	809	60	13588	3.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0009991~response to extracellular stimulus	15	1.708428246	3.E-02	12190, 12842, 109900, 12043, 100040331	809	133	13588	2.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0031667~response to nutrient levels	13	1.480637813	4.E-02	12190, 12842, 109900, 12043, 100040331	809	115	13588	2.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0007584~response to nutrient	7	0.797266515	3.E-01	12039, 100048339, 12190, 19982, 12842	809	76	13588	2.E+00	1.E+00	9.E-01	1.E+02
Annotation Cluster 83	Enrichment Score: 1.776290829638283											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_SEQ_FEATURE	domain:Ras-associating	7	0.797266515	9.E-03	17925, 270163, 54519, 54354, 244867, 21	861	34	16021	4.E+00	1.E+00	4.E-01	1.E+01
INTERPRO	IPR000159:Ras-association	7	0.797266515	2.E-02	17925, 270163, 54519, 54354, 244867, 21	860	44	17763	3.E+00	1.E+00	4.E-01	3.E+01
SMART	SM00314:RA	7	0.797266515	3.E-02	17925, 270163, 54519, 54354, 244867, 21	492	44	9131	3.E+00	1.E+00	3.E-01	3.E+01
Annotation Cluster 84	Enrichment Score: 1.7605099529759798											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0005925~focal adhesion	10	1.138952164	2.E-03	22323, 12549, 13800, 22793, 236920, 545	636	57	12504	3.E+00	6.E-01	2.E-02	3.E+00
GOTERM_CC_FAT	GO:0005924~cell-substrate adherens junction	10	1.138952164	3.E-03	22323, 12549, 13800, 22793, 236920, 545	636	61	12504	3.E+00	7.E-01	3.E-02	5.E+00
GOTERM_CC_FAT	GO:0016323~basolateral plasma membrane	16	1.822323462	5.E-03	22323, 13649, 13800, 20525, 22793, 2369	636	141	12504	2.E+00	9.E-01	4.E-02	7.E+00
GOTERM_CC_FAT	GO:0030055~cell-substrate junction	10	1.138952164	6.E-03	22323, 12549, 13800, 22793, 236920, 545	636	66	12504	3.E+00	9.E-01	4.E-02	8.E+00
GOTERM_CC_FAT	GO:0005912~adherens junction	13	1.480637813	7.E-03	22323, 69524, 13800, 22793, 236920, 545	636	106	12504	2.E+00	9.E-01	5.E-02	1.E+01
GOTERM_CC_FAT	GO:0070161~anchoring junction	13	1.480637813	2.E-02	22323, 69524, 13800, 22793, 236920, 545	636	123	12504	2.E+00	1.E+00	1.E-01	3.E+01
SP_PIR_KEYWORDS	cell junction	22	2.505694761	4.E-01	22323, 13800, 69524, 16456, 19894, 9419	869	392	17854	1.E+00	1.E+00	7.E-01	1.E+02
GOTERM_CC_FAT	GO:0030054~cell junction	24	2.733485194	6.E-01	22323, 13800, 19894, 69524, 16456, 9419	636	470	12504	1.E+00	1.E+00	9.E-01	1.E+02
Annotation Cluster 85	Enrichment Score: 1.7383268575187347											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0016477~cell migration	24	2.733485194	2.E-02	117600, 13649, 11806, 16414, 57257, 187	809	240	13588	2.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0051674~localization of cell	27	3.075170843	2.E-02	117600, 13649, 238055, 18792, 21869, 16	809	284	13588	2.E+00	1.E+00	2.E-01	3.E+01



GOTERM_BP_FAT	GO:0048870--cell motility	27	3.075170843	2.E-02	117600, 13649, 238055, 18792, 21869, 16	809	284	13588	2.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0006928--cell motion	33	3.758542141	2.E-02	117600, 22323, 13649, 11658, 238055, 18	809	367	13588	2.E+00	1.E+00	2.E-01	3.E+01
Annotation Cluster 86	Enrichment Score: 1.7152993357962114											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR004161:Translation elongation factor EFTu/EF1A, domain 2	6	0.683371298	1.E-03	26905, 13627, 13628, 13629, 14852, 2269	860	17	17763	7.E+00	7.E-01	4.E-02	2.E+00
INTERPRO	IPR000795:Protein synthesis factor, GTP-binding	6	0.683371298	1.E-03	26905, 13627, 13628, 13629, 14852, 2269	860	18	17763	7.E+00	8.E-01	5.E-02	2.E+00
GOTERM_CC_FAT	GO:0005853--eukaryotic translation elongation factor 1 complex	3	0.341685649	1.E-02	13628, 66656, 55949	636	4	12504	1.E+01	1.E+00	8.E-02	2.E+01
SP_PIR_KEYWORDS	elongation factor	5	0.569476082	4.E-02	13627, 13628, 13629, 66656, 55949	869	27	17854	4.E+00	1.E+00	2.E-01	4.E+01
INTERPRO	IPR004160:Translation elongation factor EFTu/EF1A, C-terminal	3	0.341685649	5.E-02	13627, 13628, 14852	860	8	17763	8.E+00	1.E+00	7.E-01	6.E+01
GOTERM_MF_FAT	GO:0003746--translation elongation factor activity	5	0.569476082	1.E-01	13627, 13628, 13629, 66656, 55949	754	31	13288	3.E+00	1.E+00	6.E-01	8.E+01
GOTERM_BP_FAT	GO:0006414--translational elongation	5	0.569476082	3.E-01	56040, 13627, 13628, 66656, 55949	809	43	13588	2.E+00	1.E+00	8.E-01	1.E+02
Annotation Cluster 87	Enrichment Score: 1.704610956027809											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0035295--tube development	31	3.530751708	5.E-04	22323, 14178, 19206, 232906, 15376, 148	809	264	13588	2.E+00	8.E-01	1.E-02	9.E-01
GOTERM_BP_FAT	GO:0060541--respiratory system development	13	1.480637813	7.E-02	14178, 15376, 14180, 19378, 16948, 5684	809	124	13588	2.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0030324--lung development	12	1.366742597	7.E-02	15402, 24064, 14178, 11486, 14465, 7431	809	111	13588	2.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0030323--respiratory tube development	12	1.366742597	7.E-02	15402, 24064, 14178, 11486, 14465, 7431	809	113	13588	2.E+00	1.E+00	5.E-01	7.E+01
Annotation Cluster 88	Enrichment Score: 1.669849649820838											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0031570--DNA integrity checkpoint	8	0.911161731	3.E-03	245000, 11920, 67177, 26416, 12649, 124	809	33	13588	4.E+00	1.E+00	5.E-02	5.E+00
GOTERM_BP_FAT	GO:0000075--cell cycle checkpoint	10	1.138952164	3.E-03	245000, 11920, 67177, 26416, 12649, 124	809	52	13588	3.E+00	1.E+00	5.E-02	6.E+00
GOTERM_BP_FAT	GO:0042770--DNA damage response, signal transduction	9	1.025056948	2.E-02	12051, 12190, 245000, 11920, 26416, 126	809	57	13588	3.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0000077--DNA damage checkpoint	6	0.683371298	3.E-02	245000, 11920, 26416, 12649, 12443, 125	809	30	13588	3.E+00	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0007093--mitotic cell cycle checkpoint	5	0.569476082	5.E-02	11920, 12443, 56150, 68193, 12534	809	24	13588	3.E+00	1.E+00	4.E-01	6.E+01
BIOCARTA	m_atrbcrPathway:Role of BRCA1, BRCA2 and ATR in Cancer Sus	5	0.569476082	4.E-01	12190, 245000, 11920, 12649, 19356	188	19	1171	2.E+00	1.E+00	7.E-01	1.E+02
Annotation Cluster 89	Enrichment Score: 1.6695841099813824											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0030335--positive regulation of cell migration	8	0.911161731	6.E-03	18708, 16367, 73167, 12043, 11855, 2033	809	37	13588	4.E+00	1.E+00	8.E-02	9.E+00
GOTERM_BP_FAT	GO:0030334--regulation of cell migration	13	1.480637813	8.E-03	14674, 73167, 12043, 11855, 384783, 187	809	92	13588	2.E+00	1.E+00	1.E-01	1.E+01
GOTERM_BP_FAT	GO:0051272--positive regulation of cell motion	8	0.911161731	1.E-02	18708, 16367, 73167, 12043, 11855, 2033	809	41	13588	3.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0051270--regulation of cell motion	14	1.59453303	1.E-02	14674, 73167, 12043, 11855, 384783, 187	809	107	13588	2.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0040017--positive regulation of locomotion	8	0.911161731	1.E-02	18708, 16367, 73167, 12043, 11855, 2033	809	44	13588	3.E+00	1.E+00	2.E-01	2.E+01
GOTERM_BP_FAT	GO:0040012--regulation of locomotion	13	1.480637813	3.E-02	14674, 73167, 12043, 11855, 384783, 187	809	110	13588	2.E+00	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0002053--positive regulation of mesenchymal cell proliferator	4	0.455580866	1.E-01	16367, 14180, 11855, 384783	809	22	13588	3.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0010464--regulation of mesenchymal cell proliferation	4	0.455580866	2.E-01	16367, 14180, 11855, 384783	809	23	13588	3.E+00	1.E+00	7.E-01	1.E+02
Annotation Cluster 90	Enrichment Score: 1.6449537070876337											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR005952:Phosphoglycerate mutase 1	3	0.341685649	7.E-03	18648, 12183, 56012	860	3	17763	2.E+01	1.E+00	2.E-01	1.E+01
UP_SEQ_FEATURE	site:Interaction with carboxyl group of phosphoglycerates	3	0.341685649	8.E-03	18648, 12183, 56012	861	3	16021	2.E+01	1.E+00	3.E-01	1.E+01
GOTERM_MF_FAT	GO:0004083--2,3-bisphospho-D-glycerate 2-phosphohydrolase ac	3	0.341685649	9.E-03	18648, 12183, 56012	754	3	13288	2.E+01	1.E+00	1.E-01	1.E+01
GOTERM_MF_FAT	GO:0004082--bisphosphoglycerate mutase activity	3	0.341685649	9.E-03	18648, 12183, 56012	754	3	13288	2.E+01	1.E+00	1.E-01	1.E+01
GOTERM_MF_FAT	GO:0034416--bisphosphoglycerate phosphatase activity	3	0.341685649	9.E-03	18648, 12183, 56012	754	3	13288	2.E+01	1.E+00	1.E-01	1.E+01
GOTERM_MF_FAT	GO:0004619--phosphoglycerate mutase activity	3	0.341685649	9.E-03	18648, 12183, 56012	754	3	13288	2.E+01	1.E+00	1.E-01	1.E+01
GOTERM_MF_FAT	GO:0016868--intramolecular transferase activity, phosphotransfera	4	0.455580866	2.E-02	18648, 72157, 12183, 56012	754	10	13288	7.E+00	1.E+00	2.E-01	2.E+01
PIR_SUPERFAMILY	PIRSF001490:cofactor-dependent phosphoglycerate mutase	3	0.341685649	3.E-02	18648, 12183, 56012	576	4	8136	1.E+01	1.E+00	8.E-01	3.E+01
SP_PIR_KEYWORDS	Isomerase	12	1.366742597	3.E-02	18453, 14226, 72157, 14827, 12183, 5601	869	118	17854	2.E+00	1.E+00	1.E-01	3.E+01
INTERPRO	IPR001345:Phosphoglycerate/bisphosphoglycerate mutase	3	0.341685649	7.E-02	18648, 12183, 56012	860	9	17763	7.E+00	1.E+00	7.E-01	3.E+01
UP_SEQ_FEATURE	active site:Tele-phosphohistidine intermediate	3	0.341685649	8.E-02	18648, 12183, 56012	861	9	16021	6.E+00	1.E+00	9.E-01	8.E+01
INTERPRO	IPR013078:Phosphoglycerate mutase	3	0.341685649	1.E-01	18648, 12183, 56012	860	11	17763	6.E+00	1.E+00	8.E-01	8.E+01
GOTERM_MF_FAT	GO:0016866--intramolecular transferase activity	4	0.455580866	2.E-01	18648, 72157, 12183, 56012	754	24	13288	3.E+00	1.E+00	7.E-01	9.E+01
Annotation Cluster 91	Enrichment Score: 1.6241208186537013											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0051402--neuron apoptosis	6	0.683371298	2.E-03	11920, 12028, 19164, 12043, 12568, 1000	809	16	13588	6.E+00	1.E+00	3.E-02	3.E+00
GOTERM_BP_FAT	GO:0043525--positive regulation of neuron apoptosis	5	0.569476082	2.E-02	16994, 11920, 12028, 14815, 12568	809	19	13588	4.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0043523--regulation of neuron apoptosis	10	1.138952164	5.E-02	16994, 12048, 11920, 12028, 15461, 1204	809	80	13588	2.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0010212--response to ionizing radiation	6	0.683371298	2.E-01	12190, 11920, 12028, 12018, 12043, 1081	809	48	13588	2.E+00	1.E+00	7.E-01	1.E+02
Annotation Cluster 92	Enrichment Score: 1.6199386931959372											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR



SP_PIR_KEYWORDS	GTP binding	8	0.911161731	1.E-03	19354, 14674, 14675, 14678, 11854, 1254	869	35	17854	5.E+00	4.E-01	8.E-03	2.E+00
SP_PIR_KEYWORDS	nucleotide binding	10	1.138952164	4.E-03	110957, 19354, 14674, 14675, 14678, 146	869	64	17854	3.E+00	8.E-01	2.E-02	5.E+00
SP_PIR_KEYWORDS	P-loop	10	1.138952164	4.E-03	110957, 19354, 14674, 14675, 14678, 146	869	65	17854	3.E+00	8.E-01	2.E-02	6.E+00
INTERPRO	IPR001019:Guanine nucleotide binding protein (G-protein), alpha	5	0.569476082	6.E-03	14674, 14675, 14678, 14673, 14682	860	16	17763	6.E+00	1.E+00	2.E-01	1.E+01
GOTERM_CC_FAT	GO:0019897~extrinsic to plasma membrane	9	1.025056948	6.E-03	269589, 14674, 14675, 11816, 14673, 836	636	55	12504	3.E+00	9.E-01	4.E-02	8.E+00
PIR_SUPERFAMILY	PIRSF002400:GTP-binding regulatory protein Gs alpha chain	5	0.569476082	1.E-02	14674, 14675, 14678, 14673, 14682	576	14	8136	5.E+00	1.E+00	6.E-01	2.E+01
GOTERM_CC_FAT	GO:0005834~heterotrimeric G-protein complex	4	0.455580866	3.E-01	14674, 14675, 14673, 14682	636	35	12504	2.E+00	1.E+00	6.E-01	1.E+02
GOTERM_BP_FAT	GO:0007186~G-protein coupled receptor protein signaling pathw	11	1.25284738	1.E+00	12765, 18126, 14674, 14675, 14678, 1406	809	1877	13588	1.E-01	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	transducer	14	1.59453303	1.E+00	12765, 14674, 14675, 14678, 384783, 187	869	1467	17854	2.E-01	1.E+00	1.E+00	1.E+02
Annotation Cluster 93	Enrichment Score: 1.6148497698562085											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	calmodulin-binding	13	1.480637813	4.E-03	102093, 18679, 18682, 18126, 14432, 775	869	103	17854	3.E+00	9.E-01	2.E-02	6.E+00
GOTERM_MF_FAT	GO:0005516~calmodulin binding	13	1.480637813	3.E-02	102093, 18679, 18682, 18126, 14432, 775	754	114	13288	2.E+00	1.E+00	3.E-01	3.E+01
UP_SEQ_FEATURE	region of interest:Calmodulin-binding	6	0.683371298	1.E-01	18126, 102093, 110094, 18679, 19056, 18	861	49	16021	2.E+00	1.E+00	1.E+00	9.E+01
Annotation Cluster 94	Enrichment Score: 1.606839310217028											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
BIOCARTA	m_p27Pathway:Regulation of p27 Phosphorylation during Cell Cy	7	0.797266515	6.E-03	13555, 19645, 12447, 26965, 12566, 5412	188	12	1171	4.E+00	7.E-01	6.E-02	8.E+00
BIOCARTA	m_fbw7Pathway:Cyclin E Destruction Pathway	5	0.569476082	4.E-02	13555, 19645, 12447, 26965, 12566	188	9	1171	3.E+00	1.E+00	2.E-01	4.E+01
BIOCARTA	m_skp2e2fPathway:E2f1 Destruction Pathway	5	0.569476082	6.E-02	13555, 19645, 12447, 26965, 12566	188	10	1171	3.E+00	1.E+00	2.E-01	5.E+01
Annotation Cluster 95	Enrichment Score: 1.5896842392464907											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0035004~phosphoinositide 3-kinase activity	5	0.569476082	2.E-03	18709, 18708, 11920, 30955, 18707	754	11	13288	8.E+00	8.E-01	3.E-02	4.E+00
GOTERM_MF_FAT	GO:0016303~1-phosphatidylinositol-3-kinase activity	5	0.569476082	2.E-03	18709, 18708, 11920, 30955, 18707	754	11	13288	8.E+00	8.E-01	3.E-02	4.E+00
KEGG_PATHWAY	mmu04960:Aldosterone-regulated sodium reabsorption	11	1.25284738	8.E-03	18709, 18751, 18708, 16367, 16333, 1633	580	42	5738	3.E+00	7.E-01	3.E-02	9.E+00
INTERPRO	IPR000403:Phosphatidylinositol 3- and 4-kinase, catalytic	5	0.569476082	8.E-03	56717, 245000, 11920, 30955, 18707	860	17	17763	6.E+00	1.E+00	2.E-01	1.E+01
INTERPRO	IPR018936:Phosphatidylinositol 3- and 4-kinase, conserved site	5	0.569476082	8.E-03	56717, 245000, 11920, 30955, 18707	860	17	17763	6.E+00	1.E+00	2.E-01	1.E+01
UP_SEQ_FEATURE	domain:PI3K/PI4K	5	0.569476082	9.E-03	56717, 245000, 11920, 30955, 18707	861	16	16021	6.E+00	1.E+00	4.E-01	1.E+01
SMART	SM00146:PI3Kc	5	0.569476082	1.E-02	56717, 245000, 11920, 30955, 18707	492	17	9131	5.E+00	9.E-01	1.E-01	1.E+01
GOTERM_CC_FAT	GO:0005942~phosphoinositide 3-kinase complex	4	0.455580866	2.E-02	18709, 18708, 30955, 18707	636	12	12504	7.E+00	1.E+00	1.E-01	2.E+01
INTERPRO	IPR003151:PIK-related kinase, FAT	3	0.341685649	2.E-02	56717, 245000, 11920	860	5	17763	1.E+01	1.E+00	4.E-01	3.E+01
INTERPRO	IPR003152:PIK-related kinase, FATC	3	0.341685649	3.E-02	56717, 245000, 11920	860	6	17763	1.E+01	1.E+00	5.E-01	4.E+01
INTERPRO	IPR014009:PIK-related kinase	3	0.341685649	3.E-02	56717, 245000, 11920	860	6	17763	1.E+01	1.E+00	5.E-01	4.E+01
UP_SEQ_FEATURE	domain:FATC	3	0.341685649	4.E-02	56717, 245000, 11920	861	6	16021	9.E+00	1.E+00	7.E-01	5.E+01
UP_SEQ_FEATURE	domain:FAT	3	0.341685649	4.E-02	56717, 245000, 11920	861	6	16021	9.E+00	1.E+00	7.E-01	5.E+01
GOTERM_BP_FAT	GO:0030258~lipid modification	7	0.797266515	6.E-02	18708, 74147, 26416, 30955, 11364, 1870	809	47	13588	3.E+00	1.E+00	4.E-01	7.E+01
GOTERM_MF_FAT	GO:0001727~lipid kinase activity	5	0.569476082	6.E-02	18709, 18708, 11920, 30955, 18707	754	27	13288	3.E+00	1.E+00	4.E-01	6.E+01
GOTERM_MF_FAT	GO:0004428~inositol or phosphatidylinositol kinase activity	5	0.569476082	1.E-01	18709, 18708, 11920, 30955, 18707	754	35	13288	3.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0046854~phosphoinositide phosphorylation	3	0.341685649	2.E-01	18708, 30955, 18707	809	13	13588	4.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0046834~lipid phosphorylation	3	0.341685649	2.E-01	18708, 30955, 18707	809	14	13588	4.E+00	1.E+00	7.E-01	1.E+02
KEGG_PATHWAY	mmu04070:Phosphatidylinositol signaling system	11	1.25284738	2.E-01	320207, 18797, 18795, 18751, 18709, 188	580	75	5738	1.E+00	1.E+00	4.E-01	1.E+02
Annotation Cluster 96	Enrichment Score: 1.5534352400233888											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_SEQ_FEATURE	binding site:NAD or substrate	3	0.341685649	8.E-03	16828, 16833, 16832	861	3	16021	2.E+01	1.E+00	3.E-01	1.E+01
UP_SEQ_FEATURE	binding site:NAD	8	0.911161731	1.E-02	15107, 100042746, 13382, 100041325, 10	861	46	16021	3.E+00	1.E+00	4.E-01	2.E+01
INTERPRO	IPR011304:L-lactate dehydrogenase	3	0.341685649	1.E-02	16828, 16833, 16832	860	4	17763	2.E+01	1.E+00	3.E-01	2.E+01
INTERPRO	IPR018177:L-lactate dehydrogenase, active site	3	0.341685649	1.E-02	16828, 16833, 16832	860	4	17763	2.E+01	1.E+00	3.E-01	2.E+01
GOTERM_MF_FAT	GO:0004459~L-lactate dehydrogenase activity	3	0.341685649	2.E-02	16828, 16833, 16832	754	4	13288	1.E+01	1.E+00	2.E-01	2.E+01
KEGG_PATHWAY	mmu00640:Propanoate metabolism	8	0.911161731	3.E-02	16828, 74147, 93747, 68738, 16833, 1683	580	30	5738	3.E+00	1.E+00	8.E-02	3.E+01
GOTERM_MF_FAT	GO:0004457~lactate dehydrogenase activity	3	0.341685649	3.E-02	16828, 16833, 16832	754	5	13288	1.E+01	1.E+00	3.E-01	4.E+01
INTERPRO	IPR001557:L-lactate/malate dehydrogenase	3	0.341685649	4.E-02	16828, 16833, 16832	860	7	17763	9.E+00	1.E+00	6.E-01	5.E+01
INTERPRO	IPR015955:Lactate dehydrogenase/glycoside hydrolase, family 4, (	3	0.341685649	5.E-02	16828, 16833, 16832	860	8	17763	8.E+00	1.E+00	7.E-01	6.E+01
INTERPRO	IPR001236:Lactate/malate dehydrogenase	3	0.341685649	5.E-02	16828, 16833, 16832	860	8	17763	8.E+00	1.E+00	7.E-01	6.E+01
PIR_SUPERFAMILY	PIRSF000102:Lac_mal_DH	3	0.341685649	8.E-02	16828, 16833, 16832	576	7	8136	6.E+00	1.E+00	1.E+00	7.E+01
KEGG_PATHWAY	mmu00270:Cysteine and methionine metabolism	7	0.797266515	1.E-01	16828, 232087, 13436, 16833, 16832, 229	580	33	5738	2.E+00	1.E+00	2.E-01	8.E+01
Annotation Cluster 97	Enrichment Score: 1.5388565164053842											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR005476:Transketolase, C-terminal	3	0.341685649	2.E-02	68263, 100048676, 12040, 21881	860	5	17763	1.E+01	1.E+00	4.E-01	3.E+01
INTERPRO	IPR015941:Transketolase C-terminal-like	3	0.341685649	2.E-02	68263, 100048676, 12040, 21881	860	5	17763	1.E+01	1.E+00	4.E-01	3.E+01
INTERPRO	IPR005475:Transketolase, central region	3	0.341685649	5.E-02	68263, 100048676, 12040, 21881	860	8	17763	8.E+00	1.E+00	7.E-01	6.E+01







GOTERM_BP_FAT	GO:0001782~B cell homeostasis	4	0.455580866	6.E-02 12028, 12018, 12043, 18707	809	15	13588	4.E+00	1.E+00	4.E-01	6.E+01
KEGG_PATHWAY	mmu05014:Amyotrophic lateral sclerosis (ALS)	11	1.25284738	6.E-02 672195, 12015, 12048, 12028, 12122, 264	580	57	5738	2.E+00	1.E+00	1.E-01	5.E+01
GOTERM_BP_FAT	GO:0007005~mitochondrion organization	11	1.25284738	6.E-02 382985, 18181, 12048, 13052, 12028, 121	809	97	13588	2.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0008584~male gonad development	6	0.683371298	8.E-02 12048, 12028, 12043, 14180, 21869, 1162	809	39	13588	3.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0014070~response to organic cyclic substance	6	0.683371298	1.E-01 12048, 12043, 12568, 16847, 20191, 1338	809	42	13588	2.E+00	1.E+00	5.E-01	9.E+01
GOTERM_BP_FAT	GO:0043270~positive regulation of ion transport	4	0.455580866	1.E-01 234779, 12028, 12018, 11651	809	20	13588	3.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0045136~development of secondary sexual characteristics	3	0.341685649	1.E-01 12028, 21869, 17979	809	11	13588	5.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0009791~post-embryonic development	9	1.025056948	1.E-01 12028, 109900, 12018, 19164, 12043, 238	809	87	13588	2.E+00	1.E+00	7.E-01	9.E+01
GOTERM_BP_FAT	GO:0010212~response to ionizing radiation	6	0.683371298	2.E-01 12190, 11920, 12028, 12018, 12043, 1081	809	48	13588	2.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0051928~positive regulation of calcium ion transport	3	0.341685649	2.E-01 234779, 12028, 12018	809	12	13588	4.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0043524~negative regulation of neuron apoptosis	6	0.683371298	2.E-01 12048, 12028, 15461, 12043, 108138, 118	809	50	13588	2.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0046660~female sex differentiation	7	0.797266515	2.E-01 12190, 12048, 12028, 12043, 16847, 2186	809	64	13588	2.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0007006~mitochondrial membrane organization	4	0.455580866	2.E-01 12028, 12122, 12018, 12043	809	26	13588	3.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0046546~development of primary male sexual characteristics	6	0.683371298	2.E-01 12048, 12028, 12043, 14180, 21869, 1162	809	53	13588	2.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0006839~mitochondrial transport	5	0.569476082	2.E-01 12028, 12122, 12018, 19164, 12043	809	42	13588	2.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0046661~male sex differentiation	6	0.683371298	3.E-01 12048, 12028, 12043, 14180, 21869, 1162	809	57	13588	2.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0008406~gonad development	8	0.911161731	3.E-01 12190, 12048, 12028, 12043, 14180, 1684	809	88	13588	2.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0022602~ovulation cycle process	5	0.569476082	3.E-01 12048, 12028, 12043, 16847, 21869	809	47	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0042698~ovulation cycle	5	0.569476082	3.E-01 12048, 12028, 12043, 16847, 21869	809	48	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0008585~female gonad development	5	0.569476082	4.E-01 12190, 12048, 12028, 12043, 16847	809	53	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0045137~development of primary sexual characteristics	8	0.911161731	4.E-01 12190, 12048, 12028, 12043, 14180, 1684	809	104	13588	1.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0046545~development of primary female sexual characteristic	5	0.569476082	4.E-01 12190, 12048, 12028, 12043, 16847	809	57	13588	1.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0007548~sex differentiation	9	1.025056948	5.E-01 12190, 12048, 12028, 12043, 14180, 1684	809	130	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0009636~response to toxin	3	0.341685649	5.E-01 12028, 12018, 12043	809	29	13588	2.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0048511~rhythmic process	7	0.797266515	5.E-01 12048, 12028, 232087, 12567, 12043, 168	809	98	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0001541~ovarian follicle development	3	0.341685649	6.E-01 12048, 12028, 12043	809	33	13588	2.E+00	1.E+00	1.E+00	1.E+02
BIOCARTA	m_deathPathwayInduction of apoptosis through DR3 and DR4/5	5	0.569476082	7.E-01 672195, 12122, 12043, 13063, 22030, 123	188	29	1171	1.E+00	1.E+00	9.E-01	1.E+02

Annotation Cluster 102	Enrichment Score: 1.434524155022859											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0047497~mitochondrion transport along microtubule	3	0.341685649	1.E-02	59040, 16561, 214952	809	3	13588	2.E+01	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0034643~mitochondrion localization, microtubule-mediated	3	0.341685649	1.E-02	59040, 16561, 214952	809	3	13588	2.E+01	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0051654~establishment of mitochondrion localization	3	0.341685649	1.E-02	59040, 16561, 214952	809	3	13588	2.E+01	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0051640~organelle localization	9	1.025056948	1.E-02	245049, 77579, 19164, 12540, 11891, 171	809	54	13588	3.E+00	1.E+00	2.E-01	2.E+01
GOTERM_BP_FAT	GO:0051656~establishment of organelle localization	7	0.797266515	1.E-02	77579, 19164, 12540, 11891, 59040, 1656	809	34	13588	3.E+00	1.E+00	2.E-01	2.E+01
GOTERM_BP_FAT	GO:0051646~mitochondrion localization	3	0.341685649	8.E-02	59040, 16561, 214952	809	8	13588	6.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0010970~microtubule-based transport	3	0.341685649	3.E-01	59040, 16561, 214952	809	18	13588	3.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0007018~microtubule-based movement	6	0.683371298	7.E-01	22142, 19348, 71819, 59040, 16561, 2149	809	101	13588	1.E+00	1.E+00	1.E+00	1.E+02

Annotation Cluster 103	Enrichment Score: 1.4225280012955557											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0032469~endoplasmic reticulum calcium ion homeostasis	4	0.455580866	4.E-03	12028, 12018, 19164, 12043	809	6	13588	1.E+01	1.E+00	6.E-02	6.E+00
GOTERM_BP_FAT	GO:0042326~negative regulation of phosphorylation	6	0.683371298	2.E-02	15170, 12703, 12028, 12018, 19164, 2023	809	27	13588	4.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0031400~negative regulation of protein modification process	7	0.797266515	2.E-02	15170, 12703, 12028, 12018, 19164, 1256	809	38	13588	3.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0045936~negative regulation of phosphate metabolic process	6	0.683371298	3.E-02	15170, 12703, 12028, 12018, 19164, 2023	809	29	13588	3.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0010563~negative regulation of phosphorus metabolic process	6	0.683371298	3.E-02	15170, 12703, 12028, 12018, 19164, 2023	809	29	13588	3.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0001933~negative regulation of protein amino acid phosphorylation	5	0.569476082	4.E-02	15170, 12703, 12028, 12018, 19164	809	23	13588	4.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0051248~negative regulation of protein metabolic process	9	1.025056948	9.E-02	15170, 13685, 12703, 12028, 12018, 1916	809	78	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0032269~negative regulation of cellular protein metabolic process	8	0.911161731	1.E-01	15170, 13685, 12703, 12028, 12018, 1916	809	72	13588	2.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0006839~mitochondrial transport	5	0.569476082	2.E-01	12028, 12122, 12018, 19164, 12043	809	42	13588	2.E+00	1.E+00	8.E-01	1.E+02

Annotation Cluster 104		Enrichment Score: 1.417411677076899										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0009314~response to radiation	16	1.822323462	2.E-02	12190, 14151, 232087, 17869, 12043, 108	809	143	13588	2.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0009628~response to abiotic stimulus	24	2.733485194	3.E-02	12190, 14151, 12842, 12955, 232087, 178	809	251	13588	2.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0009411~response to UV	6	0.683371298	5.E-02	13872, 12190, 14151, 12028, 12043, 1257	809	35	13588	3.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0009416~response to light stimulus	11	1.25284738	7.E-02	13872, 11785, 12190, 14151, 12028, 2320	809	98	13588	2.E+00	1.E+00	4.E-01	7.E+01

Annotation Cluster 105		Enrichment Score: 1.402884388322403											
Category	Term	Count	%	PValue	Genes		List Total	Pop Hits	Pop Total	Fold Enrichment Bonferroni		Benjamini	FDR
PIR_SUPERFAMILY	PIRSF002367:apolipoprotein A-I	6	0.683371298	3.E-05	11813	11814, 11806, 11807, 11816, 1180	576	7	8136	1.E+01	2.E-02	5.E-03	5.E-02
SP_PIR_KEYWORDS	chylomicron	6	0.683371298	6.E-05	11813	11814, 669888, 11816, 238055, 11	869	10	17854	1.E+01	2.E-02	5.E-04	8.E-02
GOTERM_CC_FAT	GO:0042627~chylomicron	5	0.569476082	4.E-04	11813	11814, 669888, 11816, 11808	636	8	12504	1.E+01	1.E-01	4.E-03	5.E-01
SP_PIR_KEYWORDS	hdl	5	0.569476082	1.E-03	11813	11814, 669888, 11816, 238055	869	11	17854	9.E+00	5.E-01	9.E-03	2.E+00
GOTERM_CC_FAT	GO:0032994~protein-lipid complex	7	0.797266515	2.E-03	11813	11814, 669888, 11806, 11807, 118	636	27	12504	5.E+00	5.E-01	2.E-02	3.E+00



GOTERM_CC_FAT	GO:0034358~plasma lipoprotein particle	7	0.797266515	2.E-03	11813, 11814, 669888, 11806, 11807, 118	636	27	12504	5.E+00	5.E-01	2.E-02	3.E+00
SP_PIR_KEYWORDS	lipid binding	4	0.455580866	5.E-03	11807, 11816, 238055, 11808	869	8	17854	1.E+01	9.E-01	3.E-02	7.E+00
SP_PIR_KEYWORDS	lipid transport	8	0.911161731	1.E-02	11813, 11814, 11806, 11807, 11816, 2380	869	51	17854	3.E+00	1.E+00	5.E-02	1.E+01
GOTERM_CC_FAT	GO:0034361~very-low-density lipoprotein particle	4	0.455580866	1.E-02	11813, 11814, 669888, 11816	636	10	12504	8.E+00	1.E+00	7.E-02	2.E+01
GOTERM_CC_FAT	GO:0034385~triglyceride-rich lipoprotein particle	4	0.455580866	1.E-02	11813, 11814, 669888, 11816	636	10	12504	8.E+00	1.E+00	7.E-02	2.E+01
INTERPRO	IPR013326:Apolipoprotein/apolipophorin	3	0.341685649	1.E-02	11806, 11816, 11808	860	4	17763	2.E+01	1.E+00	3.E-01	2.E+01
INTERPRO	IPR000074:Apolipoprotein A1/A4/E	3	0.341685649	1.E-02	11806, 11816, 11808	860	4	17763	2.E+01	1.E+00	3.E-01	2.E+01
GOTERM_BP_FAT	GO:0030300~regulation of intestinal cholesterol absorption	3	0.341685649	2.E-02	11806, 11807, 11808	809	4	13588	1.E+01	1.E+00	2.E-01	3.E+01
GOTERM_MF_FAT	GO:0008034~lipoprotein binding	5	0.569476082	3.E-02	11806, 11807, 11816, 21899, 12491	754	21	13288	4.E+00	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0032371~regulation of sterol transport	3	0.341685649	3.E-02	11806, 11807, 11808	809	5	13588	1.E+01	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0032374~regulation of cholesterol transport	3	0.341685649	3.E-02	11806, 11807, 11808	809	5	13588	1.E+01	1.E+00	3.E-01	4.E+01
GOTERM_CC_FAT	GO:0034364~high-density lipoprotein particle	4	0.455580866	4.E-02	11806, 11807, 11816, 11808	636	16	12504	5.E+00	1.E+00	2.E-01	5.E+01
GOTERM_BP_FAT	GO:0032368~regulation of lipid transport	3	0.341685649	5.E-02	11806, 11807, 11808	809	6	13588	8.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0044058~regulation of digestive system process	3	0.341685649	5.E-02	11806, 11807, 11808	809	6	13588	8.E+00	1.E+00	3.E-01	6.E+01
SP_PIR_KEYWORDS	hdl	4	0.455580866	5.E-02	11806, 11807, 11816, 11808	869	17	17854	5.E+00	1.E+00	2.E-01	5.E+01
GOTERM_BP_FAT	GO:0051346~negative regulation of hydrolase activity	4	0.455580866	1.E-01	24064, 11806, 11807, 16847	809	22	13588	3.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0006869~lipid transport	11	1.25284738	2.E-01	11813, 17777, 11814, 11806, 11807, 1181	809	119	13588	2.E+00	1.E+00	7.E-01	1.E+02
UP_SEQ_FEATURE	repeat:6	7	0.797266515	2.E-01	13669, 13800, 20345, 11806, 11816, 1180	861	71	16021	2.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0010876~lipid localization	11	1.25284738	2.E-01	11813, 17777, 11814, 11806, 11807, 1181	809	128	13588	1.E+00	1.E+00	8.E-01	1.E+02
UP_SEQ_FEATURE	repeat:5	7	0.797266515	3.E-01	13669, 13800, 20345, 11806, 11816, 1180	861	84	16021	2.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:8	5	0.569476082	4.E-01	13669, 20345, 11806, 11816, 11808	861	58	16021	2.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0008203~cholesterol metabolic process	6	0.683371298	4.E-01	14151, 11814, 11806, 11807, 11816, 1684	809	70	13588	1.E+00	1.E+00	9.E-01	1.E+02
UP_SEQ_FEATURE	repeat:2	10	1.138952164	4.E-01	19944, 22323, 18019, 13669, 13800, 2034	861	151	16021	1.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:10	4	0.455580866	5.E-01	13669, 20345, 11806, 11808	861	46	16021	2.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:4	7	0.797266515	5.E-01	13669, 13800, 20345, 11806, 11816, 1180	861	101	16021	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0016125~sterol metabolic process	6	0.683371298	5.E-01	14151, 11814, 11806, 11807, 11816, 1684	809	77	13588	1.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:7	5	0.569476082	5.E-01	13669, 13800, 20345, 11816, 11808	861	67	16021	1.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:1	9	1.025056948	5.E-01	19944, 22323, 18019, 13800, 20345, 1180	861	148	16021	1.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:9	3	0.341685649	7.E-01	13669, 20345, 11808	861	46	16021	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0008202~steroid metabolic process	9	1.025056948	7.E-01	14151, 11814, 11806, 11807, 11816, 2088	809	161	13588	9.E-01	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:3	5	0.569476082	9.E-01	13800, 20345, 11816, 11808, 19989	861	119	16021	8.E-01	1.E+00	1.E+00	1.E+02

Annotation Cluster 106	Enrichment Score: 1.3726853580547287											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_SEQ_FEATURE	binding site:NAD	8	0.911161731		1.E-02 15107, 100042746, 13382, 100041325, 10	861	46	16021	3.E+00	1.E+00	4.E-01	2.E+01
UP_SEQ_FEATURE	nucleotide phosphate-binding region:NAD	10	1.138952164		2.E-02 15107, 100042746, 19378, 56847, 13382,	861	73	16021	3.E+00	1.E+00	5.E-01	2.E+01
INTERPRO	IPR016040:NAD(P)-binding domain	9	1.025056948		4.E-01 15107, 100042746, 100041325, 99586, 10	860	151	17763	1.E+00	1.E+00	1.E+00	1.E+02

Annotation Cluster 107	Enrichment Score: 1.3504229391669522											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR000941:Enolase	3	0.341685649		1.E-02 433182, 13807, 13806, 13808, 100044223	860	4	17763	2.E+01	1.E+00	3.E-01	2.E+01
GOTERM_CC_FAT	GO:0000015~phosphopyruvate hydratase complex	3	0.341685649		1.E-02 433182, 13807, 13806, 13808, 100044223	636	4	12504	1.E+01	1.E+00	8.E-02	2.E+01
GOTERM_MF_FAT	GO:0004634~phosphopyruvate hydratase activity	3	0.341685649		2.E-02 433182, 13807, 13806, 13808, 100044223	754	4	13288	1.E+01	1.E+00	2.E-01	2.E+01
PIR_SUPERFAMILY	PIRSF001400:Enolase	3	0.341685649		3.E-02 433182, 13807, 13806, 13808, 100044223	576	4	8136	1.E+01	1.E+00	8.E-01	3.E+01
GOTERM_MF_FAT	GO:0016836~hydro-lyase activity	6	0.683371298		9.E-02 22276, 74147, 433182, 13807, 13806, 937	754	42	13288	3.E+00	1.E+00	5.E-01	8.E+01
KEGG_PATHWAY	mmu03018:RNA degradation	3	0.341685649		1.E+00 433182, 13807, 13806, 13808, 100044223	580	60	5738	5.E-01	1.E+00	1.E+00	1.E+02

Annotation Cluster 108	Enrichment Score: 1.3472163014390013											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
BIOCARTA	m_crebPathway:Transcription factor CREB and its extracellular sig	9	1.025056948		1.E-02 18751, 18708, 18747, 14784, 20662, 2641	188	21	1171	3.E+00	9.E-01	8.E-02	1.E+01
BIOCARTA	m_hcmvPathway:Human Cytomegalovirus and Map Kinase Pathwa	6	0.683371298		6.E-02 18708, 19645, 26416, 26395, 11651, 1291	188	14	1171	3.E+00	1.E+00	2.E-01	5.E+01
BIOCARTA	m_nfaiPathway:NFAT and Hypertrophy of the heart (Transcription	10	1.138952164		1.E-01 18708, 18747, 12315, 12314, 26416, 2639	188	38	1171	2.E+00	1.E+00	4.E-01	8.E+01

Annotation Cluster 109	Enrichment Score: 1.3424526643232897											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0050900~leukocyte migration	9	1.025056948		3.E-03 20310, 14127, 20345, 56744, 12490, 1641	809	43	13588	4.E+00	1.E+00	5.E-02	6.E+00
GOTERM_BP_FAT	GO:0030595~leukocyte chemotaxis	7	0.797266515		4.E-03 20310, 14127, 56744, 16414, 20202, 1680	809	27	13588	4.E+00	1.E+00	6.E-02	8.E+00
GOTERM_BP_FAT	GO:0060326~cell chemotaxis	7	0.797266515		4.E-03 20310, 14127, 56744, 16414, 20202, 1680	809	27	13588	4.E+00	1.E+00	6.E-02	8.E+00
GOTERM_BP_FAT	GO:0030593~neutrophil chemotaxis	4	0.455580866		8.E-02 20310, 14127, 16414, 16409	809	17	13588	4.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0060935~chemotaxis	10	1.138952164		2.E-01 20310, 14127, 12765, 19354, 56744, 1641	809	109	13588	2.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0042330~taxis	10	1.138952164		2.E-01 20310, 14127, 12765, 19354, 56744, 1641	809	109	13588	2.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0007626~locomotory behavior	18	2.050113895		3.E-01 12765, 109900, 15430, 16414, 16803, 218	809	239	13588	1.E+00	1.E+00	8.E-01	1.E+02
SP_PIR_KEYWORDS	chemotaxis	5	0.569476082		4.E-01 20310, 12765, 56744, 20202, 20201	869	62	17854	2.E+00	1.E+00	7.E-01	1.E+02

Annotation Cluster 110    Enrichment Score: 1.3395127020293038



Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_BP_FAT	GO:0007090~regulation of S phase of mitotic cell cycle	4	0.455580866	2.E-02	11785, 12190, 67177, 27214	809	809	11	13588	6.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0033261~regulation of S phase	4	0.455580866	3.E-02	11785, 12190, 67177, 27214	809	809	12	13588	6.E+00	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0051052~regulation of DNA metabolic process	7	0.797266515	1.E-01	11785, 12190, 57441, 22130, 67177, 1853	809	809	58	13588	2.E+00	1.E+00	6.E-01	9.E+01
Annotation Cluster 111													
Enrichment Score: 1.334921931526416													
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_BP_FAT	GO:0050730~regulation of peptidyl-tyrosine phosphorylation	10	1.138952164	4.E-03	56717, 18596, 15170, 13649, 12703, 1841	809	809	53	13588	3.E+00	1.E+00	6.E-02	6.E+00
GOTERM_BP_FAT	GO:0051247~positive regulation of protein metabolic process	14	1.59453303	1.E-02	17999, 12043, 11651, 16396, 216080, 151	809	809	109	13588	2.E+00	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0032270~positive regulation of cellular protein metabolic pro	12	1.366742597	4.E-02	56717, 18413, 12567, 19164, 11651, 1204	809	809	100	13588	2.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0031401~positive regulation of protein modification process	10	1.138952164	4.E-02	56717, 18413, 19164, 12043, 216080, 209	809	809	78	13588	2.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0001934~positive regulation of protein amino acid phosphory	8	0.911161731	5.E-02	56717, 18413, 19164, 12043, 20963, 1645	809	809	56	13588	2.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0050731~positive regulation of peptidyl-tyrosine phosphoryla	6	0.683371298	5.E-02	56717, 18413, 20963, 16452, 15163, 1709	809	809	35	13588	3.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0042509~regulation of tyrosine phosphorylation of STAT prot	4	0.455580866	6.E-02	12703, 16452, 15163, 17096	809	809	15	13588	4.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0042327~positive regulation of phosphorylation	8	0.911161731	6.E-02	56717, 18413, 19164, 12043, 20963, 1645	809	809	60	13588	2.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0045937~positive regulation of phosphate metabolic process	8	0.911161731	7.E-02	56717, 18413, 19164, 12043, 20963, 1645	809	809	62	13588	2.E+00	1.E+00	5.E-01	7.E+01
GOTERM_BP_FAT	GO:0010562~positive regulation of phosphorus metabolic proces	8	0.911161731	7.E-02	56717, 18413, 19164, 12043, 20963, 1645	809	809	62	13588	2.E+00	1.E+00	5.E-01	7.E+01
GOTERM_BP_FAT	GO:0042531~positive regulation of tyrosine phosphorylation of S	3	0.341685649	1.E-01	16452, 15163, 17096	809	809	9	13588	6.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0046425~regulation of JAK-STAT cascade	4	0.455580866	1.E-01	12703, 16452, 15163, 17096	809	809	19	13588	4.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0046427~positive regulation of JAK-STAT cascade	3	0.341685649	1.E-01	16452, 15163, 17096	809	809	11	13588	5.E+00	1.E+00	6.E-01	9.E+01
Annotation Cluster 112													
Enrichment Score: 1.3328673648379736													
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_MF_FAT	GO:0016681~oxidoreductase activity, acting on diphenols and rel	4	0.455580866	3.E-03	66694, 67530, 66594, 66576	754	754	6	13288	1.E+01	9.E-01	4.E-02	5.E+00
GOTERM_MF_FAT	GO:0016679~oxidoreductase activity, acting on diphenols and rel	4	0.455580866	3.E-03	66694, 67530, 66594, 66576	754	754	6	13288	1.E+01	9.E-01	4.E-02	5.E+00
GOTERM_MF_FAT	GO:0008121~ubiquinol-cytochrome-c reductase activity	4	0.455580866	3.E-03	66694, 67530, 66594, 66576	754	754	6	13288	1.E+01	9.E-01	4.E-02	5.E+00
GOTERM_BP_FAT	GO:0006122~mitochondrial electron transport, ubiquinol to cytoc	4	0.455580866	4.E-03	67530, 66594, 66576, 22273	809	809	6	13588	1.E+01	1.E+00	6.E-02	6.E+00
KEGG_PATHWAY	mmu04260:Cardiac muscle contraction	10	1.138952164	4.E-01	66694, 67530, 11464, 67003, 66445, 2019	580	580	78	5738	1.E+00	1.E+00	6.E-01	1.E+02
GOTERM_MF_FAT	GO:0015078~hydrogen ion transmembrane transporter activity	5	0.569476082	7.E-01	66694, 67530, 67942, 66594, 66576	754	754	82	13288	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_MF_FAT	GO:0015077~monovalent inorganic cation transmembrane transp	5	0.569476082	7.E-01	66694, 67530, 67942, 66594, 66576	754	754	87	13288	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_MF_FAT	GO:0022890~inorganic cation transmembrane transporter activity	5	0.569476082	9.E-01	66694, 67530, 67942, 66594, 66576	754	754	127	13288	7.E-01	1.E+00	1.E+00	1.E+02
Annotation Cluster 113													
Enrichment Score: 1.3325629104489696													
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_BP_FAT	GO:0046626~regulation of insulin receptor signaling pathway	4	0.455580866	2.E-02	12703, 20779, 12702, 11625	809	809	10	13588	7.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0046627~negative regulation of insulin receptor signaling pat	3	0.341685649	6.E-02	12703, 12702, 11625	809	809	7	13588	7.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0048585~negative regulation of response to stimulus	8	0.911161731	9.E-02	56717, 15170, 12703, 16197, 12702, 1148	809	809	65	13588	2.E+00	1.E+00	5.E-01	8.E+01
Annotation Cluster 114													
Enrichment Score: 1.327149803400171													
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
UP_SEQ_FEATURE	short sequence motif:Box 1 motif	8	0.911161731	3.E-04	16195, 12983, 16197, 13857, 18414, 1616	861	861	25	16021	6.E+00	4.E-01	2.E-02	4.E-01
GOTERM_MF_FAT	GO:0004896~cytokine receptor activity	11	1.25284738	9.E-04	12765, 16195, 12983, 16197, 50498, 1385	754	754	55	13288	4.E+00	5.E-01	1.E-02	1.E+00
UP_SEQ_FEATURE	short sequence motif:WSXWS motif	8	0.911161731	1.E-03	16195, 12983, 16197, 13857, 18414, 1616	861	861	31	16021	5.E+00	9.E-01	7.E-02	2.E+00
GOTERM_MF_FAT	GO:0019955~cytokine binding	14	1.59453303	1.E-03	12765, 18414, 21937, 16195, 18824, 1298	754	754	88	13288	3.E+00	6.E-01	2.E-02	2.E+00
INTERPRO	IPR003531:Short hematopoietin receptor, family 1, conserved site	4	0.455580866	1.E-02	12983, 16197, 16190, 16847	860	860	10	17763	8.E+00	1.E+00	3.E-01	2.E+01
INTERPRO	IPR003529:Long hematopoietin receptor, gp130 family 2, conserv	3	0.341685649	4.E-02	16195, 18414, 16847	860	860	7	17763	9.E+00	1.E+00	6.E-01	5.E+01
INTERPRO	IPR008957:Fibronectin, type III-like fold	15	1.708428246	7.E-02	18414, 545156, 23920, 16195, 13836, 129	860	860	187	17763	2.E+00	1.E+00	7.E-01	7.E+01
SP_PIR_KEYWORDS	cytokine receptor	4	0.455580866	8.E-02	12983, 16197, 16190, 21937	869	869	21	17854	4.E+00	1.E+00	3.E-01	7.E+01
INTERPRO	IPR003961:Fibronectin, type III	14	1.59453303	1.E-01	18414, 545156, 23920, 16195, 13836, 129	860	860	191	17763	2.E+00	1.E+00	9.E-01	9.E+01
SMART	SM00060:FN3	14	1.59453303	2.E-01	18414, 545156, 23920, 16195, 13836, 129	492	492	191	9131	1.E+00	1.E+00	8.E-01	1.E+02
UP_SEQ_FEATURE	domain:Fibronectin type-III 2	9	1.025056948	3.E-01	13836, 16195, 23920, 12983, 50498, 1841	861	861	120	16021	1.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	domain:Fibronectin type-III 1	9	1.025056948	3.E-01	13836, 16195, 23920, 12983, 50498, 1841	861	861	121	16021	1.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	domain:Fibronectin type-III	4	0.455580866	5.E-01	16197, 13857, 16190, 545156	861	861	51	16021	1.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	domain:Fibronectin type-III 3	5	0.569476082	6.E-01	16195, 23920, 18414, 16001, 16847	861	861	74	16021	1.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	domain:Fibronectin type-III 4	3	0.341685649	8.E-01	16195, 18414, 16847	861	861	56	16021	1.E+00	1.E+00	1.E+00	1.E+02
KEGG_PATHWAY	mmu04060:Cytokine-cytokine receptor interaction	18	2.050113895	1.E+00	12765, 13649, 18414, 21934, 21937, 1699	580	580	244	5738	7.E-01	1.E+00	1.E+00	1.E+02
Annotation Cluster 115													
Enrichment Score: 1.3214439064295591													
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_MF_FAT	GO:0008353~RNA polymerase II carboxy-terminal domain kinase	7	0.797266515	2.E-05	13872, 107951, 17420, 14884, 14885, 125	754	754	12	13288	1.E+01	2.E-02	5.E-04	3.E-02
GOTERM_CC_FAT	GO:0005675~holo TFIIH complex	5	0.569476082	1.E-03	13872, 17420, 14884, 14885, 66671	636	636	10	12504	1.E+01	3.E-01	1.E-02	1.E+00
KEGG_PATHWAY	mmu03420:Nucleotide excision repair	10	1.138952164	3.E-02	13872, 19891, 19358, 68240, 17420, 1488	580	580	43	5738	2.E+00	1.E+00	7.E-02	3.E+01
GOTERM_BP_FAT	GO:0006366~transcription from RNA polymerase II promoter	8	0.911161731	1.E-01	13872, 69920, 16911, 17420, 17869, 1488	809	809	74	13588	2.E+00	1.E+00	7.E-01	9.E+01
GOTERM_CC_FAT	GO:0016591~DNA-directed RNA polymerase II, holoenzyme	6	0.683371298	2.E-01	13872, 69920, 17420, 14884, 14885, 6667	636	636	56	12504	2.E+00	1.E+00	5.E-01	9.E+01
GOTERM_MF_FAT	GO:0008094~DNA-dependent ATPase activity	5	0.569476082	2.E-01	13872, 17420, 14884, 14885, 66671	754	754	38	13288	2.E+00	1.E+00	7.E-01	9.E+01



GOTERM_BP_FAT	GO:0006351~transcription, DNA-dependent	11	1.25284738	2.E-01	13872, 69920, 69890, 22130, 16911, 1742	809	122	13588	2.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0032774~RNA biosynthetic process	11	1.25284738	2.E-01	13872, 69920, 69890, 22130, 16911, 1742	809	126	13588	1.E+00	1.E+00	8.E-01	1.E+02
GOTERM_MF_FAT	GO:0042623~ATPase activity, coupled	12	1.366742597	7.E-01	13872, 110957, 17925, 77579, 17420, 148	754	223	13288	9.E-01	1.E+00	1.E+00	1.E+02
GOTERM_MF_FAT	GO:0016887~ATPase activity	13	1.480637813	9.E-01	18195, 16561, 110957, 13872, 77579, 179	754	281	13288	8.E-01	1.E+00	1.E+00	1.E+02

Annotation Cluster 116	Enrichment Score: 1.3172524279927527											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	glucose metabolism	6	0.683371298		1.E-03 16333, 16334, 11651, 72157, 14381, 1438	869	17	17854	7.E+00	4.E-01	7.E-03	1.E+00
GOTERM_BP_FAT	GO:0015758~glucose transport	5	0.569476082		8.E-02 16333, 20525, 16334, 22612, 11651	809	28	13588	3.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0008645~hexose transport	5	0.569476082		1.E-01 16333, 20525, 16334, 22612, 11651	809	30	13588	3.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0015749~monosaccharide transport	5	0.569476082		1.E-01 16333, 20525, 16334, 22612, 11651	809	31	13588	3.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0008643~carbohydrate transport	6	0.683371298		3.E-01 16333, 20525, 11807, 16334, 22612, 1165	809	60	13588	2.E+00	1.E+00	8.E-01	1.E+02

Annotation Cluster 117	Enrichment Score: 1.309080406319458											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
BIOCARTA	m_Par1Pathway:Thrombin signaling and protease-activated recep	9	1.025056948		2.E-03 18751, 18708, 14674, 14065, 14682, 1680	188	17	1171	3.E+00	4.E-01	3.E-02	3.E+00
BIOCARTA	m_pkcPathway:Activation of PKC through G protein coupled recep	3	0.341685649		2.E-01 18751, 14682, 18795	188	5	1171	4.E+00	1.E+00	5.E-01	9.E+01
BIOCARTA	m_CCR3Pathway:CCR3 signaling in Eosinophils	6	0.683371298		3.E-01 18751, 26395, 15461, 14682, 11848, 1879	188	22	1171	2.E+00	1.E+00	6.E-01	1.E+02

Annotation Cluster 118	Enrichment Score: 1.3036608835425374											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0001816~cytokine production	9	1.025056948		3.E-03 18019, 17874, 21898, 16822, 13383, 1680	809	43	13588	4.E+00	1.E+00	5.E-02	6.E+00
GOTERM_BP_FAT	GO:0042089~cytokine biosynthetic process	3	0.341685649		2.E-01 17874, 54123, 23882	809	13	13588	4.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0042107~cytokine metabolic process	3	0.341685649		2.E-01 17874, 54123, 23882	809	14	13588	4.E+00	1.E+00	7.E-01	1.E+02

Annotation Cluster 119	Enrichment Score: 1.2994058637242456											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0042592~homeostatic process	62	7.061503417		1.E-05 19206, 238055, 14782, 20191, 12815, 159	809	584	13588	2.E+00	3.E-02	5.E-04	2.E-02
GOTERM_BP_FAT	GO:0010522~regulation of calcium ion transport into cytosol	5	0.569476082		7.E-04 14226, 12028, 12018, 12043, 20191	809	8	13588	1.E+01	9.E-01	2.E-02	1.E+00
GOTERM_BP_FAT	GO:0010959~regulation of metal ion transport	10	1.138952164		2.E-03 17999, 234779, 14226, 14678, 12028, 120	809	48	13588	3.E+00	1.E+00	3.E-02	3.E+00
GOTERM_BP_FAT	GO:0032844~regulation of homeostatic process	11	1.25284738		3.E-03 14127, 16818, 21349, 11486, 14226, 1202	809	60	13588	3.E+00	1.E+00	4.E-02	5.E+00
GOTERM_BP_FAT	GO:0043269~regulation of ion transport	11	1.25284738		3.E-03 16994, 17999, 234779, 14226, 14678, 120	809	62	13588	3.E+00	1.E+00	5.E-02	6.E+00
GOTERM_BP_FAT	GO:0032469~endoplasmic reticulum calcium ion homeostasis	4	0.455580866		4.E-03 12028, 12018, 19164, 12043	809	6	13588	1.E+01	1.E+00	6.E-02	6.E+00
GOTERM_BP_FAT	GO:0019725~cellular homeostasis	34	3.872437358		4.E-03 11816, 14782, 20191, 103988, 214952, 16	809	343	13588	2.E+00	1.E+00	6.E-02	8.E+00
GOTERM_BP_FAT	GO:0051924~regulation of calcium ion transport	7	0.797266515		1.E-02 234779, 14226, 14678, 12028, 12018, 120	809	34	13588	3.E+00	1.E+00	2.E-01	2.E+01
GOTERM_BP_FAT	GO:0051279~regulation of release of sequestered calcium ion int	3	0.341685649		3.E-02 14226, 12028, 20191	809	5	13588	1.E+01	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0048878~chemical homeostasis	31	3.530751708		4.E-02 14151, 19206, 11816, 238055, 20191, 103	809	365	13588	1.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0030183~B cell differentiation	7	0.797266515		5.E-02 12051, 18708, 11486, 234779, 12028, 120	809	46	13588	3.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0006874~cellular calcium ion homeostasis	10	1.138952164		9.E-02 18751, 16818, 13857, 11816, 14226, 1202	809	91	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0055074~calcium ion homeostasis	10	1.138952164		1.E-01 18751, 16818, 13857, 11816, 14226, 1202	809	95	13588	2.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0043270~positive regulation of ion transport	4	0.455580866		1.E-01 234779, 12028, 12018, 11651	809	20	13588	3.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0006875~cellular metal ion homeostasis	10	1.138952164		1.E-01 18751, 16818, 13857, 11816, 14226, 1202	809	100	13588	2.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0051928~positive regulation of calcium ion transport	3	0.341685649		2.E-01 234779, 12028, 12018	809	12	13588	4.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0042391~regulation of membrane potential	11	1.25284738		2.E-01 19317, 12018, 19164, 12043, 14360, 2271	809	119	13588	2.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0055082~cellular chemical homeostasis	21	2.391799544		2.E-01 19317, 11816, 14226, 12043, 20191, 1338	809	268	13588	1.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0055065~metal ion homeostasis	10	1.138952164		2.E-01 18751, 16818, 13857, 11816, 14226, 1202	809	106	13588	2.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0006839~mitochondrial transport	5	0.569476082		2.E-01 12028, 12122, 12018, 19164, 12043	809	42	13588	2.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0006873~cellular ion homeostasis	19	2.164009112		3.E-01 19317, 11816, 14226, 12043, 20191, 1338	809	261	13588	1.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0055066~di-, tri-valent inorganic cation homeostasis	11	1.25284738		4.E-01 18751, 16818, 14151, 13857, 11816, 1422	809	146	13588	1.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0050801~ion homeostasis	20	2.277904328		4.E-01 19317, 14151, 11816, 14226, 12043, 2019	809	293	13588	1.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0030005~cellular di-, tri-valent inorganic cation homeostasis	10	1.138952164		4.E-01 18751, 16818, 13857, 11816, 14226, 1202	809	134	13588	1.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0030003~cellular cation homeostasis	10	1.138952164		6.E-01 18751, 16818, 13857, 11816, 14226, 1202	809	152	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0055080~cation homeostasis	11	1.25284738		7.E-01 18751, 16818, 14151, 13857, 11816, 1422	809	184	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0006816~calcium ion transport	4	0.455580866		1.E+00 18751, 16818, 14226, 20191	809	121	13588	6.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0015674~di-, tri-valent inorganic cation transport	4	0.455580866		1.E+00 18751, 16818, 14226, 20191	809	161	13588	4.E-01	1.E+00	1.E+00	1.E+02

Annotation Cluster 120	Enrichment Score: 1.2986723555782913											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0019205~nucleobase, nucleoside, nucleotide kinase activity	7	0.797266515		1.E-02 80914, 68556, 22245, 14923, 11636, 6658	754	36	13288	3.E+00	1.E+00	1.E-01	2.E+01
GOTERM_MF_FAT	GO:0019201~nucleotide kinase activity	4	0.455580866		4.E-02 14923, 11636, 66588, 11637	754	14	13288	5.E+00	1.E+00	3.E-01	5.E+01
INTERPRO	IPR000850:Adenylyate kinase	3	0.341685649		5.E-02 11636, 66588, 11637	860	8	17763	8.E+00	1.E+00	7.E-01	6.E+01
GOTERM_MF_FAT	GO:0016776~phosphotransferase activity, phosphate group as ac	4	0.455580866		2.E-01 14923, 11636, 66588, 11637	754	27	13288	3.E+00	1.E+00	8.E-01	1.E+02

Annotation Cluster 121	Enrichment Score: 1.2978315098627702											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR



GOTERM_BP_FAT	GO:0051640--organelle localization	9	1.025056948	1.E-02	245049, 77579, 19164, 12540, 11891, 171	809	54	13588	3.E+00	1.E+00	2.E-01	2.E+01
GOTERM_BP_FAT	GO:0051648--vesicle localization	4	0.455580866	6.E-02	245049, 19164, 11891, 171531	809	15	13588	4.E+00	1.E+00	4.E-01	6.E+01
GOTERM_MF_FAT	GO:0017022--myosin binding	3	0.341685649	2.E-01	245049, 11891, 171531	754	13	13288	4.E+00	1.E+00	7.E-01	9.E+01
Annotation Cluster 122	Enrichment Score: 1.2906923063969205											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0004748--ribonucleoside-diphosphate reductase activity	3	0.341685649	9.E-03	382985, 20133, 20135	754	3	13288	2.E+01	1.E+00	1.E-01	1.E+01
GOTERM_MF_FAT	GO:0016728--oxidoreductase activity, acting on CH or CH2 group:	3	0.341685649	9.E-03	382985, 20133, 20135	754	3	13288	2.E+01	1.E+00	1.E-01	1.E+01
GOTERM_MF_FAT	GO:0016725--oxidoreductase activity, acting on CH or CH2 group:	3	0.341685649	3.E-02	382985, 20133, 20135	754	5	13288	1.E+01	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0009263--deoxyribonucleotide biosynthetic process	3	0.341685649	8.E-02	382985, 20133, 20135	809	8	13588	6.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0009262--deoxyribonucleotide metabolic process	4	0.455580866	2.E-01	382985, 11486, 20133, 20135	809	23	13588	3.E+00	1.E+00	7.E-01	1.E+02
KEGG_PATHWAY	mmu00480:Glutathione metabolism	6	0.683371298	6.E-01	382985, 20133, 14782, 20135, 14381, 143	580	52	5738	1.E+00	1.E+00	8.E-01	1.E+02
Annotation Cluster 123	Enrichment Score: 1.290062910192549											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0050798--activated T cell proliferation	5	0.569476082	4.E-04	16408, 16411, 16414, 14360, 16409	809	7	13588	1.E+01	7.E-01	1.E-02	7.E-01
GOTERM_BP_FAT	GO:0046651--lymphocyte proliferation	10	1.138952164	7.E-04	16408, 12445, 16197, 16411, 14226, 1202	809	42	13588	4.E+00	9.E-01	1.E-02	1.E+00
GOTERM_BP_FAT	GO:0070661--leukocyte proliferation	10	1.138952164	8.E-04	16408, 12445, 16197, 16411, 14226, 1202	809	43	13588	4.E+00	9.E-01	2.E-02	1.E+00
GOTERM_BP_FAT	GO:0032943--mononuclear cell proliferation	10	1.138952164	8.E-04	16408, 12445, 16197, 16411, 14226, 1202	809	43	13588	4.E+00	9.E-01	2.E-02	1.E+00
GOTERM_BP_FAT	GO:0042098--T cell proliferation	8	0.911161731	1.E-03	16408, 12445, 16411, 14226, 12028, 1641	809	28	13588	5.E+00	1.E+00	2.E-02	2.E+00
BIOCARTA	m_monocytePathway:Monocyte and its Surface Molecules	7	0.797266515	4.E-03	16408, 20343, 16414, 12505, 16412, 2033	188	11	1171	4.E+00	5.E-01	4.E-02	4.E+00
BIOCARTA	m_neutrophilPathway:Neutrophil and Its Surface Molecules	6	0.683371298	4.E-03	16408, 20343, 16414, 12505, 20339, 1640	188	8	1171	5.E+00	6.E-01	4.E-02	5.E+00
BIOCARTA	m_lymphocytePathway:Adhesion Molecules on Lymphocyte	6	0.683371298	7.E-03	16408, 20343, 16414, 12505, 16412, 2033	188	9	1171	4.E+00	8.E-01	6.E-02	9.E+00
GOTERM_CC_FAT	GO:0043235--receptor complex	11	1.25284738	9.E-03	16408, 15170, 12475, 16411, 21898, 1641	636	83	12504	3.E+00	1.E+00	6.E-02	1.E+01
GOTERM_BP_FAT	GO:0007159--leukocyte adhesion	4	0.455580866	5.E-02	16408, 20345, 16414, 16409	809	14	13588	5.E+00	1.E+00	3.E-01	6.E+01
GOTERM_CC_FAT	GO:0008305--integrin complex	5	0.569476082	5.E-02	16408, 16411, 16414, 16412, 16409	636	28	12504	4.E+00	1.E+00	2.E-01	5.E+01
GOTERM_BP_FAT	GO:0007229--integrin-mediated signaling pathway	9	1.025056948	8.E-02	16408, 22324, 16411, 232906, 57257, 164	809	76	13588	2.E+00	1.E+00	5.E-01	8.E+01
PIR_SUPERFAMILY	PIRSF002497: integrin alpha with I domain	3	0.341685649	1.E-01	16408, 16411, 16409	576	8	8136	5.E+00	1.E+00	1.E+00	8.E+01
INTERPRO	IPR013513: Integrin alpha chain, C-terminal, cytoplasmic region	3	0.341685649	1.E-01	16408, 16411, 16409	860	14	17763	4.E+00	1.E+00	9.E-01	9.E+01
UP_SEQ_FEATURE	short sequence motif:GFFKR motif	3	0.341685649	2.E-01	16408, 16411, 16409	861	13	16021	4.E+00	1.E+00	1.E+00	9.E+01
UP_SEQ_FEATURE	domain:VWFA	6	0.683371298	2.E-01	16408, 16411, 16414, 16412, 12263, 1640	861	54	16021	2.E+00	1.E+00	1.E+00	1.E+02
INTERPRO	IPR013649: Integrin alpha-2	3	0.341685649	2.E-01	16408, 16411, 16409	860	18	17763	3.E+00	1.E+00	1.E+00	1.E+02
INTERPRO	IPR018184: Integrin alpha chain, C-terminal cytoplasmic region, co	3	0.341685649	2.E-01	16408, 16411, 16409	860	18	17763	3.E+00	1.E+00	1.E+00	1.E+02
INTERPRO	IPR000413: Integrin alpha chain	3	0.341685649	2.E-01	16408, 16411, 16409	860	18	17763	3.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:FG-GAP 2	3	0.341685649	2.E-01	16408, 16411, 16409	861	17	16021	3.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:FG-GAP 1	3	0.341685649	2.E-01	16408, 16411, 16409	861	17	16021	3.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:FG-GAP 6	3	0.341685649	2.E-01	16408, 16411, 16409	861	17	16021	3.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:FG-GAP 5	3	0.341685649	2.E-01	16408, 16411, 16409	861	17	16021	3.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:FG-GAP 4	3	0.341685649	2.E-01	16408, 16411, 16409	861	17	16021	3.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:FG-GAP 3	3	0.341685649	2.E-01	16408, 16411, 16409	861	17	16021	3.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:FG-GAP 7	3	0.341685649	2.E-01	16408, 16411, 16409	861	17	16021	3.E+00	1.E+00	1.E+00	1.E+02
INTERPRO	IPR013519: Integrin alpha beta-propellor	3	0.341685649	2.E-01	16408, 16411, 16409	860	19	17763	3.E+00	1.E+00	1.E+00	1.E+02
SMART	SM00191: Int_alpha	3	0.341685649	3.E-01	16408, 16411, 16409	492	19	9131	3.E+00	1.E+00	9.E-01	1.E+02
INTERPRO	IPR013517: FG-GAP	3	0.341685649	3.E-01	16408, 16411, 16409	860	23	17763	3.E+00	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	integrin	5	0.569476082	3.E-01	16408, 16411, 16414, 16412, 16409	869	61	17854	2.E+00	1.E+00	7.E-01	1.E+02
INTERPRO	IPR002035: von Willebrand factor, type A	6	0.683371298	4.E-01	16408, 16411, 16414, 16412, 12263, 1640	860	88	17763	1.E+00	1.E+00	1.E+00	1.E+02
SMART	SM00327: VWFA	6	0.683371298	5.E-01	16408, 16411, 16414, 16412, 12263, 1640	492	88	9131	1.E+00	1.E+00	1.E+00	1.E+02
Annotation Cluster 124	Enrichment Score: 1.2737764501591693											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR000270: Octicosapeptide/Phox/Bem1p	4	0.455580866	3.E-02	17970, 21787, 17972, 17966	860	14	17763	6.E+00	1.E+00	5.E-01	4.E+01
SMART	SM00666: PB1	4	0.455580866	4.E-02	17970, 21787, 17972, 17966	492	14	9131	5.E+00	1.E+00	3.E-01	4.E+01
UP_SEQ_FEATURE	domain:OPR	3	0.341685649	2.E-01	17970, 17972, 17966	861	13	16021	4.E+00	1.E+00	1.E+00	9.E+01
Annotation Cluster 125	Enrichment Score: 1.2723235729562123											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0000151--ubiquitin ligase complex	9	1.025056948	1.E-02	17999, 26965, 52563, 99152, 16396, 2140	636	60	12504	3.E+00	1.E+00	7.E-02	1.E+01
GOTERM_CC_FAT	GO:0005680--anaphase-promoting complex	3	0.341685649	1.E-01	52563, 66440, 668450, 68999	636	11	12504	5.E+00	1.E+00	4.E-01	8.E+01
GOTERM_CC_FAT	GO:0000152--nuclear ubiquitin ligase complex	3	0.341685649	1.E-01	52563, 66440, 668450, 68999	636	13	12504	5.E+00	1.E+00	4.E-01	9.E+01
Annotation Cluster 126	Enrichment Score: 1.2533530444218055											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0015629--actin cytoskeleton	22	2.505694761	2.E-03	215280, 73750, 19894, 13800, 232906, 94	636	205	12504	2.E+00	5.E-01	2.E-02	2.E+00
SP_PIR_KEYWORDS	actin-binding	17	1.936218679	9.E-02	22323, 227753, 215280, 13800, 76448, 14	869	226	17854	2.E+00	1.E+00	3.E-01	7.E+01
GOTERM_MF_FAT	GO:0003779--actin binding	21	2.391799544	2.E-01	22323, 215280, 227753, 13800, 19894, 94	754	288	13288	1.E+00	1.E+00	8.E-01	1.E+02



GOTERM_MF_FAT	GO:0008092~cytoskeletal protein binding	27	3.075170843	3.E-01	22323, 227753, 215280, 94190, 16800, 14	754	414	13288	1.E+00	1.E+00	9.E-01	1.E+02
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Annotation Cluster 127	Enrichment Score: 1.2314888521955016											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0048599~oocyte development	5	0.569476082	2.E-02	12190, 12043, 12531, 20112, 67141	809	17	13588	5.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0001556~oocyte maturation	4	0.455580866	2.E-02	12190, 12531, 20112, 67141	809	10	13588	7.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0009994~oocyte differentiation	5	0.569476082	2.E-02	12190, 12043, 12531, 20112, 67141	809	18	13588	5.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0021700~developmental maturation	12	1.366742597	4.E-02	12190, 108672, 12229, 19713, 19164, 116	809	101	13588	2.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0007292~female gamete generation	8	0.911161731	5.E-02	12190, 20779, 11920, 12043, 12531, 1684	809	56	13588	2.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0048477~oogenesis	6	0.683371298	8.E-02	12190, 20779, 12043, 12531, 20112, 6714	809	39	13588	3.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0007281~germ cell development	10	1.138952164	1.E-01	12190, 56717, 12048, 12028, 11651, 1204	809	101	13588	2.E+00	1.E+00	7.E-01	9.E+01
GOTERM_BP_FAT	GO:0048469~cell maturation	8	0.911161731	2.E-01	12190, 12229, 19713, 12531, 20112, 1338	809	75	13588	2.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0048610~reproductive cellular process	12	1.366742597	5.E-01	12190, 56717, 12048, 12028, 11651, 1204	809	173	13588	1.E+00	1.E+00	1.E+00	1.E+02

Annotation Cluster 128	Enrichment Score: 1.2283277311433651											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	camp	6	0.683371298	1.E-02	18747, 19085, 19088, 18576, 18575, 1857	869	28	17854	4.E+00	1.E+00	5.E-02	1.E+01
SP_PIR_KEYWORDS	cAMP binding	3	0.341685649	2.E-02	18747, 19085, 19088	869	5	17854	1.E+01	1.E+00	1.E-01	3.E+01
SP_PIR_KEYWORDS	heterotetramer	3	0.341685649	9.E-01	18747, 19085, 19088	869	87	17854	7.E-01	1.E+00	1.E+00	1.E+02

Annotation Cluster 129	Enrichment Score: 1.1982204900535645											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0044427~chromosomal part	30	3.416856492	2.E-03	60406, 245000, 12649, 433759, 22209, 50	636	318	12504	2.E+00	5.E-01	2.E-02	2.E+00
GOTERM_CC_FAT	GO:0005694~chromosome	31	3.530751708	1.E-02	60406, 245000, 12649, 433759, 22209, 50	636	378	12504	2.E+00	1.E+00	7.E-02	1.E+01
GOTERM_CC_FAT	GO:0044454~nuclear chromosome part	12	1.366742597	2.E-02	60406, 18393, 19891, 17216, 13006, 2450	636	103	12504	2.E+00	1.E+00	9.E-02	2.E+01
GOTERM_CC_FAT	GO:0000228~nuclear chromosome	13	1.480637813	2.E-02	19891, 60406, 245000, 50793, 22209, 180	636	121	12504	2.E+00	1.E+00	1.E-01	2.E+01
GOTERM_CC_FAT	GO:0000803~sex chromosome	4	0.455580866	1.E-01	245000, 22209, 12566, 20467	636	22	12504	4.E+00	1.E+00	3.E-01	8.E+01
GOTERM_CC_FAT	GO:0001741~XY body	3	0.341685649	1.E-01	245000, 22209, 20467	636	11	12504	5.E+00	1.E+00	4.E-01	8.E+01
GOTERM_CC_FAT	GO:0000792~heterochromatin	6	0.683371298	1.E-01	18393, 245000, 433759, 22209, 13436, 20	636	51	12504	2.E+00	1.E+00	4.E-01	8.E+01
GOTERM_CC_FAT	GO:0005720~nuclear heterochromatin	4	0.455580866	3.E-01	245000, 22209, 13436, 20467	636	35	12504	2.E+00	1.E+00	6.E-01	1.E+02
GOTERM_CC_FAT	GO:0001739~sex chromatin	3	0.341685649	3.E-01	245000, 22209, 20467	636	21	12504	3.E+00	1.E+00	7.E-01	1.E+02
GOTERM_CC_FAT	GO:0000790~nuclear chromatin	5	0.569476082	3.E-01	60406, 245000, 22209, 13436, 20467	636	55	12504	2.E+00	1.E+00	7.E-01	1.E+02
GOTERM_CC_FAT	GO:0000785~chromatin	10	1.138952164	5.E-01	60406, 319168, 18393, 621893, 319169, 2	636	165	12504	1.E+00	1.E+00	8.E-01	1.E+02

Annotation Cluster 130	Enrichment Score: 1.1487206598501347											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
KEGG_PATHWAY	mmu04120~Ubiquitin mediated proteolysis	29	3.302961276	2.E-04	56550, 218793, 26965, 246710, 22209, 59	580	136	5738	2.E+00	3.E-02	7.E-04	2.E-01
GOTERM_MF_FAT	GO:0004842~ubiquitin-protein ligase activity	13	1.480637813	1.E-02	56550, 74287, 218793, 17999, 26965, 222	754	104	13288	2.E+00	1.E+00	1.E-01	2.E+01
INTERPRO	IPR000608~Ubiquitin-conjugating enzyme, E2	7	0.797266515	1.E-02	100041766, 56550, 218793, 100047012, 2	860	42	17763	3.E+00	1.E+00	3.E-01	2.E+01
UP_SEQ_FEATURE	active site:Glycyl thioester intermediate	9	1.025056948	2.E-02	100041766, 56550, 218793, 17999, 10004	861	61	16021	3.E+00	1.E+00	5.E-01	2.E+01
SMART	SM00212~UBCc	7	0.797266515	2.E-02	100041766, 56550, 218793, 100047012, 2	492	42	9131	3.E+00	1.E+00	2.E-01	3.E+01
GOTERM_MF_FAT	GO:0019787~small conjugating protein ligase activity	14	1.59453303	2.E-02	56550, 74287, 218793, 17999, 26965, 222	754	125	13288	2.E+00	1.E+00	2.E-01	3.E+01
INTERPRO	IPR016135~Ubiquitin-conjugating enzyme/RWD-like	7	0.797266515	3.E-02	100041766, 56550, 218793, 100047012, 2	860	50	17763	3.E+00	1.E+00	5.E-01	4.E+01
SP_PIR_KEYWORDS	ubl conjugation pathway	32	3.644646925	7.E-02	56550, 74287, 218793, 26965, 22209, 590	869	484	17854	1.E+00	1.E+00	3.E-01	7.E+01
GOTERM_BP_FAT	GO:0009057~macromolecule catabolic process	48	5.466970387	1.E-01	218793, 238055, 59008, 16341, 52563, 12	809	654	13588	1.E+00	1.E+00	5.E-01	9.E+01
GOTERM_MF_FAT	GO:0016879~ligase activity, forming carbon-nitrogen bonds	16	1.822323462	1.E-01	56550, 74287, 218793, 17999, 26965, 222	754	193	13288	1.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0044265~cellular macromolecule catabolic process	44	5.011389522	1.E-01	56550, 74287, 218793, 11816, 26965, 222	809	609	13588	1.E+00	1.E+00	6.E-01	9.E+01
GOTERM_MF_FAT	GO:0016881~acid-amino acid ligase activity	14	1.59453303	1.E-01	56550, 74287, 218793, 17999, 26965, 222	754	166	13288	1.E+00	1.E+00	7.E-01	9.E+01
GOTERM_BP_FAT	GO:0030163~protein catabolic process	40	4.555808656	2.E-01	56550, 74287, 218793, 26965, 22209, 116	809	556	13588	1.E+00	1.E+00	7.E-01	1.E+02
PIR_SUPERFAMILY	PIRSF001567~ubiquitin-protein ligase E2	3	0.341685649	2.E-01	22209, 66105, 22194	576	13	8136	3.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0051603~proteolysis involved in cellular protein catabolic pro	37	4.214123007	2.E-01	56550, 74287, 218793, 26965, 22209, 590	809	534	13588	1.E+00	1.E+00	8.E-01	1.E+02
SP_PIR_KEYWORDS	ligase	18	2.050113895	2.E-01	56550, 74287, 218793, 17999, 22209, 168	869	290	17854	1.E+00	1.E+00	6.E-01	1.E+02
GOTERM_BP_FAT	GO:0044257~cellular protein catabolic process	37	4.214123007	3.E-01	56550, 74287, 218793, 26965, 22209, 590	809	537	13588	1.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0019941~modification-dependent protein catabolic process	34	3.872437358	3.E-01	56550, 74287, 218793, 26965, 22209, 590	809	508	13588	1.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0043632~modification-dependent macromolecule catabolic p	34	3.872437358	3.E-01	56550, 74287, 218793, 26965, 22209, 590	809	508	13588	1.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0006508~proteolysis	55	6.264236902	9.E-01	218793, 59008, 22273, 73078, 52563, 670	809	1034	13588	9.E-01	1.E+00	1.E+00	1.E+02

Annotation Cluster 131	Enrichment Score: 1.1464538970839588											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0010906~regulation of glucose metabolic process	4	0.455580866	5.E-02	14447, 14815, 103988, 208727	809	14	13588	5.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0006109~regulation of carbohydrate metabolic process	4	0.455580866	6.E-02	14447, 14815, 103988, 208727	809	15	13588	4.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0010675~regulation of cellular carbohydrate metabolic proces	4	0.455580866	6.E-02	14447, 14815, 103988, 208727	809	15	13588	4.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0043467~regulation of generation of precursor metabolites ai	3	0.341685649	2.E-01	14447, 103988, 208727	809	13	13588	4.E+00	1.E+00	7.E-01	1.E+02

Annotation Cluster 132    Enrichment Score: 1.1416367411951072



Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_BP_FAT	GO:0044242~cellular lipid catabolic process	10	1.138952164	5.E-03	18783, 18803, 11814, 669888, 74147, 234	809	809	56	13588	3.E+00	1.E+00	8.E-02	9.E+00
UP_SEQ_FEATURE	domain:C2	9	1.025056948	3.E-02	18751, 18783, 18803, 17999, 234779, 163	861	861	68	16021	2.E+00	1.E+00	7.E-01	4.E+01
INTERPRO	IPR001711:Phospholipase C, phosphatidylinositol-specific, Y doma	4	0.455580866	3.E-02	18803, 234779, 18797, 18795	860	860	15	17763	6.E+00	1.E+00	5.E-01	4.E+01
INTERPRO	IPR001192:Phospholipase C, phosphoinositol-specific, C-terminal (	4	0.455580866	3.E-02	18803, 234779, 18797, 18795	860	860	15	17763	6.E+00	1.E+00	5.E-01	4.E+01
UP_SEQ_FEATURE	domain:PI-PLC Y-box	4	0.455580866	4.E-02	18803, 234779, 18797, 18795	861	861	14	16021	5.E+00	1.E+00	7.E-01	5.E+01
SMART	SM00149:PLCYc	4	0.455580866	4.E-02	18803, 234779, 18797, 18795	492	492	15	9131	5.E+00	1.E+00	4.E-01	4.E+01
GOTERM_MF_FAT	GO:0004435~phosphoinositide phospholipase C activity	4	0.455580866	5.E-02	18803, 234779, 18797, 18795	754	754	15	13288	5.E+00	1.E+00	4.E-01	5.E+01
UP_SEQ_FEATURE	domain:PI-PLC X-box	4	0.455580866	5.E-02	18803, 234779, 18797, 18795	861	861	16	16021	5.E+00	1.E+00	8.E-01	6.E+01
GOTERM_BP_FAT	GO:0016042~lipid catabolic process	14	1.59453303	6.E-02	11813, 11814, 11816, 238055, 18797, 113	809	809	134	13588	2.E+00	1.E+00	4.E-01	6.E+01
INTERPRO	IPR000909:Phospholipase C, phosphatidylinositol-specific , X regic	4	0.455580866	6.E-02	18803, 234779, 18797, 18795	860	860	19	17763	4.E+00	1.E+00	7.E-01	6.E+01
GOTERM_BP_FAT	GO:0009395~phospholipid catabolic process	4	0.455580866	8.E-02	18783, 18803, 234779, 18797	809	809	17	13588	4.E+00	1.E+00	5.E-01	8.E+01
SMART	SM00148:PLCXc	4	0.455580866	8.E-02	18803, 234779, 18797, 18795	492	492	19	9131	4.E+00	1.E+00	5.E-01	6.E+01
SP_PIR_KEYWORDS	lipid degradation	8	0.911161731	9.E-02	18783, 18803, 11813, 11814, 669888, 234	869	869	79	17854	2.E+00	1.E+00	3.E-01	7.E+01
GOTERM_MF_FAT	GO:0004629~phospholipase C activity	4	0.455580866	9.E-02	18803, 234779, 18797, 18795	754	754	19	13288	4.E+00	1.E+00	5.E-01	8.E+01
GOTERM_MF_FAT	GO:0008081~phosphoric diester hydrolase activity	8	0.911161731	1.E-01	18803, 234779, 20598, 18576, 18575, 185	754	754	72	13288	2.E+00	1.E+00	6.E-01	8.E+01
INTERPRO	IPR017946:PLC-like phosphodiesterase, TIM beta/alpha-barrel don	4	0.455580866	1.E-01	18803, 234779, 18797, 18795	860	860	25	17763	3.E+00	1.E+00	9.E-01	9.E+01
KEGG_PATHWAY	mmu04070:Phosphatidylinositol signaling system	11	1.25284738	2.E-01	320207, 18797, 18795, 18751, 18709, 188	580	580	75	5738	1.E+00	1.E+00	4.E-01	1.E+02
GOTERM_MF_FAT	GO:0004620~phospholipase activity	6	0.683371298	3.E-01	18783, 18803, 234779, 20598, 18797, 187	754	754	63	13288	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_MF_FAT	GO:0016298~lipase activity	7	0.797266515	3.E-01	18783, 18803, 669888, 234779, 20598, 18	754	754	84	13288	1.E+00	1.E+00	9.E-01	1.E+02
KEGG_PATHWAY	mmu00562:inositol phosphate metabolism	7	0.797266515	5.E-01	18803, 234779, 30955, 21991, 18797, 187	580	580	54	5738	1.E+00	1.E+00	7.E-01	1.E+02
Annotation Cluster 133	Enrichment Score: 1.139902247892908												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_BP_FAT	GO:0002252~immune effector process	16	1.822323462	8.E-03	15170, 15018, 108138, 13035, 16803, 133	809	809	126	13588	2.E+00	1.E+00	1.E-01	1.E+01
GOTERM_BP_FAT	GO:0002443~leukocyte mediated immunity	12	1.366742597	2.E-02	12051, 14127, 15170, 17874, 230558, 118	809	809	89	13588	2.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0002460~adaptive immune response based on somatic recomb	11	1.25284738	3.E-02	12051, 14127, 17874, 21899, 230558, 118	809	809	84	13588	2.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0002250~adaptive immune response	11	1.25284738	3.E-02	12051, 14127, 17874, 21899, 230558, 118	809	809	84	13588	2.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0002449~lymphocyte mediated immunity	10	1.138952164	4.E-02	12051, 14127, 15170, 17874, 230558, 118	809	809	76	13588	2.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0016064~immunoglobulin mediated immune response	7	0.797266515	2.E-01	12051, 14127, 17874, 230558, 108138, 12	809	809	63	13588	2.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0019724~B cell mediated immunity	7	0.797266515	2.E-01	12051, 14127, 17874, 230558, 108138, 12	809	809	65	13588	2.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0002455~humoral immune response mediated by circulating	3	0.341685649	6.E-01	12051, 230558, 12263	809	809	35	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0006959~humoral immune response	3	0.341685649	8.E-01	12051, 230558, 12263	809	809	54	13588	9.E-01	1.E+00	1.E+00	1.E+02
Annotation Cluster 134	Enrichment Score: 1.1359178983376383												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_BP_FAT	GO:0010882~regulation of cardiac muscle contraction by calcium	3	0.341685649	1.E-02	14226, 20191, 208727	809	809	3	13588	2.E+01	1.E+00	1.E-01	2.E+01
GOTERM_BP_FAT	GO:0055117~regulation of cardiac muscle contraction	3	0.341685649	5.E-02	14226, 20191, 208727	809	809	6	13588	8.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0006942~regulation of striated muscle contraction	3	0.341685649	1.E-01	14226, 20191, 208727	809	809	10	13588	5.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0008016~regulation of heart contraction	6	0.683371298	2.E-01	11486, 14226, 14678, 74318, 20191, 2087	809	809	50	13588	2.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0006937~regulation of muscle contraction	5	0.569476082	2.E-01	11486, 14226, 20191, 17969, 208727	809	809	41	13588	2.E+00	1.E+00	8.E-01	1.E+02
Annotation Cluster 135	Enrichment Score: 1.1302862389713233												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_CC_FAT	GO:0031968~organelle outer membrane	10	1.138952164	3.E-02	56717, 12015, 14732, 12048, 12028, 1916	636	636	87	12504	2.E+00	1.E+00	2.E-01	4.E+01
GOTERM_CC_FAT	GO:0019867~outer membrane	10	1.138952164	4.E-02	56717, 12015, 14732, 12048, 12028, 1916	636	636	90	12504	2.E+00	1.E+00	2.E-01	4.E+01
GOTERM_CC_FAT	GO:0005741~mitochondrial outer membrane	9	1.025056948	5.E-02	56717, 12015, 14732, 12048, 12028, 1527	636	636	80	12504	2.E+00	1.E+00	2.E-01	5.E+01
SP_PIR_KEYWORDS	mitochondrion outer membrane	8	0.911161731	5.E-02	56717, 12015, 14732, 12028, 15275, 1204	869	869	69	17854	2.E+00	1.E+00	2.E-01	5.E+01
UP_SEQ_FEATURE	topological domain:Mitochondrial intermembrane	3	0.341685649	7.E-01	14732, 59040, 214952	861	861	47	16021	1.E+00	1.E+00	1.E+00	1.E+02
Annotation Cluster 136	Enrichment Score: 1.1279745882609098												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
KEGG_PATHWAY	mmu04540:Gap junction	17	1.936218679	1.E-02	22142, 18747, 13649, 14678, 18797, 1879	580	580	86	5738	2.E+00	8.E-01	4.E-02	1.E+01
KEGG_PATHWAY	mmu04720:Long-term potentiation	14	1.59453303	2.E-02	18747, 18797, 12914, 18795, 18751, 1151	580	580	70	5738	2.E+00	1.E+00	7.E-02	2.E+01
KEGG_PATHWAY	mmu04730:Long-term depression	14	1.59453303	3.E-02	14674, 14678, 18797, 18795, 18751, 1878	580	580	72	5738	2.E+00	1.E+00	8.E-02	3.E+01
KEGG_PATHWAY	mmu04912:GnRH signaling pathway	17	1.936218679	3.E-02	18747, 13649, 18797, 18795, 18751, 1878	580	580	97	5738	2.E+00	1.E+00	9.E-02	3.E+01
BIOCARTA	m_CCR3Pathway:CCR3 signaling in Eosinophils	6	0.683371298	3.E-01	18751, 26395, 15461, 14682, 11848, 1879	188	188	22	1171	2.E+00	1.E+00	6.E-01	1.E+02
KEGG_PATHWAY	mmu04916:Melanogenesis	12	1.366742597	4.E-01	18747, 14678, 12912, 18797, 12914, 1879	580	580	100	5738	1.E+00	1.E+00	6.E-01	1.E+02
KEGG_PATHWAY	mmu04270:Vascular smooth muscle contraction	13	1.480637813	6.E-01	18747, 14674, 18797, 16801, 11848, 1879	580	580	120	5738	1.E+00	1.E+00	7.E-01	1.E+02
Annotation Cluster 137	Enrichment Score: 1.125344100238476												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_BP_FAT	GO:0001501~skeletal system development	26	2.961275626	3.E-02	69121, 17869, 21934, 12815, 15402, 1859	809	809	285	13588	2.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0001649~osteoblast differentiation	7	0.797266515	6.E-02	78294, 12842, 12161, 14180, 208727, 160	809	809	47	13588	3.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0001503~ossification	11	1.25284738	1.E-01	78294, 12842, 12161, 69121, 12043, 1418	809	809	106	13588	2.E+00	1.E+00	5.E-01	8.E+01



GOTERM_BP_FAT	GO:0060348--bone development	11	1.25284738	2.E-01	78294, 12842, 12161, 69121, 12043, 1418	809	118	13588	2.E+00	1.E+00	7.E-01	1.E+02
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Annotation Cluster 138	Enrichment Score: 1.1219384238383714											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0042159--lipoprotein catabolic process	4	0.455580866	4.E-03	11816, 11920, 12491, 238055	809	6	13588	1.E+01	1.E+00	6.E-02	6.E+00
SP_PIR_KEYWORDS	lipid binding	4	0.455580866	5.E-03	11807, 11816, 238055, 11808	869	8	17854	1.E+01	9.E-01	3.E-02	7.E+00
SP_PIR_KEYWORDS	lipid transport	8	0.911161731	1.E-02	11813, 11814, 11806, 11807, 11816, 2380	869	51	17854	3.E+00	1.E+00	5.E-02	1.E+01
GOTERM_MF_FAT	GO:0008034--lipoprotein binding	5	0.569476082	3.E-02	11806, 11807, 11816, 21899, 12491	754	21	13288	4.E+00	1.E+00	3.E-01	4.E+01
GOTERM_BP_FAT	GO:0030301--cholesterol transport	4	0.455580866	2.E-01	11806, 11816, 12491, 238055	809	23	13588	3.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0015918--sterol transport	4	0.455580866	2.E-01	11806, 11816, 12491, 238055	809	23	13588	3.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0006869--lipid transport	11	1.25284738	2.E-01	11813, 17777, 11814, 11806, 11807, 1181	809	119	13588	2.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0055092--sterol homeostasis	4	0.455580866	2.E-01	17777, 11807, 11816, 238055	809	26	13588	3.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0042632--cholesterol homeostasis	4	0.455580866	2.E-01	17777, 11807, 11816, 238055	809	26	13588	3.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0010876--lipid localization	11	1.25284738	2.E-01	11813, 17777, 11814, 11806, 11807, 1181	809	128	13588	1.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0055088--lipid homeostasis	4	0.455580866	3.E-01	17777, 11807, 11816, 238055	809	34	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_MF_FAT	GO:0005319--lipid transporter activity	4	0.455580866	5.E-01	17777, 11806, 11816, 238055	754	44	13288	2.E+00	1.E+00	1.E+00	1.E+02

Annotation Cluster 139	Enrichment Score: 1.1070145799307387											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0008629--induction of apoptosis by intracellular signals	7	0.797266515	2.E-02	12051, 12190, 66593, 11920, 12028, 1786	809	35	13588	3.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0042770--DNA damage response, signal transduction	9	1.025056948	2.E-02	12051, 12190, 245000, 11920, 26416, 126	809	57	13588	3.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0008630--DNA damage response, signal transduction resulting in	4	0.455580866	2.E-01	12051, 12190, 11920, 170770	809	23	13588	3.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0042771--DNA damage response, signal transduction by p53	3	0.341685649	2.E-01	12051, 12190, 170770	809	14	13588	4.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0030330--DNA damage response, signal transduction by p53	3	0.341685649	3.E-01	12051, 12190, 170770	809	19	13588	3.E+00	1.E+00	9.E-01	1.E+02

Annotation Cluster 140	Enrichment Score: 1.099632338162649											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0043547--positive regulation of GTPase activity	4	0.455580866	4.E-02	71709, 11856, 19765, 19417	809	13	13588	5.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0032319--regulation of Rho GTPase activity	4	0.455580866	5.E-02	56717, 71709, 19765, 19417	809	14	13588	5.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0032321--positive regulation of Rho GTPase activity	3	0.341685649	8.E-02	71709, 19765, 19417	809	8	13588	6.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0032320--positive regulation of Ras GTPase activity	3	0.341685649	1.E-01	71709, 19765, 19417	809	10	13588	5.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0032318--regulation of Ras GTPase activity	8	0.911161731	2.E-01	56717, 24064, 71709, 228998, 19765, 194	809	80	13588	2.E+00	1.E+00	7.E-01	1.E+02

Annotation Cluster 141	Enrichment Score: 1.0893608625171893											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0060537--muscle tissue development	17	1.936218679	7.E-03	15430, 18479, 16412, 13383, 20467, 1136	809	136	13588	2.E+00	1.E+00	9.E-02	1.E+01
GOTERM_BP_FAT	GO:0031032--actomyosin structure organization	6	0.683371298	1.E-02	26934, 77579, 11464, 71994, 16412, 1145	809	25	13588	4.E+00	1.E+00	2.E-01	2.E+01
GOTERM_BP_FAT	GO:0014706--striated muscle tissue development	15	1.708428246	2.E-02	15430, 18479, 16412, 20467, 11364, 1184	809	127	13588	2.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0055007--cardiac muscle cell differentiation	6	0.683371298	2.E-02	77579, 14465, 11464, 16412, 11364, 1420	809	28	13588	4.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0007517--muscle organ development	18	2.050113895	3.E-02	12955, 15430, 18479, 16412, 13383, 2046	809	176	13588	2.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0035051--cardiac cell differentiation	6	0.683371298	4.E-02	77579, 14465, 11464, 16412, 11364, 1420	809	33	13588	3.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0042692--muscle cell differentiation	13	1.480637813	5.E-02	19317, 18479, 16412, 11364, 19645, 1305	809	117	13588	2.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0048738--cardiac muscle tissue development	8	0.911161731	5.E-02	13052, 77579, 14465, 11464, 16412, 2046	809	57	13588	2.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0051146--striated muscle cell differentiation	10	1.138952164	8.E-02	19645, 13052, 77579, 14465, 11464, 1641	809	89	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0030239--myofibril assembly	4	0.455580866	1.E-01	77579, 11464, 16412, 11459	809	19	13588	4.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0007519--skeletal muscle tissue development	8	0.911161731	1.E-01	15438, 26416, 15430, 18479, 11459, 1256	809	72	13588	2.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0060538--skeletal muscle organ development	8	0.911161731	1.E-01	15438, 26416, 15430, 18479, 11459, 1256	809	74	13588	2.E+00	1.E+00	7.E-01	9.E+01
GOTERM_BP_FAT	GO:0055001--muscle cell development	7	0.797266515	2.E-01	13052, 77579, 11464, 16412, 18479, 1145	809	61	13588	2.E+00	1.E+00	7.E-01	9.E+01
GOTERM_BP_FAT	GO:0055006--cardiac cell development	3	0.341685649	2.E-01	77579, 11464, 14200	809	14	13588	4.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0055013--cardiac muscle cell development	3	0.341685649	2.E-01	77579, 11464, 14200	809	14	13588	4.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0055002--striated muscle cell development	6	0.683371298	2.E-01	13052, 77579, 11464, 16412, 18479, 1145	809	54	13588	2.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0007422--peripheral nervous system development	4	0.455580866	3.E-01	15438, 18413, 15430, 12568	809	30	13588	2.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0010927--cellular component assembly involved in morphoge	4	0.455580866	4.E-01	77579, 11464, 16412, 11459	809	36	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0048747--muscle fiber development	3	0.341685649	7.E-01	13052, 18479, 11459	809	38	13588	1.E+00	1.E+00	1.E+00	1.E+02

Annotation Cluster 142	Enrichment Score: 1.0868027536771288											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0042060--wound healing	13	1.480637813	3.E-02	14674, 18793, 14026, 14060, 14432, 5674	809	112	13588	2.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0007596--blood coagulation	9	1.025056948	6.E-02	14060, 14674, 56744, 18815, 74145, 1406	809	70	13588	2.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0050817--coagulation	9	1.025056948	6.E-02	14060, 14674, 56744, 18815, 74145, 1406	809	70	13588	2.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0007599--hemostasis	9	1.025056948	6.E-02	14060, 14674, 56744, 18815, 74145, 1406	809	71	13588	2.E+00	1.E+00	4.E-01	7.E+01
SP_PIR_KEYWORDS	blood coagulation	5	0.569476082	1.E-01	14060, 18815, 74145, 14065, 14064	869	37	17854	3.E+00	1.E+00	3.E-01	8.E+01
GOTERM_BP_FAT	GO:0050878--regulation of body fluid levels	9	1.025056948	2.E-01	14060, 14674, 56744, 18815, 74145, 1406	809	89	13588	2.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0030168--platelet activation	3	0.341685649	2.E-01	14674, 56744, 14026	809	16	13588	3.E+00	1.E+00	8.E-01	1.E+02



Annotation Cluster 143		Enrichment Score: 1.0751657371809962											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
UP_SEQ_FEATURE	domain:WW 2	5	0.569476082	6.E-02	17999, 223666, 75415, 16396, 22601	861	28	16021	3.E+00	1.E+00	9.E-01	7.E+01	
UP_SEQ_FEATURE	domain:WW 1	5	0.569476082	6.E-02	17999, 223666, 75415, 16396, 22601	861	28	16021	3.E+00	1.E+00	9.E-01	7.E+01	
INTERPRO	IPR001202:WW/Rsp5/WWP	6	0.683371298	1.E-01	11785, 17999, 223666, 75415, 16396, 226	860	51	17763	2.E+00	1.E+00	8.E-01	8.E+01	
SMART	SM00456:WW	6	0.683371298	1.E-01	11785, 17999, 223666, 75415, 16396, 226	492	51	9131	2.E+00	1.E+00	7.E-01	8.E+01	
Annotation Cluster 144		Enrichment Score: 1.0750106496500804											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_CC_FAT	GO:0042641~actomyosin	5	0.569476082	5.E-02	13800, 77579, 11459, 208727, 19200	636	27	12504	4.E+00	1.E+00	2.E-01	5.E+01	
GOTERM_CC_FAT	GO:0001725~stress fiber	4	0.455580866	1.E-01	13800, 77579, 11459, 19200	636	23	12504	3.E+00	1.E+00	4.E-01	8.E+01	
GOTERM_CC_FAT	GO:0032432~actin filament bundle	4	0.455580866	1.E-01	13800, 77579, 11459, 19200	636	24	12504	3.E+00	1.E+00	4.E-01	8.E+01	
Annotation Cluster 145		Enrichment Score: 1.0712593929659058											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_BP_FAT	GO:0060674~placenta blood vessel development	5	0.569476082	2.E-02	12702, 18815, 26395, 11651, 16477	809	18	13588	5.E+00	1.E+00	2.E-01	3.E+01	
GOTERM_BP_FAT	GO:0060711~labyrinthine layer development	6	0.683371298	5.E-02	12702, 14784, 18815, 26395, 11651, 1647	809	35	13588	3.E+00	1.E+00	4.E-01	6.E+01	
GOTERM_BP_FAT	GO:0001890~placenta development	10	1.138952164	7.E-02	13649, 12702, 11486, 13857, 14784, 1881	809	87	13588	2.E+00	1.E+00	5.E-01	7.E+01	
GOTERM_BP_FAT	GO:0001892~embryonic placenta development	7	0.797266515	2.E-01	13649, 12702, 14784, 18815, 26395, 1165	809	61	13588	2.E+00	1.E+00	7.E-01	9.E+01	
GOTERM_BP_FAT	GO:0060706~cell differentiation involved in embryonic placenta d	3	0.341685649	2.E-01	12702, 18815, 11651	809	12	13588	4.E+00	1.E+00	7.E-01	1.E+02	
GOTERM_BP_FAT	GO:0060716~labyrinthine layer blood vessel development	3	0.341685649	2.E-01	18815, 11651, 16477	809	14	13588	4.E+00	1.E+00	7.E-01	1.E+02	
Annotation Cluster 146		Enrichment Score: 1.0660101988260942											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_BP_FAT	GO:0006800~oxygen and reactive oxygen species metabolic proc	11	1.25284738	4.E-04	18126, 672195, 17970, 68349, 50493, 120	809	47	13588	4.E+00	7.E-01	1.E-02	7.E-01	
INTERPRO	IPR009056:Cytochrome c, monohaem	3	0.341685649	7.E-03	672195, 66445, 13063, 13067	860	3	17763	2.E+01	1.E+00	2.E-01	1.E+01	
UP_SEQ_FEATURE	binding site:Heme (covalent)	3	0.341685649	8.E-03	672195, 66445, 13063, 13067	861	3	16021	2.E+01	1.E+00	3.E-01	1.E+01	
GOTERM_BP_FAT	GO:0042743~hydrogen peroxide metabolic process	5	0.569476082	3.E-02	672195, 50493, 13063, 13077, 17969, 130	809	20	13588	4.E+00	1.E+00	2.E-01	4.E+01	
SP_PIR_KEYWORDS	metalloprotein	6	0.683371298	1.E-01	18746, 672195, 11486, 13063, 13077, 177	869	56	17854	2.E+00	1.E+00	4.E-01	9.E+01	
SP_PIR_KEYWORDS	electron transfer	4	0.455580866	1.E-01	672195, 13063, 13077, 17711, 13067	869	27	17854	3.E+00	1.E+00	4.E-01	9.E+01	
SP_PIR_KEYWORDS	chromoprotein	4	0.455580866	3.E-01	672195, 13063, 13077, 17711, 13067	869	40	17854	2.E+00	1.E+00	7.E-01	1.E+02	
UP_SEQ_FEATURE	metal ion-binding site:Iron (heme axial ligand)	5	0.569476082	8.E-01	18126, 672195, 66445, 13063, 13077, 130	861	99	16021	9.E-01	1.E+00	1.E+00	1.E+02	
SP_PIR_KEYWORDS	heme	6	0.683371298	8.E-01	18126, 672195, 66445, 13063, 13077, 177	869	142	17854	9.E-01	1.E+00	1.E+00	1.E+02	
GOTERM_MF_FAT	GO:0020037~heme binding	6	0.683371298	9.E-01	18126, 672195, 14151, 66445, 13063, 130	754	144	13288	7.E-01	1.E+00	1.E+00	1.E+02	
GOTERM_MF_FAT	GO:0046906~tetrapyrrole binding	6	0.683371298	9.E-01	18126, 672195, 14151, 66445, 13063, 130	754	151	13288	7.E-01	1.E+00	1.E+00	1.E+02	
Annotation Cluster 147		Enrichment Score: 1.0590411399942026											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_BP_FAT	GO:0030900~forebrain development	18	2.050113895	2.E-02	13649, 232906, 433759, 19378, 56847, 14	809	167	13588	2.E+00	1.E+00	2.E-01	3.E+01	
GOTERM_BP_FAT	GO:0021537~telencephalon development	10	1.138952164	3.E-02	13649, 77579, 433759, 12028, 19164, 148	809	72	13588	2.E+00	1.E+00	2.E-01	4.E+01	
GOTERM_BP_FAT	GO:0021795~cerebral cortex cell migration	4	0.455580866	7.E-02	13649, 19164, 12568, 21869	809	16	13588	4.E+00	1.E+00	4.E-01	7.E+01	
GOTERM_BP_FAT	GO:0021987~cerebral cortex development	6	0.683371298	7.E-02	13649, 12028, 19164, 12568, 21869, 1162	809	37	13588	3.E+00	1.E+00	4.E-01	7.E+01	
GOTERM_BP_FAT	GO:0022029~telencephalon cell migration	4	0.455580866	9.E-02	13649, 19164, 12568, 21869	809	18	13588	4.E+00	1.E+00	5.E-01	8.E+01	
GOTERM_BP_FAT	GO:0021543~pallium development	7	0.797266515	9.E-02	13649, 433759, 12028, 19164, 12568, 218	809	53	13588	2.E+00	1.E+00	5.E-01	8.E+01	
GOTERM_BP_FAT	GO:0021885~forebrain cell migration	4	0.455580866	1.E-01	13649, 19164, 12568, 21869	809	19	13588	4.E+00	1.E+00	5.E-01	8.E+01	
GOTERM_BP_FAT	GO:0021761~limbic system development	5	0.569476082	1.E-01	433759, 12028, 56847, 12568, 21869	809	33	13588	3.E+00	1.E+00	6.E-01	9.E+01	
GOTERM_BP_FAT	GO:0001764~neuron migration	7	0.797266515	2.E-01	11785, 77579, 12028, 19164, 14360, 1256	809	70	13588	2.E+00	1.E+00	8.E-01	1.E+02	
GOTERM_BP_FAT	GO:0021766~hippocampus development	3	0.341685649	4.E-01	433759, 12568, 21869	809	24	13588	2.E+00	1.E+00	9.E-01	1.E+02	
Annotation Cluster 148		Enrichment Score: 1.0511099662257786											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
INTERPRO	IPR005792:Protein disulphide isomerase	3	0.341685649	1.E-02	18453, 12304, 14827	860	4	17763	2.E+01	1.E+00	3.E-01	2.E+01	
INTERPRO	IPR006662:Thioredoxin-like subdomain	4	0.455580866	1.E-02	18453, 12304, 14827, 67402	860	11	17763	8.E+00	1.E+00	3.E-01	2.E+01	
INTERPRO	IPR005788:Disulphide isomerase	3	0.341685649	3.E-02	18453, 12304, 14827	860	6	17763	1.E+01	1.E+00	5.E-01	4.E+01	
GOTERM_MF_FAT	GO:0016860~intramolecular oxidoreductase activity	6	0.683371298	6.E-02	18453, 12304, 14751, 74147, 21991, 1482	754	38	13288	3.E+00	1.E+00	4.E-01	6.E+01	
UP_SEQ_FEATURE	domain:Thioredoxin 2	3	0.341685649	6.E-02	18453, 12304, 14827	861	8	16021	7.E+00	1.E+00	9.E-01	7.E+01	
UP_SEQ_FEATURE	domain:Thioredoxin 1	3	0.341685649	6.E-02	18453, 12304, 14827	861	8	16021	7.E+00	1.E+00	9.E-01	7.E+01	
GOTERM_MF_FAT	GO:0016864~intramolecular oxidoreductase activity, transposing	3	0.341685649	7.E-02	18453, 12304, 14827	754	8	13288	7.E+00	1.E+00	5.E-01	7.E+01	
GOTERM_MF_FAT	GO:0003756~protein disulfide isomerase activity	3	0.341685649	7.E-02	18453, 12304, 14827	754	8	13288	7.E+00	1.E+00	5.E-01	7.E+01	
GOTERM_MF_FAT	GO:0016862~intramolecular oxidoreductase activity, interconvertir	3	0.341685649	9.E-02	18453, 12304, 14827	754	9	13288	6.E+00	1.E+00	5.E-01	8.E+01	
INTERPRO	IPR017936:Thioredoxin-like	5	0.569476082	9.E-02	18453, 12304, 14827, 54683, 67402	860	36	17763	3.E+00	1.E+00	8.E-01	8.E+01	
INTERPRO	IPR017937:Thioredoxin, conserved site	4	0.455580866	1.E-01	18453, 12304, 14827, 67402	860	25	17763	3.E+00	1.E+00	9.E-01	9.E+01	
INTERPRO	IPR013766:Thioredoxin domain	4	0.455580866	1.E-01	18453, 12304, 14827, 67402	860	26	17763	3.E+00	1.E+00	9.E-01	9.E+01	
INTERPRO	IPR012335:Thioredoxin fold	7	0.797266515	4.E-01	18453, 12304, 93692, 14827, 54683, 6740	860	106	17763	1.E+00	1.E+00	1.E+00	1.E+02	
UP_SEQ_FEATURE	short sequence motif:Prevents secretion from ER	4	0.455580866	6.E-01	18453, 12304, 14827, 68675	861	59	16021	1.E+00	1.E+00	1.E+00	1.E+02	



GOTERM_CC_FAT	GO:0005788--endoplasmic reticulum lumen	4	0.455580866	7.E-01	18453, 12304, 14827, 81500	636	72	12504	1.E+00	1.E+00	1.E+00	1.E+02
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Annotation Cluster 149	Enrichment Score: 1.0441495920139918											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0002696--positive regulation of leukocyte activation	13	1.480637813	1.E-02	19370, 21898, 16408, 16818, 17874, 1412	809	99	13588	2.E+00	1.E+00	2.E-01	2.E+01
GOTERM_BP_FAT	GO:0050867--positive regulation of cell activation	13	1.480637813	2.E-02	19370, 21898, 16408, 16818, 17874, 1412	809	101	13588	2.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0050670--regulation of lymphocyte proliferation	11	1.25284738	2.E-02	16408, 15170, 17874, 246779, 11486, 218	809	80	13588	2.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0032944--regulation of mononuclear cell proliferation	11	1.25284738	2.E-02	16408, 15170, 17874, 246779, 11486, 218	809	80	13588	2.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0002694--regulation of leukocyte activation	17	1.936218679	2.E-02	19370, 15170, 21898, 16396, 13383, 1640	809	154	13588	2.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0070663--regulation of leukocyte proliferation	11	1.25284738	2.E-02	16408, 15170, 17874, 246779, 11486, 218	809	82	13588	2.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0050865--regulation of cell activation	17	1.936218679	2.E-02	19370, 15170, 21898, 16396, 13383, 1640	809	156	13588	2.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0051251--positive regulation of lymphocyte activation	12	1.366742597	2.E-02	19370, 21898, 16408, 16818, 17874, 1201	809	94	13588	2.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0051249--regulation of lymphocyte activation	16	1.822323462	2.E-02	19370, 15170, 21898, 16396, 13383, 1640	809	144	13588	2.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0045582--positive regulation of T cell differentiation	6	0.683371298	4.E-02	16818, 12015, 16197, 11486, 16190, 2096	809	32	13588	3.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0045621--positive regulation of lymphocyte differentiation	6	0.683371298	5.E-02	16818, 12015, 16197, 11486, 16190, 2096	809	34	13588	3.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0050871--positive regulation of B cell activation	6	0.683371298	7.E-02	12015, 11486, 21898, 106759, 12575, 209	809	37	13588	3.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0050671--positive regulation of lymphocyte proliferation	7	0.797266515	7.E-02	16408, 17874, 11486, 21898, 106759, 125	809	50	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0032946--positive regulation of mononuclear cell proliferation	7	0.797266515	7.E-02	16408, 17874, 11486, 21898, 106759, 125	809	50	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0070665--positive regulation of leukocyte proliferation	7	0.797266515	9.E-02	16408, 17874, 11486, 21898, 106759, 125	809	52	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0050864--regulation of B cell activation	7	0.797266515	1.E-01	15170, 12015, 11486, 21898, 106759, 125	809	55	13588	2.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0050863--regulation of T cell activation	11	1.25284738	1.E-01	16408, 15170, 16818, 12015, 16197, 2467	809	108	13588	2.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0045619--regulation of lymphocyte differentiation	7	0.797266515	1.E-01	15170, 16818, 12015, 16197, 11486, 1619	809	58	13588	2.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0030890--positive regulation of B cell proliferation	4	0.455580866	1.E-01	11486, 21898, 106759, 12575	809	22	13588	3.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0045580--regulation of T cell differentiation	6	0.683371298	2.E-01	16818, 12015, 16197, 11486, 16190, 2096	809	48	13588	2.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0050870--positive regulation of T cell activation	7	0.797266515	2.E-01	16408, 16818, 12015, 16197, 11486, 1619	809	66	13588	2.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0045577--regulation of B cell differentiation	3	0.341685649	2.E-01	15170, 12015, 20963	809	16	13588	3.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0050850--positive regulation of calcium-mediated signaling	3	0.341685649	2.E-01	16408, 11486, 20963	809	16	13588	3.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0042129--regulation of T cell proliferation	6	0.683371298	3.E-01	16408, 15170, 246779, 16396, 13383, 209	809	59	13588	2.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0050848--regulation of calcium-mediated signaling	3	0.341685649	3.E-01	16408, 11486, 20963	809	18	13588	3.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0030888--regulation of B cell proliferation	4	0.455580866	3.E-01	11486, 21898, 106759, 12575	809	32	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0046638--positive regulation of alpha-beta T cell differentiat	3	0.341685649	3.E-01	11486, 16190, 20963	809	19	13588	3.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0046634--regulation of alpha-beta T cell activation	4	0.455580866	3.E-01	11486, 16396, 16190, 20963	809	34	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0046637--regulation of alpha-beta T cell differentiation	3	0.341685649	4.E-01	11486, 16190, 20963	809	22	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0046635--positive regulation of alpha-beta T cell activation	3	0.341685649	5.E-01	11486, 16190, 20963	809	26	13588	2.E+00	1.E+00	1.E+00	1.E+02
KEGG_PATHWAY	mmu05340:Primary immunodeficiency	4	0.455580866	7.E-01	16818, 12229, 16197, 11486	580	36	5738	1.E+00	1.E+00	9.E-01	1.E+02

Annotation Cluster 150	Enrichment Score: 1.0392045114086983											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	camp	6	0.683371298	1.E-02	18747, 19085, 19088, 18576, 18575, 1857	869	28	17854	4.E+00	1.E+00	5.E-02	1.E+01
GOTERM_MF_FAT	GO:0016208--AMP binding	4	0.455580866	1.E-01	19085, 19088, 68738, 18575	754	20	13288	4.E+00	1.E+00	6.E-01	8.E+01
GOTERM_MF_FAT	GO:0030552--cAMP binding	3	0.341685649	2.E-01	19085, 19088, 18575	754	14	13288	4.E+00	1.E+00	7.E-01	1.E+02
GOTERM_MF_FAT	GO:0030551--cyclic nucleotide binding	3	0.341685649	4.E-01	19085, 19088, 18575	754	22	13288	2.E+00	1.E+00	9.E-01	1.E+02

Annotation Cluster 151	Enrichment Score: 1.0359257383709075											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0022612--gland morphogenesis	11	1.25284738	3.E-02	13649, 20779, 14178, 19206, 12043, 1481	809	84	13588	2.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0060603--mammary gland duct morphogenesis	5	0.569476082	7.E-02	20779, 19206, 14815, 17979, 12234	809	26	13588	3.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0060443--mammary gland morphogenesis	5	0.569476082	1.E-01	20779, 19206, 14815, 17979, 12234	809	33	13588	3.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0060444--branching involved in mammary gland duct morphc	3	0.341685649	3.E-01	20779, 17979, 12234	809	19	13588	3.E+00	1.E+00	9.E-01	1.E+02

Annotation Cluster 152	Enrichment Score: 1.0234502445499685											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR000494:EGF receptor, L domain	3	0.341685649	4.E-02	13649, 23920, 16001	860	7	17763	9.E+00	1.E+00	6.E-01	5.E+01
INTERPRO	IPR006211:Furin-like cysteine rich region	3	0.341685649	4.E-02	13649, 23920, 16001	860	7	17763	9.E+00	1.E+00	6.E-01	5.E+01
GOTERM_MF_FAT	GO:0004714--transmembrane receptor protein tyrosine kinase act	7	0.797266515	1.E-01	13836, 18596, 13649, 23920, 19713, 1600	754	56	13288	2.E+00	1.E+00	5.E-01	8.E+01
INTERPRO	IPR006212:Furin-like repeat	3	0.341685649	2.E-01	13649, 23920, 16001	860	17	17763	4.E+00	1.E+00	1.E+00	1.E+02
SMART	SM00261:FU	3	0.341685649	2.E-01	13649, 23920, 16001	492	17	9131	3.E+00	1.E+00	8.E-01	1.E+02

Annotation Cluster 153	Enrichment Score: 1.0192297409324558											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_SEQ_FEATURE	metal ion-binding site:Potassium	5	0.569476082	1.E-04	18746, 12039, 18770, 232087, 11720	861	6	16021	2.E+01	2.E-01	1.E-02	2.E-01
SP_PIR_KEYWORDS	potassium	5	0.569476082	8.E-01	18746, 12039, 18770, 232087, 11720	869	118	17854	9.E-01	1.E+00	1.E+00	1.E+02
GOTERM_MF_FAT	GO:0030955--potassium ion binding	5	0.569476082	9.E-01	18746, 12039, 18770, 232087, 11720	754	118	13288	7.E-01	1.E+00	1.E+00	1.E+02
GOTERM_MF_FAT	GO:0031420--alkali metal ion binding	7	0.797266515	1.E+00	18746, 12039, 18770, 232087, 20505, 205	754	206	13288	6.E-01	1.E+00	1.E+00	1.E+02



Annotation Cluster 154		Enrichment Score: 1.003895646080884											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_CC_FAT	GO:0000775~chromosome, centromeric region	12	1.366742597	3.E-02	18393, 67052, 19053, 20871, 12236, 1800	636	111	12504	2.E+00	1.E+00	1.E-01	3.E+01	
GOTERM_CC_FAT	GO:0000793~condensed chromosome	10	1.138952164	9.E-02	18393, 13006, 67052, 12236, 18005, 1712	636	107	12504	2.E+00	1.E+00	3.E-01	7.E+01	
GOTERM_CC_FAT	GO:0000776~kinetochore	7	0.797266515	9.E-02	18393, 67052, 12236, 17120, 56150, 2046	636	62	12504	2.E+00	1.E+00	3.E-01	7.E+01	
GOTERM_CC_FAT	GO:0000777~condensed chromosome kinetochore	6	0.683371298	1.E-01	18393, 67052, 12236, 17120, 56150, 1291	636	53	12504	2.E+00	1.E+00	4.E-01	9.E+01	
SP_PIR_KEYWORDS	kinetochore	6	0.683371298	2.E-01	67052, 18817, 12236, 18005, 17120, 5615	869	61	17854	2.E+00	1.E+00	5.E-01	9.E+01	
GOTERM_CC_FAT	GO:0000779~condensed chromosome, centromeric region	6	0.683371298	2.E-01	18393, 67052, 12236, 17120, 56150, 1291	636	60	12504	2.E+00	1.E+00	5.E-01	9.E+01	
Annotation Cluster 155		Enrichment Score: 1.0023259318990503											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_BP_FAT	GO:0006525~arginine metabolic process	4	0.455580866	1.E-02	18126, 18416, 109900, 11847	809	9	13588	7.E+00	1.E+00	2.E-01	2.E+01	
SP_PIR_KEYWORDS	urea cycle	3	0.341685649	4.E-02	18416, 109900, 11847	869	7	17854	9.E+00	1.E+00	2.E-01	5.E+01	
GOTERM_BP_FAT	GO:0019627~urea metabolic process	3	0.341685649	1.E-01	18416, 109900, 11847	809	9	13588	6.E+00	1.E+00	5.E-01	8.E+01	
GOTERM_BP_FAT	GO:0000050~urea cycle	3	0.341685649	1.E-01	18416, 109900, 11847	809	9	13588	6.E+00	1.E+00	5.E-01	8.E+01	
GOTERM_BP_FAT	GO:0043604~amide biosynthetic process	3	0.341685649	1.E-01	18416, 109900, 11847	809	10	13588	5.E+00	1.E+00	6.E-01	9.E+01	
GOTERM_BP_FAT	GO:0009064~glutamine family amino acid metabolic process	5	0.569476082	3.E-01	18126, 18416, 109900, 11847, 14645	809	43	13588	2.E+00	1.E+00	8.E-01	1.E+02	
KEGG_PATHWAY	mmu00330:Arginine and proline metabolism	6	0.683371298	6.E-01	18126, 14661, 18416, 109900, 11847, 146	580	53	5738	1.E+00	1.E+00	8.E-01	1.E+02	
Annotation Cluster 156		Enrichment Score: 0.9889162757344856											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_BP_FAT	GO:0032386~regulation of intracellular transport	8	0.911161731	1.E-02	18747, 18826, 14226, 68092, 192176, 125	809	42	13588	3.E+00	1.E+00	1.E-01	2.E+01	
GOTERM_BP_FAT	GO:0032880~regulation of protein localization	12	1.366742597	2.E-02	16994, 18747, 18826, 14570, 104215, 192	809	90	13588	2.E+00	1.E+00	2.E-01	3.E+01	
GOTERM_BP_FAT	GO:0051051~negative regulation of transport	10	1.138952164	3.E-02	16994, 11486, 17999, 14678, 104215, 184	809	72	13588	2.E+00	1.E+00	2.E-01	4.E+01	
GOTERM_BP_FAT	GO:0033157~regulation of intracellular protein transport	5	0.569476082	1.E-01	18747, 18826, 192176, 12568, 24069	809	30	13588	3.E+00	1.E+00	5.E-01	8.E+01	
GOTERM_BP_FAT	GO:0070201~regulation of establishment of protein localization	8	0.911161731	1.E-01	16994, 18747, 18826, 104215, 192176, 12	809	71	13588	2.E+00	1.E+00	6.E-01	9.E+01	
GOTERM_BP_FAT	GO:0046822~regulation of nucleocytoplasmic transport	5	0.569476082	2.E-01	18747, 68092, 192176, 12568, 24069	809	35	13588	2.E+00	1.E+00	7.E-01	9.E+01	
GOTERM_BP_FAT	GO:0046824~positive regulation of nucleocytoplasmic transport	3	0.341685649	2.E-01	18747, 68092, 192176	809	12	13588	4.E+00	1.E+00	7.E-01	1.E+02	
GOTERM_BP_FAT	GO:0051223~regulation of protein transport	7	0.797266515	2.E-01	16994, 18747, 18826, 192176, 12568, 220	809	65	13588	2.E+00	1.E+00	7.E-01	1.E+02	
GOTERM_BP_FAT	GO:0032388~positive regulation of intracellular transport	3	0.341685649	2.E-01	18747, 68092, 192176	809	15	13588	3.E+00	1.E+00	8.E-01	1.E+02	
GOTERM_BP_FAT	GO:0051224~negative regulation of protein transport	3	0.341685649	3.E-01	192176, 12568, 24069	809	19	13588	3.E+00	1.E+00	9.E-01	1.E+02	
GOTERM_BP_FAT	GO:0051222~positive regulation of protein transport	3	0.341685649	6.E-01	16994, 18747, 192176	809	36	13588	1.E+00	1.E+00	1.E+00	1.E+02	
Annotation Cluster 157		Enrichment Score: 0.9782336912804246											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_BP_FAT	GO:0031016~pancreas development	6	0.683371298	7.E-02	15376, 18609, 19378, 16001, 18576, 1600	809	37	13588	3.E+00	1.E+00	4.E-01	7.E+01	
GOTERM_BP_FAT	GO:0031017~exocrine pancreas development	3	0.341685649	8.E-02	18609, 16001, 16000	809	8	13588	6.E+00	1.E+00	5.E-01	8.E+01	
GOTERM_BP_FAT	GO:0035272~exocrine system development	5	0.569476082	2.E-01	13649, 14178, 18609, 16001, 16000	809	41	13588	2.E+00	1.E+00	8.E-01	1.E+02	
Annotation Cluster 158		Enrichment Score: 0.9687479811151865											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_BP_FAT	GO:0010604~positive regulation of macromolecule metabolic pro	54	6.150341686	7.E-03	22130, 21869, 12912, 12914, 16543, 2193	809	633	13588	1.E+00	1.E+00	9.E-02	1.E+01	
GOTERM_BP_FAT	GO:0031328~positive regulation of cellular biosynthetic process	47	5.353075171	1.E-02	17536, 22130, 15376, 17869, 12912, 2186	809	552	13588	1.E+00	1.E+00	1.E-01	2.E+01	
GOTERM_BP_FAT	GO:0009891~positive regulation of biosynthetic process	47	5.353075171	1.E-02	17536, 22130, 15376, 17869, 12912, 2186	809	557	13588	1.E+00	1.E+00	2.E-01	2.E+01	
GOTERM_BP_FAT	GO:0010557~positive regulation of macromolecule biosynthetic p	43	4.897494305	3.E-02	17536, 22130, 15376, 17869, 21869, 1291	809	530	13588	1.E+00	1.E+00	3.E-01	5.E+01	
GOTERM_BP_FAT	GO:0045944~positive regulation of transcription from RNA polym	30	3.416856492	6.E-02	17536, 22130, 15376, 17869, 21869, 1291	809	358	13588	1.E+00	1.E+00	4.E-01	6.E+01	
GOTERM_BP_FAT	GO:0051173~positive regulation of nitrogen compound metabol	41	4.669703872	6.E-02	17536, 22130, 15376, 17869, 21869, 1291	809	526	13588	1.E+00	1.E+00	4.E-01	7.E+01	
GOTERM_BP_FAT	GO:0045893~positive regulation of transcription, DNA-dependent	33	3.758542141	8.E-02	17536, 22130, 15376, 17869, 21869, 1291	809	416	13588	1.E+00	1.E+00	5.E-01	8.E+01	
GOTERM_BP_FAT	GO:0051254~positive regulation of RNA metabolic process	33	3.758542141	9.E-02	17536, 22130, 15376, 17869, 21869, 1291	809	419	13588	1.E+00	1.E+00	5.E-01	8.E+01	
GOTERM_BP_FAT	GO:0045941~positive regulation of transcription	35	3.986332574	1.E-01	17536, 22130, 15376, 17869, 21869, 1291	809	475	13588	1.E+00	1.E+00	7.E-01	9.E+01	
GOTERM_BP_FAT	GO:0006357~regulation of transcription from RNA polymerase II p	44	5.011389522	2.E-01	60406, 17536, 22130, 15376, 433759, 197	809	616	13588	1.E+00	1.E+00	7.E-01	1.E+02	
GOTERM_BP_FAT	GO:0010628~positive regulation of gene expression	35	3.986332574	2.E-01	17536, 22130, 15376, 17869, 21869, 1291	809	488	13588	1.E+00	1.E+00	7.E-01	1.E+02	
GOTERM_BP_FAT	GO:0045935~positive regulation of nucleobase, nucleoside, nucle	35	3.986332574	3.E-01	17536, 22130, 15376, 17869, 21869, 1291	809	510	13588	1.E+00	1.E+00	8.E-01	1.E+02	
GOTERM_MF_FAT	GO:0016563~transcription activator activity	18	2.050113895	3.E-01	101206, 12043, 20375, 14462, 12815, 218	754	259	13288	1.E+00	1.E+00	9.E-01	1.E+02	
GOTERM_MF_FAT	GO:0030528~transcription regulator activity	64	7.28929385	8.E-01	22130, 101206, 14815, 12815, 12912, 218	754	1206	13288	9.E-01	1.E+00	1.E+00	1.E+02	
GOTERM_BP_FAT	GO:0006355~regulation of transcription, DNA-dependent	71	8.086560364	1.E+00	22130, 14815, 12912, 21869, 12914, 1654	809	1465	13588	8.E-01	1.E+00	1.E+00	1.E+02	
GOTERM_BP_FAT	GO:0051252~regulation of RNA metabolic process	71	8.086560364	1.E+00	22130, 14815, 12912, 21869, 12914, 1654	809	1488	13588	8.E-01	1.E+00	1.E+00	1.E+02	
Annotation Cluster 159		Enrichment Score: 0.9426522015448877											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
INTERPRO	IPR011765:Peptidase M16, N-terminal	3	0.341685649	3.E-02	73078, 67003, 22273	860	6	17763	1.E+01	1.E+00	5.E-01	4.E+01	
INTERPRO	IPR011237:Peptidase M16, core	3	0.341685649	4.E-02	73078, 67003, 22273	860	7	17763	9.E+00	1.E+00	6.E-01	5.E+01	
INTERPRO	IPR007863:Peptidase M16, C-terminal	3	0.341685649	4.E-02	73078, 67003, 22273	860	7	17763	9.E+00	1.E+00	6.E-01	5.E+01	
INTERPRO	IPR001431:Peptidase M16, zinc-binding site	3	0.341685649	4.E-02	73078, 67003, 22273	860	7	17763	9.E+00	1.E+00	6.E-01	5.E+01	
GOTERM_MF_FAT	GO:0004222~metalloendopeptidase activity	3	0.341685649	1.E+00	73078, 67003, 22273	754	114	13288	5.E-01	1.E+00	1.E+00	1.E+02	



GOTERM_MF_FAT	GO:0008237~metallopeptidase activity	4	0.455580866	1.E+00	73078, 67003, 59029, 22273	754	187	13288	4.E-01	1.E+00	1.E+00	1.E+02
Annotation Cluster 160	Enrichment Score: 0.938075424389345											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0005158~insulin receptor binding	4	0.455580866	7.E-02	18708, 16367, 27261, 384783	754	17	13288	4.E+00	1.E+00	5.E-01	7.E+01
INTERPRO	IPR002404Insulin receptor substrate-1, PTB	3	0.341685649	1.E-01	16367, 27261, 384783	860	13	17763	5.E+00	1.E+00	9.E-01	9.E+01
UP_SEQ_FEATURE	domainIRS-type PTB	3	0.341685649	1.E-01	16367, 27261, 384783	861	12	16021	5.E+00	1.E+00	1.E+00	9.E+01
SMART	SM00310:PTBI	3	0.341685649	2.E-01	16367, 27261, 384783	492	13	9131	4.E+00	1.E+00	7.E-01	9.E+01
Annotation Cluster 161	Enrichment Score: 0.9321395095510709											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0031589~cell-substrate adhesion	8	0.911161731	5.E-02	19944, 665032, 50768, 12043, 16414, 118	809	57	13588	2.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0007160~cell-matrix adhesion	7	0.797266515	7.E-02	50768, 12043, 16414, 11856, 16412, 1256	809	50	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0048041~focal adhesion formation	3	0.341685649	8.E-02	50768, 12043, 11856	809	8	13588	6.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0034330~cell junction organization	5	0.569476082	1.E-01	13052, 50768, 12043, 11856, 12540	809	32	13588	3.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0007044~cell-substrate junction assembly	3	0.341685649	2.E-01	50768, 12043, 11856	809	14	13588	4.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0034329~cell junction assembly	3	0.341685649	4.E-01	50768, 12043, 11856	809	21	13588	2.E+00	1.E+00	9.E-01	1.E+02
Annotation Cluster 162	Enrichment Score: 0.929721043961941											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0002822~regulation of adaptive immune response based on :	9	1.025056948	2.E-02	14972, 14127, 15170, 15018, 16197, 1148	809	56	13588	3.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0002819~regulation of adaptive immune response	9	1.025056948	2.E-02	14972, 14127, 15170, 15018, 16197, 1148	809	56	13588	3.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0002706~regulation of lymphocyte mediated immunity	9	1.025056948	4.E-02	19370, 14972, 14127, 15170, 15018, 1619	809	65	13588	2.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0048585~negative regulation of response to stimulus	8	0.911161731	9.E-02	56717, 15170, 12703, 16197, 12702, 1148	809	65	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0002823~negative regulation of adaptive immune response b	3	0.341685649	2.E-01	15170, 16197, 19056	809	13	13588	4.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0002820~negative regulation of adaptive immune response	3	0.341685649	2.E-01	15170, 16197, 19056	809	13	13588	4.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0002707~negative regulation of lymphocyte mediated immun	3	0.341685649	2.E-01	15170, 16197, 19056	809	14	13588	4.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0002704~negative regulation of leukocyte mediated immunity	3	0.341685649	2.E-01	15170, 16197, 19056	809	14	13588	4.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0002683~negative regulation of immune system process	7	0.797266515	3.E-01	15170, 16197, 11486, 16396, 16190, 1905	809	76	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0002698~negative regulation of immune effector process	3	0.341685649	3.E-01	15170, 16197, 19056	809	20	13588	3.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0050777~negative regulation of immune response	3	0.341685649	5.E-01	15170, 16197, 19056	809	26	13588	2.E+00	1.E+00	1.E+00	1.E+02
Annotation Cluster 163	Enrichment Score: 0.9242944095001885											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0001914~regulation of T cell mediated cytotoxicity	5	0.569476082	3.E-03	14972, 15018, 16197, 19056, 12010	809	11	13588	8.E+00	1.E+00	5.E-02	5.E+00
GOTERM_BP_FAT	GO:0001910~regulation of leukocyte mediated cytotoxicity	7	0.797266515	8.E-03	19370, 14972, 15018, 16197, 27007, 3790	809	30	13588	4.E+00	1.E+00	1.E-01	1.E+01
GOTERM_BP_FAT	GO:0031341~regulation of cell killing	7	0.797266515	8.E-03	19370, 14972, 15018, 16197, 27007, 3790	809	30	13588	4.E+00	1.E+00	1.E-01	1.E+01
SP_PIR_KEYWORDS	mhc i	4	0.455580866	1.E-02	15007, 14972, 15018, 12010	869	11	17854	7.E+00	1.E+00	6.E-02	2.E+01
GOTERM_BP_FAT	GO:0002697~regulation of immune effector process	12	1.366742597	1.E-02	19370, 15170, 14972, 15018, 27007, 1680	809	88	13588	2.E+00	1.E+00	2.E-01	2.E+01
GOTERM_BP_FAT	GO:0002474~antigen processing and presentation of peptide ant	5	0.569476082	2.E-02	15007, 14972, 14127, 15018, 12010	809	17	13588	5.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0002822~regulation of adaptive immune response based on :	9	1.025056948	2.E-02	14972, 14127, 15170, 15018, 16197, 1148	809	56	13588	3.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0002819~regulation of adaptive immune response	9	1.025056948	2.E-02	14972, 14127, 15170, 15018, 16197, 1148	809	56	13588	3.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0002699~positive regulation of immune effector process	8	0.911161731	2.E-02	19370, 14972, 14127, 15018, 27007, 3790	809	46	13588	3.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0002709~regulation of T cell mediated immunity	5	0.569476082	2.E-02	14972, 15018, 16197, 19056, 12010	809	18	13588	5.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0002703~regulation of leukocyte mediated immunity	10	1.138952164	2.E-02	19370, 14972, 14127, 15170, 15018, 1619	809	70	13588	2.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0002706~regulation of lymphocyte mediated immunity	9	1.025056948	4.E-02	19370, 14972, 14127, 15170, 15018, 1619	809	65	13588	2.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0001912~positive regulation of leukocyte mediated cytotoxici	5	0.569476082	4.E-02	19370, 14972, 15018, 27007, 379043, 120	809	23	13588	4.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0031343~positive regulation of cell killing	5	0.569476082	4.E-02	19370, 14972, 15018, 27007, 379043, 120	809	23	13588	4.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0032729~positive regulation of interferon-gamma production	4	0.455580866	8.E-02	12051, 19370, 15018, 27007, 379043	809	17	13588	4.E+00	1.E+00	5.E-01	8.E+01
UP_SEQ_FEATURE	region of interest:Alpha-3	3	0.341685649	8.E-02	15007, 14972, 15018	861	9	16021	6.E+00	1.E+00	9.E-01	8.E+01
GOTERM_BP_FAT	GO:0002708~positive regulation of lymphocyte mediated immuni	6	0.683371298	9.E-02	19370, 14972, 14127, 15018, 27007, 3790	809	40	13588	3.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0002705~positive regulation of leukocyte mediated immunity	6	0.683371298	9.E-02	19370, 14972, 14127, 15018, 27007, 3790	809	40	13588	3.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0001916~positive regulation of T cell mediated cytotoxicity	3	0.341685649	1.E-01	14972, 15018, 12010	809	9	13588	6.E+00	1.E+00	5.E-01	8.E+01
UP_SEQ_FEATURE	region of interest:Alpha-1	3	0.341685649	1.E-01	15007, 14972, 15018	861	11	16021	5.E+00	1.E+00	1.E+00	9.E+01
UP_SEQ_FEATURE	region of interest:Alpha-2	3	0.341685649	1.E-01	15007, 14972, 15018	861	11	16021	5.E+00	1.E+00	1.E+00	9.E+01
GOTERM_BP_FAT	GO:0002821~positive regulation of adaptive immune response	5	0.569476082	1.E-01	14972, 14127, 15018, 11486, 12010	809	34	13588	2.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0002824~positive regulation of adaptive immune response b2	5	0.569476082	1.E-01	14972, 14127, 15018, 11486, 12010	809	34	13588	2.E+00	1.E+00	6.E-01	9.E+01
UP_SEQ_FEATURE	domainIg-like C1-type	4	0.455580866	1.E-01	15007, 14972, 15018, 12010	861	25	16021	3.E+00	1.E+00	1.E+00	9.E+01
GOTERM_BP_FAT	GO:0048002~antigen processing and presentation of peptide ant	5	0.569476082	2.E-01	15007, 14972, 14127, 15018, 12010	809	35	13588	2.E+00	1.E+00	7.E-01	9.E+01
GOTERM_BP_FAT	GO:0002711~positive regulation of T cell mediated immunity	3	0.341685649	2.E-01	14972, 15018, 12010	809	13	13588	4.E+00	1.E+00	7.E-01	1.E+02
UP_SEQ_FEATURE	region of interest:Connecting peptide	4	0.455580866	2.E-01	15007, 14972, 15018, 18792	861	28	16021	3.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0032649~regulation of interferon-gamma production	4	0.455580866	3.E-01	12051, 19370, 15018, 27007, 379043	809	32	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_CC_FAT	GO:0042612~MHC class I protein complex	4	0.455580866	4.E-01	15007, 14972, 15018, 12010	636	42	12504	2.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0002478~antigen processing and presentation of exogenous	3	0.341685649	4.E-01	14972, 14127, 12010	809	23	13588	2.E+00	1.E+00	9.E-01	1.E+02
INTERPRO	IPR011161:MHC class I-like antigen recognition	4	0.455580866	4.E-01	19370, 15007, 14972, 15018, 379043	860	49	17763	2.E+00	1.E+00	1.E+00	1.E+02



GOTERM_CC_FAT	GO:0042611~MHC protein complex	4	0.455580866	5.E-01 15007, 14972, 15018, 12010	636	52	12504	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0019884~antigen processing and presentation of exogenous	3	0.341685649	5.E-01 14972, 14127, 12010	809	28	13588	2.E+00	1.E+00	1.E+00	1.E+02
PIR_SUPERFAMILY	PIRSF001990:class I histocompatibility antigen	3	0.341685649	5.E-01 15007, 14972, 15018	576	24	8136	2.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0019882~antigen processing and presentation	6	0.683371298	6.E-01 19370, 15007, 14972, 14127, 15018, 3790	809	87	13588	1.E+00	1.E+00	1.E+00	1.E+02
INTERPRO	IPR001039:MHC class I, alpha chain, alpha1 and alpha2	3	0.341685649	6.E-01 15007, 14972, 15018	860	41	17763	2.E+00	1.E+00	1.E+00	1.E+02
INTERPRO	IPR003597:Immunoglobulin C1-set	4	0.455580866	8.E-01 15007, 14972, 15018, 12010	860	83	17763	1.E+00	1.E+00	1.E+00	1.E+02
KEGG_PATHWAY	mmu04940:Type I diabetes mellitus	6	0.683371298	8.E-01 15007, 14972, 15018, 16333, 16334, 1493	580	63	5738	9.E-01	1.E+00	9.E-01	1.E+02
KEGG_PATHWAY	mmu04612:Antigen processing and presentation	8	0.911161731	8.E-01 15007, 14972, 15018, 15512, 15481, 1482	580	91	5738	9.E-01	1.E+00	9.E-01	1.E+02
SMART	SM00407:IGc1	4	0.455580866	8.E-01 15007, 14972, 15018, 12010	492	83	9131	9.E-01	1.E+00	1.E+00	1.E+02
INTERPRO	IPR003006:Immunoglobulin/major histocompatibility complex, cor	4	0.455580866	9.E-01 15007, 14972, 15018, 12010	860	98	17763	8.E-01	1.E+00	1.E+00	1.E+02
KEGG_PATHWAY	mmu05332:Graft-versus-host disease	4	0.455580866	9.E-01 15007, 14972, 15018, 14939	580	58	5738	7.E-01	1.E+00	1.E+00	1.E+02
KEGG_PATHWAY	mmu05330:Allograft rejection	4	0.455580866	9.E-01 15007, 14972, 15018, 14939	580	58	5738	7.E-01	1.E+00	1.E+00	1.E+02
KEGG_PATHWAY	mmu05320:Autoimmune thyroid disease	4	0.455580866	1.E+00 15007, 14972, 15018, 14939	580	72	5738	5.E-01	1.E+00	1.E+00	1.E+02

Annotation Cluster 164		Enrichment Score: 0.923704351576393										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0051924~regulation of calcium ion transport	7	0.797266515	1.E-02	234779, 14226, 14678, 12028, 12018, 120	809	34	13588	3.E+00	1.E+00	2.E-01	2.E+01
GOTERM_BP_FAT	GO:0034765~regulation of ion transmembrane transport	3	0.341685649	2.E-01	234779, 14226, 14678	809	13	13588	4.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0022898~regulation of transmembrane transporter activity	3	0.341685649	2.E-01	234779, 14226, 14678	809	13	13588	4.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0034762~regulation of transmembrane transport	3	0.341685649	2.E-01	234779, 14226, 14678	809	13	13588	4.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0032412~regulation of ion transmembrane transporter activity	3	0.341685649	2.E-01	234779, 14226, 14678	809	13	13588	4.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0032409~regulation of transporter activity	3	0.341685649	2.E-01	234779, 14226, 14678	809	14	13588	4.E+00	1.E+00	7.E-01	1.E+02

Annotation Cluster 165	Enrichment Score: 0.919994351488386											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
	GOTERM_MF_FAT	GO:0008201~heparin binding	10	1.138952164	4.E-02 19944, 12831, 19206, 19934, 11816, 6650	754	83	13288	2.E+00	1.E+00	3.E-01	5.E+01
	GOTERM_MF_FAT	GO:0001871~pattern binding	12	1.366742597	1.E-01 19944, 12831, 19206, 19934, 11816, 6650	754	128	13288	2.E+00	1.E+00	6.E-01	8.E+01
	GOTERM_MF_FAT	GO:0030247~polysaccharide binding	12	1.366742597	1.E-01 19944, 12831, 19206, 19934, 11816, 6650	754	128	13288	2.E+00	1.E+00	6.E-01	8.E+01
	GOTERM_MF_FAT	GO:0005539~glycosaminoglycan binding	11	1.25284738	1.E-01 19944, 12831, 19206, 19934, 11816, 6650	754	114	13288	2.E+00	1.E+00	6.E-01	8.E+01
	SP_PIR_KEYWORDS	heparin-binding	6	0.683371298	1.E-01 12831, 669888, 56744, 11816, 19934, 141	869	53	17854	2.E+00	1.E+00	3.E-01	8.E+01
	GOTERM_MF_FAT	GO:0030246~carbohydrate binding	20	2.277904328	4.E-01 19944, 17159, 12831, 19206, 665032, 118	754	317	13288	1.E+00	1.E+00	1.E+00	1.E+02

Annotation Cluster 166		Enrichment Score: 0.9195568833008677										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_SEQ_FEATURE	zinc finger region:GATA-type 1	3	0.341685649	4.E-02	14465, 14462, 14460	861	6	16021	9.E+00	1.E+00	7.E-01	5.E+01
UP_SEQ_FEATURE	zinc finger region:GATA-type 2	3	0.341685649	4.E-02	14465, 14462, 14460	861	6	16021	9.E+00	1.E+00	7.E-01	5.E+01
INTERPRO	IPR000679:Zinc finger, GATA-type	3	0.341685649	2.E-01	14465, 14462, 14460	860	16	17763	4.E+00	1.E+00	9.E-01	1.E+02
SMART	SM00401:ZnF_GATA	3	0.341685649	2.E-01	14465, 14462, 14460	492	16	9131	3.E+00	1.E+00	8.E-01	1.E+02
INTERPRO	IPR013088:Zinc finger, NHR/GATA-type	4	0.455580866	5.E-01	14465, 14815, 14462, 14460	860	53	17763	2.E+00	1.E+00	1.E+00	1.E+02

Annotation Cluster 167	Enrichment Score: 0.9190366010762988											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0032760~positive regulation of tumor necrosis factor product	7	0.797266515	1.E-04	14127, 17874, 12475, 21898, 24088, 1680	809	15	13588	8.E+00	3.E-01	4.E-03	2.E-01
UP_SEQ_FEATURE	domain:TLR	8	0.911161731	3.E-04	17874, 239081, 21899, 21898, 117149, 24	861	25	16021	6.E+00	4.E-01	2.E-02	4.E-01
INTERPRO	IPR000157:Toll-Interleukin receptor	7	0.797266515	8.E-04	17874, 239081, 21899, 21898, 117149, 24	860	24	17763	6.E+00	7.E-01	3.E-02	1.E+00
SMART	SM00255:TLR	7	0.797266515	1.E-03	17874, 239081, 21899, 21898, 117149, 24	492	24	9131	5.E+00	3.E-01	3.E-02	2.E+00
GOTERM_BP_FAT	GO:0070391~response to lipoteichoic acid	4	0.455580866	2.E-03	12475, 21898, 24088, 16803	809	5	13588	1.E+01	1.E+00	3.E-02	3.E+00
GOTERM_BP_FAT	GO:0045087~innate immune response	15	1.708428246	4.E-03	15170, 239081, 21899, 21898, 16803, 178	809	107	13588	2.E+00	1.E+00	6.E-02	8.E+00
SP_PIR_KEYWORDS	inflammatory response	11	1.25284738	4.E-03	20310, 17874, 12475, 239081, 246779, 17	869	78	17854	3.E+00	9.E-01	2.E-02	6.E+00
SP_PIR_KEYWORDS	immune response	18	2.050113895	8.E-03	15007, 14972, 12475, 15018, 239081, 218	869	184	17854	2.E+00	1.E+00	4.E-02	1.E+01
INTERPRO	IPR017241:Toll-like receptor	3	0.341685649	1.E-02	21899, 21898, 24088	860	4	17763	2.E+01	1.E+00	3.E-01	2.E+01
PIR_SUPERFAMILY	PIRSF037595:Toll-like_receptor	3	0.341685649	3.E-02	21899, 21898, 24088	576	4	8136	1.E+01	1.E+00	8.E-01	3.E+01
GOTERM_BP_FAT	GO:0032675~regulation of interleukin-6 production	6	0.683371298	4.E-02	14127, 17874, 21899, 21898, 24088, 1067	809	32	13588	3.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0007249~I-kappaB kinase/NF-kappaB cascade	5	0.569476082	8.E-02	57874, 12229, 21899, 21898, 117149	809	28	13588	3.E+00	1.E+00	5.E-01	8.E+01
INTERPRO	IPR004075:Interleukin-1 receptor, type I/Toll precursor	3	0.341685649	1.E-01	21899, 24088, 17082	860	12	17763	5.E+00	1.E+00	9.E-01	9.E+01
SP_PIR_KEYWORDS	innate immunity	7	0.797266515	2.E-01	239081, 246779, 21899, 21898, 230558, 1	869	75	17854	2.E+00	1.E+00	4.E-01	9.E+01
UP_SEQ_FEATURE	repeat:LRR 11	5	0.569476082	7.E-01	12475, 239081, 21899, 21898, 24088	861	88	16021	1.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:LRR 14	3	0.341685649	8.E-01	21899, 21898, 24088	861	55	16021	1.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:LRR 10	5	0.569476082	8.E-01	12475, 239081, 21899, 21898, 24088	861	103	16021	9.E-01	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:LRR 13	3	0.341685649	9.E-01	21899, 21898, 24088	861	65	16021	9.E-01	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:LRR 9	5	0.569476082	9.E-01	12475, 239081, 21899, 21898, 24088	861	122	16021	8.E-01	1.E+00	1.E+00	1.E+02
INTERPRO	IPR000483:Cysteine-rich flanking region, C-terminal	3	0.341685649	9.E-01	21899, 21898, 24088	860	83	17763	7.E-01	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:LRR 12	3	0.341685649	9.E-01	21899, 21898, 24088	861	79	16021	7.E-01	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:LRR 8	5	0.569476082	9.E-01	12475, 239081, 21899, 21898, 24088	861	133	16021	7.E-01	1.E+00	1.E+00	1.E+02
SMART	SM00082:LRRCT	3	0.341685649	9.E-01	21899, 21898, 24088	492	83	9131	7.E-01	1.E+00	1.E+00	1.E+02



INTERPRO	IPR001611:Leucine-rich repeat	6	0.683371298	1.E+00	12475, 239081, 21899, 21898, 98238, 240	860	202	17763	6.E-01	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:LRR 7	5	0.569476082	1.E+00	12475, 239081, 21899, 21898, 24088	861	157	16021	6.E-01	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:LRR 5	6	0.683371298	1.E+00	12475, 239081, 21899, 21898, 98238, 240	861	203	16021	5.E-01	1.E+00	1.E+00	1.E+02
INTERPRO	IPR003591:Leucine-rich repeat, typical subtype	3	0.341685649	1.E+00	239081, 21899, 24088	860	129	17763	5.E-01	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:LRR 6	5	0.569476082	1.E+00	12475, 239081, 21899, 21898, 24088	861	185	16021	5.E-01	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:LRR 4	6	0.683371298	1.E+00	12475, 239081, 21899, 21898, 98238, 240	861	221	16021	5.E-01	1.E+00	1.E+00	1.E+02
SMART	SM00369:LRR_TYP	3	0.341685649	1.E+00	239081, 21899, 24088	492	129	9131	4.E-01	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:LRR 3	6	0.683371298	1.E+00	12475, 239081, 21899, 21898, 98238, 240	861	245	16021	5.E-01	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	leucine-rich repeat	6	0.683371298	1.E+00	12475, 239081, 21899, 21898, 98238, 240	869	275	17854	4.E-01	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:LRR 2	6	0.683371298	1.E+00	12475, 239081, 21899, 21898, 98238, 240	861	266	16021	4.E-01	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:LRR 1	6	0.683371298	1.E+00	12475, 239081, 21899, 21898, 98238, 240	861	266	16021	4.E-01	1.E+00	1.E+00	1.E+02

Annotation Cluster 168	Enrichment Score: 0.9166175390872011											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0046907~intracellular transport	41	4.669703872	3.E-03	215280, 269589, 11852, 14026, 171531, 2	809	431	13588	2.E+00	1.E+00	5.E-02	6.E+00
GOTERM_BP_FAT	GO:0034613~cellular protein localization	25	2.84738041	8.E-02	269589, 171531, 236643, 320051, 231103	809	299	13588	1.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0070727~cellular macromolecule localization	25	2.84738041	9.E-02	269589, 171531, 236643, 320051, 231103	809	301	13588	1.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0006886~intracellular protein transport	21	2.391799544	2.E-01	269589, 19894, 56338, 54401, 380714, 12	809	276	13588	1.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0008104~protein localization	50	5.69476082	3.E-01	238055, 171531, 69875, 108672, 320051	809	753	13588	1.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0045184~establishment of protein localization	41	4.669703872	5.E-01	269589, 11852, 238055, 14567, 14569, 17	809	656	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0015031~protein transport	39	4.44191344	6.E-01	269589, 11852, 238055, 14567, 14569, 17	809	651	13588	1.E+00	1.E+00	1.E+00	1.E+02

Annotation Cluster 169	Enrichment Score: 0.9137964582582717											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0009119~ribonucleoside metabolic process	7	0.797266515	3.E-02	22017, 11486, 72269, 232087, 56749, 222	809	39	13588	3.E+00	1.E+00	2.E-01	4.E+01
GOTERM_BP_FAT	GO:0009164~nucleoside catabolic process	3	0.341685649	5.E-02	11486, 72269, 99586	809	6	13588	8.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0009116~nucleoside metabolic process	8	0.911161731	5.E-02	22017, 11486, 72269, 232087, 56749, 708	809	56	13588	2.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0046131~pyrimidine ribonucleoside metabolic process	4	0.455580866	6.E-02	72269, 56749, 22271, 99586	809	15	13588	4.E+00	1.E+00	4.E-01	6.E+01
GOTERM_BP_FAT	GO:0034656~nucleobase, nucleoside and nucleotide catabolic process	6	0.683371298	6.E-02	11486, 17970, 72269, 17969, 22271, 9958	809	36	13588	3.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0034655~nucleobase, nucleoside, nucleotide and nucleic acid	6	0.683371298	6.E-02	11486, 17970, 72269, 17969, 22271, 9958	809	36	13588	3.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0044270~nitrogen compound catabolic process	6	0.683371298	1.E-01	11486, 17970, 72269, 17969, 22271, 9958	809	42	13588	2.E+00	1.E+00	5.E-01	9.E+01
GOTERM_BP_FAT	GO:0006213~pyrimidine nucleoside metabolic process	4	0.455580866	1.E-01	72269, 56749, 22271, 99586	809	22	13588	3.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0006220~pyrimidine nucleotide metabolic process	4	0.455580866	2.E-01	56749, 22271, 66588, 99586	809	27	13588	2.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0009166~nucleotide catabolic process	4	0.455580866	3.E-01	11486, 17970, 17969, 22271	809	31	13588	2.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0042278~purine nucleoside metabolic process	3	0.341685649	4.E-01	22017, 11486, 232087	809	24	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0046128~purine ribonucleoside metabolic process	3	0.341685649	4.E-01	22017, 11486, 232087	809	24	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0046700~heterocycle catabolic process	3	0.341685649	8.E-01	11486, 72269, 99586	809	46	13588	1.E+00	1.E+00	1.E+00	1.E+02

Annotation Cluster 170	Enrichment Score: 0.9129354467250989											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_SEQ_FEATURE	domain:Leucine-zipper	12	1.366742597	3.E-02	104394, 13555, 242705, 13559, 17869, 16	861	107	16021	2.E+00	1.E+00	7.E-01	4.E+01
INTERPRO	IPR011616:bZIP transcription factor, bZIP-1	5	0.569476082	5.E-02	16477, 14281, 14282, 18022, 12912	860	30	17763	3.E+00	1.E+00	7.E-01	6.E+01
INTERPRO	IPR004827:Basic-leucine zipper (bZIP) transcription factor	6	0.683371298	1.E-01	16477, 14281, 14282, 18022, 12912, 1713	860	54	17763	2.E+00	1.E+00	9.E-01	9.E+01
SMART	SM00338:BRLZ	6	0.683371298	2.E-01	16477, 14281, 14282, 18022, 12912, 1713	492	54	9131	2.E+00	1.E+00	7.E-01	9.E+01
SP_PIR_KEYWORDS	leucine zipper	3	0.341685649	2.E-01	14281, 14282, 17135	869	16	17854	4.E+00	1.E+00	5.E-01	9.E+01
UP_SEQ_FEATURE	DNA-binding region:Basic motif	12	1.366742597	2.E-01	21349, 17119, 17869, 16477, 14281, 1428	861	154	16021	1.E+00	1.E+00	1.E+00	1.E+02
BIOCARTA	m_arenr12Pathway/Oxidative Stress Induced Gene Expression Via	5	0.569476082	4.E-01	18751, 26416, 14281, 12912, 17135	188	19	1171	2.E+00	1.E+00	7.E-01	1.E+02

Annotation Cluster 171	Enrichment Score: 0.9041140592537277											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR013126:Heat shock protein 70	3	0.341685649	1.E-01	15505, 15512, 15481	860	11	17763	6.E+00	1.E+00	8.E-01	8.E+01
INTERPRO	IPR001023:Heat shock protein Hsp70	3	0.341685649	1.E-01	15505, 15512, 15481	860	11	17763	6.E+00	1.E+00	8.E-01	8.E+01
INTERPRO	IPR018181:Heat shock protein 70, conserved site	3	0.341685649	1.E-01	15505, 15512, 15481	860	13	17763	5.E+00	1.E+00	9.E-01	9.E+01
SP_PIR_KEYWORDS	molecular chaperone	3	0.341685649	1.E-01	15505, 15512, 15481	869	14	17854	4.E+00	1.E+00	4.E-01	9.E+01
SP_PIR_KEYWORDS	stress response	5	0.569476082	2.E-01	15505, 15512, 15481, 22218, 15507	869	45	17854	2.E+00	1.E+00	5.E-01	9.E+01

Annotation Cluster 172	Enrichment Score: 0.8978597385083382											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR003096:SM22/calponin	4	0.455580866	1.E-02	73341, 22324, 71994, 57257	860	10	17763	8.E+00	1.E+00	3.E-01	2.E+01
INTERPRO	IPR001715:Calponin-like actin-binding	6	0.683371298	2.E-01	73341, 22324, 18826, 71994, 57257, 1921	860	68	17763	2.E+00	1.E+00	1.E+00	1.E+02
SMART	SM00033:CH	6	0.683371298	3.E-01	73341, 22324, 18826, 71994, 57257, 1921	492	68	9131	2.E+00	1.E+00	9.E-01	1.E+02
UP_SEQ_FEATURE	domain:CH	4	0.455580866	3.E-01	73341, 22324, 71994, 57257	861	39	16021	2.E+00	1.E+00	1.E+00	1.E+02

Annotation Cluster 173	Enrichment Score: 0.8831511105056102											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR



UP_SEQ_FEATURE	domain:MPN	3	0.341685649	1.E-01 66085, 68135, 59029	861	11	16021	5.E+00	1.E+00	1.E+00	9.E+01	
INTERPRO	IPR000555:Mov34/MPN/PAD-1	3	0.341685649	1.E-01 66085, 68135, 59029	860	13	17763	5.E+00	1.E+00	9.E-01	9.E+01	
SMART	SM00232:JAB_MPN	3	0.341685649	2.E-01 66085, 68135, 59029	492	13	9131	4.E+00	1.E+00	7.E-01	9.E+01	
Annotation Cluster 174	Enrichment Score: 0.8818378952179214											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR000591:Pleckstrin/G-protein, interacting region	4	0.455580866	9.E-02 277360, 218581, 211896, 76131	860	22	17763	4.E+00	1.E+00	8.E-01	8.E+01	
SMART	SM00049:DEP	4	0.455580866	1.E-01 277360, 218581, 211896, 76131	492	22	9131	3.E+00	1.E+00	7.E-01	8.E+01	
UP_SEQ_FEATURE	domain:DEP	3	0.341685649	2.E-01 218581, 211896, 76131	861	17	16021	3.E+00	1.E+00	1.E+00	1.E+02	
Annotation Cluster 175	Enrichment Score: 0.8591594570520011											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0010035~response to inorganic substance	10	1.138952164	1.E-01 12842, 19053, 12443, 26462, 17420, 5049	809	92	13588	2.E+00	1.E+00	5.E-01	8.E+01	
GOTERM_BP_FAT	GO:0000302~response to reactive oxygen species	5	0.569476082	2.E-01 12842, 19053, 26462, 50493, 12043	809	36	13588	2.E+00	1.E+00	7.E-01	1.E+02	
GOTERM_BP_FAT	GO:0042542~response to hydrogen peroxide	4	0.455580866	2.E-01 12842, 19053, 50493, 12043	809	24	13588	3.E+00	1.E+00	7.E-01	1.E+02	
Annotation Cluster 176	Enrichment Score: 0.8378703701405043											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0051047~positive regulation of secretion	7	0.797266515	9.E-02 14127, 14661, 12568, 12912, 83671, 1039	809	53	13588	2.E+00	1.E+00	5.E-01	8.E+01	
GOTERM_BP_FAT	GO:0046883~regulation of hormone secretion	5	0.569476082	2.E-01 14661, 18413, 18576, 12912, 103988	809	36	13588	2.E+00	1.E+00	7.E-01	1.E+02	
GOTERM_BP_FAT	GO:0046887~positive regulation of hormone secretion	3	0.341685649	2.E-01 14661, 12912, 103988	809	14	13588	4.E+00	1.E+00	7.E-01	1.E+02	
Annotation Cluster 177	Enrichment Score: 0.8343036572644715											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0045619~regulation of lymphocyte differentiation	7	0.797266515	1.E-01 15170, 16818, 12015, 16197, 11486, 1619	809	58	13588	2.E+00	1.E+00	6.E-01	9.E+01	
GOTERM_BP_FAT	GO:0050856~regulation of T cell receptor signaling pathway	3	0.341685649	1.E-01 15170, 16818, 11486	809	11	13588	5.E+00	1.E+00	6.E-01	9.E+01	
GOTERM_BP_FAT	GO:0050854~regulation of antigen receptor-mediated signaling p	3	0.341685649	2.E-01 15170, 16818, 11486	809	13	13588	4.E+00	1.E+00	7.E-01	1.E+02	
Annotation Cluster 178	Enrichment Score: 0.8241139492880126											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_SEQ_FEATURE	region of interest:Catalytic	9	1.025056948	3.E-03 11370, 235339, 15275, 15277, 18576, 185	861	47	16021	4.E+00	1.E+00	2.E-01	5.E+00	
SP_PIR_KEYWORDS	camp	6	0.683371298	1.E-02 18747, 19085, 19088, 18576, 18575, 1857	869	28	17854	4.E+00	1.E+00	5.E-02	1.E+01	
GOTERM_MF_FAT	GO:008081~phosphoric diester hydrolase activity	8	0.911161731	1.E-01 18803, 234779, 20598, 18576, 18575, 185	754	72	13288	2.E+00	1.E+00	6.E-01	8.E+01	
INTERPRO	IPR002073:3'5'-cyclic nucleotide phosphodiesterase	3	0.341685649	3.E-01 18576, 18575, 18574	860	21	17763	3.E+00	1.E+00	1.E+00	1.E+02	
SP_PIR_KEYWORDS	cGMP	3	0.341685649	3.E-01 18576, 18575, 18574	869	21	17854	3.E+00	1.E+00	6.E-01	1.E+02	
INTERPRO	IPR003607:Metal-dependent phosphohydrolase, HD region	3	0.341685649	3.E-01 18576, 18575, 18574	860	24	17763	3.E+00	1.E+00	1.E+00	1.E+02	
SMART	SM00471:HDc	3	0.341685649	4.E-01 18576, 18575, 18574	492	24	9131	2.E+00	1.E+00	9.E-01	1.E+02	
UP_SEQ_FEATURE	metal ion-binding site:Divalent metal cation 1	3	0.341685649	4.E-01 18576, 18575, 18574	861	25	16021	2.E+00	1.E+00	1.E+00	1.E+02	
UP_SEQ_FEATURE	metal ion-binding site:Divalent metal cation 2	3	0.341685649	4.E-01 18576, 18575, 18574	861	25	16021	2.E+00	1.E+00	1.E+00	1.E+02	
GOTERM_MF_FAT	GO:0044114~3',5'-cyclic-nucleotide phosphodiesterase activity	3	0.341685649	4.E-01 18576, 18575, 18574	754	24	13288	2.E+00	1.E+00	9.E-01	1.E+02	
GOTERM_MF_FAT	GO:0044112~cyclic-nucleotide phosphodiesterase activity	3	0.341685649	4.E-01 18576, 18575, 18574	754	25	13288	2.E+00	1.E+00	9.E-01	1.E+02	
Annotation Cluster 179	Enrichment Score: 0.8100791874774212											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	fatty acid metabolism	9	1.025056948	9.E-03 11370, 66885, 15107, 11409, 74147, 9374	869	61	17854	3.E+00	1.E+00	4.E-02	1.E+01	
KEGG_PATHWAY	mmu00071:Fatty acid metabolism	9	1.025056948	8.E-02 11370, 66885, 15107, 11409, 74147, 9374	580	45	5738	2.E+00	1.E+00	2.E-01	6.E+01	
UP_SEQ_FEATURE	site:Important for catalytic activity	3	0.341685649	1.E-01 15107, 74147, 93747	861	12	16021	5.E+00	1.E+00	1.E+00	9.E+01	
KEGG_PATHWAY	mmu00650:Butanoate metabolism	7	0.797266515	2.E-01 68263, 15107, 11409, 74147, 18597, 1859	580	37	5738	2.E+00	1.E+00	3.E-01	9.E+01	
KEGG_PATHWAY	mmu00062:Fatty acid elongation in mitochondria	3	0.341685649	2.E-01 15107, 93747, 231086	580	8	5738	4.E+00	1.E+00	4.E-01	9.E+01	
KEGG_PATHWAY	mmu00380:Tryptophan metabolism	4	0.455580866	8.E-01 15107, 74147, 93747, 13077	580	40	5738	1.E+00	1.E+00	9.E-01	1.E+02	
KEGG_PATHWAY	mmu00310:Lysine degradation	3	0.341685649	9.E-01 15107, 74147, 93747	580	41	5738	7.E-01	1.E+00	1.E+00	1.E+02	
Annotation Cluster 180	Enrichment Score: 0.8100422757087479											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0010035~response to inorganic substance	10	1.138952164	1.E-01 12842, 19053, 12443, 26462, 17420, 5049	809	92	13588	2.E+00	1.E+00	5.E-01	8.E+01	
GOTERM_BP_FAT	GO:0051592~response to calcium ion	4	0.455580866	1.E-01 12443, 17420, 18575, 11704	809	19	13588	4.E+00	1.E+00	5.E-01	8.E+01	
GOTERM_BP_FAT	GO:0010038~response to metal ion	5	0.569476082	4.E-01 12443, 17420, 230163, 18575, 11704	809	53	13588	2.E+00	1.E+00	9.E-01	1.E+02	
Annotation Cluster 181	Enrichment Score: 0.7956201304854009											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0009894~regulation of catabolic process	8	0.911161731	3.E-02 56717, 17999, 14447, 282663, 11651, 192	809	50	13588	3.E+00	1.E+00	2.E-01	4.E+01	
GOTERM_BP_FAT	GO:0042176~regulation of protein catabolic process	5	0.569476082	1.E-01 17999, 282663, 11651, 192176, 16396	809	32	13588	3.E+00	1.E+00	6.E-01	9.E+01	
GOTERM_BP_FAT	GO:0009896~positive regulation of catabolic process	4	0.455580866	2.E-01 17999, 14447, 11651, 16396	809	23	13588	3.E+00	1.E+00	7.E-01	1.E+02	
GOTERM_BP_FAT	GO:0032446~protein modification by small protein conjugation	8	0.911161731	2.E-01 74287, 17999, 11651, 12043, 14852, 1639	809	79	13588	2.E+00	1.E+00	7.E-01	1.E+02	
GOTERM_BP_FAT	GO:0016567~protein ubiquitination	7	0.797266515	2.E-01 74287, 17999, 11651, 12043, 14852, 1639	809	66	13588	2.E+00	1.E+00	7.E-01	1.E+02	



GOTERM_BP_FAT	GO:0045732~positive regulation of protein catabolic process	3	0.341685649	2.E-01 17999, 11651, 16396	809	14	13588	4.E+00	1.E+00	7.E-01	1.E+02	
GOTERM_BP_FAT	GO:0000209~protein polyubiquitination	3	0.341685649	3.E-01 12043, 16396, 216080	809	17	13588	3.E+00	1.E+00	8.E-01	1.E+02	
GOTERM_BP_FAT	GO:0070647~protein modification by small protein conjugation o	8	0.911161731	4.E-01 74287, 17999, 11651, 12043, 14852, 1639	809	104	13588	1.E+00	1.E+00	9.E-01	1.E+02	
Annotation Cluster 182	Enrichment Score: 0.7901556232069346											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	translation regulation	7	0.797266515	8.E-02 13684, 13685, 19317, 13665, 11651, 6809	869	63	17854	2.E+00	1.E+00	3.E-01	7.E+01	
GOTERM_BP_FAT	GO:0006446~regulation of translational initiation	4	0.455580866	1.E-01 13685, 13665, 68092, 73830	809	21	13588	3.E+00	1.E+00	6.E-01	9.E+01	
GOTERM_BP_FAT	GO:0006417~regulation of translation	9	1.025056948	2.E-01 13684, 13685, 19317, 13665, 12567, 1165	809	100	13588	2.E+00	1.E+00	8.E-01	1.E+02	
GOTERM_BP_FAT	GO:0010608~posttranscriptional regulation of gene expression	12	1.366742597	3.E-01 13684, 11785, 13685, 19317, 13665, 1256	809	148	13588	1.E+00	1.E+00	8.E-01	1.E+02	
Annotation Cluster 183	Enrichment Score: 0.7674373884303614											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	cytolysis	6	0.683371298	4.E-04 14939, 14941, 230558, 14940, 14944, 149	869	14	17854	9.E+00	2.E-01	3.E-03	5.E-01	
SP_PIR_KEYWORDS	serine proteinase	9	1.025056948	1.E-03 14939, 18815, 14941, 14940, 13035, 1879	869	43	17854	4.E+00	4.E-01	7.E-03	1.E+00	
GOTERM_BP_FAT	GO:0019835~cytolysis	6	0.683371298	1.E-02 14939, 14941, 230558, 14940, 14944, 149	809	23	13588	4.E+00	1.E+00	1.E-01	2.E+01	
UP_SEQ_FEATURE	domain:Peptidase S1	11	1.25284738	7.E-02 18048, 14939, 18815, 14941, 14940, 1303	861	111	16021	2.E+00	1.E+00	9.E-01	7.E+01	
INTERPRO	IPR001314:Peptidase S1A, chymotrypsin	11	1.25284738	2.E-01 18048, 14939, 18815, 14941, 14940, 1303	860	143	17763	2.E+00	1.E+00	9.E-01	9.E+01	
SP_PIR_KEYWORDS	T-cell	4	0.455580866	2.E-01 14939, 14941, 14940, 14943	869	31	17854	3.E+00	1.E+00	5.E-01	9.E+01	
INTERPRO	IPR018114:Peptidase S1/S6, chymotrypsin/Hap_ active site	11	1.25284738	2.E-01 18048, 14939, 18815, 14941, 14940, 1303	860	151	17763	2.E+00	1.E+00	1.E+00	1.E+02	
PIR_SUPERFAMILY	PIRSF001135:trypsin	8	0.911161731	2.E-01 18048, 14939, 14941, 14940, 13035, 1722	576	68	8136	2.E+00	1.E+00	1.E+00	1.E+02	
INTERPRO	IPR001254:Peptidase S1 and S6, chymotrypsin/Hap	11	1.25284738	2.E-01 18048, 14939, 18815, 14941, 14940, 1303	860	159	17763	1.E+00	1.E+00	1.E+00	1.E+02	
GOTERM_MF_FAT	GO:0004252~serine-type endopeptidase activity	14	1.59453303	3.E-01 14939, 14941, 18195, 14940, 18792, 1303	754	189	13288	1.E+00	1.E+00	9.E-01	1.E+02	
SMART	SM00020:Tryp_SPc	11	1.25284738	4.E-01 18048, 14939, 18815, 14941, 14940, 1303	492	159	9131	1.E+00	1.E+00	9.E-01	1.E+02	
SP_PIR_KEYWORDS	Serine protease	10	1.138952164	4.E-01 14939, 18815, 14941, 14940, 13035, 1879	869	164	17854	1.E+00	1.E+00	8.E-01	1.E+02	
GOTERM_MF_FAT	GO:0008236~serine-type peptidase activity	14	1.59453303	4.E-01 14939, 14941, 18195, 14940, 18792, 1303	754	212	13288	1.E+00	1.E+00	9.E-01	1.E+02	
GOTERM_MF_FAT	GO:0017171~serine hydrolase activity	14	1.59453303	4.E-01 14939, 14941, 18195, 14940, 18792, 1303	754	213	13288	1.E+00	1.E+00	9.E-01	1.E+02	
SP_PIR_KEYWORDS	zymogen	11	1.25284738	5.E-01 14939, 18815, 74145, 14941, 14940, 1303	869	199	17854	1.E+00	1.E+00	8.E-01	1.E+02	
UP_SEQ_FEATURE	propeptide:Activation peptide	5	0.569476082	6.E-01 14939, 74145, 13035, 17227, 14944	861	78	16021	1.E+00	1.E+00	1.E+00	1.E+02	
UP_SEQ_FEATURE	active site:Charge relay system	11	1.25284738	6.E-01 669888, 14939, 18815, 14941, 14940, 130	861	198	16021	1.E+00	1.E+00	1.E+00	1.E+02	
GOTERM_MF_FAT	GO:0004175~endopeptidase activity	22	2.505694761	8.E-01 14939, 329777, 14941, 14940, 18195, 130	754	421	13288	9.E-01	1.E+00	1.E+00	1.E+02	
SP_PIR_KEYWORDS	Protease	17	1.936218679	1.E+00 14939, 329777, 14941, 14940, 13035, 590	869	509	17854	7.E-01	1.E+00	1.E+00	1.E+02	
GOTERM_MF_FAT	GO:0070011~peptidase activity, acting on L-amino acid peptides	23	2.619589977	1.E+00 14939, 329777, 14941, 14940, 18195, 130	754	603	13288	7.E-01	1.E+00	1.E+00	1.E+02	
GOTERM_MF_FAT	GO:0008233~peptidase activity	23	2.619589977	1.E+00 14939, 329777, 14941, 14940, 18195, 130	754	629	13288	6.E-01	1.E+00	1.E+00	1.E+02	
Annotation Cluster 184	Enrichment Score: 0.7581700675738703											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR002913:Lipid-binding START	3	0.341685649	2.E-01 236920, 50768, 243362	860	15	17763	4.E+00	1.E+00	9.E-01	9.E+01	
UP_SEQ_FEATURE	domain:START	3	0.341685649	2.E-01 236920, 50768, 243362	861	14	16021	4.E+00	1.E+00	1.E+00	1.E+02	
SMART	SM00234:START	3	0.341685649	2.E-01 236920, 50768, 243362	492	15	9131	4.E+00	1.E+00	8.E-01	9.E+01	
Annotation Cluster 185	Enrichment Score: 0.757003140324816											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0009416~response to light stimulus	11	1.25284738	7.E-02 13872, 11785, 12190, 14151, 12028, 2320	809	98	13588	2.E+00	1.E+00	4.E-01	7.E+01	
GOTERM_BP_FAT	GO:0007611~learning or memory	10	1.138952164	8.E-02 17159, 11785, 14661, 11514, 19085, 1916	809	89	13588	2.E+00	1.E+00	5.E-01	8.E+01	
GOTERM_BP_FAT	GO:0008542~visual learning	4	0.455580866	2.E-01 11785, 12568, 18574, 20238	809	29	13588	2.E+00	1.E+00	8.E-01	1.E+02	
GOTERM_BP_FAT	GO:0007632~visual behavior	4	0.455580866	3.E-01 11785, 12568, 18574, 20238	809	31	13588	2.E+00	1.E+00	8.E-01	1.E+02	
GOTERM_BP_FAT	GO:0007612~learning	5	0.569476082	4.E-01 11785, 19088, 12568, 18574, 20238	809	57	13588	1.E+00	1.E+00	9.E-01	1.E+02	
Annotation Cluster 186	Enrichment Score: 0.7515386360254843											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	DNA binding	23	2.619589977	8.E-03 78294, 15376, 15430, 14815, 20375, 1428	869	258	17854	2.E+00	1.E+00	4.E-02	1.E+01	
INTERPRO	IPR001827:Homeobox protein, antennapedia type, conserved site	5	0.569476082	3.E-02 15402, 15415, 15407, 15416, 18609	860	24	17763	4.E+00	1.E+00	5.E-01	4.E+01	
INTERPRO	IPR017995:Homeobox protein, antennapedia type	4	0.455580866	3.E-02 15402, 15415, 15416, 18609	860	14	17763	6.E+00	1.E+00	5.E-01	4.E+01	
GOTERM_BP_FAT	GO:0001501~skeletal system development	26	2.961275626	3.E-02 69121, 17869, 21934, 12815, 15402, 1859	809	285	13588	2.E+00	1.E+00	3.E-01	5.E+01	
UP_SEQ_FEATURE	short sequence motif:Antp-type hexapeptide	5	0.569476082	4.E-02 15402, 15415, 15407, 15416, 18609	861	24	16021	4.E+00	1.E+00	8.E-01	5.E+01	
GOTERM_BP_FAT	GO:0048706~embryonic skeletal system development	9	1.025056948	1.E-01 15402, 15438, 15415, 15407, 15416, 1540	809	83	13588	2.E+00	1.E+00	6.E-01	9.E+01	
GOTERM_BP_FAT	GO:0048705~skeletal system morphogenesis	12	1.366742597	2.E-01 15402, 18596, 15438, 12842, 15415, 1540	809	130	13588	2.E+00	1.E+00	7.E-01	9.E+01	
GOTERM_BP_FAT	GO:0048704~embryonic skeletal system morphogenesis	7	0.797266515	2.E-01 15402, 15438, 15415, 15407, 15416, 1543	809	64	13588	2.E+00	1.E+00	7.E-01	1.E+02	
INTERPRO	IPR017970:Homeobox, conserved site	15	1.708428246	2.E-01 17536, 15430, 14843, 13799, 21869, 1540	860	222	17763	1.E+00	1.E+00	1.E+00	1.E+02	
INTERPRO	IPR001356:Homeobox	15	1.708428246	3.E-01 17536, 15430, 14843, 13799, 21869, 1540	860	254	17763	1.E+00	1.E+00	1.E+00	1.E+02	
GOTERM_BP_FAT	GO:0048562~embryonic organ morphogenesis	12	1.366742597	4.E-01 15402, 13836, 15438, 24064, 15415, 1540	809	161	13588	1.E+00	1.E+00	9.E-01	1.E+02	
INTERPRO	IPR012287:Homeodomain-related	15	1.708428246	4.E-01 17536, 15430, 14843, 13799, 21869, 1540	860	259	17763	1.E+00	1.E+00	1.E+00	1.E+02	
GOTERM_BP_FAT	GO:0003002~regionalization	15	1.708428246	4.E-01 19206, 15376, 19378, 15430, 14843, 2186	809	214	13588	1.E+00	1.E+00	9.E-01	1.E+02	
SP_PIR_KEYWORDS	Homeobox	15	1.708428246	4.E-01 17536, 15430, 14843, 13799, 21869, 1540	869	263	17854	1.E+00	1.E+00	8.E-01	1.E+02	



GOTERM_BP_FAT	GO:0009952~anterior/posterior pattern formation	11	1.25284738	4.E-01	15402, 15438, 15415, 15407, 15416, 1192	809	153	13588	1.E+00	1.E+00	9.E-01	1.E+02
UP_SEQ_FEATURE	DNA-binding region:Homeobox	11	1.25284738	5.E-01	15402, 15438, 15415, 15407, 15416, 1860	861	180	16021	1.E+00	1.E+00	1.E+00	1.E+02
SMART	SM00389:HOX	15	1.708428246	5.E-01	17536, 15430, 14843, 13799, 21869, 1540	492	254	9131	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_MF_FAT	GO:0043565~sequence-specific DNA binding	32	3.644646925	6.E-01	17536, 15376, 14815, 17869, 21869, 1291	754	556	13288	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0007389~pattern specification process	17	1.936218679	6.E-01	14674, 19206, 15376, 66042, 19378, 1543	809	284	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_MF_FAT	GO:0003700~transcription factor activity	41	4.669703872	8.E-01	17536, 69890, 18181, 433759, 15376, 178	754	776	13288	9.E-01	1.E+00	1.E+00	1.E+02

Annotation Cluster 187	Enrichment Score: 0.7514565874809875											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
BIOCARTA	m_cdMacPathway:Cadmium induces DNA synthesis and proliferat	6	0.683371298	6.E-02	18751, 26395, 15461, 17869, 14281, 1879	188	14	1171	3.E+00	1.E+00	2.E-01	5.E+01
BIOCARTA	m_CCR3Pathway:CCR3 signaling in Eosinophils	6	0.683371298	3.E-01	18751, 26395, 15461, 14682, 11848, 1879	188	22	1171	2.E+00	1.E+00	6.E-01	1.E+02
BIOCARTA	m_bArrestin-srcPathway:Roles of ???-arrestin-dependent Recruitm	5	0.569476082	4.E-01	14191, 20779, 26395, 15461, 18795	188	19	1171	2.E+00	1.E+00	7.E-01	1.E+02

Annotation Cluster 188	Enrichment Score: 0.7293664004811959											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_SEQ_FEATURE	region of interest:Bait region	3	0.341685649	2.E-02	17836, 17837, 11287	861	4	16021	1.E+01	1.E+00	5.E-01	2.E+01
SP_PIR_KEYWORDS	bait region	3	0.341685649	3.E-02	17836, 17837, 11287	869	6	17854	1.E+01	1.E+00	1.E-01	4.E+01
SP_PIR_KEYWORDS	thioester bond	3	0.341685649	4.E-02	17836, 17837, 11287	869	7	17854	9.E+00	1.E+00	2.E-01	5.E+01
UP_SEQ_FEATURE	cross-link:isoglutamyl cysteine thioester (Cys-Gln)	3	0.341685649	5.E-02	17836, 17837, 11287	861	7	16021	8.E+00	1.E+00	8.E-01	6.E+01
INTERPRO	IPR019565:Alpha-2-macroglobulin, thiol-ester bond-forming	3	0.341685649	5.E-02	17836, 17837, 11287	860	8	17763	8.E+00	1.E+00	7.E-01	6.E+01
INTERPRO	IPR001599:Alpha-2-macroglobulin	3	0.341685649	7.E-02	17836, 17837, 11287	860	9	17763	7.E+00	1.E+00	7.E-01	7.E+01
INTERPRO	IPR009048:Alpha-macroglobulin, receptor-binding	3	0.341685649	7.E-02	17836, 17837, 11287	860	9	17763	7.E+00	1.E+00	7.E-01	7.E+01
INTERPRO	IPR011626:A-macroglobulin complement component	3	0.341685649	7.E-02	17836, 17837, 11287	860	9	17763	7.E+00	1.E+00	7.E-01	7.E+01
INTERPRO	IPR011625:Alpha-2-macroglobulin, N-terminal 2	3	0.341685649	7.E-02	17836, 17837, 11287	860	9	17763	7.E+00	1.E+00	7.E-01	7.E+01
INTERPRO	IPR002890:Alpha-2-macroglobulin, N-terminal	3	0.341685649	8.E-02	17836, 17837, 11287	860	10	17763	6.E+00	1.E+00	8.E-01	8.E+01
INTERPRO	IPR019742:Alpha-2-macroglobulin, conserved site	3	0.341685649	1.E-01	17836, 17837, 11287	860	11	17763	6.E+00	1.E+00	8.E-01	8.E+01
PIR_SUPERFAMILY	PIRSF001635:alpha-2-macroglobulin	3	0.341685649	1.E-01	17836, 17837, 11287	576	9	8136	5.E+00	1.E+00	1.E+00	9.E+01
SP_PIR_KEYWORDS	Serine protease inhibitor	6	0.683371298	4.E-01	17836, 17837, 18787, 282663, 18788, 112	869	82	17854	2.E+00	1.E+00	7.E-01	1.E+02
GOTERM_MF_FAT	GO:0004857~enzyme inhibitor activity	15	1.708428246	5.E-01	56338, 16952, 282663, 94175, 18788, 112	754	243	13288	1.E+00	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	protease inhibitor	6	0.683371298	6.E-01	17836, 17837, 18787, 282663, 18788, 112	869	109	17854	1.E+00	1.E+00	9.E-01	1.E+02
GOTERM_MF_FAT	GO:0004867~serine-type endopeptidase inhibitor activity	7	0.797266515	6.E-01	17836, 17837, 18787, 282663, 94175, 187	754	115	13288	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_MF_FAT	GO:0004869~cysteine-type endopeptidase inhibitor activity	3	0.341685649	7.E-01	30939, 94175, 11625	754	39	13288	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_MF_FAT	GO:0004866~endopeptidase inhibitor activity	9	1.025056948	7.E-01	17836, 17837, 30939, 18787, 282663, 941	754	161	13288	1.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	site:Reactive bond	3	0.341685649	8.E-01	18787, 282663, 18788	861	52	16021	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_MF_FAT	GO:0030414~peptidase inhibitor activity	9	1.025056948	8.E-01	17836, 17837, 30939, 18787, 282663, 941	754	176	13288	9.E-01	1.E+00	1.E+00	1.E+02
INTERPRO	IPR000215:Protease inhibitor I4, serpin	3	0.341685649	9.E-01	18787, 282663, 18788	860	69	17763	9.E-01	1.E+00	1.E+00	1.E+02
SMART	SM00093:SERPIN	3	0.341685649	9.E-01	18787, 282663, 18788	492	69	9131	8.E-01	1.E+00	1.E+00	1.E+02
PIR_SUPERFAMILY	PIRSF001630:serpin	3	0.341685649	9.E-01	18787, 282663, 18788	576	53	8136	8.E-01	1.E+00	1.E+00	1.E+02

Annotation Cluster 189	Enrichment Score: 0.7200031424686949											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR001251:Cellular retinaldehyde-binding/triple function, C-termin	4	0.455580866	1.E-01	73167, 228359, 109904, 545156	860	26	17763	3.E+00	1.E+00	9.E-01	9.E+01
SMART	SM00516:SEC14	4	0.455580866	2.E-01	73167, 228359, 109904, 545156	492	26	9131	3.E+00	1.E+00	7.E-01	9.E+01
UP_SEQ_FEATURE	domain:CRAL-TRIO	3	0.341685649	3.E-01	73167, 228359, 545156	861	22	16021	3.E+00	1.E+00	1.E+00	1.E+02

Annotation Cluster 190	Enrichment Score: 0.712659008749761											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
BIOCARTA	m_fibrinolysisPathway:Fibrinolysis Pathway	5	0.569476082	3.E-02	18787, 18815, 74145, 18792, 18788	188	8	1171	4.E+00	1.E+00	1.E-01	3.E+01
BIOCARTA	m_plateletAppPathway:Platelet Amyloid Precursor Protein Pathway	3	0.341685649	4.E-01	18787, 18815, 18792	188	9	1171	2.E+00	1.E+00	8.E-01	1.E+02
KEGG_PATHWAY	mmu04610:Complement and coagulation cascades	8	0.911161731	6.E-01	14060, 18787, 18815, 74145, 18793, 2305	580	75	5738	1.E+00	1.E+00	8.E-01	1.E+02

Annotation Cluster 191	Enrichment Score: 0.7091328351742802											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0033043~regulation of organelle organization	15	1.708428246	7.E-02	227753, 16800, 56150, 13383, 14026, 123	809	154	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0051693~actin filament capping	4	0.455580866	1.E-01	227753, 14026, 12345, 19684	809	19	13588	4.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0032271~regulation of protein polymerization	7	0.797266515	1.E-01	56717, 227753, 13383, 14026, 12345, 196	809	57	13588	2.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0030835~negative regulation of actin filament depolymerizati	4	0.455580866	1.E-01	227753, 14026, 12345, 19684	809	21	13588	3.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0030833~regulation of actin filament polymerization	6	0.683371298	1.E-01	56717, 227753, 13383, 14026, 12345, 196	809	45	13588	2.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0032956~regulation of actin cytoskeleton organization	7	0.797266515	1.E-01	56717, 227753, 13383, 14026, 12345, 196	809	60	13588	2.E+00	1.E+00	7.E-01	9.E+01
GOTERM_BP_FAT	GO:0043242~negative regulation of protein complex disassembly	5	0.569476082	2.E-01	227753, 16800, 14026, 12345, 19684	809	35	13588	2.E+00	1.E+00	7.E-01	9.E+01
GOTERM_BP_FAT	GO:0032970~regulation of actin filament-based process	7	0.797266515	2.E-01	56717, 227753, 13383, 14026, 12345, 196	809	61	13588	2.E+00	1.E+00	7.E-01	9.E+01
GOTERM_BP_FAT	GO:0010639~negative regulation of organelle organization	7	0.797266515	2.E-01	227753, 11920, 16800, 56150, 14026, 123	809	62	13588	2.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0030834~regulation of actin filament depolymerization	4	0.455580866	2.E-01	227753, 14026, 12345, 19684	809	24	13588	3.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0008064~regulation of actin polymerization or depolymerizati	6	0.683371298	2.E-01	56717, 227753, 13383, 14026, 12345, 196	809	50	13588	2.E+00	1.E+00	7.E-01	1.E+02
SP_PIR_KEYWORDS	actin capping	3	0.341685649	2.E-01	227753, 12345, 19684	869	16	17854	4.E+00	1.E+00	5.E-01	9.E+01



GOTERM_BP_FAT	GO:0030837~negative regulation of actin filament polymerization	4	0.455580866	2.E-01 227753, 14026, 12345, 19684	809	25	13588	3.E+00	1.E+00	7.E-01	1.E+02	
GOTERM_BP_FAT	GO:0030832~regulation of actin filament length	6	0.683371298	2.E-01 56717, 227753, 13383, 14026, 12345, 196	809	51	13588	2.E+00	1.E+00	7.E-01	1.E+02	
GOTERM_BP_FAT	GO:0051129~negative regulation of cellular component organizat	9	1.025056948	2.E-01 227753, 11920, 104215, 19164, 16800, 56	809	93	13588	2.E+00	1.E+00	7.E-01	1.E+02	
GOTERM_BP_FAT	GO:0043254~regulation of protein complex assembly	7	0.797266515	2.E-01 56717, 227753, 13383, 14026, 12345, 196	809	65	13588	2.E+00	1.E+00	7.E-01	1.E+02	
GOTERM_BP_FAT	GO:0051495~positive regulation of cytoskeleton organization	4	0.455580866	2.E-01 56717, 13383, 11848, 12576	809	26	13588	3.E+00	1.E+00	7.E-01	1.E+02	
GOTERM_BP_FAT	GO:0031333~negative regulation of protein complex assembly	4	0.455580866	2.E-01 227753, 14026, 12345, 19684	809	27	13588	2.E+00	1.E+00	8.E-01	1.E+02	
GOTERM_BP_FAT	GO:0032272~negative regulation of protein polymerization	4	0.455580866	2.E-01 227753, 14026, 12345, 19684	809	27	13588	2.E+00	1.E+00	8.E-01	1.E+02	
GOTERM_BP_FAT	GO:0051493~regulation of cytoskeleton organization	9	1.025056948	2.E-01 56717, 227753, 16800, 13383, 14026, 123	809	99	13588	2.E+00	1.E+00	8.E-01	1.E+02	
GOTERM_BP_FAT	GO:0043244~regulation of protein complex disassembly	5	0.569476082	3.E-01 227753, 16800, 14026, 12345, 19684	809	43	13588	2.E+00	1.E+00	8.E-01	1.E+02	
GOTERM_BP_FAT	GO:0044087~regulation of cellular component biogenesis	8	0.911161731	3.E-01 56717, 227753, 13383, 14026, 12345, 196	809	89	13588	2.E+00	1.E+00	8.E-01	1.E+02	
GOTERM_BP_FAT	GO:0032273~positive regulation of protein polymerization	3	0.341685649	3.E-01 56717, 13383, 12576	809	19	13588	3.E+00	1.E+00	9.E-01	1.E+02	
GOTERM_BP_FAT	GO:0051494~negative regulation of cytoskeleton organization	5	0.569476082	3.E-01 227753, 16800, 14026, 12345, 19684	809	48	13588	2.E+00	1.E+00	9.E-01	1.E+02	
GOTERM_BP_FAT	GO:0010638~positive regulation of organelle organization	5	0.569476082	4.E-01 16994, 56717, 13383, 11848, 12576	809	52	13588	2.E+00	1.E+00	9.E-01	1.E+02	
GOTERM_BP_FAT	GO:0031334~positive regulation of protein complex assembly	3	0.341685649	4.E-01 56717, 13383, 12576	809	24	13588	2.E+00	1.E+00	9.E-01	1.E+02	
GOTERM_BP_FAT	GO:0051130~positive regulation of cellular component organizati	8	0.911161731	6.E-01 16994, 56717, 14127, 13383, 21844, 1162	809	122	13588	1.E+00	1.E+00	1.E+00	1.E+02	
Annotation Cluster 192	Enrichment Score: 0.7042255471066875											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0051271~negative regulation of cell motion	5	0.569476082	1.E-01 11486, 74144, 12043, 106952, 12576	809	32	13588	3.E+00	1.E+00	6.E-01	9.E+01	
GOTERM_BP_FAT	GO:0030336~negative regulation of cell migration	4	0.455580866	2.E-01 11486, 74144, 12043, 106952	809	28	13588	2.E+00	1.E+00	8.E-01	1.E+02	
GOTERM_BP_FAT	GO:0040013~negative regulation of locomotion	4	0.455580866	3.E-01 11486, 74144, 12043, 106952	809	31	13588	2.E+00	1.E+00	8.E-01	1.E+02	
Annotation Cluster 193	Enrichment Score: 0.7020237458204156											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_SEQ_FEATURE	zinc finger region:ZZ-type	3	0.341685649	2.E-01 74287, 17966, 12914	861	14	16021	4.E+00	1.E+00	1.E+00	1.E+02	
INTERPRO	IPR000433:Zinc finger, ZZ-type	3	0.341685649	2.E-01 74287, 17966, 12914	860	17	17763	4.E+00	1.E+00	1.E+00	1.E+02	
SMART	SM00291:ZnF_ZZ	3	0.341685649	2.E-01 74287, 17966, 12914	492	17	9131	3.E+00	1.E+00	8.E-01	1.E+02	
Annotation Cluster 194	Enrichment Score: 0.7008310660142734											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR000751:M-phase inducer phosphatase	3	0.341685649	7.E-03 12532, 12531, 12530	860	3	17763	2.E+01	1.E+00	2.E-01	1.E+01	
SP_PIR_KEYWORDS	phosphoric monoester hydrolase	6	0.683371298	4.E-02 15170, 12532, 12531, 12183, 19056, 1905	869	38	17854	3.E+00	1.E+00	1.E-01	4.E+01	
UP_SEQ_FEATURE	domain:Rhodanese	3	0.341685649	2.E-01 12532, 12531, 12530	861	15	16021	4.E+00	1.E+00	1.E+00	1.E+02	
SP_PIR_KEYWORDS	protein phosphatase	9	1.025056948	2.E-01 15170, 19053, 19253, 14208, 12532, 1253	869	120	17854	2.E+00	1.E+00	5.E-01	1.E+02	
SP_PIR_KEYWORDS	tyrosine-specific phosphatase	3	0.341685649	3.E-01 15170, 12532, 12531	869	20	17854	3.E+00	1.E+00	6.E-01	1.E+02	
GOTERM_MF_FAT	GO:0016791~phosphatase activity	17	1.936218679	3.E-01 15170, 19253, 14208, 67916, 12183, 5601	754	238	13288	1.E+00	1.E+00	9.E-01	1.E+02	
INTERPRO	IPR001763:Rhodanese-like	3	0.341685649	3.E-01 12532, 12531, 12530	860	22	17763	3.E+00	1.E+00	1.E+00	1.E+02	
SMART	SM00450:RHOD	3	0.341685649	3.E-01 12532, 12531, 12530	492	22	9131	3.E+00	1.E+00	9.E-01	1.E+02	
GOTERM_MF_FAT	GO:0004721~phosphoprotein phosphatase activity	11	1.25284738	4.E-01 15170, 16818, 19053, 19253, 14208, 2639	754	152	13288	1.E+00	1.E+00	9.E-01	1.E+02	
GOTERM_BP_FAT	GO:0006470~protein amino acid dephosphorylation	9	1.025056948	4.E-01 15170, 19253, 19012, 14208, 12043, 1253	809	114	13588	1.E+00	1.E+00	9.E-01	1.E+02	
GOTERM_BP_FAT	GO:0016311~dephosphorylation	9	1.025056948	6.E-01 15170, 19253, 19012, 14208, 12043, 1253	809	141	13588	1.E+00	1.E+00	1.E+00	1.E+02	
GOTERM_MF_FAT	GO:0004725~protein tyrosine phosphatase activity	6	0.683371298	7.E-01 15170, 19253, 26395, 12532, 12531, 1253	754	101	13288	1.E+00	1.E+00	1.E+00	1.E+02	
Annotation Cluster 195	Enrichment Score: 0.6924643180148207											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0009156~ribonucleoside monophosphate biosynthetic proces	5	0.569476082	2.E-02 11486, 56749, 11717, 11566, 99586	809	17	13588	5.E+00	1.E+00	2.E-01	3.E+01	
GOTERM_BP_FAT	GO:0009161~ribonucleoside monophosphate metabolic process	5	0.569476082	2.E-02 11486, 56749, 11717, 11566, 99586	809	19	13588	4.E+00	1.E+00	2.E-01	3.E+01	
GOTERM_BP_FAT	GO:0009119~ribonucleoside metabolic process	7	0.797266515	3.E-02 22017, 11486, 72269, 232087, 56749, 222	809	39	13588	3.E+00	1.E+00	2.E-01	4.E+01	
GOTERM_BP_FAT	GO:0046112~nucleobase biosynthetic process	3	0.341685649	1.E-01 11486, 56749, 99586	809	9	13588	6.E+00	1.E+00	5.E-01	8.E+01	
GOTERM_BP_FAT	GO:0009112~nucleobase metabolic process	4	0.455580866	1.E-01 11486, 56749, 11717, 99586	809	19	13588	4.E+00	1.E+00	5.E-01	8.E+01	
GOTERM_BP_FAT	GO:0009124~nucleoside monophosphate biosynthetic process	6	0.683371298	1.E-01 11486, 11514, 56749, 11717, 11566, 9958	809	45	13588	2.E+00	1.E+00	6.E-01	9.E+01	
GOTERM_BP_FAT	GO:0009168~purine ribonucleoside monophosphate biosynthetic	3	0.341685649	2.E-01 11486, 11717, 11566	809	13	13588	4.E+00	1.E+00	7.E-01	1.E+02	
GOTERM_BP_FAT	GO:0009127~purine nucleoside monophosphate biosynthetic pro	3	0.341685649	2.E-01 11486, 11717, 11566	809	13	13588	4.E+00	1.E+00	7.E-01	1.E+02	
GOTERM_BP_FAT	GO:0044271~nitrogen compound biosynthetic process	23	2.619589977	2.E-01 382985, 14151, 18416, 109900, 232087, 1	809	302	13588	1.E+00	1.E+00	7.E-01	1.E+02	
GOTERM_BP_FAT	GO:0009167~purine ribonucleoside monophosphate metabolic pr	3	0.341685649	2.E-01 11486, 11717, 11566	809	15	13588	3.E+00	1.E+00	8.E-01	1.E+02	
GOTERM_BP_FAT	GO:0009126~purine nucleoside monophosphate metabolic proce	3	0.341685649	2.E-01 11486, 11717, 11566	809	15	13588	3.E+00	1.E+00	8.E-01	1.E+02	
GOTERM_BP_FAT	GO:0009165~nucleotide biosynthetic process	14	1.59453303	2.E-01 382985, 11717, 11564, 11566, 99586, 114	809	174	13588	1.E+00	1.E+00	8.E-01	1.E+02	
GOTERM_BP_FAT	GO:0034404~nucleobase, nucleoside and nucleotide biosynthetic	14	1.59453303	3.E-01 382985, 11717, 11564, 11566, 99586, 114	809	179	13588	1.E+00	1.E+00	8.E-01	1.E+02	
GOTERM_BP_FAT	GO:0034654~nucleobase, nucleoside, nucleotide and nucleic acid	14	1.59453303	3.E-01 382985, 11717, 11564, 11566, 99586, 114	809	179	13588	1.E+00	1.E+00	8.E-01	1.E+02	
GOTERM_BP_FAT	GO:0009123~nucleoside monophosphate metabolic process	6	0.683371298	3.E-01 11486, 11514, 56749, 11717, 11566, 9958	809	59	13588	2.E+00	1.E+00	8.E-01	1.E+02	
KEGG_PATHWAY	mmu00230:Purine metabolism	19	2.164009112	3.E-01 18746, 382985, 14923, 11717, 11564, 115	580	157	5738	1.E+00	1.E+00	5.E-01	1.E+02	
GOTERM_BP_FAT	GO:0009259~ribonucleotide metabolic process	9	1.025056948	5.E-01 11486, 56749, 11717, 11564, 227197, 679	809	125	13588	1.E+00	1.E+00	1.E+00	1.E+02	
GOTERM_BP_FAT	GO:0006163~purine nucleotide metabolic process	10	1.138952164	6.E-01 11486, 11514, 14923, 11717, 11564, 2271	809	160	13588	1.E+00	1.E+00	1.E+00	1.E+02	
GOTERM_BP_FAT	GO:0009260~ribonucleotide biosynthetic process	7	0.797266515	7.E-01 11486, 56749, 11717, 11564, 67942, 1156	809	111	13588	1.E+00	1.E+00	1.E+00	1.E+02	
GOTERM_BP_FAT	GO:0009150~purine ribonucleotide metabolic process	7	0.797266515	7.E-01 11486, 11717, 11564, 227197, 67942, 115	809	119	13588	1.E+00	1.E+00	1.E+00	1.E+02	



GOTERM_BP_FAT	GO:0009152--purine ribonucleotide biosynthetic process	5	0.569476082	9.E-01	11486, 11717, 11564, 67942, 11566	809	107	13588	8.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0006164--purine nucleotide biosynthetic process	6	0.683371298	9.E-01	11486, 11514, 11717, 11564, 67942, 1156	809	137	13588	7.E-01	1.E+00	1.E+00	1.E+02
Annotation Cluster 196	Enrichment Score: 0.6804956546232547											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0043010--camera-type eye development	12	1.366742597	2.E-01	18771, 12955, 232906, 77579, 12028, 120	809	130	13588	2.E+00	1.E+00	7.E-01	9.E+01
GOTERM_BP_FAT	GO:0001654--eye development	13	1.480637813	2.E-01	17536, 232906, 12955, 19378, 56847, 133	809	157	13588	1.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0007423--sensory organ development	19	2.164009112	3.E-01	17536, 73750, 12955, 232906, 19378, 178	809	257	13588	1.E+00	1.E+00	8.E-01	1.E+02
Annotation Cluster 197	Enrichment Score: 0.673365429672032											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR000717:Proteasome component region PCI	3	0.341685649	2.E-01	13669, 16341, 56347	860	16	17763	4.E+00	1.E+00	9.E-01	1.E+02
SMART	SM00088:PINT	3	0.341685649	2.E-01	13669, 16341, 56347	492	16	9131	3.E+00	1.E+00	8.E-01	1.E+02
UP_SEQ_FEATURE	domain:PCI	3	0.341685649	3.E-01	13669, 16341, 56347	861	18	16021	3.E+00	1.E+00	1.E+00	1.E+02
Annotation Cluster 198	Enrichment Score: 0.6677997934527333											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0031406--carboxylic acid binding	10	1.138952164	5.E-02	70316, 18126, 11409, 235339, 17999, 184	754	85	13288	2.E+00	1.E+00	4.E-01	5.E+01
GOTERM_MF_FAT	GO:0016597--amino acid binding	4	0.455580866	3.E-01	70316, 18126, 17999, 18416	754	33	13288	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_MF_FAT	GO:0043176--amine binding	4	0.455580866	7.E-01	70316, 18126, 17999, 18416	754	61	13288	1.E+00	1.E+00	1.E+00	1.E+02
Annotation Cluster 199	Enrichment Score: 0.6616156875840783											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0043005--neuron projection	18	2.050113895	1.E-01	11658, 73750, 94190, 17869, 16800, 1847	636	245	12504	1.E+00	1.E+00	4.E-01	8.E+01
GOTERM_CC_FAT	GO:0030424--axon	9	1.025056948	2.E-01	14432, 11658, 94190, 77579, 19164, 1786	636	107	12504	2.E+00	1.E+00	5.E-01	9.E+01
GOTERM_CC_FAT	GO:0030425--dendrite	7	0.797266515	5.E-01	94190, 77579, 19164, 16800, 12568, 1796	636	110	12504	1.E+00	1.E+00	9.E-01	1.E+02
Annotation Cluster 200	Enrichment Score: 0.6575304973184858											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0031365--N-terminal protein amino acid modification	3	0.341685649	5.E-02	18108, 18107, 12914	809	6	13588	8.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0043543--protein amino acid acylation	5	0.569476082	3.E-01	11785, 18108, 18107, 108672, 12914	809	48	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_MF_FAT	GO:0016410--N-acyltransferase activity	4	0.455580866	7.E-01	18108, 18107, 17979, 12914	754	67	13288	1.E+00	1.E+00	1.E+00	1.E+02
Annotation Cluster 201	Enrichment Score: 0.6568579248165822											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0035107--appendage morphogenesis	11	1.25284738	1.E-01	15438, 19206, 12028, 12018, 15405, 1937	809	115	13588	2.E+00	1.E+00	7.E-01	9.E+01
GOTERM_BP_FAT	GO:0035108--limb morphogenesis	11	1.25284738	1.E-01	15438, 19206, 12028, 12018, 15405, 1937	809	115	13588	2.E+00	1.E+00	7.E-01	9.E+01
GOTERM_BP_FAT	GO:0048736--appendage development	11	1.25284738	2.E-01	15438, 19206, 12028, 12018, 15405, 1937	809	119	13588	2.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0060173--limb development	11	1.25284738	2.E-01	15438, 19206, 12028, 12018, 15405, 1937	809	119	13588	2.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0009954--proximal/distal pattern formation	4	0.455580866	2.E-01	15438, 15405, 19378, 15430	809	25	13588	3.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0035136--forelimb morphogenesis	4	0.455580866	2.E-01	15438, 15405, 19378, 15430	809	27	13588	2.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0030326--embryonic limb morphogenesis	9	1.025056948	2.E-01	15438, 19206, 15405, 19378, 19164, 1543	809	97	13588	2.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0035113--embryonic appendage morphogenesis	9	1.025056948	2.E-01	15438, 19206, 15405, 19378, 19164, 1543	809	97	13588	2.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0035115--embryonic forelimb morphogenesis	3	0.341685649	4.E-01	15438, 15405, 19378	809	22	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0035137--hindlimb morphogenesis	3	0.341685649	6.E-01	15438, 19206, 15430	809	34	13588	1.E+00	1.E+00	1.E+00	1.E+02
Annotation Cluster 202	Enrichment Score: 0.6553429156905405											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	cell adhesion	24	2.733485194	2.E-01	11350, 11658, 69524, 11852, 22793, 1641	869	380	17854	1.E+00	1.E+00	4.E-01	9.E+01
GOTERM_BP_FAT	GO:0007155--cell adhesion	39	4.44191344	2.E-01	12831, 11658, 69524, 11852, 22793, 6650	809	561	13588	1.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0022610--biological adhesion	39	4.44191344	2.E-01	12831, 11658, 69524, 11852, 22793, 6650	809	562	13588	1.E+00	1.E+00	8.E-01	1.E+02
KEGG_PATHWAY	mmu04514:Cell adhesion molecules (CAMs)	19	2.164009112	3.E-01	15007, 14972, 15018, 11658, 69524, 1645	580	154	5738	1.E+00	1.E+00	5.E-01	1.E+02
Annotation Cluster 203	Enrichment Score: 0.6533883803412465											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR004825:Insulin/IGF/relaxin	3	0.341685649	1.E-01	16333, 16334, 16000	860	11	17763	6.E+00	1.E+00	8.E-01	8.E+01
SMART	SM00078:IGF	3	0.341685649	1.E-01	16333, 16334, 16000	492	11	9131	5.E+00	1.E+00	7.E-01	8.E+01
GOTERM_MF_FAT	GO:0005179--hormone activity	3	0.341685649	1.E+00	16333, 16334, 16000	754	113	13288	5.E-01	1.E+00	1.E+00	1.E+02
Annotation Cluster 204	Enrichment Score: 0.6395448566841513											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0005581--collagen	5	0.569476082	1.E-02	12843, 12831, 12842, 16948, 12815	636	19	12504	5.E+00	1.E+00	8.E-02	2.E+01
INTERPRO	IPR000885:Fibrillar collagen, C-terminal	4	0.455580866	1.E-02	12843, 12831, 12842, 12815	860	11	17763	8.E+00	1.E+00	3.E-01	2.E+01
UP_SEQ_FEATURE	domain:Fibrillar collagen NC1	4	0.455580866	1.E-02	12843, 12831, 12842, 12815	861	10	16021	7.E+00	1.E+00	5.E-01	2.E+01
SMART	SM00038:COLFI	4	0.455580866	2.E-02	12843, 12831, 12842, 12815	492	11	9131	7.E+00	1.E+00	2.E-01	2.E+01



UP_SEQ_FEATURE	propeptide:C-terminal propeptide	3	0.341685649	5.E-02	12843, 12842, 12815	861	7	16021	8.E+00	1.E+00	8.E-01	6.E+01
GOTERM_MF_FAT	GO:0005201~extracellular matrix structural constituent	5	0.569476082	9.E-02	12843, 12831, 12842, 12815, 11704	754	30	13288	3.E+00	1.E+00	5.E-01	8.E+01
GOTERM_MF_FAT	GO:0048407~platelet-derived growth factor binding	3	0.341685649	9.E-02	12843, 12831, 12842	754	9	13288	6.E+00	1.E+00	5.E-01	8.E+01
UP_SEQ_FEATURE	region of interest:Triple-helical region	3	0.341685649	3.E-01	12831, 12842, 12815	861	18	16021	3.E+00	1.E+00	1.E+00	1.E+02
GOTERM_CC_FAT	GO:0044420~extracellular matrix part	7	0.797266515	3.E-01	12843, 12831, 12842, 20692, 16948, 1281	636	92	12504	1.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0030199~collagen fibril organization	3	0.341685649	4.E-01	12831, 16948, 12815	809	21	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_MF_FAT	GO:0019838~growth factor binding	6	0.683371298	4.E-01	12843, 12831, 16195, 12842, 16001, 1708	754	72	13288	1.E+00	1.E+00	9.E-01	1.E+02
SP_PIR_KEYWORDS	hydroxylation	4	0.455580866	6.E-01	12843, 12831, 12842, 12815	869	64	17854	1.E+00	1.E+00	9.E-01	1.E+02
KEGG_PATHWAY	mmu04512ECM-receptor interaction	8	0.911161731	7.E-01	12843, 12831, 12842, 12491, 20969, 1250	580	83	5738	1.E+00	1.E+00	9.E-01	1.E+02
INTERPRO	IPR008160:Collagen triple helix repeat	4	0.455580866	8.E-01	12843, 12831, 12842, 12815	860	81	17763	1.E+00	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	collagen	4	0.455580866	8.E-01	12843, 12831, 12842, 12815	869	84	17854	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0030198~extracellular matrix organization	5	0.569476082	9.E-01	12051, 11785, 12831, 16948, 12815	809	101	13588	8.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0043062~extracellular structure organization	7	0.797266515	9.E-01	12051, 11785, 12831, 16948, 18479, 1281	809	149	13588	8.E-01	1.E+00	1.E+00	1.E+02
GOTERM_CC_FAT	GO:0005604~basement membrane	3	0.341685649	9.E-01	12831, 20692, 11704	636	73	12504	8.E-01	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	extracellular matrix	7	0.797266515	1.E+00	12843, 12831, 13801, 12842, 20692, 1281	869	213	17854	7.E-01	1.E+00	1.E+00	1.E+02
GOTERM_CC_FAT	GO:0031012~extracellular matrix	9	1.025056948	1.E+00	12843, 12831, 13801, 12842, 20692, 1694	636	309	12504	6.E-01	1.E+00	1.E+00	1.E+02
GOTERM_CC_FAT	GO:0005578~proteinaceous extracellular matrix	8	0.911161731	1.E+00	12843, 12831, 13801, 12842, 20692, 1694	636	297	12504	5.E-01	1.E+00	1.E+00	1.E+02

Annotation Cluster 205	Enrichment Score: 0.6254113931720793											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0031674~I band	6	0.683371298	1.E-01	12955, 11464, 20191, 12345, 208727, 155	636	53	12504	2.E+00	1.E+00	4.E-01	9.E+01
GOTERM_CC_FAT	GO:0030018~Z disc	5	0.569476082	2.E-01	12955, 20191, 12345, 208727, 15507	636	46	12504	2.E+00	1.E+00	6.E-01	1.E+02
GOTERM_CC_FAT	GO:0030017~sarcomere	7	0.797266515	2.E-01	12955, 11464, 11459, 20191, 12345, 2087	636	80	12504	2.E+00	1.E+00	6.E-01	1.E+02
GOTERM_CC_FAT	GO:0044449~contractile fiber part	7	0.797266515	3.E-01	12955, 11464, 11459, 20191, 12345, 2087	636	86	12504	2.E+00	1.E+00	7.E-01	1.E+02
GOTERM_CC_FAT	GO:0030016~myofibril	7	0.797266515	3.E-01	12955, 11464, 11459, 20191, 12345, 2087	636	91	12504	2.E+00	1.E+00	7.E-01	1.E+02
GOTERM_CC_FAT	GO:0043292~contractile fiber	7	0.797266515	4.E-01	12955, 11464, 11459, 20191, 12345, 2087	636	95	12504	1.E+00	1.E+00	7.E-01	1.E+02

Annotation Cluster 206	Enrichment Score: 0.623332445580504											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0007398~ectoderm development	13	1.480637813	1.E-01	12831, 13649, 14178, 12842, 19206, 1537	809	133	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0008544~epidermis development	12	1.366742597	1.E-01	16994, 12831, 13649, 12842, 14178, 1920	809	125	13588	2.E+00	1.E+00	6.E-01	9.E+01
BIOCARTA	m_telPathway:Telomeres Telomerase Cellular Aging and Immort	6	0.683371298	1.E-01	13649, 19645, 11651, 12043, 17869, 1600	188	18	1171	2.E+00	1.E+00	4.E-01	9.E+01
GOTERM_BP_FAT	GO:0001942~hair follicle development	5	0.569476082	3.E-01	13649, 14178, 19164, 11651, 12043	809	50	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0022405~hair cycle process	5	0.569476082	3.E-01	13649, 14178, 19164, 11651, 12043	809	50	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0022404~molting cycle process	5	0.569476082	3.E-01	13649, 14178, 19164, 11651, 12043	809	50	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0042303~molting cycle	5	0.569476082	4.E-01	13649, 14178, 19164, 11651, 12043	809	52	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0042633~hair cycle	5	0.569476082	4.E-01	13649, 14178, 19164, 11651, 12043	809	52	13588	2.E+00	1.E+00	9.E-01	1.E+02

Annotation Cluster 207	Enrichment Score: 0.6100563952301316											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0051047~positive regulation of secretion	7	0.797266515	9.E-02	14127, 14661, 12568, 12912, 83671, 1039	809	53	13588	2.E+00	1.E+00	5.E-01	8.E+01
GOTERM_BP_FAT	GO:0045921~positive regulation of exocytosis	3	0.341685649	2.E-01	14127, 12568, 20963	809	13	13588	4.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0017157~regulation of exocytosis	4	0.455580866	3.E-01	14127, 380714, 12568, 20963	809	32	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0060627~regulation of vesicle-mediated transport	5	0.569476082	7.E-01	14127, 380714, 12568, 11625, 20963	809	83	13588	1.E+00	1.E+00	1.E+00	1.E+02

Annotation Cluster 208	Enrichment Score: 0.6044343365019649											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0043933~macromolecular complex subunit organization	29	3.302961276	1.E-01	227753, 14151, 22130, 13669, 18416, 118	809	367	13588	1.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0034621~cellular macromolecular complex subunit organizati	20	2.277904328	1.E-01	22142, 621893, 227753, 13800, 13669, 22	809	245	13588	1.E+00	1.E+00	7.E-01	9.E+01
GOTERM_BP_FAT	GO:0065003~macromolecular complex assembly	25	2.84738041	2.E-01	227753, 14151, 22130, 13669, 18416, 178	809	338	13588	1.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0034622~cellular macromolecular complex assembly	16	1.822323462	3.E-01	22142, 621893, 227753, 13669, 18479, 55	809	217	13588	1.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0070271~protein complex biogenesis	16	1.822323462	4.E-01	22142, 227753, 22130, 18416, 17869, 184	809	227	13588	1.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0064661~protein complex assembly	16	1.822323462	4.E-01	22142, 227753, 22130, 18416, 17869, 184	809	227	13588	1.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0051259~protein oligomerization	6	0.683371298	4.E-01	18416, 72269, 12028, 20133, 16001, 2013	809	72	13588	1.E+00	1.E+00	9.E-01	1.E+02

Annotation Cluster 209	Enrichment Score: 0.5864874746303814											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0033059~cellular pigmentation	3	0.341685649	2.E-01	12043, 11891, 171531	809	12	13588	4.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0030318~melanocyte differentiation	3	0.341685649	2.E-01	12043, 11891, 171531	809	16	13588	3.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0048066~pigmentation during development	4	0.455580866	3.E-01	12043, 11891, 14682, 171531	809	30	13588	2.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0050931~pigment cell differentiation	3	0.341685649	3.E-01	12043, 11891, 171531	809	17	13588	3.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0043473~pigmentation	5	0.569476082	4.E-01	12043, 17869, 11891, 14682, 171531	809	56	13588	1.E+00	1.E+00	9.E-01	1.E+02

Annotation Cluster 210	Enrichment Score: 0.5713032683895406											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR



KEGG_PATHWAY	mmu00270:Cysteine and methionine metabolism	7	0.797266515	1.E-01	16828, 232087, 13436, 16833, 16832, 229	580	33	5738	2.E+00	1.E+00	2.E-01	8.E+01
SP_PIR_KEYWORDS	one-carbon metabolism	3	0.341685649	2.E-01	232087, 229709, 11720	869	15	17854	4.E+00	1.E+00	4.E-01	9.E+01
KEGG_PATHWAY	mmu00450:Selenoamino acid metabolism	4	0.455580866	4.E-01	232087, 229709, 23971, 11720	580	23	5738	2.E+00	1.E+00	6.E-01	1.E+02
GOTERM_BP_FAT	GO:0006730~one-carbon metabolic process	7	0.797266515	7.E-01	225363, 232087, 14852, 15278, 13436, 22	809	117	13588	1.E+00	1.E+00	1.E+00	1.E+02
Annotation Cluster 211	Enrichment Score: 0.5478784905797576											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0030030~cell projection organization	27	3.075170843	6.E-02	22323, 11658, 11651, 21869, 14026, 1707	809	319	13588	1.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0030182~neuron differentiation	31	3.530751708	1.E-01	22323, 11658, 15376, 433759, 21869, 140	809	399	13588	1.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0007411~axon guidance	10	1.138952164	1.E-01	22323, 11785, 14432, 11658, 13800, 7757	809	98	13588	2.E+00	1.E+00	6.E-01	9.E+01
GOTERM_BP_FAT	GO:0048666~neuron development	23	2.619589977	2.E-01	22323, 11658, 73750, 13800, 15430, 1204	809	292	13588	1.E+00	1.E+00	7.E-01	9.E+01
GOTERM_BP_FAT	GO:0032989~cellular component morphogenesis	25	2.84738041	3.E-01	22323, 13649, 11658, 13605, 16800, 2186	809	351	13588	1.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0031175~neuron projection development	16	1.822323462	3.E-01	22323, 13800, 11658, 12043, 18479, 1291	809	218	13588	1.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0007409~axonogenesis	12	1.366742597	4.E-01	22323, 11785, 14432, 11658, 13800, 7757	809	163	13588	1.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0032990~cell part morphogenesis	15	1.708428246	4.E-01	22323, 104394, 13800, 11658, 12043, 129	809	212	13588	1.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0000902~cell morphogenesis	20	2.277904328	5.E-01	22323, 13649, 104394, 11658, 13800, 136	809	309	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0048812~neuron projection morphogenesis	12	1.366742597	5.E-01	22323, 11785, 14432, 11658, 13800, 7757	809	176	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0048667~cell morphogenesis involved in neuron differentiat	12	1.366742597	5.E-01	22323, 11785, 14432, 11658, 13800, 7757	809	182	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0048858~cell projection morphogenesis	13	1.480637813	5.E-01	22323, 104394, 13800, 11658, 12043, 140	809	202	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0000904~cell morphogenesis involved in differentiation	12	1.366742597	7.E-01	22323, 11785, 14432, 11658, 13800, 7757	809	212	13588	1.E+00	1.E+00	1.E+00	1.E+02
Annotation Cluster 212	Enrichment Score: 0.5427281605269167											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0045165~cell fate commitment	12	1.366742597	3.E-01	21349, 14432, 24064, 15376, 19164, 1204	809	147	13588	1.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0001708~cell fate specification	6	0.683371298	3.E-01	15376, 19164, 15430, 14843, 16412, 2186	809	59	13588	2.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0048663~neuron fate commitment	5	0.569476082	3.E-01	15376, 15430, 12540, 14843, 21869	809	47	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0048665~neuron fate specification	3	0.341685649	3.E-01	15376, 15430, 14843	809	19	13588	3.E+00	1.E+00	9.E-01	1.E+02
Annotation Cluster 213	Enrichment Score: 0.5425186922006667											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	manganese	11	1.25284738	2.E-01	11350, 23920, 19053, 245000, 14208, 185	869	145	17854	2.E+00	1.E+00	4.E-01	9.E+01
UP_SEQ_FEATURE	metal ion-binding site:Manganese	4	0.455580866	2.E-01	19053, 18534, 18563, 74551	861	31	16021	2.E+00	1.E+00	1.E+00	1.E+02
GOTERM_MF_FAT	GO:0030145~manganese ion binding	9	1.025056948	6.E-01	11350, 19053, 245000, 14208, 18534, 118	754	148	13288	1.E+00	1.E+00	1.E+00	1.E+02
Annotation Cluster 214	Enrichment Score: 0.5343596135044166											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR006186:Serine/threonine-specific protein phosphatase and bis(	3	0.341685649	2.E-01	19053, 19056, 19057	860	15	17763	4.E+00	1.E+00	9.E-01	9.E+01
SMART	SM00156:PP2Ac	3	0.341685649	2.E-01	19053, 19056, 19057	492	15	9131	4.E+00	1.E+00	8.E-01	9.E+01
SP_PIR_KEYWORDS	protein phosphatase	9	1.025056948	2.E-01	15170, 19053, 19253, 14208, 12532, 1253	869	120	17854	2.E+00	1.E+00	5.E-01	1.E+02
INTERPRO	IPR004843:Metallophosphoesterase	3	0.341685649	4.E-01	19053, 19056, 19057	860	29	17763	2.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	metal ion-binding site:Iron	3	0.341685649	7.E-01	19053, 19056, 19057	861	47	16021	1.E+00	1.E+00	1.E+00	1.E+02
Annotation Cluster 215	Enrichment Score: 0.5294668883946398											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0016605~PML body	4	0.455580866	7.E-02	19645, 22218, 12914, 68275	636	19	12504	4.E+00	1.E+00	3.E-01	6.E+01
BIOCARTA	m_pmlPathway:Regulation of transcriptional activity by PML	4	0.455580866	4.E-01	19645, 15461, 22218, 12914	188	15	1171	2.E+00	1.E+00	8.E-01	1.E+02
GOTERM_CC_FAT	GO:0016604~nuclear body	6	0.683371298	9.E-01	19645, 53610, 17869, 22218, 12914, 6827	636	142	12504	8.E-01	1.E+00	1.E+00	1.E+02
Annotation Cluster 216	Enrichment Score: 0.5260864195363711											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0040018~positive regulation of multicellular organism growth	4	0.455580866	2.E-01	14732, 12043, 12912, 13383	809	27	13588	2.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0040014~regulation of multicellular organism growth	7	0.797266515	3.E-01	14732, 19206, 11816, 12043, 12912, 1338	809	75	13588	2.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0045927~positive regulation of growth	5	0.569476082	4.E-01	14732, 74318, 12043, 12912, 13383	809	56	13588	1.E+00	1.E+00	9.E-01	1.E+02
Annotation Cluster 217	Enrichment Score: 0.5167942934158082											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0043113~receptor clustering	3	0.341685649	2.E-01	192176, 18479, 12568	809	13	13588	4.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0007172~signal complex assembly	3	0.341685649	2.E-01	192176, 18479, 12568	809	15	13588	3.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0043112~receptor metabolic process	3	0.341685649	5.E-01	192176, 18479, 12568	809	26	13588	2.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0043623~cellular protein complex assembly	8	0.911161731	5.E-01	22142, 227753, 192176, 18479, 12568, 67	809	108	13588	1.E+00	1.E+00	1.E+00	1.E+02
Annotation Cluster 218	Enrichment Score: 0.5137156559900705											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0046883~regulation of hormone secretion	5	0.569476082	2.E-01	14661, 18413, 18576, 12912, 103988	809	36	13588	2.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0050796~regulation of insulin secretion	3	0.341685649	4.E-01	14661, 18576, 103988	809	22	13588	2.E+00	1.E+00	9.E-01	1.E+02



GOTERM_BP_FAT	GO:0002791--regulation of peptide secretion	3	0.341685649	5.E-01	14661, 18576, 103988	809	26	13588	2.E+00	1.E+00	1.E+00	1.E+02
Annotation Cluster 219	Enrichment Score: 0.5039313925094354											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0030258--lipid modification	7	0.797266515	6.E-02	18708, 74147, 26416, 30955, 11364, 1870	809	47	13588	3.E+00	1.E+00	4.E-01	7.E+01
GOTERM_BP_FAT	GO:0034440--lipid oxidation	4	0.455580866	2.E-01	74147, 26416, 11364, 231086	809	24	13588	3.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0019395--fatty acid oxidation	4	0.455580866	2.E-01	74147, 26416, 11364, 231086	809	24	13588	3.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0006635--fatty acid beta-oxidation	3	0.341685649	2.E-01	74147, 11364, 231086	809	16	13588	3.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0009062--fatty acid catabolic process	3	0.341685649	4.E-01	74147, 11364, 231086	809	23	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0046395--carboxylic acid catabolic process	6	0.683371298	5.E-01	12039, 18126, 74147, 100048676, 12040,	809	81	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0016054--organic acid catabolic process	6	0.683371298	5.E-01	12039, 18126, 74147, 100048676, 12040,	809	81	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0009310--amine catabolic process	4	0.455580866	8.E-01	12039, 18126, 100048676, 12040, 12846	809	65	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0009063--cellular amino acid catabolic process	3	0.341685649	8.E-01	12039, 18126, 100048676, 12040	809	54	13588	9.E-01	1.E+00	1.E+00	1.E+02
Annotation Cluster 220	Enrichment Score: 0.49483264808388466											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0051327--M phase of meiotic cell cycle	9	1.025056948	2.E-01	12190, 13006, 209091, 30939, 100044764	809	88	13588	2.E+00	1.E+00	7.E-01	9.E+01
GOTERM_BP_FAT	GO:0007126--meiosis	9	1.025056948	2.E-01	12190, 13006, 209091, 30939, 100044764	809	88	13588	2.E+00	1.E+00	7.E-01	9.E+01
GOTERM_BP_FAT	GO:0051321--meiotic cell cycle	9	1.025056948	2.E-01	12190, 13006, 209091, 30939, 100044764	809	90	13588	2.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0007127--meiosis I	3	0.341685649	6.E-01	30939, 100044764, 100039474, 67141, 66	809	35	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_CC_FAT	GO:0000794--condensed nuclear chromosome	3	0.341685649	6.E-01	13006, 18005, 68275	636	42	12504	1.E+00	1.E+00	9.E-01	1.E+02
SP_PIR_KEYWORDS	meiosis	3	0.341685649	7.E-01	13006, 209091, 18005	869	50	17854	1.E+00	1.E+00	9.E-01	1.E+02
Annotation Cluster 221	Enrichment Score: 0.4909357679478802											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0001556--oocyte maturation	4	0.455580866	2.E-02	12190, 12531, 20112, 67141	809	10	13588	7.E+00	1.E+00	2.E-01	3.E+01
GOTERM_BP_FAT	GO:0003006--reproductive developmental process	24	2.733485194	4.E-02	12190, 11651, 14180, 12043, 13382, 6714	809	264	13588	2.E+00	1.E+00	3.E-01	5.E+01
GOTERM_BP_FAT	GO:0007292--female gamete generation	8	0.911161731	5.E-02	12190, 20779, 11920, 12043, 12531, 1684	809	56	13588	2.E+00	1.E+00	3.E-01	6.E+01
GOTERM_BP_FAT	GO:0007281--germ cell development	10	1.138952164	1.E-01	12190, 56717, 12048, 12028, 11651, 1204	809	101	13588	2.E+00	1.E+00	7.E-01	9.E+01
GOTERM_BP_FAT	GO:0048610--reproductive cellular process	12	1.366742597	5.E-01	12190, 56717, 12048, 12028, 11651, 1204	809	173	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0048609--reproductive process in a multicellular organism	25	2.84738041	6.E-01	12190, 22209, 238055, 11651, 15277, 129	809	409	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0032504--multicellular organism reproduction	25	2.84738041	6.E-01	12190, 22209, 238055, 11651, 15277, 129	809	409	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0007276--gamete generation	19	2.164009112	7.E-01	12190, 19317, 26934, 11651, 12043, 2380	809	331	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0019953--sexual reproduction	19	2.164009112	9.E-01	12190, 19317, 26934, 11651, 12043, 2380	809	386	13588	8.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0009566--fertilization	3	0.341685649	9.E-01	12048, 12028, 238055	809	73	13588	7.E-01	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	spermatogenesis	3	0.341685649	1.E+00	110957, 26934, 67402	869	123	17854	5.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0048232--male gamete generation	9	1.025056948	1.E+00	110957, 12190, 19317, 26934, 12048, 120	809	255	13588	6.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0007283--spermatogenesis	9	1.025056948	1.E+00	110957, 12190, 19317, 26934, 12048, 120	809	255	13588	6.E-01	1.E+00	1.E+00	1.E+02
Annotation Cluster 222	Enrichment Score: 0.4909269180331277											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0009743--response to carbohydrate stimulus	4	0.455580866	2.E-01	14226, 230163, 14645, 103988	809	26	13588	3.E+00	1.E+00	7.E-01	1.E+02
GOTERM_BP_FAT	GO:0034284--response to monosaccharide stimulus	3	0.341685649	4.E-01	14226, 14645, 103988	809	22	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0009746--response to hexose stimulus	3	0.341685649	4.E-01	14226, 14645, 103988	809	22	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0009749--response to glucose stimulus	3	0.341685649	4.E-01	14226, 14645, 103988	809	22	13588	2.E+00	1.E+00	9.E-01	1.E+02
Annotation Cluster 223	Enrichment Score: 0.4877409505255019											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0021904--dorsal/ventral neural tube patterning	3	0.341685649	2.E-01	19206, 15376, 19164	809	16	13588	3.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0009953--dorsal/ventral pattern formation	6	0.683371298	3.E-01	19206, 15376, 19164, 14843, 21869, 2406	809	64	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0021532--neural tube patterning	3	0.341685649	4.E-01	19206, 15376, 19164	809	24	13588	2.E+00	1.E+00	9.E-01	1.E+02
Annotation Cluster 224	Enrichment Score: 0.4856063203072306											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0032318--regulation of Ras GTPase activity	8	0.911161731	2.E-01	56717, 24064, 71709, 228998, 19765, 194	809	80	13588	2.E+00	1.E+00	7.E-01	1.E+02
INTERPRO	IPR001164:Arf GTPase activating protein	3	0.341685649	3.E-01	228998, 212285, 106952	860	23	17763	3.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	domain:Arf-GAP	3	0.341685649	3.E-01	228998, 212285, 106952	861	21	16021	3.E+00	1.E+00	1.E+00	1.E+02
SMART	SM00105:ArfGap	3	0.341685649	4.E-01	228998, 212285, 106952	492	23	9131	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_MF_FAT	GO:0008060--ARF GTPase activator activity	3	0.341685649	4.E-01	228998, 212285, 106952	754	23	13288	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0032012--regulation of ARF protein signal transduction	4	0.455580866	4.E-01	228998, 19159, 212285, 106952	809	38	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0032312--regulation of ARF GTPase activity	3	0.341685649	4.E-01	228998, 212285, 106952	809	23	13588	2.E+00	1.E+00	9.E-01	1.E+02
Annotation Cluster 225	Enrichment Score: 0.48413500852043945											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0044057--regulation of system process	18	2.050113895	9.E-02	18747, 11806, 11807, 14678, 14226, 1484	809	201	13588	2.E+00	1.E+00	5.E-01	8.E+01



GOTERM_BP_FAT	GO:0048167--regulation of synaptic plasticity	5	0.569476082	3.E-01	15461, 19164, 12568, 19417, 13385	809	48	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0050804--regulation of synaptic transmission	8	0.911161731	4.E-01	16994, 18747, 14678, 15461, 19164, 1256	809	100	13588	1.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0051969--regulation of transmission of nerve impulse	8	0.911161731	5.E-01	16994, 18747, 14678, 15461, 19164, 1256	809	107	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0048168--regulation of neuronal synaptic plasticity	3	0.341685649	5.E-01	15461, 19417, 13385	809	27	13588	2.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0031644--regulation of neurological system process	8	0.911161731	5.E-01	16994, 18747, 14678, 15461, 19164, 1256	809	113	13588	1.E+00	1.E+00	1.E+00	1.E+02
Annotation Cluster 226	Enrichment Score: 0.4787468300932601											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_SEQ_FEATURE	domain:PDZ 1	5	0.569476082	1.E-01	277360, 73750, 170761, 13383, 13385	861	34	16021	3.E+00	1.E+00	1.E+00	9.E+01
UP_SEQ_FEATURE	domain:PDZ 3	4	0.455580866	1.E-01	73750, 170761, 13383, 13385	861	24	16021	3.E+00	1.E+00	1.E+00	9.E+01
UP_SEQ_FEATURE	domain:PDZ 2	4	0.455580866	3.E-01	73750, 170761, 13383, 13385	861	33	16021	2.E+00	1.E+00	1.E+00	1.E+02
INTERPRO	IPR001478:PDZ/DHR/GLGF	8	0.911161731	6.E-01	277360, 73750, 170761, 70231, 13383, 21	860	148	17763	1.E+00	1.E+00	1.E+00	1.E+02
SMART	SM00228:PDZ	8	0.911161731	7.E-01	277360, 73750, 170761, 70231, 13383, 21	492	148	9131	1.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	domain:PDZ	4	0.455580866	9.E-01	70231, 21844, 74498, 24001	861	95	16021	8.E-01	1.E+00	1.E+00	1.E+02
Annotation Cluster 227	Enrichment Score: 0.4756273026927005											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0001829--trophectodermal cell differentiation	3	0.341685649	2.E-01	11486, 74318, 16477	809	16	13588	3.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0001825--blastocyst formation	3	0.341685649	4.E-01	11486, 74318, 16477	809	22	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0001824--blastocyst development	5	0.569476082	4.E-01	12190, 11486, 74318, 16477, 69270	809	54	13588	2.E+00	1.E+00	9.E-01	1.E+02
Annotation Cluster 228	Enrichment Score: 0.47027714283458777											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0006606--protein import into nucleus	6	0.683371298	2.E-01	664868, 56338, 231103, 14180, 70572, 67	809	56	13588	2.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0051170--nuclear import	6	0.683371298	3.E-01	664868, 56338, 231103, 14180, 70572, 67	809	58	13588	2.E+00	1.E+00	8.E-01	1.E+02
GOTERM_BP_FAT	GO:0034504--protein localization in nucleus	6	0.683371298	3.E-01	664868, 56338, 231103, 14180, 70572, 67	809	61	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0006913--nucleocytoplasmic transport	8	0.911161731	3.E-01	664868, 56338, 231103, 68092, 14180, 70	809	96	13588	1.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0017038--protein import	7	0.797266515	4.E-01	664868, 56338, 12122, 231103, 14180, 70	809	82	13588	1.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0051169--nuclear transport	8	0.911161731	4.E-01	664868, 56338, 231103, 68092, 14180, 70	809	98	13588	1.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0006605--protein targeting	10	1.138952164	4.E-01	664868, 56338, 54401, 12122, 231103, 14	809	133	13588	1.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0033365--protein localization in organelle	7	0.797266515	5.E-01	664868, 56338, 12122, 231103, 14180, 70	809	97	13588	1.E+00	1.E+00	1.E+00	1.E+02
Annotation Cluster 229	Enrichment Score: 0.4659941038691											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR008144:Guanylate kinase	3	0.341685649	3.E-01	14923, 13383, 13385	860	23	17763	3.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	domain:Guanylate kinase-like	3	0.341685649	3.E-01	14923, 13383, 13385	861	22	16021	3.E+00	1.E+00	1.E+00	1.E+02
INTERPRO	IPR008145:Guanylate kinase/L-type calcium channel region	3	0.341685649	3.E-01	14923, 13383, 13385	860	25	17763	2.E+00	1.E+00	1.E+00	1.E+02
SMART	SM00072:GuKc	3	0.341685649	4.E-01	14923, 13383, 13385	492	25	9131	2.E+00	1.E+00	9.E-01	1.E+02
Annotation Cluster 230	Enrichment Score: 0.4171478249977876											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_SEQ_FEATURE	domain:N-terminal Ras-GEF	3	0.341685649	2.E-01	20662, 20663, 19417	861	17	16021	3.E+00	1.E+00	1.E+00	1.E+02
INTERPRO	IPR019804:Ras guanine-nucleotide exchange factor, conserved sit	3	0.341685649	3.E-01	20662, 20663, 19417	860	24	17763	3.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	domain:Ras-GEF	3	0.341685649	4.E-01	20662, 20663, 19417	861	24	16021	2.E+00	1.E+00	1.E+00	1.E+02
INTERPRO	IPR001895:Guanine-nucleotide dissociation stimulator CDC25	3	0.341685649	4.E-01	20662, 20663, 19417	860	28	17763	2.E+00	1.E+00	1.E+00	1.E+02
INTERPRO	IPR000651:Guanine nucleotide exchange factor for Ras-like GTPas	3	0.341685649	4.E-01	20662, 20663, 19417	860	30	17763	2.E+00	1.E+00	1.E+00	1.E+02
INTERPRO	IPR008937:Ras guanine nucleotide exchange factor	3	0.341685649	4.E-01	20662, 20663, 19417	860	31	17763	2.E+00	1.E+00	1.E+00	1.E+02
SMART	SM00147:RasGEF	3	0.341685649	4.E-01	20662, 20663, 19417	492	28	9131	2.E+00	1.E+00	9.E-01	1.E+02
SMART	SM00229:RasGEFN	3	0.341685649	5.E-01	20662, 20663, 19417	492	30	9131	2.E+00	1.E+00	1.E+00	1.E+02
Annotation Cluster 231	Enrichment Score: 0.4149981396169685											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_SEQ_FEATURE	domain:Sushi 2	4	0.455580866	3.E-01	14060, 20343, 20339, 12263	861	33	16021	2.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	domain:Sushi 1	4	0.455580866	3.E-01	14060, 20343, 20339, 12263	861	33	16021	2.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	domain:Sushi 3	3	0.341685649	4.E-01	14060, 20339, 12263	861	24	16021	2.E+00	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	sushi	4	0.455580866	4.E-01	14060, 20343, 20339, 12263	869	46	17854	2.E+00	1.E+00	7.E-01	1.E+02
INTERPRO	IPR000436:Sushi/SCR/CCP	4	0.455580866	5.E-01	14060, 20343, 20339, 12263	860	53	17763	2.E+00	1.E+00	1.E+00	1.E+02
INTERPRO	IPR016060:Complement control module	4	0.455580866	5.E-01	14060, 20343, 20339, 12263	860	54	17763	2.E+00	1.E+00	1.E+00	1.E+02
SMART	SM00032:CCP	4	0.455580866	5.E-01	14060, 20343, 20339, 12263	492	53	9131	1.E+00	1.E+00	1.E+00	1.E+02
Annotation Cluster 232	Enrichment Score: 0.3897163418029444											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0043010--camera-type eye development	12	1.366742597	2.E-01	18771, 12955, 232906, 77579, 12028, 120	809	130	13588	2.E+00	1.E+00	7.E-01	9.E+01
GOTERM_BP_FAT	GO:0048593--camera-type eye morphogenesis	4	0.455580866	5.E-01	12028, 12018, 56847, 17268	809	48	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0048592--eye morphogenesis	4	0.455580866	8.E-01	12028, 12018, 56847, 17268	809	73	13588	9.E-01	1.E+00	1.E+00	1.E+02



Annotation Cluster 233	Enrichment Score: 0.3683053717776443													
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR		
INTERPRO	IPR000626:Ubiquitin	4	0.455580866		4.E-01 78294, 19358, 22218, 14109	860	860	47	17763	2.E+00	1.E+00	1.E+00	1.E+02	
INTERPRO	IPR019954:Ubiquitin conserved site	3	0.341685649		4.E-01 78294, 19358, 14109	860	860	29	17763	2.E+00	1.E+00	1.E+00	1.E+02	
INTERPRO	IPR019955:Ubiquitin supergroup	4	0.455580866		4.E-01 78294, 19358, 22218, 14109	860	860	50	17763	2.E+00	1.E+00	1.E+00	1.E+02	
SMART	SM00213:UBQ	4	0.455580866		5.E-01 78294, 19358, 22218, 14109	492	492	47	9131	2.E+00	1.E+00	1.E+00	1.E+02	
Annotation Cluster 234	Enrichment Score: 0.3673002383621402													
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR		
UP_SEQ_FEATURE	domain:Ig-like V-type 2	3	0.341685649		3.E-01 270152, 16456, 11658	861	861	19	16021	3.E+00	1.E+00	1.E+00	1.E+02	
UP_SEQ_FEATURE	domain:Ig-like V-type 1	3	0.341685649		3.E-01 270152, 16456, 11658	861	861	20	16021	3.E+00	1.E+00	1.E+00	1.E+02	
INTERPRO	IPR013106:Immunoglobulin V-set	9	1.025056948		1.E+00 270152, 16456, 11658, 69524, 13052, 839	860	860	364	17763	5.E-01	1.E+00	1.E+00	1.E+02	
Annotation Cluster 235	Enrichment Score: 0.3582998275203344													
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR		
GOTERM_BP_FAT	GO:0050863~regulation of T cell activation	11	1.25284738		1.E-01 16408, 15170, 16818, 12015, 16197, 2467	809	809	108	13588	2.E+00	1.E+00	6.E-01	9.E+01	
GOTERM_BP_FAT	GO:0042129~regulation of T cell proliferation	6	0.683371298		3.E-01 16408, 15170, 246779, 16396, 13383, 209	809	809	59	13588	2.E+00	1.E+00	8.E-01	1.E+02	
GOTERM_BP_FAT	GO:0002683~negative regulation of immune system process	7	0.797266515		3.E-01 15170, 16197, 11486, 16396, 16190, 1905	809	809	76	13588	2.E+00	1.E+00	9.E-01	1.E+02	
GOTERM_BP_FAT	GO:0050868~negative regulation of T cell activation	4	0.455580866		5.E-01 15170, 16396, 16190, 13383	809	809	42	13588	2.E+00	1.E+00	1.E+00	1.E+02	
GOTERM_BP_FAT	GO:0042130~negative regulation of T cell proliferation	3	0.341685649		5.E-01 15170, 16396, 13383	809	809	28	13588	2.E+00	1.E+00	1.E+00	1.E+02	
GOTERM_BP_FAT	GO:0051250~negative regulation of lymphocyte activation	4	0.455580866		6.E-01 15170, 16396, 16190, 13383	809	809	52	13588	1.E+00	1.E+00	1.E+00	1.E+02	
GOTERM_BP_FAT	GO:0002695~negative regulation of leukocyte activation	4	0.455580866		6.E-01 15170, 16396, 16190, 13383	809	809	53	13588	1.E+00	1.E+00	1.E+00	1.E+02	
GOTERM_BP_FAT	GO:0050866~negative regulation of cell activation	4	0.455580866		6.E-01 15170, 16396, 16190, 13383	809	809	53	13588	1.E+00	1.E+00	1.E+00	1.E+02	
GOTERM_BP_FAT	GO:0032945~negative regulation of mononuclear cell proliferation	3	0.341685649		6.E-01 15170, 16396, 13383	809	809	35	13588	1.E+00	1.E+00	1.E+00	1.E+02	
GOTERM_BP_FAT	GO:0070664~negative regulation of leukocyte proliferation	3	0.341685649		6.E-01 15170, 16396, 13383	809	809	35	13588	1.E+00	1.E+00	1.E+00	1.E+02	
GOTERM_BP_FAT	GO:0050672~negative regulation of lymphocyte proliferation	3	0.341685649		6.E-01 15170, 16396, 13383	809	809	35	13588	1.E+00	1.E+00	1.E+00	1.E+02	
Annotation Cluster 236	Enrichment Score: 0.35777488501643784													
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR		
UP_SEQ_FEATURE	DNA-binding region:Basic motif	12	1.366742597		2.E-01 21349, 17119, 17869, 16477, 14281, 1428	861	861	154	16021	1.E+00	1.E+00	1.E+00	1.E+02	
INTERPRO	IPR001092:Basic helix-loop-helix dimerisation region bHLH	7	0.797266515		5.E-01 21349, 17119, 17869, 17978, 17187, 1797	860	860	111	17763	1.E+00	1.E+00	1.E+00	1.E+02	
UP_SEQ_FEATURE	domain:Helix-loop-helix motif	7	0.797266515		5.E-01 21349, 17119, 17869, 17978, 17187, 1797	861	861	109	16021	1.E+00	1.E+00	1.E+00	1.E+02	
SMART	SM00353:HLH	7	0.797266515		6.E-01 21349, 17119, 17869, 17978, 17187, 1797	492	492	111	9131	1.E+00	1.E+00	1.E+00	1.E+02	
INTERPRO	IPR011598:Helix-loop-helix DNA-binding	5	0.569476082		6.E-01 21349, 17119, 17869, 17978, 17187	860	860	85	17763	1.E+00	1.E+00	1.E+00	1.E+02	
Annotation Cluster 237	Enrichment Score: 0.34347578125851086													
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR		
GOTERM_BP_FAT	GO:0001894~tissue homeostasis	5	0.569476082		3.E-01 18596, 12028, 12043, 12815, 68275	809	809	50	13588	2.E+00	1.E+00	9.E-01	1.E+02	
GOTERM_BP_FAT	GO:0048873~homeostasis of number of cells within a tissue	3	0.341685649		4.E-01 12028, 12043, 68275	809	809	21	13588	2.E+00	1.E+00	9.E-01	1.E+02	
GOTERM_BP_FAT	GO:0060249~anatomical structure homeostasis	6	0.683371298		6.E-01 18596, 12028, 18815, 12043, 12815, 6827	809	809	83	13588	1.E+00	1.E+00	1.E+00	1.E+02	
GOTERM_BP_FAT	GO:0048871~multicellular organismal homeostasis	5	0.569476082		6.E-01 18596, 12028, 12043, 12815, 68275	809	809	71	13588	1.E+00	1.E+00	1.E+00	1.E+02	
Annotation Cluster 238	Enrichment Score: 0.3423109852946941													
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR		
GOTERM_BP_FAT	GO:0001822~kidney development	9	1.025056948		3.E-01 382985, 18596, 19713, 12028, 109900, 12	809	809	107	13588	1.E+00	1.E+00	9.E-01	1.E+02	
GOTERM_BP_FAT	GO:0001655~urogenital system development	11	1.25284738		4.E-01 382985, 18596, 19713, 12028, 109900, 12	809	809	146	13588	1.E+00	1.E+00	9.E-01	1.E+02	
GOTERM_BP_FAT	GO:0001657~ureteric bud development	4	0.455580866		5.E-01 19713, 12043, 12505, 13383	809	809	42	13588	2.E+00	1.E+00	1.E+00	1.E+02	
GOTERM_BP_FAT	GO:0001658~branching involved in ureteric bud morphogenesis	3	0.341685649		5.E-01 12043, 12505, 13383	809	809	28	13588	2.E+00	1.E+00	1.E+00	1.E+02	
GOTERM_BP_FAT	GO:0060675~ureteric bud morphogenesis	3	0.341685649		5.E-01 12043, 12505, 13383	809	809	28	13588	2.E+00	1.E+00	1.E+00	1.E+02	
GOTERM_BP_FAT	GO:0001656~metanephros development	4	0.455580866		7.E-01 19713, 12043, 12505, 13383	809	809	58	13588	1.E+00	1.E+00	1.E+00	1.E+02	
Annotation Cluster 239	Enrichment Score: 0.3350437330376809													
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR		
UP_SEQ_FEATURE	domain:SAM	7	0.797266515		2.E-01 13836, 54383, 50768, 243362, 16822, 212	861	861	68	16021	2.E+00	1.E+00	1.E+00	9.E+01	
INTERPRO	IPR001660:Sterile alpha motif SAM	5	0.569476082		6.E-01 13836, 54383, 16822, 212285, 106952	860	860	87	17763	1.E+00	1.E+00	1.E+00	1.E+02	
INTERPRO	IPR013761:Sterile alpha motif-type	4	0.455580866		7.E-01 13836, 54383, 212285, 106952	860	860	72	17763	1.E+00	1.E+00	1.E+00	1.E+02	
SMART	SM00454:SAM	5	0.569476082		7.E-01 13836, 54383, 16822, 212285, 106952	492	492	87	9131	1.E+00	1.E+00	1.E+00	1.E+02	
Annotation Cluster 240	Enrichment Score: 0.3262846891217245													
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR		
GOTERM_BP_FAT	GO:0048704~embryonic skeletal system morphogenesis	7	0.797266515		2.E-01 15402, 15438, 15415, 15407, 15416, 1543	809	809	64	13588	2.E+00	1.E+00	7.E-01	1.E+02	
GOTERM_BP_FAT	GO:0008344~adult locomotory behavior	4	0.455580866		7.E-01 15438, 15416, 15430, 20238	809	809	62	13588	1.E+00	1.E+00	1.E+00	1.E+02	
GOTERM_BP_FAT	GO:0030534~adult behavior	5	0.569476082		8.E-01 15438, 15416, 15430, 12568, 20238	809	809	93	13588	9.E-01	1.E+00	1.E+00	1.E+02	



Annotation Cluster 241		Enrichment Score: 0.2981946791521004											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_BP_FAT	GO:0050729~positive regulation of inflammatory response	3	0.341685649		4.E-01 14127, 16803, 21937	809	24	13588	2.E+00	1.E+00	9.E-01	1.E+02	
GOTERM_BP_FAT	GO:0050727~regulation of inflammatory response	5	0.569476082		4.E-01 14127, 11486, 16803, 11625, 21937	809	57	13588	1.E+00	1.E+00	9.E-01	1.E+02	
GOTERM_BP_FAT	GO:0032103~positive regulation of response to external stimulus	3	0.341685649		7.E-01 14127, 16803, 21937	809	39	13588	1.E+00	1.E+00	1.E+00	1.E+02	
Annotation Cluster 242		Enrichment Score: 0.2846902783242877											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_BP_FAT	GO:0009084~glutamine family amino acid biosynthetic process	3	0.341685649		2.E-01 18416, 109900, 14645	809	15	13588	3.E+00	1.E+00	8.E-01	1.E+02	
GOTERM_BP_FAT	GO:0009064~glutamine family amino acid metabolic process	5	0.569476082		3.E-01 18126, 18416, 109900, 11847, 14645	809	43	13588	2.E+00	1.E+00	8.E-01	1.E+02	
GOTERM_BP_FAT	GO:0008652~cellular amino acid biosynthetic process	4	0.455580866		5.E-01 18416, 109900, 232087, 14645	809	44	13588	2.E+00	1.E+00	1.E+02	1.E+02	
KEGG_PATHWAY	mmu00330:Arginine and proline metabolism	6	0.683371298		6.E-01 18126, 14661, 18416, 109900, 11847, 146	580	53	5738	1.E+00	1.E+00	8.E-01	1.E+02	
GOTERM_BP_FAT	GO:0009309~amine biosynthetic process	5	0.569476082		6.E-01 18416, 109900, 232087, 14462, 14645	809	73	13588	1.E+00	1.E+00	1.E+00	1.E+02	
GOTERM_BP_FAT	GO:0046394~carboxylic acid biosynthetic process	8	0.911161731		7.E-01 70316, 19317, 18416, 109900, 232087, 21	809	141	13588	1.E+00	1.E+00	1.E+00	1.E+02	
GOTERM_BP_FAT	GO:0016053~organic acid biosynthetic process	8	0.911161731		7.E-01 70316, 19317, 18416, 109900, 232087, 21	809	141	13588	1.E+00	1.E+00	1.E+00	1.E+02	
GOTERM_BP_FAT	GO:0006633~fatty acid biosynthetic process	4	0.455580866		9.E-01 70316, 19317, 21991, 20963	809	81	13588	8.E-01	1.E+00	1.E+00	1.E+02	
Annotation Cluster 243		Enrichment Score: 0.27193618608758496											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_BP_FAT	GO:0060740~prostate gland epithelium morphogenesis	3	0.341685649		5.E-01 12505, 16001, 16000	809	26	13588	2.E+00	1.E+00	1.E+00	1.E+02	
GOTERM_BP_FAT	GO:0060512~prostate gland morphogenesis	3	0.341685649		5.E-01 12505, 16001, 16000	809	27	13588	2.E+00	1.E+00	1.E+00	1.E+02	
GOTERM_BP_FAT	GO:0030850~prostate gland development	3	0.341685649		7.E-01 12505, 16001, 16000	809	39	13588	1.E+00	1.E+00	1.E+00	1.E+02	
Annotation Cluster 244		Enrichment Score: 0.27181948085425545											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_BP_FAT	GO:0007611~learning or memory	10	1.138952164		8.E-02 17159, 11785, 14661, 11514, 19085, 1916	809	89	13588	2.E+00	1.E+00	5.E-01	8.E+01	
GOTERM_BP_FAT	GO:0050877~neurological system process	28	3.189066059		1.E+00 17159, 17869, 12815, 170758, 16561, 146	809	1681	13588	3.E-01	1.E+00	1.E+00	1.E+02	
GOTERM_BP_FAT	GO:0050890~cognition	19	2.164009112		1.E+00 17159, 73750, 19085, 19088, 17869, 1281	809	1480	13588	2.E-01	1.E+00	1.E+00	1.E+02	
GOTERM_BP_FAT	GO:0007600~sensory perception	10	1.138952164		1.E+00 216869, 24064, 73750, 15416, 17869, 143	809	1402	13588	1.E-01	1.E+00	1.E+00	1.E+02	
Annotation Cluster 245		Enrichment Score: 0.26995726021374433											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
INTERPRO	IPR000961:AGC-kinase, C-terminal	4	0.455580866		5.E-01 18751, 18747, 11651, 20112	860	53	17763	2.E+00	1.E+00	1.E+00	1.E+02	
UP_SEQ_FEATURE	domain:AGC-kinase C-terminal	4	0.455580866		5.E-01 18751, 18747, 11651, 20112	861	53	16021	1.E+00	1.E+00	1.E+00	1.E+02	
SMART	SM00133:S_TK_X	4	0.455580866		5.E-01 18751, 18747, 11651, 20112	492	53	9131	1.E+00	1.E+00	1.E+00	1.E+02	
INTERPRO	IPR017892:Protein kinase, C-terminal	3	0.341685649		6.E-01 18751, 11651, 20112	860	40	17763	2.E+00	1.E+00	1.E+00	1.E+02	
Annotation Cluster 246		Enrichment Score: 0.2647565842991868											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
SP_PIR_KEYWORDS	dna-binding	80	9.111617312		1.E-01 22130, 50793, 14815, 12912, 319191, 218	869	1404	17854	1.E+00	1.E+00	3.E-01	8.E+01	
SP_PIR_KEYWORDS	nucleus	200	22.77904328		1.E-01 18746, 18747, 22130, 18221, 14884, 2063	869	3808	17854	1.E+00	1.E+00	4.E-01	9.E+01	
SP_PIR_KEYWORDS	activator	27	3.075170843		3.E-01 18181, 15376, 17869, 21869, 12912, 1654	869	484	17854	1.E+00	1.E+00	7.E-01	1.E+02	
SP_PIR_KEYWORDS	transcription regulation	77	8.769931663		5.E-01 22130, 101206, 14815, 12912, 21869, 165	869	1546	17854	1.E+00	1.E+00	8.E-01	1.E+02	
GOTERM_MF_FAT	GO:0043565~sequence-specific DNA binding	32	3.644646925		6.E-01 17536, 15376, 14815, 17869, 21869, 1291	754	556	13288	1.E+00	1.E+00	1.E+00	1.E+02	
GOTERM_MF_FAT	GO:0003677~DNA binding	98	11.16173121		7.E-01 12190, 22130, 50793, 14815, 12912, 1291	754	1781	13288	1.E+00	1.E+00	1.E+00	1.E+02	
GOTERM_MF_FAT	GO:0003700~transcription factor activity	41	4.669703872		8.E-01 17536, 69890, 18181, 433759, 15376, 178	754	776	13288	1.E+00	1.E+00	1.E+00	1.E+02	
GOTERM_MF_FAT	GO:0030528~transcription regulator activity	64	7.28929385		8.E-01 22130, 101206, 14815, 12815, 12912, 218	754	1206	13288	9.E-01	1.E+00	1.E+00	1.E+02	
SP_PIR_KEYWORDS	Transcription	78	8.883826879		9.E-01 22130, 101206, 14815, 12912, 21869, 165	869	1769	17854	9.E-01	1.E+00	1.E+00	1.E+02	
GOTERM_BP_FAT	GO:0006355~regulation of transcription, DNA-dependent	71	8.086560364		1.E+00 22130, 14815, 12912, 21869, 12914, 1654	809	1465	13588	8.E-01	1.E+00	1.E+00	1.E+02	
GOTERM_BP_FAT	GO:0051252~regulation of RNA metabolic process	71	8.086560364		1.E+00 22130, 14815, 12912, 21869, 12914, 1654	809	1488	13588	8.E-01	1.E+00	1.E+00	1.E+02	
GOTERM_BP_FAT	GO:0045449~regulation of transcription	107	12.18678815		1.E+00 22130, 101206, 14815, 12912, 12914, 165	809	2227	13588	8.E-01	1.E+00	1.E+00	1.E+02	
GOTERM_BP_FAT	GO:0006350~transcription	79	8.997722096		1.E+00 22130, 101206, 14815, 12912, 21869, 165	809	1772	13588	7.E-01	1.E+00	1.E+00	1.E+02	
Annotation Cluster 247		Enrichment Score: 0.26328482415169907											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_BP_FAT	GO:0010605~negative regulation of macromolecule metabolic pr	36	4.10022779		2.E-01 60406, 12190, 13685, 22130, 67184, 4337	809	506	13588	1.E+00	1.E+00	7.E-01	1.E+02	
GOTERM_BP_FAT	GO:0009890~negative regulation of biosynthetic process	28	3.189066059		4.E-01 60406, 12190, 13685, 22130, 67184, 4337	809	434	13588	1.E+00	1.E+00	9.E-01	1.E+02	
GOTERM_BP_FAT	GO:0010558~negative regulation of macromolecule biosynthetic p	27	3.075170843		4.E-01 60406, 12190, 13685, 22130, 67184, 4337	809	418	13588	1.E+00	1.E+00	9.E-01	1.E+02	
GOTERM_BP_FAT	GO:0031327~negative regulation of cellular biosynthetic process	27	3.075170843		5.E-01 60406, 12190, 13685, 22130, 67184, 4337	809	430	13588	1.E+00	1.E+00	1.E+00	1.E+02	
GOTERM_BP_FAT	GO:0045934~negative regulation of nucleobase, nucleoside, nucle	25	2.84738041		5.E-01 12190, 60406, 22130, 67184, 433759, 197	809	397	13588	1.E+00	1.E+00	1.E+00	1.E+02	
GOTERM_BP_FAT	GO:0000122~negative regulation of transcription from RNA polyn	15	1.708428246		5.E-01 60406, 56338, 433759, 19720, 17869, 218	809	231	13588	1.E+00	1.E+00	1.E+00	1.E+02	
GOTERM_BP_FAT	GO:0051172~negative regulation of nitrogen compound metabol	25	2.84738041		5.E-01 12190, 60406, 22130, 67184, 433759, 197	809	401	13588	1.E+00	1.E+00	1.E+00	1.E+02	
GOTERM_BP_FAT	GO:0045892~negative regulation of transcription, DNA-dependen	18	2.050113895		7.E-01 60406, 67184, 56338, 433759, 19720, 178	809	308	13588	1.E+00	1.E+00	1.E+00	1.E+02	
GOTERM_BP_FAT	GO:0051253~negative regulation of RNA metabolic process	18	2.050113895		7.E-01 60406, 67184, 56338, 433759, 19720, 178	809	310	13588	1.E+00	1.E+00	1.E+00	1.E+02	
GOTERM_BP_FAT	GO:0016481~negative regulation of transcription	19	2.164009112		8.E-01 60406, 67184, 56338, 433759, 19720, 178	809	372	13588	9.E-01	1.E+00	1.E+00	1.E+02	



SP_PIR_KEYWORDS	repressor	16	1.822323462	9.E-01	60406, 232906, 433759, 19720, 20467, 20	869	391	17854	8.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0010629~negative regulation of gene expression	20	2.277904328	9.E-01	60406, 67184, 56338, 433759, 19720, 178	809	410	13588	8.E-01	1.E+00	1.E+00	1.E+02
Annotation Cluster 248	Enrichment Score: 0.25674776368736874											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR007125:Histone core	5	0.569476082	1.E-01	319168, 621893, 319169, 20662, 20663, 3	860	42	17763	2.E+00	1.E+00	9.E-01	9.E+01
SP_PIR_KEYWORDS	citruUination	3	0.341685649	2.E-01	319168, 621893, 319169, 319191	869	16	17854	4.E+00	1.E+00	5.E-01	9.E+01
PIR_SUPERFAMILY	PIRSF002048:histone H2A	3	0.341685649	2.E-01	319168, 621893, 319169, 319191	576	13	8136	3.E+00	1.E+00	1.E+00	1.E+02
INTERPRO	IPR002119:Histone H2A	3	0.341685649	3.E-01	319168, 621893, 319169, 319191	860	25	17763	2.E+00	1.E+00	1.E+00	1.E+02
SMART	SM00414:H2A	3	0.341685649	4.E-01	319168, 621893, 319169, 319191	492	25	9131	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_CC_FAT	GO:0032993~protein-DNA complex	5	0.569476082	5.E-01	319168, 621893, 19891, 319169, 319191	636	75	12504	1.E+00	1.E+00	9.E-01	1.E+02
SP_PIR_KEYWORDS	nucleosome core	3	0.341685649	6.E-01	319168, 621893, 319169, 319191	869	44	17854	1.E+00	1.E+00	9.E-01	1.E+02
SP_PIR_KEYWORDS	chromosomal protein	6	0.683371298	8.E-01	319168, 621893, 319169, 245000, 20877,	869	136	17854	9.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0006334~nucleosome assembly	4	0.455580866	8.E-01	319168, 621893, 319169, 17216, 319191	809	73	13588	9.E-01	1.E+00	1.E+00	1.E+02
GOTERM_CC_FAT	GO:0000786~nucleosome	3	0.341685649	8.E-01	319168, 621893, 319169, 319191	636	62	12504	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0031497~chromatin assembly	4	0.455580866	8.E-01	319168, 621893, 319169, 17216, 319191	809	75	13588	9.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0065004~protein-DNA complex assembly	4	0.455580866	8.E-01	319168, 621893, 319169, 17216, 319191	809	76	13588	9.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0034728~nucleosome organization	4	0.455580866	8.E-01	319168, 621893, 319169, 17216, 319191	809	76	13588	9.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0006323~DNA packaging	4	0.455580866	9.E-01	319168, 621893, 319169, 17216, 319191	809	101	13588	7.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0006333~chromatin assembly or disassembly	4	0.455580866	1.E+00	319168, 621893, 319169, 17216, 319191	809	109	13588	6.E-01	1.E+00	1.E+00	1.E+02
KEGG_PATHWAY	mmu05322:Systemic lupus erythematosus	6	0.683371298	1.E+00	319168, 621893, 319169, 230558, 13035,	580	103	5738	6.E-01	1.E+00	1.E+00	1.E+02
Annotation Cluster 249	Enrichment Score: 0.2510432436949626											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0010498~proteasomal protein catabolic process	3	0.341685649	5.E-01	19053, 19358, 66105	809	30	13588	2.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0043161~proteasomal ubiquitin-dependent protein catabolic	3	0.341685649	5.E-01	19053, 19358, 66105	809	30	13588	2.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0006511~ubiquitin-dependent protein catabolic process	9	1.025056948	6.E-01	19053, 19358, 26965, 99152, 16396, 6610	809	141	13588	1.E+00	1.E+00	1.E+00	1.E+02
Annotation Cluster 250	Enrichment Score: 0.2455187907022324											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0046879~hormone secretion	4	0.455580866	4.E-01	19894, 16367, 13350, 14226	809	41	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0009914~hormone transport	4	0.455580866	5.E-01	19894, 16367, 13350, 14226	809	42	13588	2.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0030073~insulin secretion	3	0.341685649	5.E-01	16367, 13350, 14226	809	27	13588	2.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0003001~generation of a signal involved in cell-cell signaling	6	0.683371298	6.E-01	19894, 16367, 13350, 14226, 19164, 2096	809	84	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0030072~peptide hormone secretion	3	0.341685649	6.E-01	16367, 13350, 14226	809	34	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0002790~peptide secretion	3	0.341685649	6.E-01	16367, 13350, 14226	809	36	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0010817~regulation of hormone levels	8	0.911161731	6.E-01	19894, 16367, 18006, 13350, 14226, 1937	809	128	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0015833~peptide transport	3	0.341685649	8.E-01	16367, 13350, 14226	809	47	13588	1.E+00	1.E+00	1.E+00	1.E+02
Annotation Cluster 251	Enrichment Score: 0.23371019078654964											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0003712~transcription cofactor activity	12	1.366742597	4.E-01	433759, 101206, 22601, 15278, 12815, 17	754	180	13288	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_MF_FAT	GO:0003714~transcription corepressor activity	5	0.569476082	6.E-01	433759, 26885, 20467, 20466, 208727	754	72	13288	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_MF_FAT	GO:0016564~transcription repressor activity	11	1.25284738	8.E-01	69890, 19645, 433759, 74318, 17978, 268	754	211	13288	9.E-01	1.E+00	1.E+00	1.E+02
Annotation Cluster 252	Enrichment Score: 0.22824410976546147											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0001704~formation of primary germ layer	4	0.455580866	4.E-01	13836, 18747, 15376, 50493	809	40	13588	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0007369~gastrulation	6	0.683371298	5.E-01	13836, 18747, 15376, 50493, 67916, 1338	809	74	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0001707~mesoderm formation	3	0.341685649	6.E-01	13836, 18747, 50493	809	36	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0048332~mesoderm morphogenesis	3	0.341685649	7.E-01	13836, 18747, 50493	809	38	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0007498~mesoderm development	3	0.341685649	9.E-01	13836, 18747, 50493	809	59	13588	9.E-01	1.E+00	1.E+00	1.E+02
Annotation Cluster 253	Enrichment Score: 0.2213588084332823											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	Tight junction	5	0.569476082	3.E-01	16456, 69524, 13052, 16800, 69847	869	61	17854	2.E+00	1.E+00	7.E-01	1.E+02
GOTERM_CC_FAT	GO:0070160~occluding junction	5	0.569476082	5.E-01	16456, 69524, 13052, 16800, 69847	636	76	12504	1.E+00	1.E+00	9.E-01	1.E+02
GOTERM_CC_FAT	GO:0005923~tight junction	5	0.569476082	5.E-01	16456, 69524, 13052, 16800, 69847	636	76	12504	1.E+00	1.E+00	9.E-01	1.E+02
GOTERM_CC_FAT	GO:0043296~apical junction complex	5	0.569476082	8.E-01	16456, 69524, 13052, 16800, 69847	636	101	12504	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_CC_FAT	GO:0016327~apicolateral plasma membrane	5	0.569476082	8.E-01	16456, 69524, 13052, 16800, 69847	636	103	12504	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_CC_FAT	GO:0005911~cell-cell junction	8	0.911161731	8.E-01	16456, 69524, 22793, 13052, 16800, 1338	636	173	12504	9.E-01	1.E+00	1.E+00	1.E+02
Annotation Cluster 254	Enrichment Score: 0.21570523724637736											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0035091~phosphoinositide binding	6	0.683371298	4.E-01	14731, 17972, 17969, 233071, 19159, 582	754	75	13288	1.E+00	1.E+00	9.E-01	1.E+02



UP_SEQ_FEATURE	domain:PX	3	0.341685649	7.E-01 17972, 17969, 58240	861	42	16021	1.E+00	1.E+00	1.E+00	1.E+02	
INTERPRO	IPR001683:Phox-like	3	0.341685649	7.E-01 17972, 17969, 58240	860	47	17763	1.E+00	1.E+00	1.E+00	1.E+02	
SMART	SM00312:PX	3	0.341685649	7.E-01 17972, 17969, 58240	492	47	9131	1.E+00	1.E+00	1.E+00	1.E+02	
Annotation Cluster 255	Enrichment Score: 0.19595837936203303											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0035257~nuclear hormone receptor binding	3	0.341685649	6.E-01 12815, 17978, 17979	754	34	13288	2.E+00	1.E+00	1.E+00	1.E+02	
GOTERM_MF_FAT	GO:0051427~hormone receptor binding	3	0.341685649	7.E-01 12815, 17978, 17979	754	39	13288	1.E+00	1.E+00	1.E+00	1.E+02	
GOTERM_MF_FAT	GO:0003713~transcription coactivator activity	6	0.683371298	7.E-01 101206, 22601, 12815, 17978, 17979, 129	754	100	13288	1.E+00	1.E+00	1.E+00	1.E+02	
Annotation Cluster 256	Enrichment Score: 0.19473733572093027											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_SEQ_FEATURE	domain:Ig-like C2-type 1	10	1.138952164	3.E-01 15896, 18596, 11658, 13052, 98752, 7414	861	130	16021	1.E+00	1.E+00	1.E+00	1.E+02	
UP_SEQ_FEATURE	domain:Ig-like C2-type 2	10	1.138952164	3.E-01 15896, 18596, 11658, 13052, 98752, 7414	861	131	16021	1.E+00	1.E+00	1.E+00	1.E+02	
INTERPRO	IPR013151:Immunoglobulin	10	1.138952164	5.E-01 18729, 18596, 16456, 11658, 18724, 9875	860	178	17763	1.E+00	1.E+00	1.E+00	1.E+02	
INTERPRO	IPR003598:Immunoglobulin subtype 2	10	1.138952164	6.E-01 18596, 16456, 69524, 13052, 83964, 7414	860	187	17763	1.E+00	1.E+00	1.E+00	1.E+02	
SMART	SM00408:IGc2	10	1.138952164	7.E-01 18596, 16456, 69524, 13052, 83964, 7414	492	187	9131	1.E+00	1.E+00	1.E+00	1.E+02	
UP_SEQ_FEATURE	domain:Ig-like C2-type 3	5	0.569476082	7.E-01 18596, 11658, 12978, 12483, 17082	861	87	16021	1.E+00	1.E+00	1.E+00	1.E+02	
SP_PIR_KEYWORDS	Immunoglobulin domain	20	2.277904328	7.E-01 11658, 69524, 16456, 17123, 545156, 120	869	443	17854	9.E-01	1.E+00	1.E+00	1.E+02	
INTERPRO	IPR003599:Immunoglobulin subtype	13	1.480637813	8.E-01 18729, 69524, 11658, 18724, 57781, 2701	860	313	17763	9.E-01	1.E+00	1.E+00	1.E+02	
INTERPRO	IPR013783:Immunoglobulin-like fold	26	2.961275626	9.E-01 14972, 18729, 15018, 69524, 11658, 1872	860	644	17763	8.E-01	1.E+00	1.E+00	1.E+02	
SMART	SM00409:IG	13	1.480637813	9.E-01 18729, 69524, 11658, 18724, 57781, 2701	492	313	9131	8.E-01	1.E+00	1.E+00	1.E+02	
INTERPRO	IPR007110:Immunoglobulin-like	21	2.391799544	1.E+00 15007, 14972, 18729, 15018, 11658, 6952	860	604	17763	7.E-01	1.E+00	1.E+00	1.E+02	
INTERPRO	IPR013106:Immunoglobulin V-set	9	1.025056948	1.E+00 270152, 16456, 11658, 69524, 13052, 839	860	364	17763	5.E-01	1.E+00	1.E+00	1.E+02	
Annotation Cluster 257	Enrichment Score: 0.18898614271382327											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0045664~regulation of neuron differentiation	7	0.797266515	6.E-01 15376, 11853, 19164, 12043, 17268, 2184	809	102	13588	1.E+00	1.E+00	1.E+00	1.E+02	
GOTERM_BP_FAT	GO:0045665~negative regulation of neuron differentiation	3	0.341685649	6.E-01 15376, 11853, 17268	809	34	13588	1.E+00	1.E+00	1.E+00	1.E+02	
GOTERM_BP_FAT	GO:0060284~regulation of cell development	10	1.138952164	6.E-01 12028, 15376, 11853, 19164, 12043, 1081	809	159	13588	1.E+00	1.E+00	1.E+00	1.E+02	
GOTERM_BP_FAT	GO:0051960~regulation of nervous system development	9	1.025056948	7.E-01 15376, 11853, 19164, 12043, 108138, 172	809	148	13588	1.E+00	1.E+00	1.E+00	1.E+02	
GOTERM_BP_FAT	GO:0050767~regulation of neurogenesis	8	0.911161731	7.E-01 15376, 11853, 19164, 12043, 108138, 172	809	132	13588	1.E+00	1.E+00	1.E+00	1.E+02	
GOTERM_BP_FAT	GO:0010720~positive regulation of cell development	3	0.341685649	8.E-01 12043, 108138, 21844	809	47	13588	1.E+00	1.E+00	1.E+00	1.E+02	
Annotation Cluster 258	Enrichment Score: 0.1875525052501266											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0016044~membrane organization	17	1.936218679	6.E-01 22324, 94190, 12122, 13430, 12043, 5725	809	272	13588	1.E+00	1.E+00	1.E+00	1.E+02	
GOTERM_BP_FAT	GO:0006909~phagocytosis	4	0.455580866	6.E-01 14127, 22324, 12491, 16803	809	49	13588	1.E+00	1.E+00	1.E+00	1.E+02	
GOTERM_BP_FAT	GO:0016192~vesicle-mediated transport	28	3.189066059	6.E-01 227753, 22324, 269589, 11852, 94190, 13	809	466	13588	1.E+00	1.E+00	1.E+00	1.E+02	
GOTERM_BP_FAT	GO:0006897~endocytosis	10	1.138952164	8.E-01 14127, 22324, 108672, 94190, 13430, 154	809	188	13588	9.E-01	1.E+00	1.E+00	1.E+02	
GOTERM_BP_FAT	GO:0010324~membrane invagination	10	1.138952164	8.E-01 14127, 22324, 108672, 94190, 13430, 154	809	188	13588	9.E-01	1.E+00	1.E+00	1.E+02	
Annotation Cluster 259	Enrichment Score: 0.18290035391753873											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_SEQ_FEATURE	domain:RRM	7	0.797266515	4.E-01 22384, 27979, 75705, 27041, 53356, 1538	861	99	16021	1.E+00	1.E+00	1.E+00	1.E+02	
INTERPRO	IPR012677:Nucleotide-binding, alpha-beta plait	11	1.25284738	6.E-01 27041, 53356, 53610, 677113, 15381, 268	860	213	17763	1.E+00	1.E+00	1.E+00	1.E+02	
INTERPRO	IPR000504:RNA recognition motif, RNP-1	9	1.025056948	8.E-01 22384, 27979, 75705, 27041, 53356, 1538	860	212	17763	9.E-01	1.E+00	1.E+00	1.E+02	
SMART	SM00360:RRM	9	1.025056948	9.E-01 22384, 27979, 75705, 27041, 53356, 1538	492	212	9131	8.E-01	1.E+00	1.E+00	1.E+02	
Annotation Cluster 260	Enrichment Score: 0.1726875009173184											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	EF hand	5	0.569476082	4.E-02 18826, 12315, 12314, 12313, 20692, 2020	869	28	17854	4.E+00	1.E+00	2.E-01	5.E+01	
INTERPRO	IPR018247:EF-HAND 1	10	1.138952164	7.E-01 70316, 18803, 18826, 12315, 12314, 1231	860	211	17763	1.E+00	1.E+00	1.E+00	1.E+02	
INTERPRO	IPR011992:EF-Hand type	10	1.138952164	8.E-01 18826, 12315, 12314, 12313, 20692, 2020	860	227	17763	9.E-01	1.E+00	1.E+00	1.E+02	
INTERPRO	IPR018249:EF-HAND 2	8	0.911161731	9.E-01 18803, 18826, 12315, 12314, 12313, 2020	860	205	17763	8.E-01	1.E+00	1.E+00	1.E+02	
INTERPRO	IPR018248:EF hand	5	0.569476082	9.E-01 18826, 12315, 12314, 12313, 20202, 2020	860	132	17763	8.E-01	1.E+00	1.E+00	1.E+02	
INTERPRO	IPR002048:Calcium-binding EF-hand	5	0.569476082	9.E-01 18826, 12315, 12314, 12313, 20191, 5904	860	137	17763	8.E-01	1.E+00	1.E+00	1.E+02	
UP_SEQ_FEATURE	domain:EF-hand 2	6	0.683371298	9.E-01 18826, 12315, 12314, 12313, 20202, 2020	861	160	16021	7.E-01	1.E+00	1.E+00	1.E+02	
UP_SEQ_FEATURE	domain:EF-hand 1	6	0.683371298	9.E-01 18826, 12315, 12314, 12313, 20202, 2020	861	161	16021	7.E-01	1.E+00	1.E+00	1.E+02	
UP_SEQ_FEATURE	calcium-binding region:2	4	0.455580866	9.E-01 18826, 12315, 12314, 12313, 59040, 2149	861	110	16021	7.E-01	1.E+00	1.E+00	1.E+02	
SMART	SM00054:EFh	5	0.569476082	9.E-01 18826, 12315, 12314, 12313, 20191, 5904	492	137	9131	7.E-01	1.E+00	1.E+00	1.E+02	
UP_SEQ_FEATURE	calcium-binding region:1	4	0.455580866	1.E+00 18826, 12315, 12314, 12313, 59040, 2149	861	120	16021	6.E-01	1.E+00	1.E+00	1.E+02	
Annotation Cluster 261	Enrichment Score: 0.1662905003110668											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR



INTERPRO	IPR001609:Myosin head, motor region	3	0.341685649	6.E-01 17925, 77579, 270163	860	38	17763	2.E+00	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	motor protein	7	0.797266515	6.E-01 17925, 77579, 19348, 270163, 13430, 718	869	123	17854	1.E+00	1.E+00	9.E-01	1.E+02
SMART	SM00242:MYSc	3	0.341685649	6.E-01 17925, 77579, 270163	492	38	9131	1.E+00	1.E+00	1.E+00	1.E+02
INTERPRO	IPR000481Q calmodulin-binding region	5	0.569476082	7.E-01 14432, 17925, 77579, 270163, 19417	860	92	17763	1.E+00	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	myosin	3	0.341685649	7.E-01 17925, 77579, 270163	869	47	17854	1.E+00	1.E+00	9.E-01	1.E+02
SMART	SM00015:IQ	5	0.569476082	7.E-01 14432, 17925, 77579, 270163, 19417	492	92	9131	1.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	domainIQ	3	0.341685649	8.E-01 14432, 77579, 19417	861	53	16021	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_MF_FAT	GO:0003774--motor activity	7	0.797266515	8.E-01 17925, 77579, 19348, 270163, 13430, 718	754	138	13288	9.E-01	1.E+00	1.E+00	1.E+02
GOTERM_CC_FAT	GO:0016459--myosin complex	3	0.341685649	8.E-01 17925, 77579, 270163	636	61	12504	1.E+00	1.E+00	1.E+00	1.E+02

Annotation Cluster 262		Enrichment Score: 0.1567005224987925										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	motor protein	7	0.797266515		6.E-01 17925, 77579, 19348, 270163, 13430, 718	869	123	17854	1.E+00	1.E+00	9.E-01	1.E+02
INTERPRO	IPR019821:Kinesin, motor region, conserved site	3	0.341685649		6.E-01 19348, 71819, 16561	860	42	17763	1.E+00	1.E+00	1.E+00	1.E+02
INTERPRO	IPR001752:Kinesin, motor region	3	0.341685649		6.E-01 19348, 71819, 16561	860	44	17763	1.E+00	1.E+00	1.E+00	1.E+02
SMART	SM00129:KISc	3	0.341685649		7.E-01 19348, 71819, 16561	492	44	9131	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0007018--microtubule-based movement	6	0.683371298		7.E-01 22142, 19348, 71819, 59040, 16561, 2149	809	101	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_MF_FAT	GO:0003774--motor activity	7	0.797266515		8.E-01 17925, 77579, 19348, 270163, 13430, 718	754	138	13288	9.E-01	1.E+00	1.E+00	1.E+02
GOTERM_MF_FAT	GO:0003777--microtubule motor activity	3	0.341685649		9.E-01 19348, 71819, 16561	754	73	13288	7.E-01	1.E+00	1.E+00	1.E+02

Annotation Cluster 263		Enrichment Score: 0.15008690899146943										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0034754~cellular hormone metabolic process	4	0.455580866	6.E-01	11806, 19378, 14815, 56847	809	52	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0010817~regulation of hormone levels	8	0.911161731	6.E-01	19894, 16367, 11806, 13350, 14226, 1937	809	128	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0042445~hormone metabolic process	4	0.455580866	9.E-01	11806, 19378, 14815, 56847	809	90	13588	7.E-01	1.E+00	1.E+00	1.E+02

Annotation Cluster 264		Enrichment Score: 0.14852605967312896											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_BP_FAT	GO:0060485~mesenchyme development	4	0.455580866		6.E-01 15402, 19713, 19378, 12043	809	809	50	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0014031~mesenchymal cell development	3	0.341685649		8.E-01 19713, 19378, 12043	809	809	47	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0048762~mesenchymal cell differentiation	3	0.341685649		8.E-01 19713, 19378, 12043	809	809	49	13588	1.E+00	1.E+00	1.E+00	1.E+02

Annotation Cluster 265		Enrichment Score: 0.13878981851953825										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	s-adenosyl-l-methionine	5	0.569476082		6.E-01 18113, 22017, 15278, 13436, 12846	869	88	17854	1.E+00	1.E+00	9.E-01	1.E+02
UP_SEQ_FEATURE	binding site:S-adenosyl-L-methionine	3	0.341685649		7.E-01 18113, 22017, 12846	861	42	16021	1.E+00	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	methyltransferase	5	0.569476082		9.E-01 18113, 22017, 15278, 13436, 12846	869	142	17854	7.E-01	1.E+00	1.E+00	1.E+02

Annotation Cluster 266		Enrichment Score: 0.13536188399190197										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR000629:RNA helicase, ATP-dependent, DEAD-box, conserved si	3	0.341685649		4.E-01 110957, 13681, 13682	860	31	17763	2.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	short sequence motif:DEAD box	3	0.341685649		5.E-01 110957, 13681, 13682	861	30	16021	2.E+00	1.E+00	1.E+00	1.E+02
INTERPRO	IPR014014:RNA helicase, DEAD-box type, Q motif	3	0.341685649		5.E-01 110957, 13681, 13682	860	35	17763	2.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	short sequence motif:Q motif	3	0.341685649		5.E-01 110957, 13681, 13682	861	33	16021	2.E+00	1.E+00	1.E+00	1.E+02
GOTERM_MF_FAT	GO:0004386--helicase activity	8	0.911161731		6.E-01 13872, 110957, 17217, 17220, 27041, 172	754	129	13288	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_MF_FAT	GO:0042623--ATPase activity, coupled	12	1.366742597		7.E-01 13872, 110957, 17925, 77579, 17420, 148	754	223	13288	9.E-01	1.E+00	1.E+00	1.E+02
INTERPRO	IPR011545:DNA/RNA helicase, DEAD/DEAH box type, N-terminal	3	0.341685649		8.E-01 110957, 13681, 13682	860	55	17763	1.E+00	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	helicase	5	0.569476082		8.E-01 13872, 110957, 27041, 13681, 13682	869	120	17854	9.E-01	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	domain:Helicase C-terminal	4	0.455580866		8.E-01 13872, 110957, 13681, 13682	861	86	16021	9.E-01	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	domain:Helicase ATP-binding	4	0.455580866		9.E-01 13872, 110957, 13681, 13682	861	89	16021	8.E-01	1.E+00	1.E+00	1.E+02
INTERPRO	IPR014021:Helicase, superfamily 1 and 2, ATP-binding	4	0.455580866		9.E-01 13872, 110957, 13681, 13682	860	99	17763	8.E-01	1.E+00	1.E+00	1.E+02
INTERPRO	IPR001650:DNA/RNA helicase, C-terminal	4	0.455580866		9.E-01 13872, 110957, 13681, 13682	860	100	17763	8.E-01	1.E+00	1.E+00	1.E+02
GOTERM_MF_FAT	GO:0008026--ATP-dependent helicase activity	4	0.455580866		9.E-01 13872, 110957, 13681, 13682	754	86	13288	8.E-01	1.E+00	1.E+00	1.E+02
GOTERM_MF_FAT	GO:0070035--purine NTP-dependent helicase activity	4	0.455580866		9.E-01 13872, 110957, 13681, 13682	754	86	13288	8.E-01	1.E+00	1.E+00	1.E+02
INTERPRO	IPR014001:DEAD-D-like helicase, N-terminal	4	0.455580866		9.E-01 13872, 110957, 13681, 13682	860	103	17763	8.E-01	1.E+00	1.E+00	1.E+02
SMART	SM00490:HELICc	4	0.455580866		9.E-01 13872, 110957, 13681, 13682	492	99	9131	7.E-01	1.E+00	1.E+00	1.E+02
SMART	SM00487:DEXDc	4	0.455580866		9.E-01 13872, 110957, 13681, 13682	492	103	9131	7.E-01	1.E+00	1.E+00	1.E+02

Annotation Cluster 267		Enrichment Score: 0.12756275180240179										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_SEQ_FEATURE	domainIg-like C2-type 3	5	0.569476082		7.E-01 18596, 11658, 12978, 12483, 17082	861	87	16021	1.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	domainIg-like C2-type 5	3	0.341685649		7.E-01 18596, 12978, 12483	861	48	16021	1.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	domainIg-like C2-type 4	3	0.341685649		8.E-01 18596, 12978, 12483	861	56	16021	1.E+00	1.E+00	1.E+00	1.E+02

Annotation Cluster 268    Enrichment Score: 0.1167445881270034



Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	mRNA transport	4	0.455580866	6.E-01	19317, 231042, 68092, 66441	869	60	17854	1.E+00	1.E+00	9.E-01	1.E+02
GOTERM_BP_FAT	GO:0051028~mRNA transport	4	0.455580866	7.E-01	19317, 231042, 68092, 66441	809	62	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0050658~RNA transport	4	0.455580866	8.E-01	19317, 231042, 68092, 66441	809	66	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0050657~nucleic acid transport	4	0.455580866	8.E-01	19317, 231042, 68092, 66441	809	66	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0051236~establishment of RNA localization	4	0.455580866	8.E-01	19317, 231042, 68092, 66441	809	66	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0006403~RNA localization	4	0.455580866	8.E-01	19317, 231042, 68092, 66441	809	67	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0015931~nucleobase, nucleoside, nucleotide and nucleic acid	4	0.455580866	8.E-01	19317, 231042, 68092, 66441	809	74	13588	9.E-01	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	mrna splicing	8	0.911161731	8.E-01	15387, 19317, 15381, 53610, 75062, 6809	869	191	17854	9.E-01	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	mrna processing	8	0.911161731	1.E+00	15387, 19317, 15381, 53610, 75062, 6809	869	240	17854	7.E-01	1.E+00	1.E+00	1.E+02
Annotation Cluster 269	Enrichment Score: 0.11440431512215696											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0051606~detection of stimulus	6	0.683371298	6.E-01	14151, 17087, 21898, 17869, 14360, 1039	809	90	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0009582~detection of abiotic stimulus	3	0.341685649	8.E-01	14151, 17869, 14360	809	52	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0009581~detection of external stimulus	3	0.341685649	9.E-01	14151, 17869, 14360	809	60	13588	8.E-01	1.E+00	1.E+00	1.E+02
Annotation Cluster 270	Enrichment Score: 0.10541749351245247											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0006730~one-carbon metabolic process	7	0.797266515	7.E-01	225363, 232087, 14852, 15278, 13436, 22	809	117	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0043414~biopolymer methylation	4	0.455580866	8.E-01	225363, 14852, 15278, 13436	809	71	13588	9.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0032259~methylation	4	0.455580866	9.E-01	225363, 14852, 15278, 13436	809	79	13588	9.E-01	1.E+00	1.E+00	1.E+02
Annotation Cluster 271	Enrichment Score: 0.09789674497176985											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0050954~sensory perception of mechanical stimulus	6	0.683371298	6.E-01	24064, 73750, 17869, 14360, 12815, 1257	809	92	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0007605~sensory perception of sound	5	0.569476082	7.E-01	24064, 73750, 17869, 12815, 12576	809	84	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0043583~ear development	6	0.683371298	7.E-01	24064, 73750, 12043, 17869, 14180, 1257	809	104	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0048839~inner ear development	4	0.455580866	9.E-01	24064, 73750, 14180, 12576	809	88	13588	8.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0007600~sensory perception	10	1.138952164	1.E+00	216869, 24064, 73750, 15416, 17869, 143	809	1402	13588	1.E-01	1.E+00	1.E+00	1.E+02
Annotation Cluster 272	Enrichment Score: 0.09569521330211346											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0009259~ribonucleotide metabolic process	9	1.025056948	5.E-01	11486, 56749, 11717, 11564, 227197, 679	809	125	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0006163~purine nucleotide metabolic process	10	1.138952164	6.E-01	11486, 11514, 14923, 11717, 11564, 2271	809	160	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0009150~purine ribonucleotide metabolic process	7	0.797266515	7.E-01	11486, 11717, 11564, 227197, 67942, 115	809	119	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0009141~nucleoside triphosphate metabolic process	5	0.569476082	9.E-01	382985, 11486, 227197, 67942, 11636	809	115	13588	7.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0009144~purine nucleoside triphosphate metabolic process	4	0.455580866	1.E+00	11486, 227197, 67942, 11636	809	106	13588	6.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0046034~ATP metabolic process	3	0.341685649	1.E+00	227197, 67942, 11636	809	90	13588	6.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0009205~purine ribonucleoside triphosphate metabolic proce	3	0.341685649	1.E+00	227197, 67942, 11636	809	101	13588	5.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0009199~ribonucleoside triphosphate metabolic process	3	0.341685649	1.E+00	227197, 67942, 11636	809	102	13588	5.E-01	1.E+00	1.E+00	1.E+02
Annotation Cluster 273	Enrichment Score: 0.08869679529942505											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0005615~extracellular space	29	3.302961276	4.E-01	11813, 11814, 11816, 66042, 18788, 1680	636	511	12504	1.E+00	1.E+00	8.E-01	1.E+02
GOTERM_CC_FAT	GO:0044421~extracellular region part	36	4.10022779	8.E-01	12831, 11813, 11814, 11816, 66042, 1281	636	774	12504	9.E-01	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	Secreted	54	6.150341686	1.E+00	14178, 69121, 18788, 12815, 16803, 1201	869	1420	17854	8.E-01	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	signal	120	13.66742597	1.E+00	12475, 15018, 14178, 69524, 69121, 1841	869	2970	17854	8.E-01	1.E+00	1.E+00	1.E+02
GOTERM_CC_FAT	GO:0005576~extracellular region	57	6.492027335	1.E+00	14178, 19206, 69121, 18788, 12815, 1680	636	1680	12504	7.E-01	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	signal peptide	120	13.66742597	1.E+00	12475, 15018, 14178, 69524, 69121, 1841	861	2963	16021	8.E-01	1.E+00	1.E+00	1.E+02
Annotation Cluster 274	Enrichment Score: 0.08015610013704419											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0014069~postsynaptic density	4	0.455580866	5.E-01	20662, 13430, 13383, 13385	636	51	12504	2.E+00	1.E+00	9.E-01	1.E+02
GOTERM_CC_FAT	GO:0045202~synapse	15	1.708428246	8.E-01	18747, 19894, 13800, 94190, 13430, 1641	636	319	12504	9.E-01	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	synapse	7	0.797266515	1.E+00	19894, 14432, 13800, 94190, 13430, 1338	869	213	17854	7.E-01	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	postsynaptic cell membrane	3	0.341685649	1.E+00	13430, 13383, 13385	869	110	17854	6.E-01	1.E+00	1.E+00	1.E+02
GOTERM_CC_FAT	GO:0045211~postsynaptic membrane	3	0.341685649	1.E+00	13430, 13383, 13385	636	126	12504	5.E-01	1.E+00	1.E+00	1.E+02
GOTERM_CC_FAT	GO:0044456~synapse part	5	0.569476082	1.E+00	19894, 20662, 13430, 13383, 13385	636	212	12504	5.E-01	1.E+00	1.E+00	1.E+02
Annotation Cluster 275	Enrichment Score: 0.07880420542576856											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_SEQ_FEATURE	domain:LIM zinc-binding 2	3	0.341685649	8.E-01	22793, 16911, 14200	861	50	16021	1.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	domain:LIM zinc-binding 1	3	0.341685649	8.E-01	22793, 16911, 14200	861	50	16021	1.E+00	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	LIM domain	3	0.341685649	9.E-01	22793, 16911, 14200	869	73	17854	8.E-01	1.E+00	1.E+00	1.E+02



INTERPRO	IPR001781:Zinc finger, LIM-type	3	0.341685649	9.E-01	22793, 16911, 14200	860	74	17763	8.E-01	1.E+00	1.E+00	1.E+02
SMART	SM00132:LIM	3	0.341685649	9.E-01	22793, 16911, 14200	492	74	9131	8.E-01	1.E+00	1.E+00	1.E+02

Annotation Cluster 276	Enrichment Score: 0.07611710321348245											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0019932~second-messenger-mediated signaling	8	0.911161731	6.E-01	16994, 18126, 14678, 30955, 192176, 146	809	118	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0007187~G-protein signaling, coupled to cyclic nucleotide se	4	0.455580866	7.E-01	18126, 14678, 192176, 14682	809	60	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0019935~cyclic-nucleotide-mediated signaling	4	0.455580866	8.E-01	18126, 14678, 192176, 14682	809	66	13588	1.E+00	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0006140~regulation of nucleotide metabolic process	4	0.455580866	8.E-01	72269, 14678, 192176, 14682	809	75	13588	9.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0007188~G-protein signaling, coupled to cAMP nucleotide se	3	0.341685649	8.E-01	14678, 192176, 14682	809	55	13588	9.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0045761~regulation of adenylate cyclase activity	3	0.341685649	9.E-01	14678, 192176, 14682	809	60	13588	8.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0019933~cAMP-mediated signaling	3	0.341685649	9.E-01	14678, 192176, 14682	809	61	13588	8.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0031279~regulation of cyclase activity	3	0.341685649	9.E-01	14678, 192176, 14682	809	62	13588	8.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0051339~regulation of lyase activity	3	0.341685649	9.E-01	14678, 192176, 14682	809	62	13588	8.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0030817~regulation of cAMP biosynthetic process	3	0.341685649	9.E-01	14678, 192176, 14682	809	65	13588	8.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0030814~regulation of cAMP metabolic process	3	0.341685649	9.E-01	14678, 192176, 14682	809	67	13588	8.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0030808~regulation of nucleotide biosynthetic process	3	0.341685649	9.E-01	14678, 192176, 14682	809	70	13588	7.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0030802~regulation of cyclic nucleotide biosynthetic process	3	0.341685649	9.E-01	14678, 192176, 14682	809	70	13588	7.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0030799~regulation of cyclic nucleotide metabolic process	3	0.341685649	9.E-01	14678, 192176, 14682	809	73	13588	7.E-01	1.E+00	1.E+00	1.E+02

Annotation Cluster 277	Enrichment Score: 0.07554395779673438											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR018355:SPiA/RYanodine receptor subgroup	3	0.341685649	6.E-01	192658, 19720, 20191	860	45	17763	1.E+00	1.E+00	1.E+00	1.E+02
SMART	SM00449:SPRY	3	0.341685649	7.E-01	192658, 19720, 20191	492	45	9131	1.E+00	1.E+00	1.E+00	1.E+02
INTERPRO	IPR003877:SPiA/RYanodine receptor SPRY	4	0.455580866	7.E-01	192658, 20128, 19720, 20191	860	76	17763	1.E+00	1.E+00	1.E+00	1.E+02
INTERPRO	IPR003879:Butyrophilin-like	3	0.341685649	7.E-01	192658, 20128, 19720	860	54	17763	1.E+00	1.E+00	1.E+00	1.E+02
INTERPRO	IPR001870:B302 (SPRY)-like	4	0.455580866	7.E-01	192658, 20128, 19720, 20191	860	80	17763	1.E+00	1.E+00	1.E+00	1.E+02
INTERPRO	IPR001841:Zinc finger, RING-type	8	0.911161731	1.E+00	66156, 192658, 20128, 19720, 17420, 273	860	286	17763	6.E-01	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	zinc finger region:RING-type	5	0.569476082	1.E+00	66156, 20128, 19720, 17420, 22030	861	176	16021	5.E-01	1.E+00	1.E+00	1.E+02
INTERPRO	IPR018957:Zinc finger, C3HC4 RING-type	5	0.569476082	1.E+00	20128, 19720, 17420, 22030, 74126	860	219	17763	5.E-01	1.E+00	1.E+00	1.E+02
SMART	SM00184:RING	8	0.911161731	1.E+00	66156, 192658, 20128, 19720, 17420, 273	492	286	9131	5.E-01	1.E+00	1.E+00	1.E+02
INTERPRO	IPR017907:Zinc finger, RING-type, conserved site	5	0.569476082	1.E+00	20128, 19720, 17420, 22030, 74126	860	254	17763	4.E-01	1.E+00	1.E+00	1.E+02

Annotation Cluster 278	Enrichment Score: 0.07531787028237909											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0016485~protein processing	5	0.569476082	8.E-01	19206, 19164, 17869, 230558, 12263	809	90	13588	9.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0051604~protein maturation	5	0.569476082	8.E-01	19206, 19164, 17869, 230558, 12263	809	96	13588	9.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0051605~protein maturation by peptide bond cleavage	3	0.341685649	9.E-01	19164, 230558, 12263	809	65	13588	8.E-01	1.E+00	1.E+00	1.E+02

Annotation Cluster 279	Enrichment Score: 0.07008809062166196											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	zinc-finger	60	6.833712984	5.E-01	22324, 54354, 14815, 16800, 171531, 129	869	1204	17854	1.E+00	1.E+00	8.E-01	1.E+02
SP_PIR_KEYWORDS	metal-binding	130	14.80637813	6.E-01	18746, 226646, 22324, 19744, 14815, 168	869	2682	17854	1.E+00	1.E+00	9.E-01	1.E+02
SP_PIR_KEYWORDS	zinc	73	8.314350797	1.E+00	22324, 54354, 14815, 16800, 171531, 129	869	1886	17854	8.E-01	1.E+00	1.E+00	1.E+02
GOTERM_MF_FAT	GO:0046914~transition metal ion binding	107	12.18678815	1.E+00	226646, 22324, 19206, 14815, 16800, 171	754	2608	13288	7.E-01	1.E+00	1.E+00	1.E+02
GOTERM_MF_FAT	GO:0008270~zinc ion binding	77	8.769931663	1.E+00	22324, 19206, 54354, 14815, 16800, 1715	754	2105	13288	6.E-01	1.E+00	1.E+00	1.E+02
GOTERM_MF_FAT	GO:0046872~metal ion binding	158	17.99544419	1.E+00	18746, 226646, 19744, 22324, 19206, 169	754	3850	13288	7.E-01	1.E+00	1.E+00	1.E+02
GOTERM_MF_FAT	GO:0043169~cation binding	158	17.99544419	1.E+00	18746, 226646, 19744, 22324, 19206, 169	754	3885	13288	7.E-01	1.E+00	1.E+00	1.E+02
GOTERM_MF_FAT	GO:0043167~ion binding	159	18.10933941	1.E+00	18746, 226646, 19744, 22324, 18416, 192	754	3934	13288	7.E-01	1.E+00	1.E+00	1.E+02

Annotation Cluster 280	Enrichment Score: 0.06697077282979119											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	viral nucleoprotein	3	0.341685649	4.E-01	15387, 15381, 20639	869	27	17854	2.E+00	1.E+00	7.E-01	1.E+02
SP_PIR_KEYWORDS	mrna splicing	8	0.911161731	8.E-01	15387, 19317, 15381, 53610, 75062, 6809	869	191	17854	9.E-01	1.E+00	1.E+00	1.E+02
GOTERM_CC_FAT	GO:0005681~spliceosome	5	0.569476082	9.E-01	15387, 19744, 15381, 75062, 20639	636	124	12504	8.E-01	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	Spliceosome	4	0.455580866	9.E-01	15387, 15381, 75062, 20639	869	111	17854	7.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0008380~RNA splicing	9	1.025056948	9.E-01	15387, 19317, 15381, 53610, 75062, 6809	809	201	13588	8.E-01	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	mrna processing	8	0.911161731	1.E+00	15387, 19317, 15381, 53610, 75062, 6809	869	240	17854	7.E-01	1.E+00	1.E+00	1.E+02
KEGG_PATHWAY	mmu03040:Spliceosome	7	0.797266515	1.E+00	15387, 15381, 15512, 75062, 68092, 1548	580	124	5738	6.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0006397~mRNA processing	9	1.025056948	1.E+00	15387, 19317, 15381, 53610, 75062, 6809	809	262	13588	6.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0016071~mRNA metabolic process	10	1.138952164	1.E+00	15387, 19317, 16341, 15381, 53610, 7506	809	302	13588	6.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0006396~RNA processing	12	1.366742597	1.E+00	15387, 19317, 19896, 15381, 53610, 7506	809	437	13588	5.E-01	1.E+00	1.E+00	1.E+02

Annotation Cluster 281	Enrichment Score: 0.05715272448310661											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR



UP_SEQ_FEATURE	repeat:TPR 7	3	0.341685649	7.E-01 52563, 56317, 69957	861	49	16021	1.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:TPR 6	3	0.341685649	8.E-01 52563, 56317, 69957	861	55	16021	1.E+00	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:TPR 4	4	0.455580866	8.E-01 52563, 56317, 59008, 69957	861	82	16021	9.E-01	1.E+00	1.E+00	1.E+02
INTERPRO	IPR001440:Tetratrico peptide TPR-1	4	0.455580866	8.E-01 17970, 52563, 56317, 69957	860	95	17763	9.E-01	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:TPR 5	3	0.341685649	8.E-01 52563, 56317, 69957	861	61	16021	9.E-01	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:TPR 3	5	0.569476082	9.E-01 17970, 52563, 56317, 59008, 69957	861	118	16021	8.E-01	1.E+00	1.E+00	1.E+02
INTERPRO	IPR019734:Tetratrico peptide repeat	4	0.455580866	9.E-01 17970, 52563, 56317, 69957	860	112	17763	7.E-01	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	tp repeat	5	0.569476082	9.E-01 17970, 52563, 56317, 59008, 69957	869	141	17854	7.E-01	1.E+00	1.E+00	1.E+02
INTERPRO	IPR013026:Tetratrico peptide region	4	0.455580866	9.E-01 17970, 52563, 56317, 69957	860	114	17763	7.E-01	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:TPR 1	5	0.569476082	9.E-01 17970, 52563, 56317, 59008, 69957	861	130	16021	7.E-01	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:TPR 2	5	0.569476082	9.E-01 17970, 52563, 56317, 59008, 69957	861	130	16021	7.E-01	1.E+00	1.E+00	1.E+02
INTERPRO	IPR011990:Tetratrico peptide-like helical	5	0.569476082	9.E-01 17970, 52563, 56317, 59008, 69957	860	150	17763	7.E-01	1.E+00	1.E+00	1.E+02
SMART	SM00028:TPR	4	0.455580866	9.E-01 17970, 52563, 56317, 69957	492	112	9131	7.E-01	1.E+00	1.E+00	1.E+02

Annotation Cluster 282		Enrichment Score: 0.054896579550950474											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_BP_FAT	GO:0016569~covalent chromatin modification	5	0.569476082		8.E-01 11785, 433759, 74318, 13436, 12914	809	809	96	13588	9.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0051276~chromosome organization	21	2.391799544		8.E-01 12190, 621893, 57376, 22130, 433759, 18	809	809	404	13588	9.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0006325~chromatin organization	15	1.708428246		9.E-01 621893, 57376, 22130, 433759, 14815, 31	809	809	315	13588	8.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0016568~chromatin modification	11	1.25284738		9.E-01 11785, 57376, 19645, 22130, 433759, 743	809	809	236	13588	8.E-01	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	chromatin regulator	7	0.797266515		9.E-01 11785, 57376, 19645, 433759, 15376, 148	869	869	192	17854	7.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0016570~histone modification	4	0.455580866		9.E-01 11785, 433759, 74318, 12914	809	809	92	13588	7.E-01	1.E+00	1.E+00	1.E+02

Annotation Cluster 283	Enrichment Score: 0.037376374421295065											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR011992:EF-Hand type	10	1.138952164		8.E-01 18826, 12315, 12314, 12313, 20692, 2020	860	227	17763	9.E-01	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	calcium	22	2.505694761		1.E+00 227753, 16952, 238055, 18797, 214952, 2	869	731	17854	6.E-01	1.E+00	1.E+00	1.E+02
GOTERM_MF_FAT	GO:0005509~calcium ion binding	24	2.733485194		1.E+00 227753, 16952, 20191, 18797, 214952, 21	754	840	13288	5.E-01	1.E+00	1.E+00	1.E+02

Annotation Cluster 284		Enrichment Score: 0.03526401099258756										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR016186:C-type lectin-like	5	0.569476082	9.E-01	20343, 27007, 12505, 20339, 17533	860	127	17763	8.E-01	1.E+00	1.E+00	1.E+02
INTERPRO	IPR018378:C-type lectin, conserved site	4	0.455580866	9.E-01	20343, 27007, 20339, 17533	860	104	17763	8.E-01	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	Lectin	6	0.683371298	9.E-01	20345, 20343, 27007, 20339, 17533, 1248	869	167	17854	7.E-01	1.E+00	1.E+00	1.E+02
INTERPRO	IPR001304:C-type lectin	4	0.455580866	9.E-01	20343, 27007, 20339, 17533	860	118	17763	7.E-01	1.E+00	1.E+00	1.E+02
GOTERM_MF_FAT	GO:0005529~sugar binding	7	0.797266515	9.E-01	20345, 20343, 27007, 20339, 17533, 1248	754	181	13288	7.E-01	1.E+00	1.E+00	1.E+02
SMART	SM00034:CLECT	4	0.455580866	1.E+00	20343, 27007, 20339, 17533	492	118	9131	6.E-01	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	domain:C-type lectin	3	0.341685649	1.E+00	20343, 27007, 20339	861	90	16021	6.E-01	1.E+00	1.E+00	1.E+02

Annotation Cluster 285		Enrichment Score: 0.026226154464969214										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0001505~regulation of neurotransmitter levels	3	0.341685649	9.E-01	19894, 19164, 12846	809	62	13588	8.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0007267~cell-cell signaling	13	1.480637813	9.E-01	14178, 19894, 14226, 14180, 21869, 2023	809	290	13588	8.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0019226~transmission of nerve impulse	9	1.025056948	1.E+00	19317, 19894, 14226, 19164, 14360, 1256	809	226	13588	7.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0007268~synaptic transmission	6	0.683371298	1.E+00	19894, 19164, 12568, 16561, 20238, 1284	809	178	13588	6.E-01	1.E+00	1.E+00	1.E+02

Annotation Cluster 286		Enrichment Score: 0.024956873886038462										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_SEQ_FEATURE	domain:EGF-like	4	0.455580866	7.E-01	20343, 230558, 18792, 20339	861	68	16021	1.E+00	1.E+00	1.E+00	1.E+02
	IPR013032:EGF-like region, conserved site	8	0.911161731	1.E+00	13836, 20343, 16414, 230558, 16412, 187	860	310	17763	5.E-01	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	egf-like domain	4	0.455580866	1.E+00	20343, 230558, 18792, 20339	869	222	17854	4.E-01	1.E+00	1.E+00	1.E+02
	IPR000742:EGF-like, type 3	3	0.341685649	1.E+00	20343, 18792, 20339	860	199	17763	3.E-01	1.E+00	1.E+00	1.E+02
INTERPRO	IPR006210:EGF-like	3	0.341685649	1.E+00	20343, 18792, 20339	860	203	17763	3.E-01	1.E+00	1.E+00	1.E+02
	SM00181:EGF	3	0.341685649	1.E+00	20343, 18792, 20339	492	203	9131	3.E-01	1.E+00	1.E+00	1.E+02

Annotation Cluster 287		Enrichment Score: 0.012237314241252325										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR019775:WD40 repeat, conserved site	9	1.025056948		9.E-01 27979, 76646, 107995, 54709, 56371, 103	860	258	17763	7.E-01	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	wd repeat	9	1.025056948		9.E-01 27979, 76646, 107995, 54709, 56371, 103	869	263	17854	7.E-01	1.E+00	1.E+00	1.E+02
INTERPRO	IPR015943:WD40/YVTN repeat-like	10	1.138952164		1.E+00 27979, 52206, 76646, 107995, 54709, 563	860	305	17763	7.E-01	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:WD 5	7	0.797266515		1.E+00 27979, 76646, 107995, 54709, 56371, 192	861	202	16021	6.E-01	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:WD 7	4	0.455580866		1.E+00 76646, 107995, 56371, 74370	861	124	16021	6.E-01	1.E+00	1.E+00	1.E+02
INTERPRO	IPR017986:WD40 repeat, region	7	0.797266515		1.E+00 76646, 107995, 54709, 56371, 103583, 12	860	228	17763	6.E-01	1.E+00	1.E+00	1.E+02
INTERPRO	IPR001680:WD40 repeat	8	0.911161731		1.E+00 76646, 107995, 54709, 56371, 103583, 19	860	259	17763	6.E-01	1.E+00	1.E+00	1.E+02
INTERPRO	IPR019781:WD40 repeat, subgroup	7	0.797266515		1.E+00 76646, 107995, 54709, 56371, 103583, 12	860	235	17763	6.E-01	1.E+00	1.E+00	1.E+02



UP_SEQ_FEATURE	repeat:WD 4	7	0.797266515	1.E+00	27979, 76646, 107995, 54709, 56371, 192	861	218	16021	6.E-01	1.E+00	1.E+00	1.E+02
INTERPRO	IPR019782:WD40 repeat 2	6	0.683371298	1.E+00	76646, 107995, 54709, 56371, 103583, 12	860	214	17763	6.E-01	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:WD 3	7	0.797266515	1.E+00	27979, 76646, 107995, 54709, 56371, 192	861	231	16021	6.E-01	1.E+00	1.E+00	1.E+02
SMART	SM00320:WD40	8	0.911161731	1.E+00	76646, 107995, 54709, 56371, 103583, 19	492	259	9131	6.E-01	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:WD 2	7	0.797266515	1.E+00	27979, 76646, 107995, 54709, 56371, 192	861	235	16021	6.E-01	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:WD 1	7	0.797266515	1.E+00	27979, 76646, 107995, 54709, 56371, 192	861	235	16021	6.E-01	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	repeat:WD 6	4	0.455580866	1.E+00	76646, 107995, 56371, 74370	861	161	16021	5.E-01	1.E+00	1.E+00	1.E+02

Annotation Cluster 288	Enrichment Score: 0.00549827854048582											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	disulfide bond	111	12.64236902	9.E-01	12475, 15018, 69524, 18414, 14782, 1201	869	2469	17854	9.E-01	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	disulfide bond	107	12.18678815	1.E+00	12475, 15018, 69524, 18414, 14782, 1201	861	2379	16021	8.E-01	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	signal	120	13.66742597	1.E+00	12475, 15018, 14178, 69524, 69121, 1841	869	2970	17854	8.E-01	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	membrane	232	26.42369021	1.E+00	19744, 12475, 15018, 69524, 19206, 2433	869	5507	17854	9.E-01	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	signal peptide	120	13.66742597	1.E+00	12475, 15018, 14178, 69524, 69121, 1841	861	2963	16021	8.E-01	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	glycoprotein	116	13.2118451	1.E+00	12475, 15018, 14178, 69524, 19206, 6912	869	3600	17854	7.E-01	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	topological domain:Extracellular	62	7.061503417	1.E+00	12765, 15018, 69524, 19206, 18414, 2193	861	2174	16021	5.E-01	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	107	12.18678815	1.E+00	12475, 15018, 14178, 69524, 19206, 6912	861	3444	16021	6.E-01	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	receptor	56	6.378132118	1.E+00	12765, 19206, 18414, 14815, 21934, 2019	869	2465	17854	5.E-01	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	topological domain:Cytoplasmic	72	8.200455581	1.E+00	12765, 69524, 19206, 276846, 18414, 219	861	2780	16021	5.E-01	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	transmembrane	122	13.8952164	1.E+00	15018, 66377, 69524, 19206, 18414, 2019	869	5237	17854	5.E-01	1.E+00	1.E+00	1.E+02
GOTERM_CC_FAT	GO:0031224~intrinsic to membrane	146	16.62870159	1.E+00	12475, 15018, 66377, 69524, 19206, 1841	636	5914	12504	5.E-01	1.E+00	1.E+00	1.E+02
UP_SEQ_FEATURE	transmembrane region	119	13.55353075	1.E+00	15018, 66377, 69524, 19206, 18414, 1640	861	4113	16021	5.E-01	1.E+00	1.E+00	1.E+02
GOTERM_CC_FAT	GO:0016021~integral to membrane	130	14.80637813	1.E+00	12475, 15018, 66377, 69524, 19206, 1841	636	5709	12504	4.E-01	1.E+00	1.E+00	1.E+02

Annotation Cluster 289	Enrichment Score: 0.005270676620379088											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0042277~peptide binding	6	0.683371298	1.E+00	14972, 12765, 15018, 14065, 16847, 1406	754	160	13288	7.E-01	1.E+00	1.E+00	1.E+02
GOTERM_MF_FAT	GO:0001653~peptide receptor activity	3	0.341685649	1.E+00	12765, 14065, 14064	754	110	13288	5.E-01	1.E+00	1.E+00	1.E+02
GOTERM_MF_FAT	GO:0008528~peptide receptor activity, G-protein coupled	3	0.341685649	1.E+00	12765, 14065, 14064	754	110	13288	5.E-01	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	g-protein coupled receptor	3	0.341685649	1.E+00	12765, 14065, 14064	869	1411	17854	4.E-02	1.E+00	1.E+00	1.E+02
INTERPRO	IPR00276:7TM GPCR, rhodopsin-like	3	0.341685649	1.E+00	12765, 14065, 14064	860	1458	17763	4.E-02	1.E+00	1.E+00	1.E+02
INTERPRO	IPR017452:GPCR, rhodopsin-like superfamily	3	0.341685649	1.E+00	12765, 14065, 14064	860	1575	17763	4.E-02	1.E+00	1.E+00	1.E+02

Annotation Cluster 290	Enrichment Score: 0.004997126077064406											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR011333:BTB/POZ fold	5	0.569476082	1.E+00	69288, 246710, 192192, 21402, 22724	860	180	17763	6.E-01	1.E+00	1.E+00	1.E+02
INTERPRO	IPR013069:BTB/POZ	3	0.341685649	1.E+00	69288, 246710, 22724	860	128	17763	5.E-01	1.E+00	1.E+00	1.E+02
INTERPRO	IPR000210:BTB/POZ-like	4	0.455580866	1.E+00	69288, 246710, 192192, 22724	860	180	17763	5.E-01	1.E+00	1.E+00	1.E+02
SMART	SM00225:BTB	4	0.455580866	1.E+00	69288, 246710, 192192, 22724	492	180	9131	4.E-01	1.E+00	1.E+00	1.E+02

Annotation Cluster 291	Enrichment Score: 0.0024569330489607804											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0005773~vacuole	5	0.569476082	1.E+00	17159, 56722, 230163, 11891, 13382	636	204	12504	5.E-01	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	lysosome	3	0.341685649	1.E+00	17159, 56722, 11891	869	144	17854	4.E-01	1.E+00	1.E+00	1.E+02
GOTERM_CC_FAT	GO:0005764~lysosome	4	0.455580866	1.E+00	17159, 56722, 230163, 11891	636	178	12504	4.E-01	1.E+00	1.E+00	1.E+02
GOTERM_CC_FAT	GO:0000323~lytic vacuole	4	0.455580866	1.E+00	17159, 56722, 230163, 11891	636	179	12504	4.E-01	1.E+00	1.E+00	1.E+02

Annotation Cluster 292	Enrichment Score: 2.546176679181264E-4											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0006813~potassium ion transport	4	0.455580866	1.E+00	12566, 18195, 192192, 12576	809	160	13588	4.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0015672~monovalent inorganic cation transport	7	0.797266515	1.E+00	20505, 12566, 18195, 192192, 67942, 205	809	303	13588	4.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0030001~metal ion transport	10	1.138952164	1.E+00	18751, 16818, 14226, 20505, 12566, 1819	809	442	13588	4.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0006812~cation transport	12	1.366742597	1.E+00	18751, 16818, 14226, 19164, 20505, 1256	809	515	13588	4.E-01	1.E+00	1.E+00	1.E+02
GOTERM_BP_FAT	GO:0006811~ion transport	14	1.59453303	1.E+00	26934, 14226, 18195, 20191, 18751, 1681	809	712	13588	3.E-01	1.E+00	1.E+00	1.E+02
SP_PIR_KEYWORDS	ion transport	5	0.569476082	1.E+00	26934, 20505, 20191, 67942, 20504	869	543	17854	2.E-01	1.E+00	1.E+00	1.E+02

Annotation Cluster 293	Enrichment Score: 2.51978767010447E-13											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR015880:Zinc finger, C2H2-like	4	0.455580866	1.E+00	69890, 74287, 75062, 22724	860	676	17763	1.E-01	1.E+00	1.E+00	1.E+02
INTERPRO	IPR007087:Zinc finger, C2H2-type	4	0.455580866	1.E+00	14163, 69890, 74287, 22724	860	681	17763	1.E-01	1.E+00	1.E+00	1.E+02
SMART	SM00355:ZnF_C2H2	4	0.455580866	1.E+00	69890, 74287, 75062, 22724	492	676	9131	1.E-01	1.E+00	1.E+00	1.E+02