**Supplementary Online Content**

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**Table S1.** **Study Measures**

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| **Table S1. Description of study measures.** | | |
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| **Variable** | **Assessment** |
| Suicide Attempt | Affirmative endorsement of the question “Have you ever tried to kill yourself?” was indicative of a lifetime suicide attempt. |
| Trauma Exposure | The Trauma History Screen (THS) (1) was used to assess exposure to the lifetime occurrence of 14 potentially traumatic events; the NHRVS additionally assessed exposure to life-threatening illness or injury. The sum of potentially traumatic events endorsed, ranging from 0–15, was used as an index of lifetime trauma burden. |
| Combat Veteran Status | Combat veteran status was assessed with the following question: “Did you ever serve in a combat or war zone?” |
| Lifetime Depression/PTSD | Probable lifetime major depressive disorder (MDD) was assessed using a modified self-report version of the Mini International Neuropsychiatric Interview (MINI) (2). Probable lifetime PTSD was assessed using a lifetime version of the PTSD Checklist-Specific Stressor version (3), which assessed PTSD symptoms related to veterans’ ‘worst’ event on the THS; scores ≥ 50 were indicative of a positive screen. |
| Lifetime Alcohol/Drug Use Disorder | Probable lifetime alcohol use disorder (AUD) and drug use disorder (DUD) was assessed using a modified self-report version of the Mini International Neuropsychiatric Interview (MINI) (2). The MINI has been found to have comparably high validity and reliability to longer psychiatric interviews such as the Composite International Diagnostic Interview (4). |

**Table S2. DNA Extraction, Genotyping, Quality Control, Imputation, and Polygenic Risk Scoring Methodology**

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| **Table S2. DNA Extraction, genotyping, quality control, imputation, and polygenic risk scoring methods.** | | |
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| **Method** | **Description** |
| DNA Extraction, Genotyping, Quality Control, and Imputation | DNA was extracted from saliva samples collected with Oragene DNA (OG-250) kits. Samples were genotyped on the Illumina (San Diego, CA, USA) PsychChip microarray at Yale. After quality control, to account for population stratification of non-related European-American individuals, principal component (PC) analysis with the first 10 PCs was performed using Eigensoft (5). Genotype imputation was conducted using SHAPEIT (6) for pre-phasing and IMPUTE (7) for imputation. The 1,000 Genomes Project Phase 3 was used as the reference panel. After imputation, 6,724,271 SNPs were used for the PRS analysis. |
| Polygenic Risk Scoring | The PRSice-2 software was used to calculate PRS (8). A suicidality GWAS performed in 129,335 participants of European ancestry from the UK Biobank was used as the base dataset (9). In this previous study, the suicidality spectrum was defined with ‘no suicidality,’ ‘thoughts that life was not worth living,’ ‘ever contemplated self-harm,’ and ‘act of deliberate self-harm in the past.’ The NHRVS imputed dataset was used as the target for the PRS analysis. The two datasets included 5,372,255 shared variants. Multiple p-value thresholds were considered for SNP inclusion (5 x 10-8, 10-7, 10-6, 10-5, 10-4, .001, .05, .3, .5, 1). An LD cut-off of R2 = 0.3 within a 500-kb window was used to calculate the PRS while excluding the Major Histocompatibility Complex region of the genome due to its complex LD structure. |
| Drug Repurposing Analyses | The Gene2drug tool (10) was used for drug repurposing analysis. Gene2drug applies Pathway-Set Enrichment Analysis (PSEA) using gene sets to identify up-or downregulated gene pathways by drugs. This tool converts gene expression profiles from Connectivity Map (11) to pathway expression profiles then ranks p-values of their Kolgomorov-Smirnov statistics. An enrichment score (EScore) is assigned to each drug to indicate up- or downregulation and its magnitude. All Bonferroni significant clumped GO terms were used as input for Gene2drug. |

**Table S3. Description of environments associated with suicide attempt**

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| **Table S3. Description of environments associated with suicide attempt.** | | |
|  |  |  |
| **Environment Name** | **Observed No.** | **Not observed No.** |
| Life-threatening illness or injury | 534 | 1132 |
| MVA | 337 | 1329 |
| Accident at Work or Home | 188 | 1478 |
| Natural disaster | 556 | 1110 |
| Child Physical Abuse | 262 | 1404 |
| Adult Physical Abuse | 232 | 1434 |
| Child Sexual Abuse | 112 | 1554 |
| Adult Sexual Abuse | 46 | 1620 |
| Attacked with Weapon | 296 | 1370 |
| Military Trauma | 437 | 1229 |
| Sudden Death of Loved One | 1004 | 662 |
| Witnessed Death/ Serious Injury | 609 | 1057 |
| Sudden Move/ Loss of Possessions | 217 | 1449 |
| Sudden Abandonment | 304 | 1362 |
| Other | 156 | 1510 |
|  |  |  |

**Table S4. Functional annotation and gene enrichment analyses**

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| **Table S4. Functional annotation and gene enrichment analyses.** | | |
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| **Method** | **Description** |
| Functional annotation | Nominally significant results from the multivariate gene-environment interaction analysis were mapped to genes using SNP Nexus (12). This tool maps each variant using dbSNP identifiers with the closest gene based on the major gene annotation systems (e.g., Ensembl, NCBI RefSeq). The GRCh38 genome assembly was used for the reference panel. |
| Gene enrichment analysis | The 5,509 genes annotated using SNP Nexus were submitted to PANTHER (13) to test for enrichment of relevant biological processes, cellular components, and molecular functions. P values adjusted by the conservative Bonferroni correction method were considered significant (p < 3.18 × 10−6). The redundant gene ontology (GO) terms were clumped using REVIGO (14), which applies a simple clustering algorithm that relies on semantic similarity measures. |

**Table S5. Gene-environment interactions**

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| **Table S5. Gene-environment interactions** | | | | | | | | | |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **Chr** | **Pos.** | **snp** | **a0** | **a1** | **P*ass* FDR** | **P*int* FDR** | **Gene** | **Func** | **LT** | **MV** | **AC** | **ND** | **CP** | **AP** | **CS** | **AS** | **AT** | **MT** | **SD** | **WD** | **SM** | **SA** | **OT** |
| 17 | 14981870 | rs11078277 | C | T | 4.91E-03 | 0.011 | NA | NA | 0.35 | -0.45 | 0.10 | -0.18 | 0.10 | -0.27 | -0.26 | -0.10 | 0.19 | -0.16 | -0.17 | 1.04 | 0.14 | -0.34 | 2.24 |
| 8 | 55513876 | rs6986108 | A | G | 0.013 | 0.011 | RP1 | intronic | -0.50 | 0.10 | 1.40 | -0.48 | -0.36 | -0.19 | -0.13 | -0.09 | 0.34 | -0.39 | -0.37 | 0.70 | -0.24 | -0.35 | 1.75 |
| 12 | 30375418 | rs10771664 | T | C | 0.013 | 0.011 | NA | NA | -0.44 | 0.08 | 0.39 | 0.03 | -0.07 | 0.17 | 0.78 | 0.42 | 0.29 | -0.18 | 0.19 | -0.35 | -0.09 | -0.27 | -0.07 |
| 11 | 34014533 | rs12797090 | C | T | 0.015 | 0.011 | NA | NA | 0.40 | -0.13 | 0.10 | -0.21 | -0.06 | 0.28 | 0.05 | 0.00 | 0.11 | 0.07 | -0.12 | -0.05 | 0.05 | -0.13 | -0.05 |
| 17 | 7906519 | rs61749665 | T | G | 0.017 | 0.012 | GUCY2D | coding | -0.44 | -0.02 | -0.03 | 0.50 | 0.00 | 1.16 | 0.64 | -0.05 | -0.30 | -0.07 | -0.42 | -0.41 | -0.21 | 0.12 | 0.50 |
| 10 | 43588196 | rs12247456 | A | G | 0.018 | 0.012 | RET | intronic | 0.61 | -0.53 | -0.29 | -0.49 | 0.47 | 1.21 | 0.91 | 0.52 | -0.46 | -0.55 | 0.45 | -0.40 | 1.44 | 0.50 | 0.16 |
| 2 | 98789684 | rs62154925 | T | C | 4.91E-03 | 0.017 | NA | NA | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| 2 | 131609712 | rs13006853 | G | A | 0.036 | 0.022 | ARHGEF4 | intronic | -0.18 | -0.14 | 0.00 | -0.01 | -0.08 | -0.06 | -0.01 | 0.07 | -0.19 | 0.14 | 0.09 | 0.41 | 0.00 | -0.01 | 0.10 |
| 6 | 114201109 | rs17790535 | G | A | 0.036 | 0.022 | NA | NA | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| 2 | 162226838 | rs1116173 | A | G | 0.038 | 0.022 | PSMD14 | 3downstream | -0.26 | 0.28 | 0.28 | 0.01 | -0.02 | 0.28 | 0.03 | 0.23 | -0.12 | -0.18 | -0.31 | -0.19 | 0.12 | 0.05 | -0.03 |
| 5 | 39400305 | rs12153248 | T | C | 0.038 | 0.022 | DAB2 | intronic | -0.60 | -0.22 | 0.27 | -0.12 | -0.43 | -0.09 | -0.38 | 0.88 | 0.45 | -0.59 | 2.11 | -0.74 | 2.22 | 4.36 | -0.46 |
| 8 | 78913579 | rs62508203 | C | T | 0.038 | 0.022 | NA | NA | 0.70 | -0.11 | 0.19 | -0.36 | -0.24 | 0.18 | -0.07 | 0.28 | 0.25 | -0.24 | -0.38 | -0.30 | -0.03 | 0.67 | 0.04 |
| 15 | 66941084 | rs1440371 | A | G | 0.038 | 0.026 | NA | NA | -0.17 | 0.19 | -0.04 | -0.15 | -0.02 | 0.01 | 0.13 | 0.00 | 0.29 | -0.11 | -0.13 | 0.17 | -0.10 | -0.01 | 0.06 |
| 1 | 89503665 | rs4656083 | A | G | 0.038 | 0.026 | NA | NA | -0.59 | 0.69 | 0.03 | 1.31 | -0.35 | 0.10 | 1.10 | 0.62 | -0.46 | -0.54 | 0.03 | 0.21 | -0.28 | 1.29 | -0.19 |
| 5 | 49452431 | rs34482469 | A | G | 0.038 | 0.026 | NA | NA | -0.26 | 0.35 | -0.17 | 1.14 | -0.11 | -0.17 | 0.00 | 0.00 | -0.12 | 0.54 | -0.03 | -0.32 | 0.11 | -0.15 | 0.14 |
| 12 | 18878196 | rs6486914 | G | A | 0.038 | 0.026 | AC087242.1 | non-coding | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| 17 | 4433600 | rs1351231 | T | G | 0.038 | 0.026 | SPNS2 | intronic | 1.43 | -0.28 | -0.25 | 1.37 | -0.34 | -0.24 | 0.02 | -0.09 | 0.33 | -0.38 | 2.24 | 0.27 | -0.26 | -0.31 | -0.11 |
| 13 | 82576261 | rs9545947 | T | C | 0.056 | 0.032 | NA | NA | 0.00 | 0.38 | -0.19 | 0.83 | -0.06 | -0.23 | -0.06 | 0.00 | -0.21 | -0.02 | -0.19 | -0.01 | -0.21 | 0.54 | -0.01 |
| 21 | 28569092 | rs34647816 | T | C | 0.041 | 0.032 | NA | NA | -0.07 | -0.13 | -0.04 | -0.38 | 0.23 | 0.13 | 0.18 | -0.02 | 0.72 | -0.15 | 0.01 | -0.22 | 0.72 | -0.28 | 0.01 |
| 2 | 138717595 | rs13432464 | T | C | 0.048 | 0.032 | NA | NA | -0.28 | 0.59 | 0.05 | -0.19 | 0.27 | 0.14 | 0.08 | -0.04 | -0.17 | -0.29 | 1.37 | -0.31 | -0.13 | -0.25 | -0.09 |
| 3 | 64852846 | rs56018244 | C | A | 0.048 | 0.032 | NA | NA | -0.63 | 1.92 | -0.32 | -0.60 | -0.01 | 0.95 | -0.17 | 0.11 | 1.25 | -0.19 | -0.56 | -0.48 | 0.43 | -0.14 | 0.42 |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 6 | 32797809 | rs2228396 | T | C | 0.045 | 0.032 | TAP2 | coding | -0.07 | -0.04 | -0.06 | -0.01 | -0.05 | 0.14 | 0.10 | 0.00 | -0.03 | -0.04 | -0.11 | -0.09 | 0.05 | 0.14 | -0.02 |
| 21 | 16008439 | rs60937991 | C | T | 0.048 | 0.032 | SAMSN1 | non-coding | -0.17 | -0.19 | -0.06 | 0.49 | -0.31 | -0.08 | -0.07 | 0.00 | -0.23 | 0.58 | 0.18 | -0.07 | 0.18 | -0.13 | 0.77 |
| 2 | 189030565 | rs10931329 | C | T | 0.038 | 0.035 | NA | NA | -0.05 | 0.27 | -0.16 | -0.37 | -0.08 | -0.07 | -0.03 | -0.02 | 0.29 | 0.40 | -0.30 | -0.23 | 0.26 | 0.66 | -0.14 |
| 19 | 49285757 | rs73059507 | A | C | 0.056 | 0.039 | NA | NA | 0.21 | -0.07 | -0.05 | -0.10 | -0.11 | -0.05 | 0.00 | 0.17 | 0.00 | -0.06 | 0.07 | 0.16 | 0.00 | -0.09 | -0.06 |
| 4 | 186734480 | rs6858186 | A | G | 0.041 | 0.040 | NA | NA | 0.64 | 0.69 | -0.14 | -0.48 | -0.11 | 1.88 | 0.07 | -0.07 | 0.25 | -0.22 | -0.51 | -0.05 | 0.37 | -0.39 | -0.10 |
| 15 | 24227492 | rs4778270 | A | G | 0.060 | 0.041 | NA | NA | -0.18 | -0.17 | -0.12 | 0.48 | -0.05 | -0.11 | -0.09 | -0.03 | 0.03 | -0.04 | -0.26 | -0.14 | 0.54 | 0.48 | -0.07 |
| 15 | 94791525 | rs7183979 | T | C | 0.063 | 0.041 | MCTP2 | non-coding | -0.13 | -0.03 | -0.16 | -0.31 | -0.14 | 0.91 | -0.11 | 0.15 | 0.38 | -0.16 | 0.10 | 0.02 | -0.09 | 0.05 | -0.11 |
| 18 | 70132719 | rs75337901 | A | C | 0.065 | 0.041 | NA | NA | 0.00 | -0.01 | 0.00 | -0.02 | -0.02 | -0.02 | 0.00 | 0.00 | -0.02 | 0.00 | -0.02 | -0.01 | 0.00 | 0.00 | 0.00 |
| 2 | 79390204 | rs116652994 | G | A | 0.064 | 0.041 | AC011754.1 | non-coding | 0.06 | 0.00 | -0.10 | -0.15 | 0.12 | 0.00 | 0.02 | 0.00 | 0.02 | 0.32 | -0.19 | 0.00 | -0.09 | 0.17 | 0.00 |
| 6 | 40655183 | rs6458171 | A | G | 0.065 | 0.041 | NA | NA | -0.40 | -0.32 | -0.24 | -0.13 | -0.25 | -0.23 | 0.03 | 0.40 | -0.31 | 0.12 | 0.78 | -0.24 | 0.58 | -0.14 | 1.05 |
| 16 | 25681314 | rs7189315 | T | G | 0.059 | 0.041 | NA | NA | -0.43 | 0.79 | -0.14 | -0.32 | 0.09 | -0.11 | -0.11 | 0.27 | 0.40 | -0.11 | -0.52 | -0.43 | 0.47 | 0.26 | 0.66 |
| 12 | 83044190 | rs1922574 | C | T | 0.056 | 0.041 | NA | NA | -0.25 | 0.83 | -0.17 | 0.07 | -0.08 | -0.13 | 0.71 | -0.05 | -0.11 | 0.35 | -0.30 | -0.24 | -0.20 | -0.21 | -0.16 |
| 11 | 102748945 | rs636648 | G | A | 0.064 | 0.041 | NA | NA | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| 17 | 9080392 | rs71369624 | T | G | 0.065 | 0.041 | AC005695.1 | non-coding | -0.02 | 0.01 | 0.00 | -0.05 | 0.04 | 0.05 | 0.00 | 0.00 | -0.07 | 0.06 | -0.06 | 0.12 | 0.00 | 0.00 | -0.04 |
| 6 | 97284616 | rs7742049 | A | G | 0.065 | 0.041 | GPR63 | intronic | 0.31 | -0.36 | 0.10 | 0.08 | 0.90 | -0.34 | 1.43 | 0.86 | -0.41 | -0.46 | -0.63 | -0.39 | 0.08 | -0.12 | -0.04 |
| 6 | 91314706 | rs12210438 | G | A | 0.065 | 0.041 | NA | NA | -0.17 | -0.20 | 0.10 | 0.30 | 0.55 | 0.60 | -0.13 | 0.04 | 0.14 | 0.13 | -0.36 | -0.20 | -0.11 | 0.26 | -0.14 |
| 13 | 108047005 | rs9583170 | A | G | 0.070 | 0.041 | NA | NA | -0.43 | -0.22 | -0.26 | -0.33 | 0.09 | -0.06 | 0.34 | 0.47 | -0.13 | -0.14 | -0.45 | -0.20 | 0.00 | 0.61 | 1.13 |
| 1 | 102090664 | rs1843113 | A | G | 0.065 | 0.041 | NA | NA | -0.01 | -0.23 | -0.23 | -0.31 | -0.18 | 0.07 | 0.41 | 0.24 | -0.14 | 0.73 | -0.24 | 0.16 | 0.47 | 0.11 | 0.21 |
| 6 | 16737046 | rs3793118 | A | G | 0.075 | 0.041 | NA | NA | -0.13 | -0.09 | 0.02 | 0.17 | -0.02 | 0.07 | -0.02 | 0.11 | 0.02 | 0.02 | -0.08 | -0.11 | 0.03 | -0.06 | -0.07 |
| 6 | 85158209 | rs9449914 | A | C | 0.065 | 0.041 | LINC01611 | non-coding | -0.02 | -0.46 | -0.25 | 0.67 | 3.15 | -0.35 | -0.24 | 0.26 | -0.40 | -0.49 | 0.58 | 0.06 | 1.15 | -0.41 | -0.29 |
| 8 | 78640043 | rs12155517 | G | A | 0.068 | 0.041 | NA | NA | 0.33 | 0.44 | -0.07 | -0.28 | -0.06 | 0.23 | -0.11 | 0.00 | -0.10 | 0.08 | -0.11 | -0.17 | 0.08 | 0.01 | -0.14 |
| 14 | 20766144 | rs2318862 | C | A | 0.068 | 0.041 | TTC5 | intronic | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| 12 | 51310623 | rs142234766 | CT | C | 0.038 | 0.041 | NA | NA | 0.01 | -0.14 | -0.02 | -0.05 | -0.14 | -0.02 | 0.03 | 0.11 | -0.01 | -0.17 | 0.28 | -0.21 | -0.09 | -0.03 | 0.12 |
| 8 | 66940471 | rs76437827 | T | C | 0.070 | 0.041 | DNAJC5B | intronic | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| 4 | 45347310 | rs7686772 | A | C | 0.054 | 0.041 | NA | NA | -0.10 | -0.16 | -0.12 | -0.31 | -0.22 | -0.08 | -0.05 | -0.02 | -0.06 | -0.24 | 0.34 | -0.18 | 1.00 | 0.85 | -0.14 |
| 12 | 16835982 | rs12371600 | A | C | 0.077 | 0.049 | NA | NA | -0.04 | -0.13 | 0.00 | 0.03 | -0.05 | -0.01 | -0.04 | 0.29 | 0.07 | 0.02 | -0.12 | 0.00 | -0.03 | -0.08 | -0.03 |
| 2 | 151522391 | rs10803808 | G | A | 0.065 | 0.049 | NA | NA | -0.22 | -0.07 | -0.12 | -0.08 | 0.35 | 0.34 | -0.04 | 0.00 | 0.00 | 0.74 | -0.26 | 0.13 | -0.21 | 0.31 | -0.13 |
| 1 | 183273751 | rs2276879 | T | C | 0.080 | 0.049 | NA | NA | -0.01 | 0.06 | 0.21 | -0.05 | 0.19 | -0.06 | -0.06 | 0.01 | 0.05 | -0.05 | -0.16 | -0.10 | -0.07 | -0.01 | -0.05 |
| 9 | 124654567 | rs10985432 | A | G | 0.077 | 0.049 | TTLL11-IT1 | non-coding | -0.17 | 0.00 | -0.01 | -0.18 | -0.08 | 0.07 | -0.06 | 0.12 | -0.04 | 0.12 | -0.11 | -0.16 | -0.07 | -0.01 | 0.19 |
| 20 | 2448587 | rs6138178 | G | T | 0.079 | 0.049 | SNRPB | intronic | 0.00 | -0.01 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | -0.03 | -0.01 | 0.00 | 0.00 | 0.00 |
| 12 | 5764207 | rs416667 | T | C | 0.079 | 0.049 | NA | NA | -0.23 | -0.17 | -0.13 | -0.10 | 0.13 | -0.17 | -0.09 | -0.07 | -0.19 | 0.62 | 1.59 | -0.28 | -0.15 | -0.16 | -0.11 |
| 8 | 83598795 | rs62513214 | A | G | 0.082 | 0.049 | NA | NA | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| 4 | 149576902 | rs7662796 | C | T | 0.079 | 0.049 | NA | NA | 0.12 | 0.14 | 0.22 | -0.17 | -0.24 | -0.23 | -0.15 | -0.03 | 0.44 | 0.78 | -0.35 | -0.32 | 0.70 | -0.15 | 0.02 |
| 11 | 61894280 | rs1792952 | T | C | 0.065 | 0.049 | INCENP | intronic | -0.19 | -0.45 | 1.14 | -0.60 | -0.38 | 0.06 | 0.10 | -0.14 | -0.43 | -0.06 | 1.03 | 0.91 | -0.24 | 3.09 | -0.26 |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

Abbreviations: AC, Life-threatening Accident; AS, Adult Sexual Abuse; AT, Attacked with Weapon; Chr, Chromosome; CP, Childhood Physical Abuse; CS, Childhood Sexual Abuse; Func, Function; LT, Life Threatening Illness or Injury; MT, Military Trauma; MV, Motor Vehicle Accident; ND, Natural Disaster; OT, Other; Pass FDR, Passociation (FDR-corrected); Pint, Pinteraction (FDR-corrected); SA, Sudden Abandonment; SM, Sudden Move/Loss; WD, Witnessed Death.

**Table S6. Gene Ontology enrichment**

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| **Table S6. Gene Ontology enrichment** | | | | | |  |
|  |  |  |  |  |  |  |
| **GO biological process** | **GO symbol** | **Number of Genes in Pathway** | **Number of Genes** | **Direction of effect** | **Fold Enrichment** | **Enrichment *p* value** |
| cellular process | GO:0009987 | 15074 | 2730 | + | 1.11 | 2.73E-25 |
| multicellular organism development | GO:0007275 | 4525 | 1014 | + | 1.38 | 1.13E-24 |
| developmental process | GO:0032502 | 5565 | 1196 | + | 1.32 | 4.57E-24 |
| anatomical structure development | GO:0048856 | 5001 | 1096 | + | 1.35 | 4.71E-24 |
| nervous system development | GO:0007399 | 2193 | 567 | + | 1.59 | 1.15E-23 |
| system development | GO:0048731 | 4169 | 940 | + | 1.38 | 2.86E-23 |
| cell adhesion | GO:0007155 | 952 | 293 | + | 1.89 | 1.74E-20 |
| biological adhesion | GO:0022610 | 958 | 293 | + | 1.88 | 4.54E-20 |
| neurogenesis | GO:0022008 | 1361 | 374 | + | 1.69 | 5.86E-19 |
| cell morphogenesis | GO:0000902 | 675 | 224 | + | 2.04 | 6.80E-19 |
| cell development | GO:0048468 | 1623 | 427 | + | 1.62 | 9.86E-19 |
| neuron differentiation | GO:0030182 | 1008 | 296 | + | 1.80 | 3.51E-18 |
| multicellular organismal process | GO:0032501 | 6584 | 1329 | + | 1.24 | 5.43E-18 |
| cellular component organization | GO:0016043 | 5298 | 1106 | + | 1.28 | 5.56E-18 |
| neuron development | GO:0048666 | 810 | 251 | + | 1.90 | 8.09E-18 |
| plasma membrane bounded cell projection organization | GO:0120036 | 1068 | 307 | + | 1.77 | 8.36E-18 |
| generation of neurons | GO:0048699 | 1237 | 342 | + | 1.70 | 1.36E-17 |
| cell projection organization | GO:0030030 | 1119 | 317 | + | 1.74 | 1.38E-17 |
| anatomical structure morphogenesis | GO:0009653 | 2130 | 521 | + | 1.50 | 1.57E-17 |
| biological process | GO:0008150 | 17698 | 3051 | + | 1.06 | 8.84E-17 |
| neuron projection development | GO:0031175 | 651 | 208 | + | 1.96 | 3.68E-16 |
| cell morphogenesis involved in differentiation | GO:0000904 | 517 | 177 | + | 2.10 | 4.98E-16 |
| cellular component organization or biogenesis | GO:0071840 | 5496 | 1122 | + | 1.25 | 1.18E-15 |
| cellular developmental process | GO:0048869 | 3463 | 759 | + | 1.35 | 1.43E-15 |
| cell differentiation | GO:0030154 | 3403 | 746 | + | 1.35 | 3.00E-15 |
| neuron projection morphogenesis | GO:0048812 | 455 | 157 | + | 2.12 | 1.13E-14 |
| plasma membrane bounded cell projection morphogenesis | GO:0120039 | 459 | 158 | + | 2.11 | 1.40E-14 |
| cell projection morphogenesis | GO:0048858 | 463 | 158 | + | 2.10 | 1.86E-14 |
| cell part morphogenesis | GO:0032990 | 483 | 162 | + | 2.06 | 3.43E-14 |
| localization | GO:0051179 | 5081 | 1035 | + | 1.25 | 6.18E-14 |
| regulation of signaling | GO:0023051 | 3257 | 707 | + | 1.33 | 1.30E-13 |
| regulation of cell communication | GO:0010646 | 3242 | 703 | + | 1.33 | 1.73E-13 |
| regulation of biological quality | GO:0065008 | 3705 | 787 | + | 1.30 | 1.85E-13 |
| cell morphogenesis involved in neuron differentiation | GO:0048667 | 408 | 141 | + | 2.12 | 2.42E-13 |
| cellular component morphogenesis | GO:0032989 | 569 | 178 | + | 1.92 | 2.76E-13 |
| regulation of cell projection organization | GO:0031344 | 643 | 194 | + | 1.85 | 3.72E-13 |
| regulation of plasma membrane bounded cell projection organization | GO:0120035 | 626 | 190 | + | 1.86 | 4.13E-13 |
| regulation of localization | GO:0032879 | 2709 | 600 | + | 1.36 | 9.33E-13 |
| movement of cell or subcellular component | GO:0006928 | 1413 | 352 | + | 1.53 | 1.06E-12 |
| regulation of cellular component organization | GO:0051128 | 2359 | 531 | + | 1.38 | 2.73E-12 |
| cell-cell adhesion | GO:0098609 | 515 | 161 | + | 1.92 | 4.22E-12 |
| animal organ development | GO:0048513 | 3079 | 659 | + | 1.31 | 1.17E-11 |
| detection of chemical stimulus involved in sensory perception of smell | GO:0050911 | 443 | 22 | - | 0.31 | 8.10E-11 |
| detection of chemical stimulus involved in sensory perception | GO:0050907 | 488 | 27 | - | 0.34 | 1.31E-10 |
| axon development | GO:0061564 | 375 | 123 | + | 2.01 | 1.45E-10 |
| transmembrane receptor protein tyrosine kinase signaling pathway | GO:0007169 | 406 | 130 | + | 1.97 | 1.89E-10 |
| regulation of developmental process | GO:0050793 | 2368 | 519 | + | 1.35 | 2.00E-10 |
| modulation of chemical synaptic transmission | GO:0050804 | 431 | 135 | + | 1.92 | 2.59E-10 |
| axonogenesis | GO:0007409 | 337 | 113 | + | 2.06 | 2.62E-10 |
| regulation of trans-synaptic signaling | GO:0099177 | 432 | 135 | + | 1.92 | 2.71E-10 |
| locomotion | GO:0040011 | 1195 | 293 | + | 1.51 | 4.53E-10 |
| sensory perception of smell | GO:0007608 | 468 | 26 | - | 0.34 | 4.56E-10 |
| biological regulation | GO:0065007 | 12249 | 2180 | + | 1.09 | 9.88E-10 |
| cell junction organization | GO:0034330 | 477 | 142 | + | 1.83 | 1.54E-09 |
| neuron projection guidance | GO:0097485 | 228 | 84 | + | 2.26 | 1.72E-09 |
| central nervous system development | GO:0007417 | 1002 | 250 | + | 1.53 | 2.47E-09 |
| axon guidance | GO:0007411 | 227 | 83 | + | 2.25 | 2.68E-09 |
| regulation of response to stimulus | GO:0048583 | 3805 | 768 | + | 1.24 | 3.04E-09 |
| regulation of multicellular organismal process | GO:0051239 | 2578 | 548 | + | 1.31 | 3.13E-09 |
| positive regulation of cellular process | GO:0048522 | 5580 | 1075 | + | 1.18 | 3.95E-09 |
| regulation of signal transduction | GO:0009966 | 2867 | 599 | + | 1.28 | 4.05E-09 |
| regulation of neuron projection development | GO:0010975 | 443 | 132 | + | 1.83 | 5.49E-09 |
| enzyme linked receptor protein signaling pathway | GO:0007167 | 598 | 165 | + | 1.69 | 6.07E-09 |
| cell-cell adhesion via plasma-membrane adhesion molecules | GO:0098742 | 258 | 89 | + | 2.12 | 7.75E-09 |
| regulation of biological process | GO:0050789 | 11528 | 2055 | + | 1.09 | 7.80E-09 |
| positive regulation of biological process | GO:0048518 | 6062 | 1154 | + | 1.17 | 8.05E-09 |
| sensory perception of chemical stimulus | GO:0007606 | 542 | 38 | - | 0.43 | 1.39E-08 |
| detection of chemical stimulus | GO:0009593 | 524 | 36 | - | 0.42 | 1.56E-08 |
| regulation of cellular process | GO:0050794 | 11076 | 1979 | + | 1.10 | 1.60E-08 |
| cytoskeleton organization | GO:0007010 | 1169 | 278 | + | 1.46 | 1.64E-08 |
| regulation of cellular component movement | GO:0051270 | 1025 | 249 | + | 1.49 | 1.93E-08 |
| signaling | GO:0023052 | 5064 | 977 | + | 1.19 | 2.76E-08 |
| regulation of anatomical structure morphogenesis | GO:0022603 | 908 | 225 | + | 1.52 | 2.88E-08 |
| regulation of cell migration | GO:0030334 | 894 | 222 | + | 1.53 | 2.97E-08 |
| establishment of localization | GO:0051234 | 3911 | 775 | + | 1.22 | 4.40E-08 |
| positive regulation of cell projection organization | GO:0031346 | 350 | 107 | + | 1.88 | 5.59E-08 |
| regulation of cell motility | GO:2000145 | 950 | 231 | + | 1.49 | 6.85E-08 |
| cell communication | GO:0007154 | 5167 | 990 | + | 1.18 | 7.75E-08 |
| transport | GO:0006810 | 3752 | 744 | + | 1.22 | 7.91E-08 |
| homophilic cell adhesion via plasma membrane adhesion molecules | GO:0007156 | 167 | 63 | + | 2.32 | 8.80E-08 |
| synapse organization | GO:0050808 | 289 | 92 | + | 1.96 | 9.36E-08 |
| trans-synaptic signaling | GO:0099537 | 416 | 120 | + | 1.77 | 1.03E-07 |
| brain development | GO:0007420 | 761 | 192 | + | 1.55 | 1.09E-07 |
| actin filament-based process | GO:0030029 | 599 | 159 | + | 1.63 | 1.19E-07 |
| positive regulation of cellular component organization | GO:0051130 | 1119 | 262 | + | 1.44 | 1.53E-07 |
| regulation of small GTPase mediated signal transduction | GO:0051056 | 308 | 95 | + | 1.89 | 2.09E-07 |
| head development | GO:0060322 | 806 | 199 | + | 1.52 | 2.30E-07 |
| regulation of intracellular signal transduction | GO:1902531 | 1655 | 362 | + | 1.34 | 2.31E-07 |
| regulation of locomotion | GO:0040012 | 990 | 235 | + | 1.46 | 2.88E-07 |
| behavior | GO:0007610 | 558 | 148 | + | 1.63 | 3.51E-07 |
| regulation of membrane potential | GO:0042391 | 434 | 121 | + | 1.71 | 4.53E-07 |
| animal organ morphogenesis | GO:0009887 | 957 | 227 | + | 1.46 | 4.63E-07 |
| intracellular signal transduction | GO:0035556 | 1464 | 324 | + | 1.36 | 4.63E-07 |
| chemical synaptic transmission | GO:0007268 | 398 | 113 | + | 1.74 | 5.75E-07 |
| anterograde trans-synaptic signaling | GO:0098916 | 398 | 113 | + | 1.74 | 5.75E-07 |
| positive regulation of cell communication | GO:0010647 | 1632 | 354 | + | 1.33 | 6.62E-07 |
| synaptic signaling | GO:0099536 | 448 | 123 | + | 1.69 | 6.71E-07 |
| peptidyl-tyrosine modification | GO:0018212 | 154 | 56 | + | 2.23 | 1.14E-06 |
| positive regulation of signaling | GO:0023056 | 1639 | 353 | + | 1.32 | 1.16E-06 |
| regulation of transport | GO:0051049 | 1732 | 370 | + | 1.31 | 1.27E-06 |
| actin cytoskeleton organization | GO:0030036 | 539 | 140 | + | 1.60 | 1.67E-06 |
| cell migration | GO:0016477 | 840 | 200 | + | 1.46 | 1.88E-06 |
| ion transmembrane transport | GO:0034220 | 854 | 202 | + | 1.45 | 2.27E-06 |
| circulatory system process | GO:0003013 | 490 | 129 | + | 1.62 | 2.40E-06 |
| extracellular matrix organization | GO:0030198 | 266 | 81 | + | 1.87 | 2.41E-06 |
| detection of stimulus involved in sensory perception | GO:0050906 | 558 | 47 | - | 0.52 | 2.42E-06 |
| extracellular structure organization | GO:0043062 | 267 | 81 | + | 1.86 | 2.57E-06 |
| metal ion transport | GO:0030001 | 613 | 154 | + | 1.54 | 2.95E-06 |
| circulatory system development | GO:0072359 | 870 | 204 | + | 1.44 | 3.40E-06 |
| signal transduction | GO:0007165 | 4727 | 894 | + | 1.16 | 3.51E-06 |
| ion transport | GO:0006811 | 1173 | 262 | + | 1.37 | 3.52E-06 |
| peptidyl-tyrosine phosphorylation | GO:0018108 | 151 | 54 | + | 2.20 | 3.69E-06 |
| external encapsulating structure organization | GO:0045229 | 269 | 81 | + | 1.85 | 3.81E-06 |
| localization of cell | GO:0051674 | 986 | 226 | + | 1.41 | 4.23E-06 |
| cell motility | GO:0048870 | 986 | 226 | + | 1.41 | 4.23E-06 |
| positive regulation of multicellular organismal process | GO:0051240 | 1412 | 306 | + | 1.33 | 4.45E-06 |
| supramolecular fiber organization | GO:0097435 | 512 | 132 | + | 1.58 | 4.90E-06 |
| regulation of cell morphogenesis | GO:0022604 | 310 | 89 | + | 1.76 | 5.67E-06 |
| cell-cell signaling | GO:0007267 | 1030 | 233 | + | 1.39 | 6.49E-06 |
| phosphorus metabolic process | GO:0006793 | 1779 | 372 | + | 1.28 | 6.82E-06 |
| phosphate-containing compound metabolic process | GO:0006796 | 1758 | 368 | + | 1.29 | 7.11E-06 |
| forebrain development | GO:0030900 | 387 | 105 | + | 1.67 | 7.22E-06 |
| regulation of cellular component biogenesis | GO:0044087 | 950 | 217 | + | 1.40 | 7.99E-06 |
| cell surface receptor signaling pathway | GO:0007166 | 2030 | 417 | + | 1.26 | 8.09E-06 |
| chemotaxis | GO:0006935 | 504 | 129 | + | 1.57 | 9.29E-06 |
| taxis | GO:0042330 | 507 | 129 | + | 1.56 | 1.00E-05 |
| regulation of molecular function | GO:0065009 | 3060 | 599 | + | 1.20 | 1.07E-05 |
| transmembrane transport | GO:0055085 | 1182 | 260 | + | 1.35 | 1.12E-05 |
| inorganic ion transmembrane transport | GO:0098660 | 642 | 156 | + | 1.49 | 1.22E-05 |
| regulation of axonogenesis | GO:0050770 | 156 | 53 | + | 2.09 | 1.26E-05 |
| cation transmembrane transport | GO:0098655 | 641 | 155 | + | 1.49 | 1.52E-05 |
| positive regulation of developmental process | GO:0051094 | 1267 | 274 | + | 1.33 | 1.75E-05 |
| cellular response to stimulus | GO:0051716 | 6392 | 1166 | + | 1.12 | 1.80E-05 |
| regulation of cell shape | GO:0008360 | 155 | 52 | + | 2.06 | 1.89E-05 |
| cellular component assembly | GO:0022607 | 2251 | 453 | + | 1.24 | 1.95E-05 |
| adaptive immune response | GO:0002250 | 640 | 61 | - | 0.59 | 1.95E-05 |
| tube morphogenesis | GO:0035239 | 644 | 155 | + | 1.48 | 1.98E-05 |
| phagocytosis, recognition | GO:0006910 | 107 | 2 | - | 0.11 | 2.14E-05 |
| tissue development | GO:0009888 | 1597 | 334 | + | 1.28 | 2.18E-05 |
| inorganic cation transmembrane transport | GO:0098662 | 576 | 141 | + | 1.50 | 2.40E-05 |
| anatomical structure formation involved in morphogenesis | GO:0048646 | 881 | 200 | + | 1.39 | 2.41E-05 |
| cation transport | GO:0006812 | 827 | 190 | + | 1.41 | 2.51E-05 |
| positive regulation of molecular function | GO:0044093 | 1497 | 315 | + | 1.29 | 2.72E-05 |
| regulation of transmembrane transport | GO:0034762 | 569 | 139 | + | 1.50 | 2.76E-05 |
| dendrite development | GO:0016358 | 111 | 41 | + | 2.27 | 2.84E-05 |
| cell-substrate adhesion | GO:0031589 | 183 | 58 | + | 1.95 | 3.27E-05 |
| regulation of anatomical structure size | GO:0090066 | 521 | 129 | + | 1.52 | 3.43E-05 |
| positive regulation of cell migration | GO:0030335 | 522 | 129 | + | 1.52 | 3.50E-05 |
| regulation of catalytic activity | GO:0050790 | 2393 | 475 | + | 1.22 | 3.59E-05 |
| regulation of MAPK cascade | GO:0043408 | 658 | 156 | + | 1.46 | 3.72E-05 |
| negative chemotaxis | GO:0050919 | 46 | 23 | + | 3.07 | 3.74E-05 |
| response to stimulus | GO:0050896 | 8039 | 1435 | + | 1.10 | 3.89E-05 |
| positive regulation of neuron projection development | GO:0010976 | 161 | 52 | + | 1.98 | 4.13E-05 |
| regulation of ion transport | GO:0043269 | 685 | 161 | + | 1.44 | 4.16E-05 |
| regulation of cell differentiation | GO:0045595 | 1496 | 313 | + | 1.29 | 4.26E-05 |
| ribonucleoprotein complex biogenesis | GO:0022613 | 424 | 36 | - | 0.52 | 4.41E-05 |
| positive regulation of MAPK cascade | GO:0043410 | 471 | 118 | + | 1.54 | 5.21E-05 |
| regulation of multicellular organismal development | GO:2000026 | 1294 | 275 | + | 1.31 | 5.51E-05 |
| positive regulation of signal transduction | GO:0009967 | 1460 | 305 | + | 1.28 | 5.57E-05 |
| regulation of synaptic plasticity | GO:0048167 | 189 | 58 | + | 1.88 | 6.21E-05 |
| actin filament organization | GO:0007015 | 271 | 76 | + | 1.72 | 6.24E-05 |
| locomotory behavior | GO:0007626 | 181 | 56 | + | 1.90 | 6.56E-05 |
| tube development | GO:0035295 | 845 | 190 | + | 1.38 | 6.56E-05 |
| humoral immune response | GO:0006959 | 337 | 26 | - | 0.47 | 6.60E-05 |
| regulation of developmental growth | GO:0048638 | 320 | 86 | + | 1.65 | 6.69E-05 |
| regulation of GTPase activity | GO:0043087 | 348 | 92 | + | 1.62 | 7.04E-05 |
| positive regulation of catalytic activity | GO:0043085 | 1134 | 244 | + | 1.32 | 7.36E-05 |
| dendrite morphogenesis | GO:0048813 | 62 | 27 | + | 2.67 | 7.74E-05 |
| cell-matrix adhesion | GO:0007160 | 126 | 43 | + | 2.10 | 7.76E-05 |
| regulation of ion transmembrane transport | GO:0034765 | 481 | 119 | + | 1.52 | 7.86E-05 |
| immune response | GO:0006955 | 1678 | 208 | - | 0.76 | 7.96E-05 |
| positive regulation of cell motility | GO:2000147 | 547 | 132 | + | 1.48 | 8.10E-05 |
| positive regulation of intracellular signal transduction | GO:1902533 | 960 | 211 | + | 1.35 | 8.29E-05 |
| positive regulation of synaptic transmission | GO:0050806 | 135 | 45 | + | 2.05 | 8.35E-05 |
| vasculature development | GO:0001944 | 509 | 124 | + | 1.50 | 9.46E-05 |
| positive regulation of locomotion | GO:0040017 | 562 | 134 | + | 1.46 | 9.98E-05 |
| telencephalon development | GO:0021537 | 254 | 71 | + | 1.72 | 1.03E-04 |
| blood vessel development | GO:0001568 | 486 | 119 | + | 1.50 | 1.08E-04 |
| regulation of system process | GO:0044057 | 553 | 132 | + | 1.47 | 1.11E-04 |
| cell junction assembly | GO:0034329 | 258 | 72 | + | 1.71 | 1.12E-04 |
| macromolecule localization | GO:0033036 | 2308 | 454 | + | 1.21 | 1.18E-04 |
| positive regulation of cellular component movement | GO:0051272 | 560 | 133 | + | 1.46 | 1.22E-04 |
| regulation of cell adhesion | GO:0030155 | 737 | 167 | + | 1.39 | 1.34E-04 |
| protein localization | GO:0008104 | 1901 | 381 | + | 1.23 | 1.39E-04 |
| sensory perception of sound | GO:0007605 | 156 | 49 | + | 1.93 | 1.54E-04 |
| complement activation | GO:0006956 | 139 | 6 | - | 0.27 | 1.62E-04 |
| receptor-mediated endocytosis | GO:0006898 | 158 | 49 | + | 1.90 | 1.72E-04 |
| regulation of nervous system development | GO:0051960 | 438 | 108 | + | 1.51 | 1.72E-04 |
| semaphorin-plexin signaling pathway | GO:0071526 | 38 | 19 | + | 3.07 | 1.73E-04 |
| regulation of synapse structure or activity | GO:0050803 | 217 | 62 | + | 1.75 | 1.74E-04 |
| regulation of epithelial cell migration | GO:0010632 | 230 | 65 | + | 1.74 | 1.82E-04 |
| blood circulation | GO:0008015 | 399 | 100 | + | 1.54 | 1.90E-04 |
| sensory perception of mechanical stimulus | GO:0050954 | 177 | 53 | + | 1.84 | 2.48E-04 |
| protein localization to synapse | GO:0035418 | 50 | 22 | + | 2.70 | 2.51E-04 |
| regulation of cell projection assembly | GO:0060491 | 188 | 55 | + | 1.80 | 2.59E-04 |
| actin filament-based movement | GO:0030048 | 93 | 33 | + | 2.18 | 2.62E-04 |
| regulation of synapse organization | GO:0050807 | 210 | 60 | + | 1.75 | 2.66E-04 |
| regulation of cell growth | GO:0001558 | 420 | 103 | + | 1.51 | 2.71E-04 |
| learning or memory | GO:0007611 | 257 | 70 | + | 1.67 | 2.78E-04 |
| cellular response to endogenous stimulus | GO:0071495 | 1070 | 227 | + | 1.30 | 2.88E-04 |
| vesicle-mediated transport | GO:0016192 | 1329 | 274 | + | 1.27 | 2.99E-04 |
| negative regulation of biological process | GO:0048519 | 5187 | 944 | + | 1.12 | 3.10E-04 |
| memory | GO:0007613 | 119 | 39 | + | 2.01 | 3.12E-04 |
| defense response to other organism | GO:0098542 | 989 | 115 | - | 0.71 | 3.16E-04 |
| lamellipodium organization | GO:0097581 | 43 | 20 | + | 2.86 | 3.23E-04 |
| receptor localization to synapse | GO:0097120 | 43 | 20 | + | 2.86 | 3.23E-04 |
| regulation of neurotransmitter levels | GO:0001505 | 217 | 61 | + | 1.73 | 3.29E-04 |
| cellular localization | GO:0051641 | 2264 | 441 | + | 1.20 | 3.29E-04 |
| regulation of plasma membrane bounded cell projection assembly | GO:0120032 | 186 | 54 | + | 1.78 | 3.44E-04 |
| phosphorylation | GO:0016310 | 874 | 190 | + | 1.34 | 3.48E-04 |
| system process | GO:0003008 | 2040 | 401 | + | 1.21 | 3.53E-04 |
| organelle organization | GO:0006996 | 3360 | 631 | + | 1.15 | 3.86E-04 |
| retina morphogenesis in camera-type eye | GO:0060042 | 60 | 24 | + | 2.46 | 4.26E-04 |
| regulation of cellular component size | GO:0032535 | 389 | 96 | + | 1.52 | 4.34E-04 |
| protein phosphorylation | GO:0006468 | 683 | 153 | + | 1.38 | 4.50E-04 |
| negative regulation of cellular process | GO:0048523 | 4785 | 873 | + | 1.12 | 4.51E-04 |
| regulation of cell size | GO:0008361 | 185 | 53 | + | 1.76 | 4.79E-04 |
| cyclic nucleotide metabolic process | GO:0009187 | 41 | 19 | + | 2.85 | 4.82E-04 |
| lamellipodium assembly | GO:0030032 | 35 | 17 | + | 2.98 | 4.85E-04 |
| positive regulation of response to stimulus | GO:0048584 | 2080 | 406 | + | 1.20 | 4.98E-04 |
| potassium ion transmembrane transport | GO:0071805 | 158 | 47 | + | 1.83 | 5.29E-04 |
| cAMP metabolic process | GO:0046058 | 22 | 13 | + | 3.63 | 5.58E-04 |
| ribosome biogenesis | GO:0042254 | 293 | 24 | - | 0.50 | 5.75E-04 |
| integrin-mediated signaling pathway | GO:0007229 | 98 | 33 | + | 2.07 | 5.76E-04 |
| defense response to bacterium | GO:0042742 | 350 | 31 | - | 0.54 | 5.81E-04 |
| regulation of cell development | GO:0060284 | 495 | 116 | + | 1.44 | 5.90E-04 |
| muscle structure development | GO:0061061 | 477 | 112 | + | 1.44 | 5.98E-04 |
| positive regulation of phosphorylation | GO:0042327 | 807 | 175 | + | 1.33 | 6.01E-04 |
| positive regulation of cell differentiation | GO:0045597 | 833 | 180 | + | 1.33 | 6.07E-04 |
| positive regulation of epithelial cell migration | GO:0010634 | 151 | 45 | + | 1.83 | 6.10E-04 |
| positive regulation of phosphorus metabolic process | GO:0010562 | 886 | 190 | + | 1.32 | 6.22E-04 |
| positive regulation of phosphate metabolic process | GO:0045937 | 886 | 190 | + | 1.32 | 6.22E-04 |
| regulation of cation channel activity | GO:2001257 | 173 | 50 | + | 1.78 | 6.28E-04 |
| humoral immune response mediated by circulating immunoglobulin | GO:0002455 | 128 | 6 | - | 0.29 | 6.29E-04 |
| regulation of growth | GO:0040008 | 659 | 147 | + | 1.37 | 6.40E-04 |
| innate immune response | GO:0045087 | 783 | 89 | - | 0.70 | 7.15E-04 |
| cognition | GO:0050890 | 299 | 76 | + | 1.56 | 7.17E-04 |
| positive regulation of cellular component biogenesis | GO:0044089 | 514 | 119 | + | 1.42 | 7.34E-04 |
| positive regulation of developmental growth | GO:0048639 | 169 | 49 | + | 1.78 | 7.70E-04 |
| calcium ion transport | GO:0006816 | 237 | 63 | + | 1.63 | 7.82E-04 |
| heart process | GO:0003015 | 104 | 34 | + | 2.01 | 7.84E-04 |
| positive regulation of metabolic process | GO:0009893 | 3675 | 680 | + | 1.14 | 7.90E-04 |
| organonitrogen compound metabolic process | GO:1901564 | 4787 | 869 | + | 1.12 | 7.95E-04 |
| insulin-like growth factor receptor signaling pathway | GO:0048009 | 14 | 10 | + | 4.39 | 8.53E-04 |
| complement activation, classical pathway | GO:0006958 | 124 | 6 | - | 0.30 | 8.56E-04 |
| blood vessel morphogenesis | GO:0048514 | 404 | 97 | + | 1.47 | 8.68E-04 |
| regulation of vesicle-mediated transport | GO:0060627 | 529 | 121 | + | 1.40 | 8.72E-04 |
| multicellular organismal signaling | GO:0035637 | 114 | 36 | + | 1.94 | 8.83E-04 |
| positive regulation of protein modification process | GO:0031401 | 970 | 204 | + | 1.29 | 8.84E-04 |
| plasma membrane bounded cell projection assembly | GO:0120031 | 389 | 94 | + | 1.48 | 8.86E-04 |
| cell growth | GO:0016049 | 91 | 31 | + | 2.09 | 8.90E-04 |
| protein localization to cell junction | GO:1902414 | 76 | 27 | + | 2.18 | 9.23E-04 |
| cellular response to organic substance | GO:0071310 | 1980 | 385 | + | 1.19 | 9.34E-04 |
| cellular response to oxygen-containing compound | GO:1901701 | 1043 | 217 | + | 1.28 | 9.72E-04 |
| localization within membrane | GO:0051668 | 504 | 116 | + | 1.41 | 9.94E-04 |
| potassium ion transport | GO:0006813 | 167 | 48 | + | 1.77 | 1.02E-03 |
| neuron migration | GO:0001764 | 119 | 37 | + | 1.91 | 1.06E-03 |
| response to endogenous stimulus | GO:0009719 | 1342 | 271 | + | 1.24 | 1.07E-03 |
| positive regulation of cellular metabolic process | GO:0031325 | 3186 | 594 | + | 1.15 | 1.08E-03 |
| positive regulation of macromolecule metabolic process | GO:0010604 | 3382 | 628 | + | 1.14 | 1.08E-03 |
| heart development | GO:0007507 | 533 | 121 | + | 1.39 | 1.11E-03 |
| organic substance transport | GO:0071702 | 1927 | 375 | + | 1.20 | 1.13E-03 |
| positive regulation of nitrogen compound metabolic process | GO:0051173 | 2992 | 560 | + | 1.15 | 1.16E-03 |
| regulation of neurogenesis | GO:0050767 | 359 | 87 | + | 1.49 | 1.17E-03 |
| glutamate receptor signaling pathway | GO:0007215 | 48 | 20 | + | 2.56 | 1.18E-03 |
| calcium ion transmembrane transport | GO:0070588 | 183 | 51 | + | 1.71 | 1.19E-03 |
| positive regulation of GTPase activity | GO:0043547 | 256 | 66 | + | 1.58 | 1.19E-03 |
| regulation of extent of cell growth | GO:0061387 | 112 | 35 | + | 1.92 | 1.21E-03 |
| regulation of phosphate metabolic process | GO:0019220 | 1379 | 277 | + | 1.23 | 1.23E-03 |
| regulation of phosphorus metabolic process | GO:0051174 | 1379 | 277 | + | 1.23 | 1.23E-03 |
| developmental cell growth | GO:0048588 | 89 | 30 | + | 2.07 | 1.24E-03 |
| cellular component biogenesis | GO:0044085 | 2481 | 471 | + | 1.17 | 1.24E-03 |
| snRNA metabolic process | GO:0016073 | 47 | 0 | - | < 0.01 | 1.25E-03 |
| vascular process in circulatory system | GO:0003018 | 260 | 67 | + | 1.58 | 1.26E-03 |
| neuron recognition | GO:0008038 | 49 | 20 | + | 2.51 | 1.29E-03 |
| protein metabolic process | GO:0019538 | 3807 | 699 | + | 1.13 | 1.30E-03 |
| cell projection assembly | GO:0030031 | 405 | 96 | + | 1.46 | 1.38E-03 |
| angiogenesis | GO:0001525 | 310 | 77 | + | 1.53 | 1.42E-03 |
| regulation of postsynapse organization | GO:0099175 | 91 | 30 | + | 2.02 | 1.43E-03 |
| response to growth factor | GO:0070848 | 485 | 111 | + | 1.41 | 1.50E-03 |
| positive regulation of hydrolase activity | GO:0051345 | 588 | 131 | + | 1.37 | 1.51E-03 |
| regulation of phosphorylation | GO:0042325 | 1236 | 250 | + | 1.24 | 1.54E-03 |
| regulation of cation transmembrane transport | GO:1904062 | 347 | 84 | + | 1.49 | 1.56E-03 |
| collagen fibril organization | GO:0030199 | 57 | 22 | + | 2.37 | 1.59E-03 |
| neurotransmitter transport | GO:0006836 | 130 | 39 | + | 1.84 | 1.65E-03 |
| protein localization to cell periphery | GO:1990778 | 233 | 61 | + | 1.61 | 1.65E-03 |
| cellular response to organonitrogen compound | GO:0071417 | 566 | 126 | + | 1.37 | 1.81E-03 |
| positive regulation of heart growth | GO:0060421 | 36 | 16 | + | 2.73 | 1.85E-03 |
| positive regulation of kinase activity | GO:0033674 | 469 | 107 | + | 1.40 | 1.91E-03 |
| regulation of axon extension | GO:0030516 | 97 | 31 | + | 1.96 | 1.92E-03 |
| regulation of cytoskeleton organization | GO:0051493 | 531 | 119 | + | 1.38 | 1.93E-03 |
| growth | GO:0040007 | 362 | 86 | + | 1.46 | 1.96E-03 |
| Fc-gamma receptor signaling pathway | GO:0038094 | 23 | 12 | + | 3.20 | 2.02E-03 |
| sensory organ development | GO:0007423 | 558 | 124 | + | 1.36 | 2.03E-03 |
| positive regulation of axonogenesis | GO:0050772 | 81 | 27 | + | 2.05 | 2.04E-03 |
| learning | GO:0007612 | 147 | 42 | + | 1.75 | 2.10E-03 |
| detection of abiotic stimulus | GO:0009582 | 137 | 40 | + | 1.79 | 2.12E-03 |
| regulation of organelle organization | GO:0033043 | 1189 | 240 | + | 1.24 | 2.15E-03 |
| cellular response to alcohol | GO:0097306 | 90 | 29 | + | 1.98 | 2.16E-03 |
| regulation of hydrolase activity | GO:0051336 | 1033 | 212 | + | 1.26 | 2.17E-03 |
| synapse assembly | GO:0007416 | 99 | 31 | + | 1.92 | 2.23E-03 |
| proteoglycan metabolic process | GO:0006029 | 76 | 26 | + | 2.10 | 2.26E-03 |
| regulation of synaptic transmission, glutamatergic | GO:0051966 | 69 | 24 | + | 2.14 | 2.38E-03 |
| cellular response to growth factor stimulus | GO:0071363 | 455 | 104 | + | 1.40 | 2.44E-03 |
| eye morphogenesis | GO:0048592 | 152 | 43 | + | 1.74 | 2.45E-03 |
| peptide biosynthetic process | GO:0043043 | 388 | 39 | - | 0.62 | 2.45E-03 |
| neuron cell-cell adhesion | GO:0007158 | 17 | 10 | + | 3.61 | 2.46E-03 |
| positive regulation of protein phosphorylation | GO:0001934 | 723 | 154 | + | 1.31 | 2.48E-03 |
| eye development | GO:0001654 | 366 | 86 | + | 1.44 | 2.58E-03 |
| visual system development | GO:0150063 | 370 | 87 | + | 1.44 | 2.67E-03 |
| cilium organization | GO:0044782 | 336 | 80 | + | 1.46 | 2.71E-03 |
| regulation of ion transmembrane transporter activity | GO:0032412 | 259 | 65 | + | 1.54 | 2.73E-03 |
| positive regulation of phosphatidylinositol 3-kinase signaling | GO:0014068 | 79 | 26 | + | 2.02 | 2.85E-03 |
| sensory system development | GO:0048880 | 376 | 88 | + | 1.44 | 2.87E-03 |
| regulation of nervous system process | GO:0031644 | 146 | 41 | + | 1.72 | 2.91E-03 |
| synaptic transmission, glutamatergic | GO:0035249 | 28 | 13 | + | 2.85 | 2.96E-03 |
| immune response-regulating cell surface receptor signaling pathway involved in phagocytosis | GO:0002433 | 21 | 11 | + | 3.22 | 3.01E-03 |
| Fc-gamma receptor signaling pathway involved in phagocytosis | GO:0038096 | 21 | 11 | + | 3.22 | 3.01E-03 |
| actin filament-based transport | GO:0099515 | 21 | 11 | + | 3.22 | 3.01E-03 |
| positive regulation of nervous system process | GO:0031646 | 39 | 16 | + | 2.52 | 3.03E-03 |
| cellular response to peptide | GO:1901653 | 297 | 72 | + | 1.49 | 3.11E-03 |
| adenylate cyclase-modulating G protein-coupled receptor signaling pathway | GO:0007188 | 223 | 57 | + | 1.57 | 3.13E-03 |
| regulation of phosphatidylinositol 3-kinase signaling | GO:0014066 | 108 | 33 | + | 1.88 | 3.14E-03 |
| detection of stimulus | GO:0051606 | 694 | 81 | - | 0.72 | 3.17E-03 |
| microtubule-based process | GO:0007017 | 765 | 161 | + | 1.29 | 3.18E-03 |
| muscle cell development | GO:0055001 | 151 | 42 | + | 1.71 | 3.31E-03 |
| gene expression | GO:0010467 | 1992 | 271 | - | 0.84 | 3.39E-03 |
| regulation of cell junction assembly | GO:1901888 | 200 | 52 | + | 1.60 | 3.41E-03 |
| cell adhesion mediated by integrin | GO:0033627 | 25 | 12 | + | 2.95 | 3.43E-03 |
| regulation of blood circulation | GO:1903522 | 243 | 61 | + | 1.54 | 3.46E-03 |
| lymphocyte mediated immunity | GO:0002449 | 235 | 20 | - | 0.52 | 3.51E-03 |
| developmental growth | GO:0048589 | 359 | 84 | + | 1.44 | 3.60E-03 |
| response to calcium ion | GO:0051592 | 153 | 42 | + | 1.69 | 3.61E-03 |
| clathrin-dependent endocytosis | GO:0072583 | 31 | 14 | + | 2.77 | 3.65E-03 |
| cellular response to chemical stimulus | GO:0070887 | 2567 | 479 | + | 1.15 | 3.65E-03 |
| leukocyte mediated immunity | GO:0002443 | 282 | 26 | - | 0.57 | 3.68E-03 |
| B cell mediated immunity | GO:0019724 | 183 | 14 | - | 0.47 | 3.68E-03 |
| cellular nitrogen compound metabolic process | GO:0034641 | 3193 | 455 | - | 0.88 | 3.70E-03 |
| positive regulation of transport | GO:0051050 | 909 | 187 | + | 1.26 | 3.73E-03 |
| translation | GO:0006412 | 366 | 37 | - | 0.62 | 3.73E-03 |
| carboxylic acid transport | GO:0046942 | 233 | 59 | + | 1.56 | 3.74E-03 |
| cellular protein modification process | GO:0006464 | 2610 | 486 | + | 1.14 | 3.89E-03 |
| protein modification process | GO:0036211 | 2610 | 486 | + | 1.14 | 3.89E-03 |
| camera-type eye morphogenesis | GO:0048593 | 124 | 36 | + | 1.78 | 3.92E-03 |
| response to oxygen-containing compound | GO:1901700 | 1567 | 304 | + | 1.19 | 3.98E-03 |
| negative regulation of cell projection organization | GO:0031345 | 182 | 48 | + | 1.62 | 4.02E-03 |
| detection of external stimulus | GO:0009581 | 135 | 38 | + | 1.73 | 4.04E-03 |
| establishment of localization in cell | GO:0051649 | 1618 | 313 | + | 1.19 | 4.06E-03 |
| activation of GTPase activity | GO:0090630 | 115 | 34 | + | 1.82 | 4.09E-03 |
| positive regulation of cardiac muscle tissue growth | GO:0055023 | 32 | 14 | + | 2.69 | 4.14E-03 |
| negative regulation of locomotion | GO:0040013 | 317 | 75 | + | 1.45 | 4.17E-03 |
| regulation of cellular localization | GO:0060341 | 820 | 170 | + | 1.27 | 4.28E-03 |
| muscle system process | GO:0003012 | 271 | 66 | + | 1.50 | 4.30E-03 |
| positive regulation of nervous system development | GO:0051962 | 271 | 66 | + | 1.50 | 4.30E-03 |
| regulation of actin filament-based process | GO:0032970 | 398 | 91 | + | 1.40 | 4.52E-03 |
| cellular homeostasis | GO:0019725 | 833 | 172 | + | 1.27 | 4.57E-03 |
| immunoglobulin production | GO:0002377 | 155 | 11 | - | 0.44 | 4.67E-03 |
| ERBB signaling pathway | GO:0038127 | 57 | 20 | + | 2.16 | 4.71E-03 |
| response to nerve growth factor | GO:1990089 | 57 | 20 | + | 2.16 | 4.71E-03 |
| regulation of calcium-mediated signaling | GO:0050848 | 73 | 24 | + | 2.02 | 4.73E-03 |
| immunoglobulin mediated immune response | GO:0016064 | 179 | 14 | - | 0.48 | 4.75E-03 |
| regulation of heart growth | GO:0060420 | 65 | 22 | + | 2.08 | 4.76E-03 |
| epithelial cell morphogenesis | GO:0003382 | 33 | 14 | + | 2.61 | 4.78E-03 |
| RNA processing | GO:0006396 | 847 | 104 | - | 0.75 | 4.86E-03 |
| anion transport | GO:0006820 | 446 | 100 | + | 1.38 | 4.89E-03 |
| regulation of neuron differentiation | GO:0045664 | 193 | 50 | + | 1.59 | 5.06E-03 |
| positive regulation of peptidyl-tyrosine phosphorylation | GO:0050731 | 193 | 50 | + | 1.59 | 5.06E-03 |
| cellular chemical homeostasis | GO:0055082 | 741 | 155 | + | 1.28 | 5.10E-03 |
| peptide metabolic process | GO:0006518 | 519 | 58 | - | 0.69 | 5.12E-03 |
| protein localization to membrane | GO:0072657 | 432 | 97 | + | 1.38 | 5.20E-03 |
| protein acetylation | GO:0006473 | 134 | 9 | - | 0.41 | 5.20E-03 |
| regulation of calcium ion transport into cytosol | GO:0010522 | 101 | 30 | + | 1.82 | 5.24E-03 |
| cardiac muscle cell differentiation | GO:0055007 | 83 | 26 | + | 1.92 | 5.26E-03 |
| action potential | GO:0001508 | 92 | 28 | + | 1.87 | 5.30E-03 |
| dense core granule exocytosis | GO:1990504 | 7 | 6 | + | 5.26 | 5.31E-03 |
| regulation of Ras protein signal transduction | GO:0046578 | 195 | 50 | + | 1.57 | 5.35E-03 |
| establishment of cell polarity | GO:0030010 | 123 | 35 | + | 1.75 | 5.39E-03 |
| semaphorin-plexin signaling pathway involved in neuron projection guidance | GO:1902285 | 13 | 8 | + | 3.78 | 5.43E-03 |
| regulation of transmembrane transporter activity | GO:0022898 | 270 | 65 | + | 1.48 | 5.45E-03 |
| negative regulation of cell migration | GO:0030336 | 270 | 65 | + | 1.48 | 5.45E-03 |
| striated muscle tissue development | GO:0014706 | 288 | 69 | + | 1.47 | 5.49E-03 |
| proteoglycan biosynthetic process | GO:0030166 | 53 | 19 | + | 2.20 | 5.53E-03 |
| positive regulation of calcium ion transmembrane transporter activity | GO:1901021 | 40 | 16 | + | 2.46 | 5.56E-03 |
| cardiac muscle tissue development | GO:0048738 | 171 | 45 | + | 1.62 | 5.59E-03 |
| positive regulation of transferase activity | GO:0051347 | 551 | 119 | + | 1.33 | 5.60E-03 |
| netrin-activated signaling pathway | GO:0038007 | 10 | 7 | + | 4.30 | 5.62E-03 |
| cAMP biosynthetic process | GO:0006171 | 10 | 7 | + | 4.30 | 5.62E-03 |
| cellular response to forskolin | GO:1904322 | 10 | 7 | + | 4.30 | 5.62E-03 |
| response to forskolin | GO:1904321 | 10 | 7 | + | 4.30 | 5.62E-03 |
| cellular response to nitrogen compound | GO:1901699 | 626 | 133 | + | 1.30 | 5.65E-03 |
| internal protein amino acid acetylation | GO:0006475 | 114 | 7 | - | 0.38 | 5.67E-03 |
| peptidyl-lysine acetylation | GO:0018394 | 115 | 7 | - | 0.37 | 5.67E-03 |
| regulation of bone resorption | GO:0045124 | 46 | 17 | + | 2.27 | 5.76E-03 |
| regulation of cell-matrix adhesion | GO:0001952 | 125 | 35 | + | 1.72 | 5.92E-03 |
| establishment of protein localization | GO:0045184 | 1273 | 250 | + | 1.21 | 5.97E-03 |
| cytoskeleton-dependent intracellular transport | GO:0030705 | 187 | 48 | + | 1.58 | 6.04E-03 |
| cellular response to nerve growth factor stimulus | GO:1990090 | 54 | 19 | + | 2.16 | 6.06E-03 |
| neurotransmitter secretion | GO:0007269 | 78 | 25 | + | 1.97 | 6.12E-03 |
| signal release from synapse | GO:0099643 | 78 | 25 | + | 1.97 | 6.12E-03 |
| RNA metabolic process | GO:0016070 | 1403 | 186 | - | 0.81 | 6.27E-03 |
| nucleic acid metabolic process | GO:0090304 | 2007 | 277 | - | 0.85 | 6.39E-03 |
| regulation of Rho protein signal transduction | GO:0035023 | 88 | 27 | + | 1.88 | 6.43E-03 |
| regulation of metal ion transport | GO:0010959 | 394 | 89 | + | 1.39 | 6.48E-03 |
| Fc receptor mediated stimulatory signaling pathway | GO:0002431 | 24 | 11 | + | 2.82 | 6.53E-03 |
| positive regulation of dendrite extension | GO:1903861 | 24 | 11 | + | 2.82 | 6.53E-03 |
| positive regulation of phosphatidylinositol 3-kinase activity | GO:0043552 | 35 | 14 | + | 2.46 | 6.57E-03 |
| peptidyl-amino acid modification | GO:0018193 | 851 | 174 | + | 1.26 | 6.58E-03 |
| regulation of protein phosphorylation | GO:0001932 | 1086 | 216 | + | 1.22 | 6.68E-03 |
| collagen-activated signaling pathway | GO:0038065 | 17 | 9 | + | 3.25 | 6.73E-03 |
| striated muscle cell differentiation | GO:0051146 | 193 | 49 | + | 1.56 | 6.78E-03 |
| regulation of actin cytoskeleton organization | GO:0032956 | 359 | 82 | + | 1.40 | 6.78E-03 |
| positive regulation of cell adhesion | GO:0045785 | 442 | 98 | + | 1.36 | 6.87E-03 |
| snRNA processing | GO:0016180 | 36 | 0 | - | < 0.01 | 7.02E-03 |
| morphogenesis of a branching structure | GO:0001763 | 169 | 44 | + | 1.60 | 7.17E-03 |
| ncRNA metabolic process | GO:0034660 | 469 | 52 | - | 0.68 | 7.20E-03 |
| cardiac cell development | GO:0055006 | 64 | 21 | + | 2.02 | 7.33E-03 |
| ephrin receptor signaling pathway | GO:0048013 | 50 | 18 | + | 2.21 | 7.36E-03 |
| production of molecular mediator of immune response | GO:0002440 | 158 | 12 | - | 0.47 | 7.36E-03 |
| negative regulation of cellular component movement | GO:0051271 | 293 | 69 | + | 1.45 | 7.37E-03 |
| protein localization to plasma membrane | GO:0072659 | 198 | 50 | + | 1.55 | 7.38E-03 |
| regulation of neuron migration | GO:2001222 | 43 | 16 | + | 2.29 | 7.39E-03 |
| cyclic nucleotide catabolic process | GO:0009214 | 14 | 8 | + | 3.51 | 7.51E-03 |
| neuroblast division | GO:0055057 | 14 | 8 | + | 3.51 | 7.51E-03 |
| positive regulation of fibroblast migration | GO:0010763 | 14 | 8 | + | 3.51 | 7.51E-03 |
| male meiotic nuclear division | GO:0007140 | 50 | 1 | - | 0.12 | 7.54E-03 |
| internal peptidyl-lysine acetylation | GO:0018393 | 112 | 7 | - | 0.38 | 7.65E-03 |
| sensory organ morphogenesis | GO:0090596 | 262 | 63 | + | 1.48 | 7.67E-03 |
| pallium development | GO:0021543 | 173 | 45 | + | 1.60 | 7.74E-03 |
| regulation of cardiac muscle tissue growth | GO:0055021 | 58 | 20 | + | 2.12 | 7.80E-03 |
| epithelial cell development | GO:0002064 | 200 | 50 | + | 1.54 | 7.82E-03 |
| positive regulation of cell development | GO:0010720 | 298 | 70 | + | 1.44 | 7.84E-03 |
| rRNA metabolic process | GO:0016072 | 230 | 21 | - | 0.56 | 7.84E-03 |
| calcium ion import | GO:0070509 | 51 | 18 | + | 2.17 | 7.93E-03 |
| endocytosis | GO:0006897 | 509 | 110 | + | 1.33 | 8.15E-03 |
| neuromuscular junction development | GO:0007528 | 38 | 15 | + | 2.42 | 8.18E-03 |
| cardiac muscle cell development | GO:0055013 | 59 | 20 | + | 2.08 | 8.21E-03 |
| nephron development | GO:0072006 | 126 | 35 | + | 1.71 | 8.24E-03 |
| vesicle-mediated transport in synapse | GO:0099003 | 126 | 35 | + | 1.71 | 8.24E-03 |
| regulation of cell-substrate adhesion | GO:0010810 | 219 | 54 | + | 1.51 | 8.24E-03 |
| vascular endothelial growth factor receptor signaling pathway | GO:0048010 | 32 | 13 | + | 2.50 | 8.27E-03 |
| cAMP-mediated signaling | GO:0019933 | 32 | 13 | + | 2.50 | 8.27E-03 |
| cell-cell signaling involved in cardiac conduction | GO:0086019 | 27 | 12 | + | 2.73 | 8.32E-03 |
| regulation of dendrite extension | GO:1903859 | 27 | 12 | + | 2.73 | 8.32E-03 |
| protein localization to postsynaptic membrane | GO:1903539 | 27 | 12 | + | 2.73 | 8.32E-03 |
| negative regulation of axon extension | GO:0030517 | 44 | 16 | + | 2.23 | 8.34E-03 |
| response to organic substance | GO:0010033 | 2688 | 494 | + | 1.13 | 8.44E-03 |
| positive regulation of plasma membrane bounded cell projection assembly | GO:0120034 | 105 | 30 | + | 1.75 | 8.65E-03 |
| neural retina development | GO:0003407 | 68 | 22 | + | 1.99 | 8.66E-03 |
| regulation of protein localization | GO:0032880 | 853 | 173 | + | 1.25 | 8.69E-03 |
| positive regulation of small GTPase mediated signal transduction | GO:0051057 | 77 | 24 | + | 1.91 | 8.82E-03 |
| synaptic vesicle cycle | GO:0099504 | 117 | 33 | + | 1.73 | 8.82E-03 |
| positive regulation of neurogenesis | GO:0050769 | 224 | 55 | + | 1.51 | 8.92E-03 |
| regulation of cell population proliferation | GO:0042127 | 1650 | 314 | + | 1.17 | 8.96E-03 |
| cerebral cortex development | GO:0021987 | 118 | 33 | + | 1.72 | 9.07E-03 |
| positive regulation of receptor internalization | GO:0002092 | 28 | 12 | + | 2.63 | 9.31E-03 |
| focal adhesion assembly | GO:0048041 | 28 | 12 | + | 2.63 | 9.31E-03 |
| protein localization to postsynapse | GO:0062237 | 28 | 12 | + | 2.63 | 9.31E-03 |
| heparan sulfate proteoglycan metabolic process | GO:0030201 | 28 | 12 | + | 2.63 | 9.31E-03 |
| ncRNA processing | GO:0034470 | 388 | 42 | - | 0.66 | 9.36E-03 |
| nitrogen compound transport | GO:0071705 | 1578 | 301 | + | 1.17 | 9.39E-03 |
| B cell receptor signaling pathway | GO:0050853 | 130 | 9 | - | 0.43 | 9.40E-03 |
| negative regulation of developmental process | GO:0051093 | 877 | 177 | + | 1.24 | 9.59E-03 |
| positive regulation of endothelial cell migration | GO:0010595 | 109 | 31 | + | 1.75 | 9.65E-03 |
| regulation of cardiac muscle cell proliferation | GO:0060043 | 40 | 15 | + | 2.30 | 9.66E-03 |
| positive regulation of calcium-mediated signaling | GO:0050850 | 33 | 13 | + | 2.42 | 9.68E-03 |
| response to organonitrogen compound | GO:0010243 | 984 | 196 | + | 1.22 | 9.78E-03 |
| neural precursor cell proliferation | GO:0061351 | 70 | 22 | + | 1.93 | 9.82E-03 |
| positive regulation of cellular protein localization | GO:1903829 | 282 | 66 | + | 1.44 | 9.99E-03 |
| G protein-coupled glutamate receptor signaling pathway | GO:0007216 | 15 | 8 | + | 3.28 | 1.01E-02 |
| postsynaptic modulation of chemical synaptic transmission | GO:0099170 | 15 | 8 | + | 3.28 | 1.01E-02 |
| peptidyl-tyrosine dephosphorylation | GO:0035335 | 100 | 29 | + | 1.78 | 1.02E-02 |
| cilium assembly | GO:0060271 | 302 | 70 | + | 1.42 | 1.02E-02 |
| muscle tissue development | GO:0060537 | 303 | 70 | + | 1.42 | 1.03E-02 |
| tissue morphogenesis | GO:0048729 | 542 | 115 | + | 1.30 | 1.03E-02 |
| regulation of secretion | GO:0051046 | 622 | 130 | + | 1.28 | 1.03E-02 |
| microtubule cytoskeleton organization | GO:0000226 | 521 | 111 | + | 1.31 | 1.05E-02 |
| regulation of transporter activity | GO:0032409 | 287 | 67 | + | 1.43 | 1.06E-02 |
| heart contraction | GO:0060047 | 91 | 27 | + | 1.82 | 1.07E-02 |
| regulation of endothelial cell proliferation | GO:0001936 | 135 | 36 | + | 1.64 | 1.07E-02 |
| epithelial tube morphogenesis | GO:0060562 | 305 | 70 | + | 1.41 | 1.07E-02 |
| bone development | GO:0060348 | 189 | 47 | + | 1.53 | 1.08E-02 |
| cellular response to insulin stimulus | GO:0032869 | 149 | 39 | + | 1.61 | 1.09E-02 |
| synaptic vesicle exocytosis | GO:0016079 | 56 | 19 | + | 2.08 | 1.10E-02 |
| negative regulation of response to stimulus | GO:0048585 | 1559 | 297 | + | 1.17 | 1.10E-02 |
| rRNA processing | GO:0006364 | 219 | 20 | - | 0.56 | 1.10E-02 |
| sulfur compound catabolic process | GO:0044273 | 34 | 0 | - | < 0.01 | 1.10E-02 |
| neuromuscular process | GO:0050905 | 136 | 36 | + | 1.63 | 1.11E-02 |
| negative regulation of neuron projection development | GO:0010977 | 136 | 36 | + | 1.63 | 1.11E-02 |
| muscle contraction | GO:0006936 | 222 | 54 | + | 1.49 | 1.11E-02 |
| semaphorin-plexin signaling pathway involved in axon guidance | GO:1902287 | 12 | 7 | + | 3.58 | 1.13E-02 |
| cell surface receptor signaling pathway involved in cell-cell signaling | GO:1905114 | 331 | 75 | + | 1.39 | 1.14E-02 |
| immune system process | GO:0002376 | 2370 | 336 | - | 0.87 | 1.14E-02 |
| vesicle transport along actin filament | GO:0030050 | 19 | 9 | + | 2.91 | 1.15E-02 |
| negative regulation of axonogenesis | GO:0050771 | 65 | 21 | + | 1.98 | 1.15E-02 |
| positive regulation of endothelial cell proliferation | GO:0001938 | 93 | 27 | + | 1.78 | 1.15E-02 |
| gliogenesis | GO:0042063 | 224 | 54 | + | 1.48 | 1.15E-02 |
| regulation of protein localization to membrane | GO:1905475 | 179 | 45 | + | 1.54 | 1.16E-02 |
| transmembrane receptor protein tyrosine phosphatase signaling pathway | GO:0007185 | 6 | 5 | + | 5.12 | 1.19E-02 |
| regulation of translation at synapse | GO:0140243 | 6 | 5 | + | 5.12 | 1.19E-02 |
| regulation of translation at synapse, modulating synaptic transmission | GO:0099547 | 6 | 5 | + | 5.12 | 1.19E-02 |
| regulation of removal of superoxide radicals | GO:2000121 | 6 | 5 | + | 5.12 | 1.19E-02 |
| activation of store-operated calcium channel activity | GO:0032237 | 6 | 5 | + | 5.12 | 1.19E-02 |
| histone dephosphorylation | GO:0016576 | 6 | 5 | + | 5.12 | 1.19E-02 |
| cAMP catabolic process | GO:0006198 | 9 | 6 | + | 4.09 | 1.21E-02 |
| retrograde trans-synaptic signaling | GO:0098917 | 9 | 6 | + | 4.09 | 1.21E-02 |
| regulation of store-operated calcium channel activity | GO:1901339 | 9 | 6 | + | 4.09 | 1.21E-02 |
| signal release | GO:0023061 | 154 | 40 | + | 1.60 | 1.21E-02 |
| positive regulation of synaptic transmission, glutamatergic | GO:0051968 | 30 | 12 | + | 2.46 | 1.23E-02 |
| negative regulation of developmental growth | GO:0048640 | 106 | 30 | + | 1.74 | 1.24E-02 |
| regulation of protein modification process | GO:0031399 | 1483 | 283 | + | 1.17 | 1.26E-02 |
| cell-substrate junction organization | GO:0150115 | 37 | 14 | + | 2.32 | 1.29E-02 |
| branching morphogenesis of an epithelial tube | GO:0048754 | 131 | 35 | + | 1.64 | 1.29E-02 |
| negative regulation of cell motility | GO:2000146 | 285 | 66 | + | 1.42 | 1.29E-02 |
| inorganic ion import across plasma membrane | GO:0099587 | 86 | 25 | + | 1.79 | 1.32E-02 |
| inorganic cation import across plasma membrane | GO:0098659 | 86 | 25 | + | 1.79 | 1.32E-02 |
| regulation of receptor-mediated endocytosis | GO:0048259 | 108 | 30 | + | 1.71 | 1.32E-02 |
| actomyosin structure organization | GO:0031032 | 108 | 30 | + | 1.71 | 1.32E-02 |
| adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains | GO:0002460 | 245 | 24 | - | 0.60 | 1.33E-02 |
| macromolecule modification | GO:0043412 | 2825 | 514 | + | 1.12 | 1.34E-02 |
| muscle cell differentiation | GO:0042692 | 252 | 59 | + | 1.44 | 1.35E-02 |
| positive regulation of intrinsic apoptotic signaling pathway | GO:2001244 | 57 | 2 | - | 0.22 | 1.35E-02 |
| regulation of action potential | GO:0098900 | 51 | 17 | + | 2.05 | 1.36E-02 |
| regulation of postsynaptic membrane potential | GO:0060078 | 98 | 28 | + | 1.75 | 1.36E-02 |
| morphogenesis of a branching epithelium | GO:0061138 | 160 | 41 | + | 1.57 | 1.37E-02 |
| histone acetylation | GO:0016573 | 106 | 7 | - | 0.41 | 1.38E-02 |
| keratinization | GO:0031424 | 58 | 2 | - | 0.21 | 1.38E-02 |
| regulation of AMPA receptor activity | GO:2000311 | 26 | 11 | + | 2.60 | 1.40E-02 |
| nucleus localization | GO:0051647 | 26 | 11 | + | 2.60 | 1.40E-02 |
| retina layer formation | GO:0010842 | 26 | 11 | + | 2.60 | 1.40E-02 |
| regulation of synapse assembly | GO:0051963 | 99 | 28 | + | 1.74 | 1.40E-02 |
| import into cell | GO:0098657 | 175 | 44 | + | 1.54 | 1.40E-02 |
| mononuclear cell migration | GO:0071674 | 107 | 7 | - | 0.40 | 1.40E-02 |
| second-messenger-mediated signaling | GO:0019932 | 222 | 53 | + | 1.47 | 1.42E-02 |
| positive regulation of growth | GO:0045927 | 257 | 60 | + | 1.43 | 1.42E-02 |
| adherens junction organization | GO:0034332 | 45 | 16 | + | 2.18 | 1.43E-02 |
| neural crest cell differentiation | GO:0014033 | 89 | 26 | + | 1.79 | 1.43E-02 |
| postsynapse organization | GO:0099173 | 89 | 26 | + | 1.79 | 1.43E-02 |
| organic anion transport | GO:0015711 | 314 | 71 | + | 1.39 | 1.43E-02 |
| regulation of dendritic spine development | GO:0060998 | 60 | 19 | + | 1.95 | 1.44E-02 |
| actin polymerization or depolymerization | GO:0008154 | 60 | 19 | + | 1.95 | 1.44E-02 |
| regulation of kinase activity | GO:0043549 | 752 | 152 | + | 1.24 | 1.45E-02 |
| nuclear migration | GO:0007097 | 20 | 9 | + | 2.76 | 1.46E-02 |
| negative regulation of cellular component organization | GO:0051129 | 722 | 147 | + | 1.25 | 1.46E-02 |
| chemical homeostasis | GO:0048878 | 1113 | 217 | + | 1.20 | 1.46E-02 |
| epithelium development | GO:0060429 | 962 | 190 | + | 1.21 | 1.47E-02 |
| regulation of heart contraction | GO:0008016 | 193 | 47 | + | 1.50 | 1.50E-02 |
| vasodilation | GO:0042311 | 46 | 16 | + | 2.14 | 1.51E-02 |
| transmission of nerve impulse | GO:0019226 | 54 | 18 | + | 2.05 | 1.55E-02 |
| detection of mechanical stimulus | GO:0050982 | 54 | 18 | + | 2.05 | 1.55E-02 |
| positive regulation of lipid kinase activity | GO:0090218 | 39 | 14 | + | 2.20 | 1.56E-02 |
| cellular response to amyloid-beta | GO:1904646 | 39 | 14 | + | 2.20 | 1.56E-02 |
| establishment or maintenance of cell polarity | GO:0007163 | 197 | 48 | + | 1.50 | 1.57E-02 |
| liver development | GO:0001889 | 139 | 36 | + | 1.59 | 1.58E-02 |
| camera-type eye photoreceptor cell differentiation | GO:0060219 | 27 | 11 | + | 2.50 | 1.59E-02 |
| ionotropic glutamate receptor signaling pathway | GO:0035235 | 27 | 11 | + | 2.50 | 1.59E-02 |
| cytoplasmic translation | GO:0002181 | 122 | 9 | - | 0.45 | 1.59E-02 |
| developmental growth involved in morphogenesis | GO:0060560 | 115 | 31 | + | 1.66 | 1.61E-02 |
| heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules | GO:0007157 | 47 | 16 | + | 2.09 | 1.62E-02 |
| positive regulation of organ growth | GO:0046622 | 47 | 16 | + | 2.09 | 1.62E-02 |
| positive regulation of receptor-mediated endocytosis | GO:0048260 | 55 | 18 | + | 2.01 | 1.63E-02 |
| positive regulation of cell-substrate adhesion | GO:0010811 | 128 | 34 | + | 1.63 | 1.63E-02 |
| regulation of dendrite development | GO:0050773 | 104 | 29 | + | 1.71 | 1.64E-02 |
| positive regulation of endocytosis | GO:0045807 | 104 | 29 | + | 1.71 | 1.64E-02 |
| G protein-coupled receptor signaling pathway | GO:0007186 | 1216 | 163 | - | 0.82 | 1.64E-02 |
| neuron projection extension | GO:1990138 | 64 | 20 | + | 1.92 | 1.67E-02 |
| cellular response to peptide hormone stimulus | GO:0071375 | 234 | 55 | + | 1.44 | 1.67E-02 |
| radial glia guided migration of Purkinje cell | GO:0021942 | 4 | 4 | + | 6.14 | 1.68E-02 |
| positive regulation of cytoskeleton organization | GO:0051495 | 218 | 52 | + | 1.47 | 1.68E-02 |
| snRNA 3'-end processing | GO:0034472 | 31 | 0 | - | < 0.01 | 1.69E-02 |
| renal system development | GO:0072001 | 291 | 66 | + | 1.39 | 1.70E-02 |
| positive regulation of cell cycle checkpoint | GO:1901978 | 10 | 6 | + | 3.69 | 1.71E-02 |
| hindbrain radial glia guided cell migration | GO:0021932 | 10 | 6 | + | 3.69 | 1.71E-02 |
| negative regulation of bone resorption | GO:0045779 | 17 | 8 | + | 2.89 | 1.73E-02 |
| peptidyl-tyrosine autophosphorylation | GO:0038083 | 17 | 8 | + | 2.89 | 1.73E-02 |
| calcium ion import across plasma membrane | GO:0098703 | 17 | 8 | + | 2.89 | 1.73E-02 |
| membrane depolarization during cardiac muscle cell action potential | GO:0086012 | 17 | 8 | + | 2.89 | 1.73E-02 |
| substrate adhesion-dependent cell spreading | GO:0034446 | 56 | 18 | + | 1.97 | 1.73E-02 |
| positive regulation of reactive oxygen species metabolic process | GO:2000379 | 74 | 22 | + | 1.83 | 1.74E-02 |
| long-term synaptic potentiation | GO:0060291 | 48 | 16 | + | 2.05 | 1.76E-02 |
| epidermal growth factor receptor signaling pathway | GO:0007173 | 48 | 16 | + | 2.05 | 1.76E-02 |
| regulation of filopodium assembly | GO:0051489 | 48 | 16 | + | 2.05 | 1.76E-02 |
| regulation of neurotransmitter receptor activity | GO:0099601 | 65 | 20 | + | 1.89 | 1.76E-02 |
| protein transport | GO:0015031 | 1183 | 228 | + | 1.18 | 1.76E-02 |
| stem cell development | GO:0048864 | 84 | 24 | + | 1.75 | 1.78E-02 |
| regulation of organelle assembly | GO:1902115 | 189 | 46 | + | 1.49 | 1.78E-02 |
| defense response | GO:0006952 | 1387 | 189 | - | 0.84 | 1.79E-02 |
| mitotic nuclear membrane disassembly | GO:0007077 | 7 | 5 | + | 4.39 | 1.80E-02 |
| positive regulation of store-operated calcium channel activity | GO:1901341 | 7 | 5 | + | 4.39 | 1.80E-02 |
| positive regulation of protein localization to centrosome | GO:1904781 | 7 | 5 | + | 4.39 | 1.80E-02 |
| axon choice point recognition | GO:0016198 | 7 | 5 | + | 4.39 | 1.80E-02 |
| neuroblast proliferation | GO:0007405 | 28 | 11 | + | 2.41 | 1.82E-02 |
| basement membrane organization | GO:0071711 | 28 | 11 | + | 2.41 | 1.82E-02 |
| positive regulation of excitatory postsynaptic potential | GO:2000463 | 28 | 11 | + | 2.41 | 1.82E-02 |
| regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum | GO:0010880 | 28 | 11 | + | 2.41 | 1.82E-02 |
| positive regulation of protein kinase activity | GO:0045860 | 387 | 84 | + | 1.33 | 1.87E-02 |
| positive regulation of B cell activation | GO:0050871 | 171 | 15 | - | 0.54 | 1.90E-02 |
| cyclic purine nucleotide metabolic process | GO:0052652 | 23 | 10 | + | 2.67 | 1.91E-02 |
| cyclic nucleotide biosynthetic process | GO:0009190 | 23 | 10 | + | 2.67 | 1.91E-02 |
| cellular response to calcium ion | GO:0071277 | 87 | 25 | + | 1.77 | 1.91E-02 |
| regulation of endocytosis | GO:0030100 | 210 | 50 | + | 1.46 | 1.91E-02 |
| negative regulation of signaling | GO:0023057 | 1305 | 249 | + | 1.17 | 1.91E-02 |
| ribonucleoprotein complex assembly | GO:0022618 | 186 | 17 | - | 0.56 | 1.91E-02 |
| response to amyloid-beta | GO:1904645 | 49 | 16 | + | 2.01 | 1.92E-02 |
| histone H4 acetylation | GO:0043967 | 54 | 2 | - | 0.23 | 1.95E-02 |
| regulation of receptor internalization | GO:0002090 | 58 | 18 | + | 1.91 | 2.00E-02 |
| regulation of reactive oxygen species metabolic process | GO:2000377 | 151 | 38 | + | 1.55 | 2.01E-02 |
| cellular protein localization | GO:0034613 | 1376 | 261 | + | 1.17 | 2.01E-02 |
| detection of calcium ion | GO:0005513 | 14 | 7 | + | 3.07 | 2.02E-02 |
| atrial cardiac muscle cell to AV node cell signaling | GO:0086026 | 14 | 7 | + | 3.07 | 2.02E-02 |
| atrial cardiac muscle cell action potential | GO:0086014 | 14 | 7 | + | 3.07 | 2.02E-02 |
| aminoglycan metabolic process | GO:0006022 | 123 | 32 | + | 1.60 | 2.02E-02 |
| glycosaminoglycan metabolic process | GO:0030203 | 112 | 30 | + | 1.65 | 2.03E-02 |
| leukocyte chemotaxis | GO:0030595 | 145 | 12 | - | 0.51 | 2.04E-02 |
| modulation of excitatory postsynaptic potential | GO:0098815 | 43 | 15 | + | 2.14 | 2.05E-02 |
| cell communication involved in cardiac conduction | GO:0086065 | 43 | 15 | + | 2.14 | 2.05E-02 |
| cell-substrate junction assembly | GO:0007044 | 36 | 13 | + | 2.22 | 2.06E-02 |
| axon extension | GO:0048675 | 36 | 13 | + | 2.22 | 2.06E-02 |
| neuron maturation | GO:0042551 | 36 | 13 | + | 2.22 | 2.06E-02 |
| regulation of calcium ion transport | GO:0051924 | 252 | 58 | + | 1.41 | 2.07E-02 |
| neural crest cell development | GO:0014032 | 79 | 23 | + | 1.79 | 2.08E-02 |
| regulation of release of sequestered calcium ion into cytosol | GO:0051279 | 79 | 23 | + | 1.79 | 2.08E-02 |
| regulation of intrinsic apoptotic signaling pathway | GO:2001242 | 160 | 14 | - | 0.54 | 2.09E-02 |
| adrenergic receptor signaling pathway | GO:0071875 | 24 | 10 | + | 2.56 | 2.11E-02 |
| neuromuscular synaptic transmission | GO:0007274 | 24 | 10 | + | 2.56 | 2.11E-02 |
| synaptic membrane adhesion | GO:0099560 | 24 | 10 | + | 2.56 | 2.11E-02 |
| outflow tract septum morphogenesis | GO:0003148 | 24 | 10 | + | 2.56 | 2.11E-02 |
| ventricular system development | GO:0021591 | 29 | 11 | + | 2.33 | 2.11E-02 |
| response to other organism | GO:0051707 | 1372 | 188 | - | 0.84 | 2.13E-02 |
| response to external biotic stimulus | GO:0043207 | 1373 | 188 | - | 0.84 | 2.13E-02 |
| ribonucleoprotein complex subunit organization | GO:0071826 | 193 | 18 | - | 0.57 | 2.14E-02 |
| regulation of protein localization to cell periphery | GO:1904375 | 127 | 33 | + | 1.60 | 2.15E-02 |
| regulation of secretion by cell | GO:1903530 | 564 | 116 | + | 1.26 | 2.15E-02 |
| mucopolysaccharide metabolic process | GO:1903510 | 80 | 23 | + | 1.77 | 2.16E-02 |
| positive regulation of cellular protein metabolic process | GO:0032270 | 1366 | 259 | + | 1.16 | 2.17E-02 |
| glomerulus development | GO:0032835 | 52 | 17 | + | 2.01 | 2.18E-02 |
| regulation of calcium ion transmembrane transport | GO:1903169 | 156 | 39 | + | 1.54 | 2.19E-02 |
| regulation of endothelial cell migration | GO:0010594 | 171 | 42 | + | 1.51 | 2.19E-02 |
| regulation of epithelial cell proliferation | GO:0050678 | 338 | 74 | + | 1.34 | 2.19E-02 |
| calcium ion import into cytosol | GO:1902656 | 18 | 8 | + | 2.73 | 2.20E-02 |
| negative regulation of amyloid-beta formation | GO:1902430 | 18 | 8 | + | 2.73 | 2.20E-02 |
| parasympathetic nervous system development | GO:0048486 | 18 | 8 | + | 2.73 | 2.20E-02 |
| protein trimerization | GO:0070206 | 18 | 8 | + | 2.73 | 2.20E-02 |
| chondroitin sulfate biosynthetic process | GO:0030206 | 18 | 8 | + | 2.73 | 2.20E-02 |
| actin filament bundle organization | GO:0061572 | 61 | 19 | + | 1.91 | 2.20E-02 |
| secretion | GO:0046903 | 486 | 102 | + | 1.29 | 2.20E-02 |
| hepaticobiliary system development | GO:0061008 | 142 | 36 | + | 1.56 | 2.21E-02 |
| regulation of actin filament organization | GO:0110053 | 278 | 63 | + | 1.39 | 2.23E-02 |
| regulation of cell-substrate junction organization | GO:0150116 | 71 | 21 | + | 1.82 | 2.25E-02 |
| axo-dendritic transport | GO:0008088 | 71 | 21 | + | 1.82 | 2.25E-02 |
| regulation of peptidyl-tyrosine phosphorylation | GO:0050730 | 259 | 59 | + | 1.40 | 2.25E-02 |
| positive regulation of lamellipodium organization | GO:1902745 | 37 | 13 | + | 2.16 | 2.26E-02 |
| protein autophosphorylation | GO:0046777 | 188 | 45 | + | 1.47 | 2.26E-02 |
| cellular amide metabolic process | GO:0043603 | 780 | 100 | - | 0.79 | 2.27E-02 |
| neural crest cell migration | GO:0001755 | 53 | 17 | + | 1.97 | 2.28E-02 |
| regulation of bone remodeling | GO:0046850 | 53 | 17 | + | 1.97 | 2.28E-02 |
| regulation of neurotransmitter transport | GO:0051588 | 104 | 28 | + | 1.65 | 2.28E-02 |
| xenobiotic metabolic process | GO:0006805 | 110 | 8 | - | 0.45 | 2.28E-02 |
| regulation of cytosolic calcium ion concentration | GO:0051480 | 322 | 71 | + | 1.35 | 2.29E-02 |
| regulation of long-term synaptic potentiation | GO:1900271 | 45 | 15 | + | 2.05 | 2.31E-02 |
| negative regulation of cell communication | GO:0010648 | 1301 | 247 | + | 1.17 | 2.31E-02 |
| facial nerve morphogenesis | GO:0021610 | 11 | 6 | + | 3.35 | 2.33E-02 |
| facial nerve development | GO:0021561 | 11 | 6 | + | 3.35 | 2.33E-02 |
| GDP metabolic process | GO:0046710 | 11 | 6 | + | 3.35 | 2.33E-02 |
| positive regulation of nucleic acid-templated transcription | GO:1903508 | 1611 | 301 | + | 1.15 | 2.34E-02 |
| positive regulation of transcription, DNA-templated | GO:0045893 | 1611 | 301 | + | 1.15 | 2.34E-02 |
| glial cell differentiation | GO:0010001 | 174 | 42 | + | 1.48 | 2.35E-02 |
| regulation of actin filament polymerization | GO:0030833 | 174 | 42 | + | 1.48 | 2.35E-02 |
| lysosome organization | GO:0007040 | 72 | 21 | + | 1.79 | 2.36E-02 |
| lytic vacuole organization | GO:0080171 | 72 | 21 | + | 1.79 | 2.36E-02 |
| neurotrophin signaling pathway | GO:0038179 | 25 | 10 | + | 2.46 | 2.38E-02 |
| cell proliferation in forebrain | GO:0021846 | 25 | 10 | + | 2.46 | 2.38E-02 |
| cyclic-nucleotide-mediated signaling | GO:0019935 | 54 | 17 | + | 1.93 | 2.41E-02 |
| regulation of JNK cascade | GO:0046328 | 133 | 34 | + | 1.57 | 2.44E-02 |
| regulation of muscle contraction | GO:0006937 | 162 | 40 | + | 1.52 | 2.44E-02 |
| cellular calcium ion homeostasis | GO:0006874 | 425 | 90 | + | 1.30 | 2.45E-02 |
| regeneration | GO:0031099 | 163 | 40 | + | 1.51 | 2.48E-02 |
| ion homeostasis | GO:0050801 | 758 | 151 | + | 1.22 | 2.48E-02 |
| Fc receptor signaling pathway | GO:0038093 | 46 | 15 | + | 2.00 | 2.49E-02 |
| acidic amino acid transport | GO:0015800 | 38 | 13 | + | 2.10 | 2.51E-02 |
| cardiac muscle cell action potential involved in contraction | GO:0086002 | 38 | 13 | + | 2.10 | 2.51E-02 |
| microtubule-based movement | GO:0007018 | 356 | 77 | + | 1.33 | 2.52E-02 |
| regulation of muscle system process | GO:0090257 | 231 | 53 | + | 1.41 | 2.54E-02 |
| positive regulation of nucleobase-containing compound metabolic process | GO:0045935 | 1902 | 351 | + | 1.13 | 2.55E-02 |
| positive regulation of RNA biosynthetic process | GO:1902680 | 1613 | 301 | + | 1.15 | 2.56E-02 |
| cardiocyte differentiation | GO:0035051 | 109 | 29 | + | 1.63 | 2.57E-02 |
| cellular response to cAMP | GO:0071320 | 55 | 17 | + | 1.90 | 2.58E-02 |
| neuron projection extension involved in neuron projection guidance | GO:1902284 | 8 | 5 | + | 3.84 | 2.60E-02 |
| axon extension involved in axon guidance | GO:0048846 | 8 | 5 | + | 3.84 | 2.60E-02 |
| regulation of arachidonic acid secretion | GO:0090237 | 8 | 5 | + | 3.84 | 2.60E-02 |
| regulation of oligodendrocyte progenitor proliferation | GO:0070445 | 8 | 5 | + | 3.84 | 2.60E-02 |
| positive regulation of cell growth involved in cardiac muscle cell development | GO:0061051 | 8 | 5 | + | 3.84 | 2.60E-02 |
| regulation of axon extension involved in axon guidance | GO:0048841 | 32 | 12 | + | 2.30 | 2.60E-02 |
| muscle hypertrophy | GO:0014896 | 32 | 12 | + | 2.30 | 2.60E-02 |
| regulation of protein kinase B signaling | GO:0051896 | 165 | 40 | + | 1.49 | 2.60E-02 |
| regulation of supramolecular fiber organization | GO:1902903 | 384 | 82 | + | 1.31 | 2.61E-02 |
| positive regulation of endothelial cell chemotaxis | GO:2001028 | 15 | 7 | + | 2.87 | 2.62E-02 |
| apical protein localization | GO:0045176 | 15 | 7 | + | 2.87 | 2.62E-02 |
| calcium ion-regulated exocytosis of neurotransmitter | GO:0048791 | 15 | 7 | + | 2.87 | 2.62E-02 |
| neuron projection arborization | GO:0140058 | 15 | 7 | + | 2.87 | 2.62E-02 |
| protein homotrimerization | GO:0070207 | 15 | 7 | + | 2.87 | 2.62E-02 |
| atrial cardiac muscle cell to AV node cell communication | GO:0086066 | 15 | 7 | + | 2.87 | 2.62E-02 |
| carbohydrate derivative metabolic process | GO:1901135 | 922 | 180 | + | 1.20 | 2.62E-02 |
| transport across blood-brain barrier | GO:0150104 | 86 | 24 | + | 1.71 | 2.63E-02 |
| cellular glucose homeostasis | GO:0001678 | 97 | 26 | + | 1.65 | 2.66E-02 |
| camera-type eye development | GO:0043010 | 318 | 70 | + | 1.35 | 2.66E-02 |
| positive regulation of transcription by RNA polymerase II | GO:0045944 | 1185 | 226 | + | 1.17 | 2.67E-02 |
| interkinetic nuclear migration | GO:0022027 | 5 | 4 | + | 4.91 | 2.69E-02 |
| presynaptic dense core vesicle exocytosis | GO:0099525 | 5 | 4 | + | 4.91 | 2.69E-02 |
| peptidyl-lysine oxidation | GO:0018057 | 5 | 4 | + | 4.91 | 2.69E-02 |
| positive regulation of the force of heart contraction | GO:0098735 | 5 | 4 | + | 4.91 | 2.69E-02 |
| neuronal dense core vesicle exocytosis | GO:0099011 | 5 | 4 | + | 4.91 | 2.69E-02 |
| membrane depolarization during SA node cell action potential | GO:0086046 | 5 | 4 | + | 4.91 | 2.69E-02 |
| axon midline choice point recognition | GO:0016199 | 5 | 4 | + | 4.91 | 2.69E-02 |
| neuron-glial cell signaling | GO:0150099 | 5 | 4 | + | 4.91 | 2.69E-02 |
| positive regulation of nitric oxide mediated signal transduction | GO:0010750 | 5 | 4 | + | 4.91 | 2.69E-02 |
| forebrain neuroblast division | GO:0021873 | 5 | 4 | + | 4.91 | 2.69E-02 |
| positive regulation of organelle organization | GO:0010638 | 583 | 119 | + | 1.25 | 2.70E-02 |
| telencephalon glial cell migration | GO:0022030 | 26 | 10 | + | 2.36 | 2.71E-02 |
| neurotransmitter receptor transport | GO:0099637 | 26 | 10 | + | 2.36 | 2.71E-02 |
| negative regulation of axon extension involved in axon guidance | GO:0048843 | 26 | 10 | + | 2.36 | 2.71E-02 |
| cerebral cortex radial glia-guided migration | GO:0021801 | 26 | 10 | + | 2.36 | 2.71E-02 |
| regulation of tissue remodeling | GO:0034103 | 76 | 22 | + | 1.78 | 2.71E-02 |
| regulation of protein polymerization | GO:0032271 | 237 | 54 | + | 1.40 | 2.71E-02 |
| regulation of myelination | GO:0031641 | 47 | 15 | + | 1.96 | 2.72E-02 |
| ribonucleotide catabolic process | GO:0009261 | 47 | 15 | + | 1.96 | 2.72E-02 |
| cellular macromolecule localization | GO:0070727 | 1386 | 261 | + | 1.16 | 2.72E-02 |
| vascular transport | GO:0010232 | 87 | 24 | + | 1.69 | 2.73E-02 |
| small molecule metabolic process | GO:0044281 | 1547 | 289 | + | 1.15 | 2.74E-02 |
| centrosome localization | GO:0051642 | 33 | 12 | + | 2.23 | 2.77E-02 |
| regulation of chemotaxis | GO:0050920 | 221 | 51 | + | 1.42 | 2.77E-02 |
| regulation of glucose import | GO:0046324 | 56 | 17 | + | 1.86 | 2.78E-02 |
| positive regulation of protein tyrosine kinase activity | GO:0061098 | 56 | 17 | + | 1.86 | 2.78E-02 |
| lymphocyte chemotaxis | GO:0048247 | 50 | 2 | - | 0.25 | 2.78E-02 |
| microtubule-based transport | GO:0099111 | 186 | 44 | + | 1.45 | 2.80E-02 |
| import across plasma membrane | GO:0098739 | 140 | 35 | + | 1.54 | 2.81E-02 |
| kidney development | GO:0001822 | 282 | 63 | + | 1.37 | 2.82E-02 |
| regulation of Wnt signaling pathway | GO:0030111 | 325 | 71 | + | 1.34 | 2.82E-02 |
| positive regulation of mitotic cell cycle | GO:0045931 | 112 | 29 | + | 1.59 | 2.84E-02 |
| proteolysis | GO:0006508 | 1216 | 231 | + | 1.17 | 2.86E-02 |
| positive regulation of cytosolic calcium ion concentration | GO:0007204 | 284 | 63 | + | 1.36 | 2.89E-02 |
| regulation of actin polymerization or depolymerization | GO:0008064 | 190 | 45 | + | 1.45 | 2.92E-02 |
| regulation of actin filament length | GO:0030832 | 191 | 45 | + | 1.45 | 2.97E-02 |
| anion transmembrane transport | GO:0098656 | 227 | 52 | + | 1.41 | 2.97E-02 |
| cellular response to hormone stimulus | GO:0032870 | 484 | 100 | + | 1.27 | 2.98E-02 |
| microtubule organizing center localization | GO:0061842 | 34 | 12 | + | 2.17 | 2.99E-02 |
| mRNA splicing, via spliceosome | GO:0000398 | 234 | 24 | - | 0.63 | 2.99E-02 |
| RNA splicing, via transesterification reactions with bulged adenosine as nucleophile | GO:0000377 | 234 | 24 | - | 0.63 | 2.99E-02 |
| cellular ion homeostasis | GO:0006873 | 638 | 128 | + | 1.23 | 3.00E-02 |
| regulation of protein-containing complex assembly | GO:0043254 | 433 | 91 | + | 1.29 | 3.02E-02 |
| male gamete generation | GO:0048232 | 585 | 73 | - | 0.77 | 3.02E-02 |
| positive regulation of cell-matrix adhesion | GO:0001954 | 59 | 18 | + | 1.87 | 3.03E-02 |
| positive regulation of epithelial cell proliferation | GO:0050679 | 192 | 45 | + | 1.44 | 3.03E-02 |
| positive regulation of angiogenesis | GO:0045766 | 160 | 39 | + | 1.50 | 3.04E-02 |
| positive regulation of vasculature development | GO:1904018 | 160 | 39 | + | 1.50 | 3.04E-02 |
| neuromuscular process controlling balance | GO:0050885 | 50 | 16 | + | 1.97 | 3.05E-02 |
| calcium-dependent cell-cell adhesion via plasma membrane cell adhesion molecules | GO:0016339 | 42 | 14 | + | 2.05 | 3.08E-02 |
| cardiac muscle cell contraction | GO:0086003 | 42 | 14 | + | 2.05 | 3.08E-02 |
| positive regulation of protein metabolic process | GO:0051247 | 1455 | 272 | + | 1.15 | 3.08E-02 |
| regulation of B cell activation | GO:0050864 | 216 | 22 | - | 0.63 | 3.09E-02 |
| lateral ventricle development | GO:0021670 | 12 | 6 | + | 3.07 | 3.10E-02 |
| cranial nerve structural organization | GO:0021604 | 12 | 6 | + | 3.07 | 3.10E-02 |
| collagen-activated tyrosine kinase receptor signaling pathway | GO:0038063 | 12 | 6 | + | 3.07 | 3.10E-02 |
| protein oxidation | GO:0018158 | 12 | 6 | + | 3.07 | 3.10E-02 |
| regulation of dendritic spine maintenance | GO:1902950 | 12 | 6 | + | 3.07 | 3.10E-02 |
| response to nitrogen compound | GO:1901698 | 1071 | 205 | + | 1.18 | 3.10E-02 |
| startle response | GO:0001964 | 27 | 10 | + | 2.27 | 3.11E-02 |
| vesicle-mediated transport to the plasma membrane | GO:0098876 | 117 | 30 | + | 1.57 | 3.12E-02 |
| insulin receptor signaling pathway | GO:0008286 | 60 | 18 | + | 1.84 | 3.16E-02 |
| cellular cation homeostasis | GO:0030003 | 621 | 125 | + | 1.24 | 3.19E-02 |
| outer dynein arm assembly | GO:0036158 | 22 | 9 | + | 2.51 | 3.20E-02 |
| regulation of protein kinase A signaling | GO:0010738 | 22 | 9 | + | 2.51 | 3.20E-02 |
| positive regulation of protein localization to cell periphery | GO:1904377 | 70 | 20 | + | 1.75 | 3.20E-02 |
| retina development in camera-type eye | GO:0060041 | 147 | 36 | + | 1.50 | 3.20E-02 |
| RNA splicing, via transesterification reactions | GO:0000375 | 238 | 25 | - | 0.65 | 3.21E-02 |
| phospholipid transport | GO:0015914 | 93 | 25 | + | 1.65 | 3.22E-02 |
| regulation of calcineurin-NFAT signaling cascade | GO:0070884 | 35 | 12 | + | 2.11 | 3.28E-02 |
| chondroitin sulfate proteoglycan metabolic process | GO:0050654 | 35 | 12 | + | 2.11 | 3.28E-02 |
| adult behavior | GO:0030534 | 133 | 33 | + | 1.52 | 3.28E-02 |
| positive regulation of translation | GO:0045727 | 137 | 12 | - | 0.54 | 3.30E-02 |
| nuclear division | GO:0000280 | 304 | 34 | - | 0.69 | 3.31E-02 |
| preganglionic parasympathetic fiber development | GO:0021783 | 16 | 7 | + | 2.69 | 3.32E-02 |
| cell migration in hindbrain | GO:0021535 | 16 | 7 | + | 2.69 | 3.32E-02 |
| cellular response to ethanol | GO:0071361 | 16 | 7 | + | 2.69 | 3.32E-02 |
| cardiac myofibril assembly | GO:0055003 | 16 | 7 | + | 2.69 | 3.32E-02 |
| photoreceptor cell differentiation | GO:0046530 | 61 | 18 | + | 1.81 | 3.32E-02 |
| positive regulation of cell growth | GO:0030307 | 166 | 40 | + | 1.48 | 3.34E-02 |
| heart morphogenesis | GO:0003007 | 238 | 54 | + | 1.39 | 3.34E-02 |
| regulation of lamellipodium organization | GO:1902743 | 52 | 16 | + | 1.89 | 3.36E-02 |
| exocytosis | GO:0006887 | 219 | 50 | + | 1.40 | 3.37E-02 |
| negative regulation of signal transduction | GO:0009968 | 1204 | 228 | + | 1.16 | 3.39E-02 |
| cell-cell signaling by wnt | GO:0198738 | 260 | 58 | + | 1.37 | 3.40E-02 |
| Wnt signaling pathway | GO:0016055 | 260 | 58 | + | 1.37 | 3.40E-02 |
| central nervous system neuron differentiation | GO:0021953 | 184 | 43 | + | 1.44 | 3.45E-02 |
| negative regulation of cell differentiation | GO:0045596 | 641 | 128 | + | 1.23 | 3.45E-02 |
| mitochondrial transport | GO:0006839 | 207 | 21 | - | 0.62 | 3.47E-02 |
| mesenchymal cell development | GO:0014031 | 84 | 23 | + | 1.68 | 3.48E-02 |
| cellular response to organic cyclic compound | GO:0071407 | 515 | 105 | + | 1.25 | 3.48E-02 |
| protein folding | GO:0006457 | 209 | 21 | - | 0.62 | 3.50E-02 |
| forebrain generation of neurons | GO:0021872 | 62 | 18 | + | 1.78 | 3.51E-02 |
| cellular divalent inorganic cation homeostasis | GO:0072503 | 460 | 95 | + | 1.27 | 3.53E-02 |
| cell-cell junction organization | GO:0045216 | 169 | 40 | + | 1.45 | 3.54E-02 |
| mesenchyme development | GO:0060485 | 224 | 51 | + | 1.40 | 3.54E-02 |
| blood vessel diameter maintenance | GO:0097746 | 138 | 34 | + | 1.51 | 3.55E-02 |
| regulation of tube diameter | GO:0035296 | 138 | 34 | + | 1.51 | 3.55E-02 |
| innervation | GO:0060384 | 23 | 9 | + | 2.40 | 3.57E-02 |
| chondroitin sulfate proteoglycan biosynthetic process | GO:0050650 | 23 | 9 | + | 2.40 | 3.57E-02 |
| aorta development | GO:0035904 | 53 | 16 | + | 1.85 | 3.58E-02 |
| regulation of vascular associated smooth muscle contraction | GO:0003056 | 9 | 5 | + | 3.41 | 3.59E-02 |
| facial nerve structural organization | GO:0021612 | 9 | 5 | + | 3.41 | 3.59E-02 |
| adenylate cyclase-inhibiting G protein-coupled glutamate receptor signaling pathway | GO:0007196 | 9 | 5 | + | 3.41 | 3.59E-02 |
| excitatory chemical synaptic transmission | GO:0098976 | 9 | 5 | + | 3.41 | 3.59E-02 |
| negative regulation of mitochondrial fusion | GO:0010637 | 9 | 5 | + | 3.41 | 3.59E-02 |
| physiological cardiac muscle hypertrophy | GO:0003301 | 9 | 5 | + | 3.41 | 3.59E-02 |
| physiological muscle hypertrophy | GO:0003298 | 9 | 5 | + | 3.41 | 3.59E-02 |
| cell growth involved in cardiac muscle cell development | GO:0061049 | 9 | 5 | + | 3.41 | 3.59E-02 |
| glycoprotein metabolic process | GO:0009100 | 334 | 72 | + | 1.32 | 3.61E-02 |
| morphogenesis of an epithelium | GO:0002009 | 437 | 91 | + | 1.28 | 3.61E-02 |
| regulation of calcineurin-mediated signaling | GO:0106056 | 36 | 12 | + | 2.05 | 3.62E-02 |
| regulation of fibroblast migration | GO:0010762 | 36 | 12 | + | 2.05 | 3.62E-02 |
| calcium ion transport into cytosol | GO:0060402 | 74 | 21 | + | 1.74 | 3.62E-02 |
| regulation of cardiac muscle contraction | GO:0055117 | 74 | 21 | + | 1.74 | 3.62E-02 |
| calcium ion homeostasis | GO:0055074 | 438 | 91 | + | 1.28 | 3.63E-02 |
| regulation of tube size | GO:0035150 | 139 | 34 | + | 1.50 | 3.64E-02 |
| regulation of stress-activated protein kinase signaling cascade | GO:0070302 | 190 | 44 | + | 1.42 | 3.72E-02 |
| gland morphogenesis | GO:0022612 | 99 | 26 | + | 1.61 | 3.74E-02 |
| response to biotic stimulus | GO:0009607 | 1418 | 198 | - | 0.86 | 3.76E-02 |
| positive regulation of protein-containing complex assembly | GO:0031334 | 230 | 52 | + | 1.39 | 3.78E-02 |
| positive regulation of secretion | GO:0051047 | 316 | 68 | + | 1.32 | 3.79E-02 |
| regulation of response to reactive oxygen species | GO:1901031 | 30 | 11 | + | 2.25 | 3.82E-02 |
| positive regulation of peptidyl-threonine phosphorylation | GO:0010800 | 30 | 11 | + | 2.25 | 3.82E-02 |
| chondroitin sulfate metabolic process | GO:0030204 | 30 | 11 | + | 2.25 | 3.82E-02 |
| striated muscle hypertrophy | GO:0014897 | 30 | 11 | + | 2.25 | 3.82E-02 |
| regulation of cellular protein localization | GO:1903827 | 538 | 109 | + | 1.24 | 3.85E-02 |
| regulation of heart rate | GO:0002027 | 100 | 26 | + | 1.60 | 3.86E-02 |
| skeletal system development | GO:0001501 | 478 | 98 | + | 1.26 | 3.86E-02 |
| positive regulation of cation channel activity | GO:2001259 | 76 | 21 | + | 1.70 | 3.87E-02 |
| inorganic ion homeostasis | GO:0098771 | 709 | 140 | + | 1.21 | 3.88E-02 |
| myeloid leukocyte differentiation | GO:0002573 | 114 | 29 | + | 1.56 | 3.89E-02 |
| microtubule bundle formation | GO:0001578 | 114 | 29 | + | 1.56 | 3.89E-02 |
| regulation of cold-induced thermogenesis | GO:0120161 | 144 | 35 | + | 1.49 | 3.92E-02 |
| homeostatic process | GO:0042592 | 1556 | 288 | + | 1.14 | 3.93E-02 |
| smoothened signaling pathway involved in spinal cord motor neuron cell fate specification | GO:0021776 | 3 | 3 | + | 6.14 | 3.94E-02 |
| smoothened signaling pathway involved in ventral spinal cord interneuron specification | GO:0021775 | 3 | 3 | + | 6.14 | 3.94E-02 |
| membrane depolarization during atrial cardiac muscle cell action potential | GO:0098912 | 3 | 3 | + | 6.14 | 3.94E-02 |
| dense core granule priming | GO:0061789 | 3 | 3 | + | 6.14 | 3.94E-02 |
| low-density lipoprotein particle mediated signaling | GO:0055096 | 3 | 3 | + | 6.14 | 3.94E-02 |
| lipoprotein particle mediated signaling | GO:0055095 | 3 | 3 | + | 6.14 | 3.94E-02 |
| positive regulation of cell communication by electrical coupling | GO:0010650 | 3 | 3 | + | 6.14 | 3.94E-02 |
| spinal cord ventral commissure morphogenesis | GO:0021965 | 3 | 3 | + | 6.14 | 3.94E-02 |
| positive regulation of protein polymerization | GO:0032273 | 129 | 32 | + | 1.52 | 3.94E-02 |
| divalent inorganic cation homeostasis | GO:0072507 | 483 | 99 | + | 1.26 | 3.95E-02 |
| protein-containing complex subunit organization | GO:0043933 | 1337 | 250 | + | 1.15 | 3.95E-02 |
| cardiac septum morphogenesis | GO:0060411 | 66 | 19 | + | 1.77 | 3.97E-02 |
| cardiac conduction | GO:0061337 | 66 | 19 | + | 1.77 | 3.97E-02 |
| mitotic spindle assembly | GO:0090307 | 47 | 2 | - | 0.26 | 3.97E-02 |
| porphyrin-containing compound metabolic process | GO:0006778 | 48 | 2 | - | 0.26 | 3.98E-02 |
| dCMP metabolic process | GO:0046063 | 6 | 4 | + | 4.09 | 3.99E-02 |
| meiotic chromosome condensation | GO:0010032 | 6 | 4 | + | 4.09 | 3.99E-02 |
| positive regulation of heart rate by epinephrine-norepinephrine | GO:0001996 | 6 | 4 | + | 4.09 | 3.99E-02 |
| amino-acid betaine biosynthetic process | GO:0006578 | 6 | 4 | + | 4.09 | 3.99E-02 |
| glutamate secretion | GO:0014047 | 6 | 4 | + | 4.09 | 3.99E-02 |
| clustering of voltage-gated sodium channels | GO:0045162 | 6 | 4 | + | 4.09 | 3.99E-02 |
| regulation of neutrophil mediated cytotoxicity | GO:0070948 | 6 | 4 | + | 4.09 | 3.99E-02 |
| dCMP catabolic process | GO:0006249 | 6 | 4 | + | 4.09 | 3.99E-02 |
| maintenance of presynaptic active zone structure | GO:0048790 | 6 | 4 | + | 4.09 | 3.99E-02 |
| positive regulation of arachidonic acid secretion | GO:0090238 | 6 | 4 | + | 4.09 | 3.99E-02 |
| modulation of inhibitory postsynaptic potential | GO:0098828 | 6 | 4 | + | 4.09 | 3.99E-02 |
| neural crest cell migration involved in autonomic nervous system development | GO:1901166 | 6 | 4 | + | 4.09 | 3.99E-02 |
| aggrephagy | GO:0035973 | 6 | 4 | + | 4.09 | 3.99E-02 |
| regulation of modification of postsynaptic actin cytoskeleton | GO:1905274 | 6 | 4 | + | 4.09 | 3.99E-02 |
| osteoclast development | GO:0036035 | 6 | 4 | + | 4.09 | 3.99E-02 |
| positive regulation of inhibitory postsynaptic potential | GO:0097151 | 6 | 4 | + | 4.09 | 3.99E-02 |
| regulation of calcium ion transmembrane transporter activity | GO:1901019 | 89 | 24 | + | 1.66 | 3.99E-02 |
| optic nerve development | GO:0021554 | 13 | 6 | + | 2.83 | 4.00E-02 |
| modification of synaptic structure | GO:0099563 | 13 | 6 | + | 2.83 | 4.00E-02 |
| positive regulation of synaptic transmission, GABAergic | GO:0032230 | 13 | 6 | + | 2.83 | 4.00E-02 |
| positive regulation of protein kinase A signaling | GO:0010739 | 13 | 6 | + | 2.83 | 4.00E-02 |
| regulation of mitochondrial fusion | GO:0010635 | 13 | 6 | + | 2.83 | 4.00E-02 |
| response to wounding | GO:0009611 | 428 | 89 | + | 1.28 | 4.00E-02 |
| response to chemical | GO:0042221 | 4055 | 712 | + | 1.08 | 4.01E-02 |
| cellular response to zinc ion | GO:0071294 | 25 | 0 | - | < 0.01 | 4.03E-02 |
| regulation of ubiquitin protein ligase activity | GO:1904666 | 25 | 0 | - | < 0.01 | 4.03E-02 |
| positive regulation of cardiac muscle cell proliferation | GO:0060045 | 24 | 9 | + | 2.30 | 4.04E-02 |
| motor neuron axon guidance | GO:0008045 | 31 | 11 | + | 2.18 | 4.05E-02 |
| adenylate cyclase-inhibiting G protein-coupled receptor signaling pathway | GO:0007193 | 77 | 21 | + | 1.68 | 4.05E-02 |
| regulation of ERBB signaling pathway | GO:1901184 | 77 | 21 | + | 1.68 | 4.05E-02 |
| ameboidal-type cell migration | GO:0001667 | 180 | 42 | + | 1.43 | 4.07E-02 |
| regulation of neurotransmitter secretion | GO:0046928 | 90 | 24 | + | 1.64 | 4.09E-02 |
| cellular metal ion homeostasis | GO:0006875 | 552 | 111 | + | 1.24 | 4.11E-02 |
| negative regulation of protein kinase B signaling | GO:0051898 | 39 | 13 | + | 2.05 | 4.18E-02 |
| regulation of heart rate by cardiac conduction | GO:0086091 | 39 | 13 | + | 2.05 | 4.18E-02 |
| cation homeostasis | GO:0055080 | 695 | 137 | + | 1.21 | 4.18E-02 |
| amide biosynthetic process | GO:0043604 | 500 | 62 | - | 0.76 | 4.21E-02 |
| cellular aromatic compound metabolic process | GO:0006725 | 2688 | 395 | - | 0.90 | 4.24E-02 |
| eye photoreceptor cell differentiation | GO:0001754 | 48 | 15 | + | 1.92 | 4.25E-02 |
| nerve development | GO:0021675 | 78 | 21 | + | 1.65 | 4.25E-02 |
| positive regulation of Ras protein signal transduction | GO:0046579 | 68 | 19 | + | 1.72 | 4.31E-02 |
| spermatogenesis | GO:0007283 | 567 | 72 | - | 0.78 | 4.31E-02 |
| actin filament bundle assembly | GO:0051017 | 58 | 17 | + | 1.80 | 4.32E-02 |
| gland development | GO:0048732 | 414 | 86 | + | 1.28 | 4.32E-02 |
| regulation of striated muscle contraction | GO:0006942 | 92 | 24 | + | 1.60 | 4.37E-02 |
| regulation of organ growth | GO:0046620 | 92 | 24 | + | 1.60 | 4.37E-02 |
| regulation of osteoblast differentiation | GO:0045667 | 120 | 30 | + | 1.54 | 4.37E-02 |
| regulation of extrinsic apoptotic signaling pathway | GO:2001236 | 151 | 36 | + | 1.46 | 4.39E-02 |
| cardiac muscle cell action potential | GO:0086001 | 49 | 15 | + | 1.88 | 4.43E-02 |
| cellular response to low-density lipoprotein particle stimulus | GO:0071404 | 19 | 8 | + | 2.59 | 4.45E-02 |
| retinoic acid receptor signaling pathway | GO:0048384 | 19 | 8 | + | 2.59 | 4.45E-02 |
| negative regulation of bone remodeling | GO:0046851 | 19 | 8 | + | 2.59 | 4.45E-02 |
| regulation of stress-activated MAPK cascade | GO:0032872 | 187 | 43 | + | 1.41 | 4.46E-02 |
| organophosphate metabolic process | GO:0019637 | 833 | 161 | + | 1.19 | 4.46E-02 |
| glycoprotein biosynthetic process | GO:0009101 | 270 | 59 | + | 1.34 | 4.51E-02 |
| striated muscle contraction | GO:0006941 | 107 | 27 | + | 1.55 | 4.54E-02 |
| protein homooligomerization | GO:0051260 | 188 | 43 | + | 1.40 | 4.55E-02 |
| protein acylation | GO:0043543 | 174 | 17 | - | 0.60 | 4.58E-02 |
| regulation of NMDA receptor activity | GO:2000310 | 25 | 9 | + | 2.21 | 4.61E-02 |
| regulation of cardiac conduction | GO:1903779 | 25 | 9 | + | 2.21 | 4.61E-02 |
| NAD metabolic process | GO:0019674 | 25 | 9 | + | 2.21 | 4.61E-02 |
| nucleosome organization | GO:0034728 | 140 | 13 | - | 0.57 | 4.71E-02 |
| metal ion homeostasis | GO:0055065 | 622 | 123 | + | 1.21 | 4.72E-02 |
| cell-cell fusion | GO:0140253 | 33 | 11 | + | 2.05 | 4.74E-02 |
| regulation of superoxide metabolic process | GO:0090322 | 33 | 11 | + | 2.05 | 4.74E-02 |
| syncytium formation by plasma membrane fusion | GO:0000768 | 33 | 11 | + | 2.05 | 4.74E-02 |
| urogenital system development | GO:0001655 | 324 | 69 | + | 1.31 | 4.74E-02 |
| positive regulation of stem cell population maintenance | GO:1902459 | 10 | 5 | + | 3.07 | 4.78E-02 |
| establishment of centrosome localization | GO:0051660 | 10 | 5 | + | 3.07 | 4.78E-02 |
| trans-synaptic signaling by trans-synaptic complex | GO:0099545 | 10 | 5 | + | 3.07 | 4.78E-02 |
| regulation of protein localization to centrosome | GO:1904779 | 10 | 5 | + | 3.07 | 4.78E-02 |
| dendrite extension | GO:0097484 | 10 | 5 | + | 3.07 | 4.78E-02 |
| synaptic vesicle docking | GO:0016081 | 10 | 5 | + | 3.07 | 4.78E-02 |
| regulation of smooth muscle contraction | GO:0006940 | 60 | 17 | + | 1.74 | 4.78E-02 |
| organic acid transport | GO:0015849 | 255 | 56 | + | 1.35 | 4.79E-02 |
| substrate-dependent cell migration | GO:0006929 | 20 | 8 | + | 2.46 | 4.85E-02 |
| vocalization behavior | GO:0071625 | 20 | 8 | + | 2.46 | 4.85E-02 |
| positive regulation of CREB transcription factor activity | GO:0032793 | 20 | 8 | + | 2.46 | 4.85E-02 |
| neuronal stem cell population maintenance | GO:0097150 | 20 | 8 | + | 2.46 | 4.85E-02 |
| kidney epithelium development | GO:0072073 | 126 | 31 | + | 1.51 | 4.87E-02 |
| regulation of cell death | GO:0010941 | 1593 | 293 | + | 1.13 | 4.87E-02 |
| mRNA metabolic process | GO:0016071 | 564 | 72 | - | 0.78 | 4.89E-02 |
| lipid translocation | GO:0034204 | 51 | 15 | + | 1.81 | 4.95E-02 |
| calcium-ion regulated exocytosis | GO:0017156 | 42 | 13 | + | 1.90 | 4.97E-02 |
| regulation of phospholipase C activity | GO:1900274 | 42 | 13 | + | 1.90 | 4.97E-02 |
| regulation of amyloid precursor protein catabolic process | GO:1902991 | 42 | 13 | + | 1.90 | 4.97E-02 |
| nucleotide catabolic process | GO:0009166 | 73 | 20 | + | 1.68 | 4.97E-02 |
|  |  |  |  |  |  |  |

**Note.** False discovery rate (5%) adjusted P-values are provided for each functional category.

**Table S7.** Bonferroni-corrected GO terms using REVIGO

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Table S7. Bonferroni corrected GO terms using REVIGO.** | | | | |
|  |  |  |  |  |
| **GO biological process** | **GO symbol** | **Frequency** | **Uniqueness** | **Dispensability** |
| biological process | GO:0008150 | 100.00% | 1 | 0 |
| cellular process | GO:0009987 | 78.51% | 1 | 0 |
| biological regulation | GO:0065007 | 23.18% | 1 | 0 |
| regulation of cellular process | GO:0050794 | 20.07% | 0.79 | 0.44 |
| localization | GO:0051179 | 19.21% | 1 | 0 |
| transport | GO:0006810 | 18.38% | 0.96 | 0.49 |
| cellular component organization or biogenesis | GO:0071840 | 9.17% | 0.99 | 0.02 |
| cell communication | GO:0007154 | 7.97% | 0.99 | 0.01 |
| cellular component organization | GO:0016043 | 7.54% | 0.84 | 0.59 |
| signaling | GO:0023052 | 7.44% | 1 | 0 |
| intracellular signal transduction | GO:0035556 | 3.95% | 0.74 | 0.52 |
| regulation of biological quality | GO:0065008 | 2.85% | 0.85 | 0.28 |
| multicellular organismal process | GO:0032501 | 2.33% | 1 | 0 |
| positive regulation of biological process | GO:0048518 | 2.11% | 0.84 | 0.31 |
| developmental process | GO:0032502 | 2.01% | 1 | 0 |
| positive regulation of cellular process | GO:0048522 | 1.94% | 0.8 | 0.3 |
| metal ion transport | GO:0030001 | 1.91% | 0.96 | 0 |
| regulation of developmental process | GO:0050793 | 1.26% | 0.85 | 0.27 |
| regulation of response to stimulus | GO:0048583 | 1.19% | 0.85 | 0.27 |
| regulation of cellular component organization | GO:0051128 | 0.99% | 0.85 | 0.28 |
| movement of cell or subcellular component | GO:0006928 | 0.96% | 0.99 | 0.01 |
| regulation of signaling | GO:0023051 | 0.96% | 0.85 | 0.26 |
| locomotion | GO:0040011 | 0.96% | 1 | 0 |
| regulation of cell communication | GO:0010646 | 0.96% | 0.85 | 0.26 |
| regulation of anatomical structure morphogenesis | GO:0022603 | 0.88% | 0.86 | 0.25 |
| cytoskeleton organization | GO:0007010 | 0.82% | 0.85 | 0.49 |
| regulation of localization | GO:0032879 | 0.72% | 0.86 | 0.24 |
| cell projection organization | GO:0030030 | 0.67% | 0.86 | 0.4 |
| biological adhesion | GO:0022610 | 0.58% | 1 | 0 |
| cell adhesion | GO:0007155 | 0.56% | 0.94 | 0.01 |
| regulation of multicellular organismal process | GO:0051239 | 0.54% | 0.86 | 0.21 |
| actin filament-based process | GO:0030029 | 0.38% | 0.99 | 0.01 |
| actin cytoskeleton organization | GO:0030036 | 0.37% | 0.86 | 0.58 |
| detection of chemical stimulus | GO:0009593 | 0.36% | 0.91 | 0 |
| plasma membrane bounded cell projection organization | GO:0120036 | 0.36% | 0.81 | 0.45 |
| enzyme linked receptor protein signaling pathway | GO:0007167 | 0.23% | 0.79 | 0.38 |
| peptidyl-tyrosine modification | GO:0018212 | 0.22% | 0.99 | 0 |
| cell migration | GO:0016477 | 0.20% | 0.95 | 0.26 |
| regulation of locomotion | GO:0040012 | 0.19% | 0.87 | 0.19 |
| regulation of cell migration | GO:0030334 | 0.16% | 0.84 | 0.17 |
| chemical synaptic transmission | GO:0007268 | 0.15% | 0.92 | 0.01 |
| head development | GO:0060322 | 0.14% | 0.68 | 0 |
| regulation of cell projection organization | GO:0031344 | 0.12% | 0.84 | 0.67 |
| behavior | GO:0007610 | 0.12% | 1 | 0 |
| regulation of membrane potential | GO:0042391 | 0.11% | 0.89 | 0 |
| cell junction organization | GO:0034330 | 0.10% | 0.88 | 0.33 |
| regulation of plasma membrane bounded cell projection organization | GO:0120035 | 0.10% | 0.83 | 0.19 |
| circulatory system process | GO:0003013 | 0.09% | 0.76 | 0 |
| modulation of chemical synaptic transmission | GO:0050804 | 0.08% | 0.83 | 0.19 |
| regulation of trans-synaptic signaling | GO:0099177 | 0.08% | 0.83 | 0.64 |
| extracellular structure organization | GO:0043062 | 0.06% | 0.88 | 0.32 |
| extracellular matrix organization | GO:0030198 | 0.06% | 0.88 | 0.32 |
| synapse organization | GO:0050808 | 0.06% | 0.88 | 0.01 |
|  |  |  |  |  |

**Note.** Reduced Bonferroni significant (p<0.05) GO terms using REVIGO. Frequency is the proportion of the GO term in the Uniprot protein annotation database. Uniqueness measures if the term is an outlier when compared to the whole list. Dispensability is the semantic similarity treshold at which the term was removed from the list and assigned to a cluster.

**Table S8. Results of drug repurposing analyses**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Table S8. Results of drug repurposing analyses** | | | | | |
|  |  |  |  |  |  |
| **Drug** | **Enrichment Score** | **p value** | **q value** | **Go Category** | **N Pathways** |
| medrysone | 0.4374 | 2.29E-05 | 0.0221 | Biological Process | 30 |
| clofibrate | 0.4300 | 3.38E-05 | 0.0221 | Biological Process | 30 |
| propoxycaine | 0.4133 | 7.76E-05 | 0.0339 | Biological Process | 30 |
| MS-275 | 0.4055 | 1.14E-04 | 0.0372 | Biological Process | 30 |
| digoxin | 0.3904 | 2.33E-04 | 0.0555 | Biological Process | 30 |
| 5182598 | -0.3884 | 2.55E-04 | 0.0555 | Biological Process | 30 |
| decitabine | -0.3849 | 2.99E-04 | 0.0555 | Biological Process | 30 |
| naproxen | 0.3784 | 4.02E-04 | 0.0555 | Biological Process | 30 |
| verapamil | 0.3782 | 4.06E-04 | 0.0555 | Biological Process | 30 |
| R-atenolol | 0.3727 | 5.19E-04 | 0.0555 | Biological Process | 30 |
| clonidine | 0.3713 | 5.51E-04 | 0.0555 | Biological Process | 30 |
| levonorgestrel | 0.3713 | 5.51E-04 | 0.0555 | Biological Process | 30 |
| carcinine | 0.3713 | 5.51E-04 | 0.0555 | Biological Process | 30 |
| clindamycin | 0.3661 | 6.94E-04 | 0.0633 | Biological Process | 30 |
| chlorphenesin | 0.3647 | 7.36E-04 | 0.0633 | Biological Process | 30 |
| allantoin | 0.3622 | 8.20E-04 | 0.0633 | Biological Process | 30 |
| bepridil | 0.3621 | 8.22E-04 | 0.0633 | Biological Process | 30 |
| albendazole | 0.3603 | 8.91E-04 | 0.0648 | Biological Process | 30 |
| 5152487 | 0.3561 | 1.06E-03 | 0.0733 | Biological Process | 30 |
| fenoprofen | 0.3545 | 1.14E-03 | 0.0746 | Biological Process | 30 |
| fenbendazole | 0.3523 | 1.25E-03 | 0.0778 | Biological Process | 30 |
| procaine | 0.3507 | 1.34E-03 | 0.0787 | Biological Process | 30 |
| nitrendipine | 0.3499 | 1.38E-03 | 0.0787 | Biological Process | 30 |
| florfenicol | 0.3466 | 1.59E-03 | 0.0788 | Biological Process | 30 |
| tonzonium\_bromide | 0.3455 | 1.65E-03 | 0.0788 | Biological Process | 30 |
| bumetanide | -0.3451 | 1.68E-03 | 0.0788 | Biological Process | 30 |
| spiradoline | -0.3447 | 1.71E-03 | 0.0788 | Biological Process | 30 |
| iloprost | -0.3443 | 1.74E-03 | 0.0788 | Biological Process | 30 |
| strophanthidin | 0.3442 | 1.75E-03 | 0.0788 | Biological Process | 30 |
| flunarizine | 0.3423 | 1.89E-03 | 0.0821 | Biological Process | 30 |
| helveticoside | 0.3409 | 2.00E-03 | 0.0821 | Biological Process | 30 |
| acetylsalicylic\_acid | 0.3408 | 2.01E-03 | 0.0821 | Biological Process | 30 |
| azapropazone | -0.3382 | 2.22E-03 | 0.0864 | Biological Process | 30 |
| Prestwick-864 | 0.3369 | 2.35E-03 | 0.0864 | Biological Process | 30 |
| ceftazidime | 0.3366 | 2.38E-03 | 0.0864 | Biological Process | 30 |
| lanatoside\_C | 0.3366 | 2.38E-03 | 0.0864 | Biological Process | 30 |
| theophylline | -0.3347 | 2.56E-03 | 0.0899 | Biological Process | 30 |
| Prestwick-691 | -0.3343 | 2.61E-03 | 0.0899 | Biological Process | 30 |
| 5213008 | -0.3303 | 3.05E-03 | 0.1023 | Biological Process | 30 |
| oxyphenbutazone | 0.3295 | 3.15E-03 | 0.1023 | Biological Process | 30 |
| SC-560 | 0.3287 | 3.25E-03 | 0.1023 | Biological Process | 30 |
| splitomicin | -0.3284 | 3.28E-03 | 0.1023 | Biological Process | 30 |
| bretylium\_tosilate | -0.3255 | 3.68E-03 | 0.1120 | Biological Process | 30 |
| apramycin | 0.3235 | 3.98E-03 | 0.1139 | Biological Process | 30 |
| rifabutin | 0.3234 | 3.99E-03 | 0.1139 | Biological Process | 30 |
| 16-phenyltetranorprostaglandin\_E2 | 0.3233 | 4.00E-03 | 0.1139 | Biological Process | 30 |
| sulfamethoxazole | 0.3208 | 4.41E-03 | 0.1196 | Biological Process | 30 |
| homochlorcyclizine | 0.3204 | 4.48E-03 | 0.1196 | Biological Process | 30 |
| tropine | -0.3204 | 4.48E-03 | 0.1196 | Biological Process | 30 |
| CP-320650-01 | -0.3190 | 4.71E-03 | 0.1212 | Biological Process | 30 |
| ioversol | 0.3184 | 4.82E-03 | 0.1212 | Biological Process | 30 |
| roxithromycin | 0.3184 | 4.82E-03 | 0.1212 | Biological Process | 30 |
| ouabain | 0.3176 | 4.97E-03 | 0.1212 | Biological Process | 30 |
| aceclofenac | 0.3170 | 5.09E-03 | 0.1212 | Biological Process | 30 |
| cytochalasin\_B | 0.3167 | 5.14E-03 | 0.1212 | Biological Process | 30 |
| bisoprolol | 0.3165 | 5.19E-03 | 0.1212 | Biological Process | 30 |
| AG-013608 | 0.3153 | 5.42E-03 | 0.1236 | Biological Process | 30 |
| niridazole | 0.3150 | 5.48E-03 | 0.1236 | Biological Process | 30 |
| dirithromycin | 0.3144 | 5.60E-03 | 0.1243 | Biological Process | 30 |
| syrosingopine | 0.3133 | 5.85E-03 | 0.1260 | Biological Process | 30 |
| pronetalol | 0.3132 | 5.87E-03 | 0.1260 | Biological Process | 30 |
| bisacodyl | 0.3116 | 6.23E-03 | 0.1266 | Biological Process | 30 |
| sulpiride | 0.3114 | 6.28E-03 | 0.1266 | Biological Process | 30 |
| spiperone | 0.3098 | 6.66E-03 | 0.1266 | Biological Process | 30 |
| methapyrilene | 0.3097 | 6.69E-03 | 0.1266 | Biological Process | 30 |
| sulfaphenazole | 0.3094 | 6.76E-03 | 0.1266 | Biological Process | 30 |
| dantrolene | -0.3093 | 6.78E-03 | 0.1266 | Biological Process | 30 |
| colforsin | 0.3091 | 6.83E-03 | 0.1266 | Biological Process | 30 |
| kawain | 0.3090 | 6.85E-03 | 0.1266 | Biological Process | 30 |
| chloramphenicol | 0.3085 | 6.99E-03 | 0.1266 | Biological Process | 30 |
| rotenone | 0.3082 | 7.05E-03 | 0.1266 | Biological Process | 30 |
| hydrocortisone | 0.3078 | 7.17E-03 | 0.1266 | Biological Process | 30 |
| benzathine\_benzylpenicillin | 0.9982 | 0.0072 | 0.1266 | Cellular Component | 1 |
| retrorsine | -0.9982 | 0.0072 | 0.1266 | Cellular Component | 1 |
| anabasine | 0.3072 | 7.33E-03 | 0.1266 | Biological Process | 30 |
| S-propranolol | 0.3071 | 7.35E-03 | 0.1266 | Biological Process | 30 |
| mepenzolate\_bromide | 0.3066 | 7.48E-03 | 0.1271 | Biological Process | 30 |
| prazosin | 0.3058 | 7.71E-03 | 0.1274 | Biological Process | 30 |
| verteporfin | -0.3055 | 7.77E-03 | 0.1274 | Biological Process | 30 |
| oxolamine | -0.3054 | 7.82E-03 | 0.1274 | Biological Process | 30 |
| zaprinast | 0.3052 | 7.89E-03 | 0.1274 | Biological Process | 30 |
| sulfachlorpyridazine | 0.3036 | 8.35E-03 | 0.1333 | Biological Process | 30 |
| scriptaid | 0.3020 | 8.84E-03 | 0.1377 | Biological Process | 30 |
| digitoxigenin | 0.3018 | 8.90E-03 | 0.1377 | Biological Process | 30 |
| tomelukast | -0.3016 | 8.98E-03 | 0.1377 | Biological Process | 30 |
| calcium\_pantothenate | 0.3008 | 9.23E-03 | 0.1377 | Biological Process | 30 |
| STOCK1N-28457 | 0.3005 | 0.0093 | 0.1377 | Biological Process | 30 |
| lisuride | -0.3004 | 0.0094 | 0.1377 | Biological Process | 30 |
| cromoglicic\_acid | 0.2999 | 0.0095 | 0.1377 | Biological Process | 30 |
| 0297417-0002B | 0.2998 | 0.0096 | 0.1377 | Biological Process | 30 |
| arcaine | -0.2997 | 0.0096 | 0.1377 | Biological Process | 30 |
| naltrexone | 0.2994 | 0.0097 | 0.1377 | Biological Process | 30 |
| mebeverine | 0.2992 | 0.0098 | 0.1377 | Biological Process | 30 |
| ofloxacin | 0.2982 | 0.0101 | 0.1403 | Biological Process | 30 |
| nicotinic\_acid | 0.2980 | 0.0102 | 0.1403 | Biological Process | 30 |
| decamethonium\_bromide | -0.2975 | 0.0104 | 0.1412 | Biological Process | 30 |
| promethazine | 0.2966 | 0.0107 | 0.1412 | Biological Process | 30 |
| cyproterone | 0.2966 | 0.0107 | 0.1412 | Biological Process | 30 |
| mephenytoin | 0.2965 | 0.0108 | 0.1412 | Biological Process | 30 |
| copper\_sulfate | -0.9964 | 0.0108 | 0.1412 | Cellular Component | 1 |
| etofenamate | 0.2959 | 0.0110 | 0.1412 | Biological Process | 30 |
| ceforanide | -0.2955 | 0.0111 | 0.1412 | Biological Process | 30 |
| clofazimine | 0.2954 | 0.0112 | 0.1412 | Biological Process | 30 |
| sulfadimidine | 0.2950 | 0.0113 | 0.1412 | Biological Process | 30 |
| fluvastatin | 0.2950 | 0.0113 | 0.1412 | Biological Process | 30 |
| sirolimus | 0.2942 | 0.0116 | 0.1428 | Biological Process | 30 |
| perhexiline | 0.2936 | 0.0119 | 0.1428 | Biological Process | 30 |
| gefitinib | 0.2936 | 0.0119 | 0.1428 | Biological Process | 30 |
| parthenolide | 0.2935 | 0.0119 | 0.1428 | Biological Process | 30 |
| cetirizine | 0.2932 | 0.0121 | 0.1428 | Biological Process | 30 |
| N6-methyladenosine | 0.2929 | 0.0122 | 0.1428 | Biological Process | 30 |
| Prestwick-675 | -0.2928 | 0.0122 | 0.1428 | Biological Process | 30 |
| alclometasone | 0.2924 | 0.0124 | 0.1434 | Biological Process | 30 |
| etamivan | 0.2922 | 0.0125 | 0.1434 | Biological Process | 30 |
| phthalylsulfathiazole | 0.2915 | 0.0128 | 0.1459 | Biological Process | 30 |
| piperacetazine | 0.2909 | 0.0131 | 0.1475 | Biological Process | 30 |
| acacetin | 0.2894 | 0.0137 | 0.1514 | Biological Process | 30 |
| hydroquinine | 0.2894 | 0.0138 | 0.1514 | Biological Process | 30 |
| labetalol | 0.2894 | 0.0138 | 0.1514 | Biological Process | 30 |
| tetraethylenepentamine | -0.2891 | 0.0139 | 0.1517 | Biological Process | 30 |
| vitexin | -0.2884 | 0.0142 | 0.1517 | Biological Process | 30 |
| flumequine | -0.9946 | 0.0144 | 0.1517 | Cellular Component | 1 |
| diclofenamide | 0.2881 | 0.0144 | 0.1517 | Biological Process | 30 |
| pseudopelletierine | 0.2880 | 0.0144 | 0.1517 | Biological Process | 30 |
| gemfibrozil | 0.2878 | 0.0145 | 0.1517 | Biological Process | 30 |
| SB-203580 | -0.2875 | 0.0147 | 0.1517 | Biological Process | 30 |
| pentamidine | 0.2873 | 0.0148 | 0.1517 | Biological Process | 30 |
| acetylsalicylsalicylic\_acid | 0.2872 | 0.0148 | 0.1517 | Biological Process | 30 |
| ampicillin | -0.2861 | 0.0154 | 0.1566 | Biological Process | 30 |
| fluoxetine | 0.2856 | 0.0156 | 0.1572 | Biological Process | 30 |
| clomipramine | 0.2853 | 0.0158 | 0.1572 | Biological Process | 30 |
| cefixime | 0.2852 | 0.0159 | 0.1572 | Biological Process | 30 |
| oxybuprocaine | 0.2848 | 0.0161 | 0.1572 | Biological Process | 30 |
| quinostatin | 0.2848 | 0.0161 | 0.1572 | Biological Process | 30 |
| naringenin | -0.2839 | 0.0166 | 0.1609 | Biological Process | 30 |
| chlorprothixene | 0.2836 | 0.0168 | 0.1613 | Biological Process | 30 |
| solanine | 0.2830 | 0.0171 | 0.1613 | Biological Process | 30 |
| nifedipine | 0.2830 | 0.0171 | 0.1613 | Biological Process | 30 |
| dropropizine | 0.2827 | 0.0173 | 0.1613 | Biological Process | 30 |
| cefalotin | 0.2825 | 0.0174 | 0.1613 | Biological Process | 30 |
| 5114445 | 0.2820 | 0.0177 | 0.1613 | Biological Process | 30 |
| metolazone | 0.2820 | 0.0177 | 0.1613 | Biological Process | 30 |
| paracetamol | 0.2816 | 0.0180 | 0.1613 | Biological Process | 30 |
| ribostamycin | -0.9928 | 0.0180 | 0.1613 | Cellular Component | 1 |
| ticlopidine | 0.9928 | 0.0180 | 0.1613 | Cellular Component | 1 |
| fluspirilene | 0.2814 | 0.0180 | 0.1613 | Biological Process | 30 |
| 0225151-0000 | 0.2812 | 0.0182 | 0.1613 | Biological Process | 30 |
| lobeline | 0.2810 | 0.0183 | 0.1613 | Biological Process | 30 |
| cycloserine | 0.2809 | 0.0184 | 0.1613 | Biological Process | 30 |
| levamisole | 0.2804 | 0.0186 | 0.1627 | Biological Process | 30 |
| todralazine | 0.2801 | 0.0188 | 0.1633 | Biological Process | 30 |
| tyloxapol | 0.2797 | 0.0191 | 0.1646 | Biological Process | 30 |
| genistein | -0.2794 | 0.0193 | 0.1646 | Biological Process | 30 |
| dobutamine | 0.2793 | 0.0194 | 0.1646 | Biological Process | 30 |
| nadolol | -0.2789 | 0.0196 | 0.1657 | Biological Process | 30 |
| Prestwick-559 | 0.2785 | 0.0199 | 0.1662 | Biological Process | 30 |
| tetracycline | -0.2784 | 0.0199 | 0.1662 | Biological Process | 30 |
| vorinostat | 0.2778 | 0.0203 | 0.1681 | Biological Process | 30 |
| berberine | 0.2775 | 0.0205 | 0.1681 | Biological Process | 30 |
| meclofenoxate | 0.2774 | 0.0206 | 0.1681 | Biological Process | 30 |
| adenosine\_phosphate | 0.2773 | 0.0207 | 0.1681 | Biological Process | 30 |
| famprofazone | 0.2768 | 0.0210 | 0.1681 | Biological Process | 30 |
| cefamandole | -0.2768 | 0.0211 | 0.1681 | Biological Process | 30 |
| colchicine | 0.2768 | 0.0211 | 0.1681 | Biological Process | 30 |
| practolol | 0.2761 | 0.0216 | 0.1695 | Biological Process | 30 |
| hyoscyamine | -0.9910 | 0.0216 | 0.1695 | Cellular Component | 1 |
| sulfadiazine | 0.2759 | 0.0216 | 0.1695 | Biological Process | 30 |
| ribavirin | -0.2753 | 0.0221 | 0.1703 | Biological Process | 30 |
| proscillaridin | 0.2752 | 0.0222 | 0.1703 | Biological Process | 30 |
| 5186223 | -0.2751 | 0.0222 | 0.1703 | Biological Process | 30 |
| ampyrone | 0.2751 | 0.0223 | 0.1703 | Biological Process | 30 |
| proxymetacaine | 0.2741 | 0.0230 | 0.1745 | Biological Process | 30 |
| podophyllotoxin | 0.2740 | 0.0231 | 0.1745 | Biological Process | 30 |
| Prestwick-685 | 0.2736 | 0.0234 | 0.1757 | Biological Process | 30 |
| noscapine | -0.2732 | 0.0237 | 0.1765 | Biological Process | 30 |
| cyproheptadine | 0.2730 | 0.0238 | 0.1765 | Biological Process | 30 |
| alprenolol | 0.2729 | 0.0239 | 0.1765 | Biological Process | 30 |
| rolitetracycline | 0.2728 | 0.0240 | 0.1765 | Biological Process | 30 |
| ranitidine | 0.2723 | 0.0243 | 0.1772 | Biological Process | 30 |
| imatinib | -0.2720 | 0.0246 | 0.1772 | Biological Process | 30 |
| penbutolol | -0.2717 | 0.0248 | 0.1772 | Biological Process | 30 |
| terbutaline | 0.2717 | 0.0248 | 0.1772 | Biological Process | 30 |
| depudecin | 0.9892 | 0.0252 | 0.1772 | Cellular Component | 1 |
| paromomycin | -0.9892 | 0.0252 | 0.1772 | Cellular Component | 1 |
| santonin | 0.9892 | 0.0252 | 0.1772 | Cellular Component | 1 |
| tolnaftate | 0.9892 | 0.0252 | 0.1772 | Cellular Component | 1 |
| ticarcillin | 0.2709 | 0.0255 | 0.1786 | Biological Process | 30 |
| rimexolone | 0.2706 | 0.0257 | 0.1792 | Biological Process | 30 |
| 1,5-isoquinolinediol | 0.2704 | 0.0259 | 0.1792 | Biological Process | 30 |
| prochlorperazine | 0.2703 | 0.0260 | 0.1792 | Biological Process | 30 |
| metergoline | 0.2693 | 0.0268 | 0.1829 | Biological Process | 30 |
| salsolinol | 0.2692 | 0.0269 | 0.1829 | Biological Process | 30 |
| pyrantel | 0.2691 | 0.0270 | 0.1829 | Biological Process | 30 |
| nalbuphine | -0.2681 | 0.0279 | 0.1879 | Biological Process | 30 |
| piperidolate | 0.2676 | 0.0283 | 0.1879 | Biological Process | 30 |
| docosahexaenoic\_acid\_ethyl\_ester | -0.2674 | 0.0285 | 0.1879 | Biological Process | 30 |
| LM-1685 | -0.2672 | 0.0287 | 0.1879 | Biological Process | 30 |
| 11-deoxy-16,16-dimethylprostaglandin\_E2 | 0.9874 | 0.0288 | 0.1879 | Cellular Component | 1 |
| nisoxetine | 0.9874 | 0.0288 | 0.1879 | Cellular Component | 1 |
| oxybenzone | 0.9874 | 0.0288 | 0.1879 | Cellular Component | 1 |
| AR-A014418 | 0.2670 | 0.0289 | 0.1879 | Biological Process | 30 |
| minaprine | 0.2669 | 0.0290 | 0.1879 | Biological Process | 30 |
| mesoridazine | 0.2662 | 0.0296 | 0.1909 | Biological Process | 30 |
| halofantrine | -0.2656 | 0.0302 | 0.1936 | Biological Process | 30 |
| H-7 | 0.2654 | 0.0303 | 0.1936 | Biological Process | 30 |
| benfotiamine | 0.2648 | 0.0310 | 0.1947 | Biological Process | 30 |
| glibenclamide | 0.2648 | 0.0310 | 0.1947 | Biological Process | 30 |
| napelline | 0.2647 | 0.0310 | 0.1947 | Biological Process | 30 |
| prasterone | -0.2647 | 0.0311 | 0.1947 | Biological Process | 30 |
| 16,16-dimethylprostaglandin\_E2 | 0.2643 | 0.0314 | 0.1960 | Biological Process | 30 |
| propidium\_iodide | -0.2640 | 0.0318 | 0.1971 | Biological Process | 30 |
| N-acetylmuramic\_acid | 0.2635 | 0.0322 | 0.1980 | Biological Process | 30 |
| gliquidone | -0.2635 | 0.0323 | 0.1980 | Biological Process | 30 |
| tolazoline | 0.9856 | 0.0324 | 0.1980 | Cellular Component | 1 |
| levocabastine | 0.2632 | 0.0325 | 0.1980 | Biological Process | 30 |
| reserpine | 0.2630 | 0.0327 | 0.1981 | Biological Process | 30 |
| ellipticine | 0.2629 | 0.0328 | 0.1981 | Biological Process | 30 |
| iopromide | 0.2626 | 0.0331 | 0.1990 | Biological Process | 30 |
| fisetin | 0.2624 | 0.0334 | 0.1994 | Biological Process | 30 |
| 4-hydroxyphenazone | -0.2617 | 0.0341 | 0.2028 | Biological Process | 30 |
| amikacin | -0.2615 | 0.0343 | 0.2031 | Biological Process | 30 |
| meticrane | 0.2610 | 0.0349 | 0.2056 | Biological Process | 30 |
| flunixin | 0.2605 | 0.0354 | 0.2067 | Biological Process | 30 |
| trimetazidine | 0.2603 | 0.0357 | 0.2067 | Biological Process | 30 |
| cloperastine | 0.2600 | 0.0359 | 0.2067 | Biological Process | 30 |
| Prestwick-857 | -0.9838 | 0.0360 | 0.2067 | Cellular Component | 1 |
| metaraminol | -0.2599 | 0.0361 | 0.2067 | Biological Process | 30 |
| finasteride | -0.2598 | 0.0362 | 0.2067 | Biological Process | 30 |
| indoprofen | -0.2598 | 0.0362 | 0.2067 | Biological Process | 30 |
| sulfafurazole | 0.2595 | 0.0365 | 0.2080 | Biological Process | 30 |
| bephenium\_hydroxynaphthoate | 0.2592 | 0.0369 | 0.2086 | Biological Process | 30 |
| (-)-atenolol | 0.2590 | 0.0370 | 0.2086 | Biological Process | 30 |
| GW-8510 | 0.2590 | 0.0371 | 0.2086 | Biological Process | 30 |
| Prestwick-984 | 0.2582 | 0.0380 | 0.2123 | Biological Process | 30 |
| tioguanine | 0.2581 | 0.0381 | 0.2123 | Biological Process | 30 |
| chlorhexidine | 0.2575 | 0.0389 | 0.2142 | Biological Process | 30 |
| F0447-0125 | -0.2570 | 0.0394 | 0.2142 | Biological Process | 30 |
| pentolonium | 0.2570 | 0.0394 | 0.2142 | Biological Process | 30 |
| 3-nitropropionic\_acid | -0.9820 | 0.0396 | 0.2142 | Cellular Component | 1 |
| hexetidine | 0.9820 | 0.0396 | 0.2142 | Cellular Component | 1 |
| scoulerine | 0.9820 | 0.0396 | 0.2142 | Cellular Component | 1 |
| amoxicillin | 0.2568 | 0.0396 | 0.2142 | Biological Process | 30 |
| merbromin | -0.2567 | 0.0398 | 0.2142 | Biological Process | 30 |
| ipratropium\_bromide | 0.2565 | 0.0401 | 0.2142 | Biological Process | 30 |
| PF-00562151-00 | 0.2565 | 0.0401 | 0.2142 | Biological Process | 30 |
| demecolcine | 0.2561 | 0.0405 | 0.2151 | Biological Process | 30 |
| pinacidil | 0.2559 | 0.0407 | 0.2151 | Biological Process | 30 |
| dl-alpha\_tocopherol | 0.2559 | 0.0407 | 0.2151 | Biological Process | 30 |
| doxylamine | -0.2558 | 0.0409 | 0.2151 | Biological Process | 30 |
| tocainide | -0.2552 | 0.0416 | 0.2170 | Biological Process | 30 |
| estrone | -0.2551 | 0.0418 | 0.2170 | Biological Process | 30 |
| 5186324 | -0.2545 | 0.0426 | 0.2170 | Biological Process | 30 |
| benzylpenicillin | -0.2545 | 0.0426 | 0.2170 | Biological Process | 30 |
| meglumine | 0.2541 | 0.0430 | 0.2170 | Biological Process | 30 |
| chlortetracycline | 0.2541 | 0.0431 | 0.2170 | Biological Process | 30 |
| chrysin | 0.2541 | 0.0431 | 0.2170 | Biological Process | 30 |
| lidocaine | 0.2540 | 0.0431 | 0.2170 | Biological Process | 30 |
| CP-319743 | 0.9802 | 0.0432 | 0.2170 | Cellular Component | 1 |
| alfuzosin | -0.9802 | 0.0432 | 0.2170 | Cellular Component | 1 |
| pipenzolate\_bromide | 0.9802 | 0.0432 | 0.2170 | Cellular Component | 1 |
| tolbutamide | -0.2539 | 0.0433 | 0.2170 | Biological Process | 30 |
| 5255229 | 0.2538 | 0.0435 | 0.2172 | Biological Process | 30 |
| etodolac | 0.2532 | 0.0442 | 0.2191 | Biological Process | 30 |
| netilmicin | 0.2532 | 0.0442 | 0.2191 | Biological Process | 30 |
| beta-escin | 0.2529 | 0.0447 | 0.2207 | Biological Process | 30 |
| oxytetracycline | 0.2526 | 0.0450 | 0.2215 | Biological Process | 30 |
| deptropine | 0.2522 | 0.0455 | 0.2228 | Biological Process | 30 |
| hexestrol | 0.2521 | 0.0458 | 0.2228 | Biological Process | 30 |
| 5252917 | 0.2515 | 0.0465 | 0.2228 | Biological Process | 30 |
| pirinixic\_acid | -0.2514 | 0.0467 | 0.2228 | Biological Process | 30 |
| clioquinol | 0.2514 | 0.0467 | 0.2228 | Biological Process | 30 |
| benzydamine | 0.9784 | 0.0468 | 0.2228 | Cellular Component | 1 |
| methoxsalen | 0.9784 | 0.0468 | 0.2228 | Cellular Component | 1 |
| phenelzine | 0.9784 | 0.0468 | 0.2228 | Cellular Component | 1 |
| ketorolac | 0.2513 | 0.0468 | 0.2228 | Biological Process | 30 |
| alexidine | 0.2505 | 0.0479 | 0.2262 | Biological Process | 30 |
| benzthiazide | 0.2503 | 0.0483 | 0.2262 | Biological Process | 30 |
| iopanoic\_acid | 0.2502 | 0.0483 | 0.2262 | Biological Process | 30 |
| ronidazole | 0.2502 | 0.0484 | 0.2262 | Biological Process | 30 |

**Note.** Multiple testing correction was performed using a false discovery rate of 5%. Nominally significant results are shown.

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