

Spot 104 [HSP74_HUMAN](#) Mass: 95127 Score: 151 Expect: 1.6e-011 Queries matched: 34

Heat shock 70 kDa protein 4 OS=Homo sapiens GN=HSPA4 PE=1 SV=4

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1045.6000	1044.5927	1044.6179	-0.0251	765	-	773	2	--- K.SKEIEAKIK.E
1083.6411	1082.6338	1082.6124	0.0215	352	-	360	2	--- K.EKISKFFGK.E
1170.6508	1169.6435	1169.6227	0.0209	560	-	569	2	--- K.KMDQPPQAKK.A
1237.6058	1236.5985	1236.5631	0.0354	34	-	44	0	--- R.CTPACISFGPK.N
1239.6238	1238.6165	1238.5819	0.0347	74	-	84	0	--- R.AFSDPFVVEAEK.S
1321.7443	1320.7370	1320.7037	0.0333	222	-	234	0	1 K.VLATAFDTTLGGR.K
1321.7443	1320.7370	1320.7037	0.0333	222	-	234	0	--- K.VLATAFDTTLGGR.K
1418.6580	1417.6507	1417.6183	0.0324	619	-	629	0	--- K.NAVEEYVYEMR.D + Oxidation (M)
1418.6580	1417.6507	1417.6183	0.0324	619	-	629	0	--- K.NAVEEYVYEMR.D + Oxidation (M)
1446.7380	1445.7307	1445.7639	-0.0332	62	-	73	2	--- K.NTVQGFKRFHGR.A
1495.7271	1494.7198	1494.6950	0.0248	20	-	33	0	28 R.AGGIETIANEYSDR.C
1495.7271	1494.7198	1494.6950	0.0248	20	-	33	0	--- R.AGGIETIANEYSDR.C
1535.7969	1534.7896	1534.7636	0.0261	375	-	388	0	--- R.GCALQCAILSPAFK.V
1562.9065	1561.8992	1561.8827	0.0165	220	-	234	1	--- K.LKVLATAFDTTLGGR.K
1648.8413	1647.8340	1647.8072	0.0268	155	-	169	0	--- R.SVMDATQIAGLNCLR.L
1664.8304	1663.8231	1663.8021	0.0210	155	-	169	0	--- R.SVMDATQIAGLNCLR.L + Oxidation (M)
1664.8304	1663.8231	1663.8021	0.0210	155	-	169	0	--- R.SVMDATQIAGLNCLR.L + Oxidation (M)
1735.9436	1734.9363	1734.9192	0.0171	391	-	405	0	22 R.EFSITDVVPYISLR.W
1735.9436	1734.9363	1734.9192	0.0171	391	-	405	0	--- R.EFSITDVVPYISLR.W
1790.9569	1789.9496	1789.9331	0.0165	375	-	390	1	--- R.GCALQCAILSPAFKVR.E
1862.0502	1861.0429	1861.0308	0.0121	330	-	346	2	--- K.LKKEDIYAVEIVGGATR.I
1940.9500	1939.9427	1939.9825	-0.0398	2	-	19	0	--- M.SVVGIDLGFQSCYVAVAR.A
1991.1073	1990.1000	1990.0887	0.0113	389	-	405	1	13 K.VREFSITDVVPYISLR.W
1991.1073	1990.1000	1990.0887	0.0113	389	-	405	1	--- K.VREFSITDVVPYISLR.W
1997.9558	1996.9485	1996.9352	0.0133	236	-	251	1	--- K.FDEVLVNHCFEEFGKK.Y
1998.9908	1997.9835	1998.0058	-0.0222	357	-	374	1	--- K.FFGKELSTTLNADEAVTR.G
2126.0405	2125.0332	2125.0302	0.0031	235	-	251	2	--- R.KFDEVLVNHCFEEFGKK.Y

2327.2268	2326.2195	2326.2168	0.0027	354	-	374	2	26	K.ISKFFGKELSTTLNADEAVTR.G
2327.2268	2326.2195	2326.2168	0.0027	354	-	374	2	---	K.ISKFFGKELSTTLNADEAVTR.G
2416.1289	2415.1216	2415.1099	0.0117	197	-	217	0	---	R.NVVFVDMGHSAYQVSVCANR.G + Oxidation (HW)
2622.3047	2621.2974	2621.1663	0.1311	522	-	543	0	---	K.MQVDQEEPHVEEQQQTPAENK.A
2714.2200	2713.2127	2713.2475	-0.0348	20	-	44	1	---	R.AGGIETIANEYSDRCTPACISFGPK.N
2714.2200	2713.2127	2713.2475	-0.0348	20	-	44	1	---	R.AGGIETIANEYSDRCTPACISFGPK.N
2901.4661	2900.4588	2900.4377	0.0211	689	-	711	2	---	R.FQESEERPKLFEELGKQIQYMK.I + Oxidation (M)

No match to: 1000.5853, 1003.5709, 1005.6109, 1008.6066, 1009.5926, 1011.5970, 1014.6162, 1018.5878, 1021.6154, 1023.6071, 1048.6251, 1050.6127, 1054.6206, 1060.6393, 1062.6423, 1064.6024, 1066.6185, 1073.6244, 1106.5945, 1125.6571, 1288.7242, 1600.8317, 1798.8290, 1809.9117, 1939.9460, 1983.0129, 1995.0601, 2011.9929, 2193.1116, 2194.1062, 2210.0889, 2211.1050, 2225.1230, 2233.0925, 2246.2075, 2265.0332, 2299.1748, 2370.3772, 2627.4856

Spot 665 [AL1A1_HUMAN](#) Mass: 55454 Score: 317 Expect: 4.1e-028 Queries matched: 39

Retinal dehydrogenase | OS=Homo sapiens GN=ALDH1A1 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
945.6119	944.6046	944.5291	0.0756	413	-	420	1	--- K.SLDDVIKRA
1100.6615	1099.6542	1099.5985	0.0557	92	-	100	1	--- K.LADLIERDR.L
1176.6302	1175.6229	1175.5723	0.0506	69	-	78	0	(22) R.QAFQIGSPWR.T + kynurenin (W); Pyro-glu (N-term Q)
1176.6302	1175.6229	1175.5723	0.0506	69	-	78	0	--- R.QAFQIGSPWR.T + kynurenin (W); Pyro-glu (N-term Q)
1193.6569	1192.6496	1192.5989	0.0507	69	-	78	0	33 R.QAFQIGSPWR.T + kynurenin (W)
1193.6569	1192.6496	1192.5989	0.0507	69	-	78	0	--- R.QAFQIGSPWR.T + kynurenin (W)
1204.6595	1203.6522	1203.6823	-0.0300	491	-	501	2	--- K.TVTVKISQKNS.-
1205.6599	1204.6526	1204.5989	0.0537	69	-	78	0	--- R.QAFQIGSPWR.T + Oxidation (HW)
1220.7489	1219.7416	1219.6924	0.0492	411	-	420	2	--- K.FKSLDDVIKRA
1221.6885	1220.6812	1220.5938	0.0874	69	-	78	0	--- R.QAFQIGSPWR.T + DOUBLE Ox (W)
1428.7091	1427.7018	1427.6615	0.0403	132	-	143	1	--- R.YCAGWADKIQR.T + kynurenin (W)
1544.8054	1543.7981	1543.7671	0.0311	144	-	156	0	46 R.TIPDGNFFTYTR.H
1544.8054	1543.7981	1543.7671	0.0311	144	-	156	0	--- R.TIPDGNFFTYTR.H
1589.8171	1588.8098	1588.7885	0.0213	421	-	435	0	63 R.ANNTFYGLSAGVFTK.D
1589.8171	1588.8098	1588.7885	0.0213	421	-	435	0	--- R.ANNTFYGLSAGVFTK.D
1617.9603	1616.9530	1616.9249	0.0281	88	-	100	2	--- R.LLYKLADLIERDR.L
1645.8383	1644.8310	1644.8035	0.0276	309	-	321	0	27 R.IFVEESIYDEFVR.R

1645.8383	1644.8310	1644.8035	0.0276	309	-	321	0	---	R.IFVEESYDEFVVR.R
1649.8207	1648.8134	1648.7845	0.0289	23	-	36	0	---	K.IFINNEWHDSVSGK.K + kynurenin (W)
1700.8033	1699.7960	1699.7729	0.0231	477	-	490	0	---	R.ELGEYGFHEYTEVK.T
1745.9180	1744.9107	1744.8896	0.0211	420	-	435	1	---	K.RANNTFYGLSAGVFTK.D
1745.9180	1744.9107	1744.8896	0.0211	420	-	435	1	---	K.RANNTFYGLSAGVFTK.D
1746.9478	1745.9405	1745.9385	0.0020	396	-	410	1	---	R.IAKEEIFGPVQIMK.F + Oxidation (M)
1798.8280	1797.8207	1797.8944	-0.0737	129	-	143	2	---	K.TLRYCAGWADKIQGR.T + kynurenin (W)
1801.9286	1800.9213	1800.9046	0.0168	309	-	322	1	28	R.IFVEESYDEFVRR.S
1801.9286	1800.9213	1800.9046	0.0168	309	-	322	1	---	R.IFVEESYDEFVRR.S
2005.9420	2004.9347	2004.9251	0.0097	379	-	395	0	---	K.GYFVQPTVFSNVTDEM.R.I + Oxidation (M)
2011.9744	2010.9671	2010.9217	0.0454	69	-	85	1	---	R.QAFQIGSPWRMDASER.G + Oxidation (M); Oxidation (HW)
2022.1144	2021.1071	2021.1019	0.0052	396	-	412	2	---	R.IAKEEIFGPVQIMKFK.S + Oxidation (M)
2193.1003	2192.0930	2192.0545	0.0386	69	-	87	2	---	R.QAFQIGSPWRMDASERGR.L
2211.1050	2210.0977	2210.0895	0.0083	477	-	495	1	---	R.ELGEYGFHEYTEVKTVTVK.I + Pyro-glu (N-term E)
2225.1230	2224.1157	2224.0443	0.0714	69	-	87	2	---	R.QAFQIGSPWRMDASERGR.L + Oxidation (M); Oxidation (HW)
2229.1167	2228.1094	2228.1000	0.0094	477	-	495	1	---	R.ELGEYGFHEYTEVKTVTVK.I
2299.1714	2298.1641	2298.1280	0.0361	18	-	36	1	---	K.IQYTKIFINNEWHDSVSGK.K + kynurenin (W); Oxidation (HW)
2318.2473	2317.2400	2317.1412	0.0988	379	-	398	1	---	K.GYFVQPTVFSNVTDEM.RIAK.E + Oxidation (M)
2318.2473	2317.2400	2317.1412	0.0988	379	-	398	1	---	K.GYFVQPTVFSNVTDEM.RIAK.E + Oxidation (M)
2516.2944	2515.2871	2515.3070	-0.0199	413	-	435	2	---	K.SLDDVIKRANNTFYGLSAGVFTK.D
2811.2776	2810.2703	2810.4287	-0.1584	157	-	179	0	---	R.HEPIGVCQHPWNFPLVLIWK.I + Oxidation (M); 3 Oxidation (HW)
3184.7373	3183.7300	3183.7689	-0.0388	180	-	210	0	---	K.IGPALSCGNTVVVKPAEQTPLTALHVASLIK.E

No match to: 909.0518, 917.3321, 935.6059, 956.6002, 1044.1261, 1045.6201, 1066.1407, 1072.1425, 1082.1152, 1088.1123, 1106.6099, 1175.6500, 1202.6605, 1277.1505, 1337.7004, 1387.7047, 1444.6965, 1465.7488, 1526.7976, 1566.7880, 1684.8777, 1713.8188, 1783.9603, 1784.9429, 1923.9559, 1940.9500, 2083.0171, 2233.1057, 2236.1333, 2247.1199, 2300.1724, 2622.3027, 3350.5508, 3354.6848

Spot 695 [DHE3_HUMAN](#) Mass: 61701 Score: 84 Expect: 8.3e-005 Queries matched: 11

Glutamate dehydrogenase 1, mitochondrial OS=Homo sapiens GN=GLUD1 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1429.7148	1428.7075	1428.6157	0.0918	125	-	136	0	30 R.DDGSWEVIEGYR.A + kynurenin (W)

1429.7148	1428.7075	1428.6157	0.0918	125	-	136	0	---	R.DDGSWEVIEGYR.A + kynurenin (W)
1584.7910	1583.7837	1583.8493	-0.0656	1	-	13	1	---	-.MYRYLGEALLLSR.A
1737.9513	1736.9440	1736.8845	0.0595	481	-	496	0	34	K.HGGTIPIVPTAEFQDR.I
1737.9513	1736.9440	1736.8845	0.0595	481	-	496	0	---	K.HGGTIPIVPTAEFQDR.I
1894.1160	1893.1087	1893.0658	0.0429	108	-	123	0	---	R.IIKPCNHVLSLSPFIR.R
1894.1160	1893.1087	1893.0658	0.0429	108	-	123	0	---	R.IIKPCNHVLSLSPFIR.R
1922.9570	1921.9497	1922.0229	-0.0732	520	-	535	2	---	R.QIMRTAMKYNLGLDLR.T
2050.2073	2049.2000	2049.1669	0.0331	108	-	124	1	---	R.IIKPCNHVLSLSPFIRR.D
2242.1729	2241.1656	2241.1640	0.0016	400	-	420	1	14	K.IAEGANGPTTPEADKIFLER.N
2242.1729	2241.1656	2241.1640	0.0016	400	-	420	1	---	K.IAEGANGPTTPEADKIFLER.N

No match to: 905.6586, 909.1331, 913.7507, 915.7192, 920.6859, 923.7382, 941.7413, 941.7413, 948.6099, 957.7872, 959.7585, 967.7461, 969.7439, 977.7315, 984.7881, 985.7694, 1013.7063, 1016.6675, 1045.6947, 1059.7080, 1066.2075, 1072.2035, 1074.6897, 1082.1843, 1088.1919, 1126.6825, 1235.6382, 1293.1735, 1320.6952, 1320.6952, 1340.7781, 1638.9274, 1657.8635, 1688.0374, 1707.8384, 1739.9531, 1791.7799, 1798.8571, 1807.8224, 1810.8699, 1826.8590, 1940.9661, 2012.0029, 2059.0073, 2084.0190, 2193.1545, 2208.1226, 2211.1050, 2225.1216, 2233.0884, 2235.0818, 2248.1492, 2299.1670, 2383.9363, 2622.2598, 2622.2598, 2650.2571, 2705.1196, 2717.0281, 2811.2507, 3354.6223, 3354.6223

Spot 748 [TXND5_HUMAN](#) Mass: 48283 Score: 73 Expect: 0.001 Queries matched: 22

Thioredoxin domain-containing protein 5 OS=Homo sapiens GN=TXNDC5 PE=1 SV=2

Observed	Mr(expt)	Mr(cale)	Delta	Start	End	Miss	Ions	Peptide	
1045.6041	1044.5968	1044.5967	0.0001	366	-	375	1	---	K.KEFPGLAGVK.I
1079.6686	1078.6613	1078.6175	0.0438	395	-	403	0	20	R.GYPTLLLF.R.G
1079.6686	1078.6613	1078.6175	0.0438	395	-	403	0	---	R.GYPTLLLF.R.G
1156.6545	1155.6472	1155.6077	0.0396	261	-	269	0	---	R.GYPTLLWFR.D + kynurenin (W)
1156.6545	1155.6472	1155.6077	0.0396	261	-	269	0	---	R.GYPTLLWFR.D + kynurenin (W)
1168.6627	1167.6554	1167.6077	0.0478	261	-	269	0	---	R.GYPTLLWFR.D + Oxidation (HW)
1184.6600	1183.6527	1183.6026	0.0502	261	-	269	0	---	R.GYPTLLWFR.D + DOUBLE Ox (W)
1456.7847	1455.7774	1455.7510	0.0264	261	-	272	1	---	R.GYPTLLWFRD.GK + kynurenin (W)
1584.9091	1583.9018	1583.8823	0.0195	391	-	403	1	---	K.YSVRGYPTLLLF.R.G
1664.8339	1663.8266	1663.8026	0.0240	408	-	422	1	---	K.VSEHSGGRDLDLSLHR.F
1761.7872	1760.7799	1760.7570	0.0229	119	-	134	0	---	K.VDCTAHSVCSAQGVR.G
1792.9337	1791.9264	1791.8976	0.0289	407	-	422	2	---	K.KVSEHSGGRDLDLSLHR.F

1864.9563	1863.9490	1863.9326	0.0164	282	-	296	1	26	R.DLESLREYVESQLQR.T
1864.9563	1863.9490	1863.9326	0.0164	282	-	296	1	---	R.DLESLREYVESQLQR.T
1965.8699	1964.8626	1964.8469	0.0158	245	-	260	0	---	K.VDCTQHYELCSGNQVR.G
1965.8699	1964.8626	1964.8469	0.0158	245	-	260	0	---	K.VDCTQHYELCSGNQVR.G
2193.1243	2192.1170	2192.1477	-0.0307	222	-	241	0	---	K.ALAPTWEQLALGLEHSETVK.I
2225.1138	2224.1065	2224.1375	-0.0310	222	-	241	0	---	K.ALAPTWEQLALGLEHSETVK.I + 2 Oxidation (HW)
2264.0474	2263.0401	2263.0473	-0.0072	242	-	260	1	1	K.IGKVDCTQHYELCSGNQVR.G
2264.0474	2263.0401	2263.0473	-0.0072	242	-	260	1	---	K.IGKVDCTQHYELCSGNQVR.G
2322.1436	2321.1363	2321.0892	0.0471	114	-	134	1	---	K.VYVAKVDCTAHSVCSAQGVR.G
2717.0388	2716.0315	2716.2777	-0.2462	345	-	366	2	---	K.FYAPWCGHCKTLAPTWEELSKK.E + 2 kynurenin (W)

No match to: 1000.6097, 1002.6080, 1005.5906, 1010.6102, 1011.5892, 1013.6169, 1015.6248, 1020.5975, 1023.6009, 1030.6068, 1033.6121, 1036.6215, 1054.6228, 1058.6099, 1061.6210, 1066.1224, 1068.6188, 1074.5782, 1082.6569, 1106.6025, 1111.6449, 1115.6484, 1125.5725, 1166.6556, 1232.6895, 1240.6750, 1320.6155, 1320.6155, 1566.8190, 1638.8807, 1707.7875, 1791.7383, 1813.8920, 1867.9504, 1940.9500, 1993.9651, 2011.9839, 2096.9670, 2150.0862, 2210.0945, 2210.0945, 2211.1050, 2233.0894, 2238.1357, 2299.1736, 2383.9392, 2501.2307, 2501.2307, 2622.2561, 2705.1326, 2811.3069

Spot 761 [ATPB HUMAN](#) Mass: 56525 Score: 180 Expect: 2e-014 Queries matched: 17

ATP synthase subunit beta, mitochondrial OS=Homo sapiens GN=ATP5B PE=1 SV=3

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide	
1088.7170	1087.7097	1087.6277	0.0820	189	-	198	0	---	K.VVDLLAPYAK.G
1401.7567	1400.7494	1400.6969	0.0525	144	-	155	0	---	R.IMNVIGEPIDER.G + Oxidation (M)
1406.7446	1405.7373	1405.6738	0.0636	226	-	239	0	82	K.AHGGYSVFAGVGER.T
1406.7446	1405.7373	1405.6738	0.0636	226	-	239	0	---	K.AHGGYSVFAGVGER.T
1435.8121	1434.8048	1434.7466	0.0582	311	-	324	0	---	R.FTQAGSEVSALLGR.I
1601.8734	1600.8661	1600.8031	0.0630	265	-	279	0	---	K.VALVYQMNEPPGAR.A
1617.8462	1616.8389	1616.7980	0.0409	265	-	279	0	---	K.VALVYQMNEPPGAR.A + Oxidation (M)
1617.8462	1616.8389	1616.7980	0.0409	265	-	279	0	---	K.VALVYQMNEPPGAR.A + Oxidation (M)
1650.9641	1649.9568	1649.9100	0.0468	95	-	109	0	20	R.LVLEVAQHLGESTVR.T
1650.9641	1649.9568	1649.9100	0.0468	95	-	109	0	---	R.LVLEVAQHLGESTVR.T
1816.0017	1814.9944	1814.8621	0.1323	407	-	422	0	---	R.IMDPNIVGSEHYDVAR.G
1831.8818	1830.8745	1830.8570	0.0175	407	-	422	0	---	R.IMDPNIVGSEHYDVAR.G + Oxidation (M)

1831.8818	1830.8745	1830.8570	0.0175	407	-	422	0	---	R.IMDPNIVGSEHYDVAR.G + Oxidation (M)
1988.0490	1987.0417	1987.0262	0.0156	388	-	406	0	16	R.AIAELGIYPAVDPLDSTSR.I
1988.0490	1987.0417	1987.0262	0.0156	388	-	406	0	---	R.AIAELGIYPAVDPLDSTSR.I
2282.1538	2281.1465	2281.0718	0.0747	325	-	345	0	---	R.IPSAVGYQPTLATDMGTMQER.I + Oxidation (M)
2298.0913	2297.0840	2297.0667	0.0173	325	-	345	0	---	R.IPSAVGYQPTLATDMGTMQER.I + 2 Oxidation (M)

No match to: 906.5909, 909.0894, 909.6020, 917.3675, 957.6276, 960.6129, 1027.6448, 1033.6349, 1039.6790, 1045.6556, 1050.1885, 1066.1655, 1072.1705, 1082.1376, 1088.1377, 1106.6439, 1277.1757, 1293.1300, 1320.6633, 1389.8140, 1405.7743, 1428.7596, 1434.8054, 1532.9121, 1552.8407, 1554.8580, 1566.8326, 1767.8856, 1797.0338, 1798.8306, 1812.8988, 1919.1188, 1919.1188, 1939.9539, 1940.9500, 1945.0078, 1962.1259, 2009.0961, 2011.9708, 2026.1125, 2026.1125, 2037.1163, 2040.0558, 2057.0757, 2083.0232, 2194.1436, 2194.1436, 2208.1360, 2211.1050, 2225.1228, 2232.2996, 2233.0898, 2234.0942, 2239.1262, 2247.0996, 2299.1558

Spot 842 [K1C18_HUMAN](#) Mass: 48029 Score: 364 Expect: 8.1e-033 Queries matched: 42

Keratin, type I cytoskeletal 18 OS=Homo sapiens GN=KRT18 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1002.5665	1001.5592	1001.4243	0.1349	125	-	131	0	--- R.DWSHYFK.I + kynurenin (W); Oxidation (HW)
1004.5437	1003.5364	1003.5046	0.0318	100	-	107	1	--- R.SLETENRR.L
1028.5453	1027.5380	1027.4934	0.0446	215	-	222	1	--- K.KNHEEEVK.G + Oxidation (HW)
1030.5741	1029.5668	1029.4192	0.1476	125	-	131	0	--- R.DWSHYFK.I + DOUBLE Ox (W); Oxidation (HW)
1041.6277	1040.6204	1040.5978	0.0226	150	-	158	0	35 R.IVLQIDNAR.L
1041.6277	1040.6204	1040.5978	0.0226	150	-	158	0	--- R.IVLQIDNAR.L
1092.6389	1091.6316	1091.6087	0.0229	91	-	99	1	--- R.LASYLDRVR.S
1093.6069	1092.5996	1092.5563	0.0433	254	-	262	1	--- R.AQYDELARK.N
1221.6847	1220.6774	1220.6513	0.0261	373	-	382	1	--- K.LEAEIATYRR.L
1255.6586	1254.6513	1254.6278	0.0235	166	-	175	1	--- R.VKYETELAMR.Q + Oxidation (M)
1267.6650	1266.6577	1266.6316	0.0261	176	-	186	0	--- R.QSVENDIHGLR.K
1292.6866	1291.6793	1291.7135	-0.0342	371	-	381	1	--- K.VKLEAEIATYR.R
1292.6866	1291.6793	1291.7135	-0.0342	371	-	381	1	--- K.VKLEAEIATYR.R
1319.6925	1318.6852	1318.6629	0.0223	138	-	149	0	--- R.AQIFANTVDNAR.I
1395.7542	1394.7469	1394.7266	0.0203	176	-	187	1	--- R.QSVENDIHGLRK.V
1419.7701	1418.7628	1418.7405	0.0223	359	-	370	0	--- R.QAQEYEALLNIK.V
1448.8418	1447.8345	1447.8147	0.0199	371	-	382	2	--- K.VKLEAEIATYRR.L
1461.7831	1460.7758	1460.7583	0.0176	100	-	111	2	--- R.SLETENRRLESK.I

1473.7814	1472.7741	1472.7583	0.0159	318	-	330	1	---	K.ASLENSLREVEAR.Y
1497.8204	1496.8131	1496.7947	0.0185	418	-	430	2	---	K.VVSETNDTKVLRH.-
1522.7588	1521.7515	1521.7345	0.0171	302	-	314	0	29	R.TVQSLEIDLDSMR.N + Oxidation (M)
1522.7588	1521.7515	1521.7345	0.0171	302	-	314	0	---	R.TVQSLEIDLDSMR.N + Oxidation (M)
1680.8539	1679.8466	1679.8301	0.0166	248	-	261	1	---	K.IMADIRAQYDELAR.K + Oxidation (M)
1680.8539	1679.8466	1679.8301	0.0166	248	-	261	1	---	K.IMADIRAQYDELAR.K + Oxidation (M)
1808.9434	1807.9361	1807.9250	0.0111	248	-	262	2	---	K.IMADIRAQYDELARK.N + Oxidation (M)
1828.9966	1827.9893	1827.9802	0.0091	315	-	330	2	7	R.NLKASLENSLREVEAR.Y
1828.9966	1827.9893	1827.9802	0.0091	315	-	330	2	---	R.NLKASLENSLREVEAR.Y
1961.0117	1960.0044	1960.0013	0.0031	354	-	370	1	---	R.AEGQRQAQEYEALLNIK.V
2044.0344	2043.0271	2043.0095	0.0177	159	-	175	2	---	R.LAADDFRVKYETELAMR.Q + Oxidation (M)
2044.0344	2043.0271	2043.0095	0.0177	159	-	175	2	---	R.LAADDFRVKYETELAMR.Q + Oxidation (M)
2059.1008	2058.0935	2058.0857	0.0078	132	-	149	1	53	K.IIEDLRAQIFANTVDNAR.I
2059.1008	2058.0935	2058.0857	0.0078	132	-	149	1	---	K.IIEDLRAQIFANTVDNAR.I
2183.1033	2182.0960	2182.0800	0.0160	82	-	99	2	---	K.ETMQSLNDRLASYLDRVR.S + Oxidation (M)
2193.1387	2192.1314	2192.1649	-0.0335	197	-	214	1	---	R.LQLETEIEALKEELLFMK.K + Oxidation (M)
2321.2632	2320.2559	2320.2599	-0.0040	197	-	215	2	---	R.LQLETEIEALKEELLFMK.N + Oxidation (M)
2686.3606	2685.3533	2685.3795	-0.0262	331	-	353	0	---	R.YALQMEQLNGILLHLESELAQTR.A + Oxidation (HW)
2749.4006	2748.3933	2748.3929	0.0004	216	-	241	1	---	K.NHEEEVKGLQAQIASSGLTVEVDAPK.S
2756.2649	2755.2576	2755.2494	0.0083	383	-	407	0	---	R.LLEDGEDFNLGDALDSSNSMQTIQK.T + Oxidation (M)
2854.3960	2853.3887	2853.4004	-0.0117	15	-	45	0	27	R.SLGSVQAPSYGARPVSSAASVYAGAGGSGSR.I
2854.3960	2853.3887	2853.4004	-0.0117	15	-	45	0	---	R.SLGSVQAPSYGARPVSSAASVYAGAGGSGSR.I
2912.3577	2911.3504	2911.3505	-0.0001	382	-	407	1	---	R.RLEDGEDFNLGDALDSSNSMQTIQK.T + Oxidation (M)
3391.7341	3390.7268	3390.7266	0.0002	216	-	247	2	---	K.NHEEEVKGLQAQIASSGLTVEVDAPKSDLAK.I

No match to: 1008.5436, 1016.5746, 1030.0721, 1045.5947, 1082.6266, 1106.5807, 1378.7263, 1402.7487, 1427.7311, 1428.2327, 1580.7815, 1609.7728, 1791.7438, 1798.8312, 1811.9629, 1940.9500, 2010.1014, 2041.1327, 2165.0835, 2211.1050, 2225.1221, 2233.0972, 2299.1716, 2360.1335, 2383.9434, 2622.3171, 2632.3264, 2692.2947, 2836.3796, 2849.5049, 3348.7129

Spot 875 [OAT_HUMAN](#) Mass: 48846 Score: 328 Expect: 3.2e-029 Queries matched: 34

Ornithine aminotransferase, mitochondrial OS=Homo sapiens GN=OAT PE=1 SV=1

Observed	Mr(expt)	Mr(calcd)	Delta	Start	End	Miss	Ions	Peptide
----------	----------	-----------	-------	-------	-----	------	------	---------

935.6051	934.5978	934.5600	0.0379	162	-	169	2	---	K.GIQKYKAK.I
1056.7004	1055.6931	1055.5975	0.0957	363	-	372	0	---	K.LPSDVVTAVR.G
1056.7004	1055.6931	1055.5975	0.0957	363	-	372	0	---	K.LPSDVVTAVR.G
1211.6826	1210.6753	1210.6346	0.0407	156	-	165	1	---	K.WGYTVKGIQK.Y + DOUBLE Ox (W)
1241.7131	1240.7058	1240.6352	0.0706	170	-	180	0	38	K.IVFAAGNFWGR.T + kynurenin (W)
1241.7131	1240.7058	1240.7139	-0.0081	363	-	374	1	---	K.LPSDVVTAVRGK.G
1253.7186	1252.7113	1252.6928	0.0186	152	-	161	2	---	K.LARKWGYTVK.G + DOUBLE Ox (W)
1269.7061	1268.6988	1268.6301	0.0687	170	-	180	0	---	K.IVFAAGNFWGR.T + DOUBLE Ox (W)
1396.7806	1395.7733	1395.7146	0.0587	65	-	76	1	28	R.GKGIYLDVEGR.K + kynurenin (W)
1396.7806	1395.7733	1395.7146	0.0587	65	-	76	1	---	R.GKGIYLDVEGR.K + kynurenin (W)
1440.8236	1439.8163	1439.7673	0.0490	168	-	180	1	---	K.AKIVFAAGNFWGR.T + kynurenin (W)
1468.8141	1467.8068	1467.7622	0.0446	168	-	180	1	---	K.AKIVFAAGNFWGR.T + DOUBLE Ox (W)
1526.9000	1525.8927	1525.8504	0.0424	414	-	426	1	---	R.FAPPLVIKEDEL.R.E
1561.7975	1560.7902	1560.7420	0.0483	33	-	46	0	---	K.TVQGPPTSDDIFER.E
1619.9290	1618.9217	1618.8791	0.0427	399	-	413	0	---	R.DNGLLAKPTHGDIIR.F
1689.8932	1688.8859	1688.8369	0.0490	32	-	46	1	---	K.KTVQGPPTSDDIFER.E
1736.9211	1735.9138	1735.8794	0.0344	50	-	64	0	45	K.YGAHNYHPLPVALER.G
1736.9211	1735.9138	1735.8794	0.0344	50	-	64	0	---	K.YGAHNYHPLPVALER.G
1811.0103	1810.0030	1809.9737	0.0293	256	-	271	0	87	R.HQVLFIADEIQTGLAR.T
1811.0103	1810.0030	1809.9737	0.0293	256	-	271	0	---	R.HQVLFIADEIQTGLAR.T
1826.9043	1825.8970	1825.9686	-0.0716	256	-	271	0	---	R.HQVLFIADEIQTGLAR.T + Oxidation (HW)
1886.1356	1885.1283	1885.0996	0.0287	97	-	113	2	---	K.IVNALKSQVDKLTLSR.A
1889.0952	1888.0879	1888.0642	0.0237	397	-	413	1	0	R.LRDNGLLAKPTHGDIIR.F
1889.0952	1888.0879	1888.0642	0.0237	397	-	413	1	---	R.LRDNGLLAKPTHGDIIR.F
1952.9447	1951.9374	1951.9203	0.0172	114	-	129	0	---	R.AFYNNVLGEYEEYITK.L
1981.9651	1980.9578	1980.9428	0.0150	33	-	49	1	---	K.TVQGPPTSDDIFEREYK.Y
2104.1528	2103.1455	2103.1364	0.0092	275	-	292	0	16	R.WLAVDYENVRPDIVLLGK.A + kynurenin (W)
2104.1528	2103.1455	2103.1364	0.0091	375	-	392	2	---	K.GLLNAIVIKETKDWDAWK.V + kynurenin (W)
2132.1379	2131.1306	2131.1313	-0.0007	275	-	292	0	---	R.WLAVDYENVRPDIVLLGK.A + DOUBLE Ox (W)
2157.0989	2156.0916	2156.0802	0.0114	47	-	64	1	---	R.EYKYGAHNYHPLPVALER.G

2257.0254	2256.0181	2256.0058	0.0123	78	-	96	0	---	K.YFDLSSYSYAVNQGHCHPK.I
2385.1052	2384.0979	2384.1007	-0.0028	77	-	96	1	---	R.KYFDLSSYSYAVNQGHCHPK.I
2453.3550	2452.3477	2452.3576	-0.0099	414	-	434	2	---	R.FAPPLVIKEDELRESIEIINK.T
2766.2839	2765.2766	2765.4395	-0.1628	251	-	274	2	---	R.ELCTRHQVLFIADEIQTGLARTGR.W + Pyro-glu (N-term E)

No match to: 920.5743, 1008.6250, 1044.1500, 1044.5540, 1045.6439, 1066.1550, 1072.1588, 1082.1158, 1106.1091, 1106.6218, 1132.6876, 1259.6543, 1259.6543, 1277.1565, 1285.7885, 1388.7902, 1798.8367, 1806.8925, 1823.0164, 1923.9963, 1940.9500, 1944.9482, 1994.0256, 2006.0809, 2011.9730, 2083.0217, 2193.1152, 2206.1636, 2211.1050, 2225.1172, 2232.1709, 2233.0916, 2235.0952, 2282.1685, 2299.1724, 2811.2827, 3339.6692, 3352.5388, 3812.7483

Spot 879 [IDHC_HUMAN](#) Mass: 46915 Score: 229 Expect: 2.6e-019 Queries matched: 30

Isocitrate dehydrogenase [NADP] cytoplasmic OS=Homo sapiens GN=IDH1 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
907.5652	906.5579	906.4348	0.1231	244	-	249	0	13 K.IWYEHR.L + kynurenin (W)
907.5652	906.5579	906.4348	0.1231	244	-	249	0	---
918.6248	917.6175	917.5586	0.0589	21	-	27	0	---
935.5576	934.5503	934.4297	0.1206	244	-	249	0	---
976.6771	975.6698	975.5501	0.1197	101	-	109	0	19 R.NILGGTVFR.E
976.6771	975.6698	975.5501	0.1197	101	-	109	0	---
1009.5677	1008.5604	1008.4413	0.1191	133	-	140	0	53 R.HAYGDQYR.A
1009.5677	1008.5604	1008.4413	0.1191	133	-	140	0	---
1068.6776	1067.6703	1067.5651	0.1052	204	-	212	0	---
1175.8232	1174.8159	1174.6961	0.1198	21	-	29	1	---
1341.7744	1340.7671	1340.6684	0.0987	302	-	314	0	---
1441.9692	1440.9619	1440.8816	0.0803	120	-	132	0	36 R.LVSGVWKPIIIGR.H + kynurenin (W)
1441.9692	1440.9619	1440.8816	0.0803	120	-	132	0	---
1469.9629	1468.9556	1468.8765	0.0791	120	-	132	0	(33) R.LVSGVWKPIIIGR.H + DOUBLE Ox (W)
1469.9629	1468.9556	1468.8765	0.0791	120	-	132	0	---
1690.9933	1689.9860	1689.9235	0.0625	101	-	115	1	---
1725.8862	1724.8789	1724.8270	0.0519	237	-	249	1	20 K.SQFEAQKIWYEHR.L + kynurenin (W)
1725.8862	1724.8789	1724.8270	0.0519	237	-	249	1	---
1753.8943	1752.8870	1752.8219	0.0651	237	-	249	1	---
1822.9530	1821.9457	1821.8931	0.0527	73	-	87	2	---

1864.9849	1863.9776	1863.9406	0.0370	223	-	236	2	---	R.FKDIFQEIYDKQYK.S
1882.9675	1881.9602	1881.9221	0.0382	322	-	338	0	41	K.GQETSTNPIASIFAWTR.G + kynurenin (W)
1882.9675	1881.9602	1881.9221	0.0382	322	-	338	0	---	K.GQETSTNPIASIFAWTR.G + kynurenin (W)
1895.0286	1894.0213	1893.9221	0.0993	322	-	338	0	---	K.GQETSTNPIASIFAWTR.G + Oxidation (HW)
1910.9619	1909.9546	1909.9170	0.0376	322	-	338	0	---	K.GQETSTNPIASIFAWTR.G + DOUBLE Ox (W)
2180.0481	2179.0408	2179.0143	0.0266	389	-	406	1	---	R.SDYLNTEFMDKLGLENLKI + Oxidation (M)
2406.2166	2405.2093	2405.2266	-0.0173	30	-	49	0	1	K.LIFPYVELDLHSYDLGIENR.D
2406.2166	2405.2093	2405.2266	-0.0173	30	-	49	0	---	K.LIFPYVELDLHSYDLGIENR.D
2421.1860	2420.1787	2420.1933	-0.0146	389	-	408	2	---	R.SDYLNTEFMDKLGLENLKI.L + Oxidation (M)
3378.6111	3377.6038	3377.6779	-0.0740	30	-	58	1	---	K.LIFPYVELDLHSYDLGIENRDATNDQVTK.D

No match to: 904.9641, 909.1044, 918.9701, 923.7097, 941.7115, 946.9749, 958.6962, 959.7203, 965.6043, 970.6986, 987.6614, 995.7206, 1021.5577, 1030.7559, 1045.6877, 1066.1722, 1072.1904, 1082.1500, 1088.1573, 1277.1782, 1424.8395, 1440.9612, 1450.9292, 1452.9785, 1798.8486, 1826.8439, 1881.9861, 1891.9631, 1940.9563, 1962.9512, 2011.9691, 2064.1021, 2193.0986, 2211.1045, 2225.1218, 2233.0869, 2236.1680, 2249.0923, 2299.1655, 2622.2747, 3339.6204, 3353.6719, 3812.6799

Spot 1149 [ROA2_HUMAN](#) Mass: 37464 Score: 222 Expect: 1.3e-018 Queries matched: 22

Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide	
1013.5621	1012.5548	1012.4362	0.1186	204	-	213	0	34 R.GGNFGFGDSR.G	
1013.5621	1012.5548	1012.4362	0.1186	204	-	213	0	---	R.GGNFGFGDSR.G
1057.7058	1056.6985	1056.5815	0.1170	4	-	12	0	---	K.TLETVPLER.K
1313.6879	1312.6806	1312.5908	0.0898	201	-	213	1	4	R.SGRGGNFGFGDSR.G
1313.6879	1312.6806	1312.5908	0.0898	201	-	213	1	---	R.SGRGGNFGFGDSR.G
1320.6682	1319.6609	1319.6833	-0.0224	100	-	112	0	---	R.EESGKPGAHVTVK.K + Pyro-glu (N-term E)
1338.8079	1337.8006	1337.6939	0.1068	100	-	112	0	---	R.EESGKPGAHVTVK.K
1377.7162	1376.7089	1376.6221	0.0869	214	-	228	0	77	R.GGGGNFGPGPSNFR.G
1377.7162	1376.7089	1376.6221	0.0869	214	-	228	0	---	R.GGGGNFGPGPSNFR.G
1410.7725	1409.7652	1409.6800	0.0853	174	-	185	0	53	K.YHTINGHNAEVR.K
1410.7725	1409.7652	1409.6800	0.0853	174	-	185	0	---	K.YHTINGHNAEVR.K
1538.8525	1537.8452	1537.7749	0.0703	174	-	186	1	2	K.YHTINGHNAEVRK.A
1538.8525	1537.8452	1537.7749	0.0703	174	-	186	1	---	K.YHTINGHNAEVRK.A

1664.8615	1663.8542	1663.7947	0.0595	187	-	200	1	---	K.ALSRQEMQEVQSSR.S + Oxidation (M)
1798.8519	1797.8446	1797.9148	-0.0702	23	-	38	0	---	K.LFIGGLSFETTEESLR.N
1867.9562	1866.9489	1866.8536	0.0953	153	-	168	1	---	K.RGFGFVTFDDHDPVVK.I + Oxidation (HW)
2205.9014	2204.8941	2204.8928	0.0013	326	-	350	0	---	R.NMGPPYGGGNYPGGGSGGGYGGGR.S + Oxidation (M)
2205.9014	2204.8941	2204.8928	0.0013	326	-	350	0	---	R.NMGPPYGGGNYPGGGSGGGYGGGR.S + Oxidation (M)
2211.1040	2210.0967	2209.9188	0.1779	121	-	137	1	---	K.EDTEEHHLRDYFEEYK.I + 2 Oxidation (HW); Pyro-glu (N-term E)
2277.1472	2276.1399	2276.1477	-0.0077	154	-	173	1	7	R.GFGFVTFDDHDPVVKIVLQK.Y
2277.1472	2276.1399	2276.1477	-0.0077	154	-	173	1	---	R.GFGFVTFDDHDPVVKIVLQK.Y
2495.0205	2494.0132	2494.0321	-0.0188	239	-	266	0	---	R.GFGDGYNGYGGGPGGGNFGGSPGYGGGR.G

No match to: 905.5921, 912.5243, 914.6615, 917.4235, 948.5579, 949.5769, 1045.6838, 1066.1896, 1072.1885, 1082.1627, 1088.1650, 1179.7026, 1235.6379, 1277.1875, 1277.8040, 1327.7094, 1333.7125, 1376.7594, 1434.8671, 1493.8107, 1560.8728, 1566.7909, 1584.7885, 1585.8521, 1600.8383, 1638.9214, 1688.0198, 1707.8345, 1713.9028, 1791.7732, 1796.8590, 1809.8669, 1922.9681, 1940.9589, 1993.9933, 2011.9847, 2083.0171, 2141.9099, 2143.1597, 2193.1082, 2225.1182, 2233.1011, 2235.1201, 2299.1665, 2383.9380, 2501.2295, 2622.2607, 2622.2607, 2705.1143, 2717.0342, 3353.6729

Spot 1156 [ACTB HUMAN](#) Mass: 42052 Score: 70 Expect: 0.0021 Queries matched: 12

Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide	
1036.6647	1035.6574	1035.6440	0.0134	327	-	335	1	---	K.IKIIAPPER.K
1129.6660	1128.6587	1128.6502	0.0085	207	-	215	2	---	R.EIVRDIKEK.L
1132.6213	1131.6140	1131.5196	0.0944	197	-	206	0	---	R.GYSFTTTAER.E
1516.7474	1515.7401	1515.6953	0.0448	360	-	372	0	---	K.QEYDESGPSIVHR.K
1516.7474	1515.7401	1515.6953	0.0448	360	-	372	0	---	K.QEYDESGPSIVHR.K
1790.9183	1789.9110	1789.8846	0.0264	239	-	254	0	26	K.SYELPDGQVITIGNER.F
1790.9183	1789.9110	1789.8846	0.0264	239	-	254	0	---	K.SYELPDGQVITIGNER.F
1954.0850	1953.0777	1953.0571	0.0207	96	-	113	0	32	R.VAPEEHPVLLTEAPLNPK.A
1954.0850	1953.0777	1953.0571	0.0207	96	-	113	0	---	R.VAPEEHPVLLTEAPLNPK.A
2622.2715	2621.2642	2621.3199	-0.0557	337	-	359	0	---	K.YSVWIGGSILASLSTFQQMWISK.Q + Oxidation (M); kynurenin (W)
2622.2715	2621.2642	2621.3199	-0.0557	337	-	359	0	---	K.YSVWIGGSILASLSTFQQMWISK.Q + kynurenin (W); Oxidation (HW)
2650.2651	2649.2578	2649.3148	-0.0570	337	-	359	0	---	K.YSVWIGGSILASLSTFQQMWISK.Q + Oxidation (M); 2 Oxidation (HW)

No match to: 1000.6295, 1002.6183, 1003.6252, 1006.6227, 1008.6249, 1010.6094, 1012.6433, 1015.6338, 1016.6201, 1017.6006, 1020.6214, 1023.6190, 1026.6344, 1028.6238, 1030.6423, 1032.6426, 1040.6539, 1042.6316, 1045.6306, 1048.6307, 1051.6298, 1057.6527, 1063.6547, 1066.1418, 1066.6198, 1081.6604, 1082.1134, 1095.6318, 1098.0848, 1098.6416, 1106.6151, 1112.6573, 1149.6997, 1160.6987, 1165.6952, 1264.6722, 1320.6378, 1320.6378, 1365.7936, 1475.8291, 1493.7859, 1549.7611, 1707.8199, 1763.9148, 1763.9148, 1808.8419, 1826.8391, 1940.9539, 2011.9885, 2082.0483, 2193.1260, 2193.1260, 2210.1045, 2211.1047, 2225.1106, 2233.0847, 2234.0911, 2234.0911, 2299.1753, 2415.2122, 3353.6250

Spot 1533 [PSA7_HUMAN](#) Mass: 28041 Score: 145 Expect: 6.4e-011 Queries matched: 22

Proteasome subunit alpha type-7 OS=Homo sapiens GN=PSMA7 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1007.6086	1006.6013	1006.5447	0.0566	167	-	174	1	--- K.SVREFLEK.N
1033.6158	1032.6085	1032.5087	0.0998	235	-	242	2	--- K.EKEENEKK.K
1045.6023	1044.5950	1044.5563	0.0387	49	-	57	1	--- K.SVAKLQDER.T
1109.6208	1108.6135	1108.5373	0.0762	116	-	124	1	--- K.QRYTQSNR.R
1142.5880	1141.5807	1141.5410	0.0397	87	-	95	1	--- R.ARVECQSHR.L
1142.5880	1141.5807	1141.5410	0.0397	87	-	95	1	--- R.ARVECQSHR.L
1184.7356	1183.7283	1183.6924	0.0359	37	-	47	1	--- R.GRDIVVLGVEK.K
1634.8821	1633.8748	1633.8563	0.0186	96	-	109	0	16 R.LTVEDPVTVEYITR.Y
1634.8821	1633.8748	1633.8563	0.0186	96	-	109	0	--- R.LTVEDPVTVEYITR.Y
1670.8109	1669.8036	1669.7736	0.0300	144	-	157	0	24 R.LYQTDPSGTYHAWK.A + kynurenin (W)
1670.8109	1669.8036	1669.7736	0.0300	144	-	157	0	--- R.LYQTDPSGTYHAWK.A + kynurenin (W)
2065.0911	2064.0838	2064.0792	0.0046	125	-	143	0	26 R.RPFGISALIVGFDFDGTPR.L
2065.0911	2064.0838	2064.0792	0.0046	125	-	143	0	--- R.RPFGISALIVGFDFDGTPR.L
2194.1152	2193.1079	2193.1416	-0.0337	175	-	193	1	--- K.NYTDEAIETDDLTIKLVK.A
2200.0449	2199.0376	2198.9758	0.0618	62	-	81	0	--- K.ICALDDNVCMAFAGLTADAR.I + Oxidation (M)
2200.0449	2199.0376	2198.9758	0.0618	62	-	81	0	--- K.ICALDDNVCMAFAGLTADAR.I + Oxidation (M)
2265.0415	2264.0342	2264.0974	-0.0632	144	-	163	1	--- R.LYQTDPSGTYHAWKANAIGR.G + Oxidation (HW)
2328.0667	2327.0594	2327.0708	-0.0113	61	-	81	1	--- R.KICALDDNVCMAFAGLTADAR.I + Oxidation (M)
2328.0667	2327.0594	2327.0708	-0.0113	61	-	81	1	--- R.KICALDDNVCMAFAGLTADAR.I + Oxidation (M)
2577.3130	2576.3057	2576.3274	-0.0217	6	-	28	1	--- R.AITVFSPDGHLFQVEYAQEAQVKK.G
2594.3943	2593.3870	2593.4115	-0.0245	96	-	117	2	--- R.LTVEDPVTVEYITRYIASLKQR.Y
3304.6855	3303.6782	3303.7250	-0.0468	6	-	36	2	--- R.AITVFSPDGHLFQVEYAQEAQVKKGSTAVGVR.G

No match to: 1000.5882, 1002.5970, 1004.6077, 1008.6019, 1011.6121, 1012.6088, 1014.5938, 1015.6074, 1017.6130, 1019.5919, 1020.5941, 1023.5964, 1027.6005, 1029.5858, 1031.6066, 1038.6147, 1048.5802, 1048.5802, 1051.6143, 1054.6305, 1055.5939, 1066.1151, 1068.6288, 1074.6530, 1082.0895, 1088.6476, 1098.0620, 1105.6548, 1106.0886, 1106.5969, 1139.6687, 1150.6543, 1160.6379, 1282.7355, 1478.8025, 1480.8275, 1798.8346, 1939.9697, 1940.9500, 1976.0106, 2011.9879, 2083.0249, 2193.1089, 2211.1050, 2225.1160, 2233.0947, 2299.1731, 2622.2859, 2811.2910, 2811.2910, 3812.7241

Spot 1580 [GSTAI HUMAN](#) Mass: 25672 Score: 415 Expect: 6.4e-038 Queries matched: 24

Glutathione S-transferase A1 OS=Homo sapiens GN=GSTAI1 PE=1 SV=3

Observed	Mr(expt)	Mr(calcd)	Delta	Start	End	Miss	Ions	Peptide
992.6935	991.6862	991.5702	0.1160	70	- 78	0	---	R.AILNYIASK.Y
1029.7166	1028.7093	1028.5767	0.1326	196	- 204	1	43	K.KFLQPGSPR.K
1029.7166	1028.7093	1028.5767	0.1326	196	- 204	1	---	K.KFLQPGSPR.K
1113.7128	1112.7055	1112.5866	0.1190	79	- 87	1	---	K.YNLYGKDIK.E
1171.7081	1170.7008	1170.5821	0.1187	130	- 138	1	45	K.NRYFPAFEK.V
1171.7081	1170.7008	1170.5821	0.1187	130	- 138	1	---	K.NRYFPAFEK.V
1217.6984	1216.6911	1216.5836	0.1075	142	- 152	0	75	K.SHGQDYLVGNK.L
1217.6984	1216.6911	1216.5836	0.1075	142	- 152	0	---	K.SHGQDYLVGNK.L
1398.8326	1397.8253	1397.7303	0.0951	79	- 89	2	29	K.YNLYGKDIKER.A
1398.8326	1397.8253	1397.7303	0.0951	79	- 89	2	---	K.YNLYGKDIKER.A
1466.8375	1465.8302	1465.7452	0.0850	21	- 33	0	---	R.WLLAAAGVEFEEK.F + kynurenin (W)
1489.9164	1488.9091	1488.7837	0.1254	2	- 13	1	---	M.AEKPKLHYFNAR.G + Oxidation (HW)
1494.8248	1493.8175	1493.7401	0.0774	21	- 33	0	---	R.WLLAAAGVEFEEK.F + DOUBLE Ox (W)
1545.8307	1544.8234	1544.7504	0.0730	205	- 217	1	---	R.KPPMDEKSLEEAR.K + Oxidation (M)
1557.9048	1556.8975	1556.8310	0.0665	139	- 152	1	---	K.VLKSHGQDYLVGNK.L
1573.8824	1572.8751	1572.8008	0.0743	142	- 155	1	73	K.SHGQDYLVGNKLSR.A
1573.8824	1572.8751	1572.8259	0.0492	139	- 152	1	---	K.VLKSHGQDYLVGNK.L + Oxidation (HW)
1673.9158	1672.9085	1672.8454	0.0632	205	- 218	2	---	R.KPPMDEKSLEEAR.K + Oxidation (M)
1730.9985	1729.9912	1729.9402	0.0510	70	- 84	1	63	R.AILNYIASKYNLYGK.D
1730.9985	1729.9912	1729.9402	0.0510	70	- 84	1	---	R.AILNYIASKYNLYGK.D
1855.0438	1854.0365	1853.9926	0.0439	21	- 36	1	---	R.WLLAAAGVEFEEKFIK.S + kynurenin (W)
1882.1332	1881.1259	1881.0836	0.0424	188	- 204	2	---	R.ISNLPVKKFLQPGSPR.K
2083.0295	2082.0222	2082.0091	0.0131	16	- 33	1	---	R.MESTRWLLAAAGVEFEEK.F + Oxidation (HW)
2087.1609	2086.1536	2086.1462	0.0074	70	- 87	2	---	R.AILNYIASKYNLYGKDIK.E

No match to: 901.6248, 901.6248, 905.6132, 906.6392, 920.6128, 920.6128, 924.6083, 932.6165, 935.5781, 942.5835, 946.6240, 963.6338, 977.6261, 1045.6948, 1066.2052, 1072.2188, 1088.1907, 1091.6375, 1106.6646, 1154.7310, 1193.6927, 1199.7023, 1395.8457, 1477.8477, 1515.8887, 1555.8641, 1599.8765, 1713.9073, 1781.8724, 1798.8571, 1809.8773, 1812.8868, 1826.8525, 1940.9666, 1944.9573, 1972.0187, 2011.9939, 2193.0828, 2211.1050, 2225.1184, 2233.0981, 2235.1128, 2237.2083, 2299.1638, 2321.2454, 2372.2883, 2622.2539, 2650.2527, 3353.6289

Spot 1671 [PSB3_HUMAN](#) Mass: 23219 Score: 173 Expect: 1e-013 Queries matched: 20

Proteasome subunit beta type-3 OS=Homo sapiens GN=PSMB3 PE=1 SV=2

Observed	Mr(expt)	Mr(calcd)	Delta	Start	End	Miss	Ions	Peptide
1145.6416	1144.6343	1144.5771	0.0572	18	- 27	1	---	K.NCVAIAADRR.F
1195.7225	1194.7152	1194.6760	0.0392	69	- 77	1	---	K.FRLNLYELK.E
1195.7225	1194.7152	1194.6760	0.0392	69	- 77	1	---	K.FRLNLYELK.E
1234.7168	1233.7095	1233.6717	0.0378	71	- 80	1	---	R.LNLYELKEGR.Q
1436.8900	1435.8827	1435.8551	0.0277	67	- 77	2	---	R.LKFRLNLYELK.E
1537.8745	1536.8672	1536.8412	0.0260	69	- 80	2	---	K.FRLNLYELKEGR.Q
1537.8745	1536.8672	1536.8412	0.0260	69	- 80	2	---	K.FRLNLYELKEGR.Q
1629.8187	1628.8114	1628.7868	0.0246	28	- 41	0	30	R.FGIQAQMVTTDFQK.I + Oxidation (M)
1629.8187	1628.8114	1628.7868	0.0246	28	- 41	0	---	R.FGIQAQMVTTDFQK.I + Oxidation (M)
1766.9222	1765.9149	1765.8926	0.0223	100	- 115	0	52	R.FGPPYYTEPVIAGLDPK.T
1766.9222	1765.9149	1765.8926	0.0223	100	- 115	0	---	R.FGPPYYTEPVIAGLDPK.T
1791.7417	1790.7344	1790.8187	-0.0842	1	- 17	1	---	-.MSIMSYNGGAVMAMKKG.N + Oxidation (M)
1807.8328	1806.8255	1806.8136	0.0119	1	- 17	1	---	-.MSIMSYNGGAVMAMKKG.N + 2 Oxidation (M)
1889.0581	1888.0508	1888.0417	0.0091	49	- 66	0	22	R.LYIGLAGLATDVQTVQR.L
1889.0581	1888.0508	1888.0417	0.0091	49	- 66	0	---	R.LYIGLAGLATDVQTVQR.L
1922.9993	1921.9920	1921.9937	-0.0017	99	- 115	1	---	K.RFGPPYYTEPVIAGLDPK.T
2130.2305	2129.2232	2129.2208	0.0025	49	- 68	1	---	R.LYIGLAGLATDVQTVQR.LK.F
2282.1379	2281.1306	2281.2463	-0.1157	178	- 198	2	---	R.DAVSGMGVIVHIEKDKITTR.T
2330.2236	2329.2163	2329.2173	-0.0010	81	- 99	1	---	R.QIKPYTLMSMVANLLYEKR.F + 2 Oxidation (M)
2705.1399	2704.1326	2704.4370	-0.3043	42	- 66	1	---	K.IFPMGDRLYIGLAGLATDVQTVQR.L

No match to: 1000.6152, 1000.6152, 1002.6139, 1004.6134, 1008.6147, 1010.5927, 1013.5957, 1015.6116, 1017.5989, 1019.6063, 1024.6237, 1026.6123, 1028.5992, 1031.6154, 1033.6083, 1045.6053, 1049.6187, 1055.6101, 1055.6101, 1057.6379, 1060.6169, 1067.6100, 1074.6031, 1082.0903, 1106.0941, 1106.5999, 1125.5774, 1125.5774, 1142.6329, 1161.6609, 1235.5773, 1584.7423, 1657.8221, 1694.8754, 1779.0535, 1798.8226, 1940.9500, 2011.9860, 2083.0215, 2193.0681, 2194.0823, 2211.1050, 2225.1182, 2233.0774, 2235.1389, 2265.0269, 2299.1838, 2313.1926, 2383.9346, 2622.2512, 2811.2749, 3353.6465, 3812.6997

Spot 1931 [PROF1_HUMAN](#) Mass: 15216 Score: 299 Expect: 2.6e-026 Queries matched: 18

Profilin-1 OS=Homo sapiens GN=PFN1 PE=1 SV=2

Observed	Mr(expt)	Mr(calcd)	Delta	Start	End	Miss	Ions	Peptide
----------	----------	-----------	-------	-------	-----	------	------	---------

1151.7721	1150.7648	1150.6458	0.1190	117	-	127	1	---	K.EGVHGGLINKK.C
1182.6157	1181.6084	1181.4957	0.1127	128	-	136	0	39	K.CYEMASHLR.R + Oxidation (M)
1182.6157	1181.6084	1181.4957	0.1127	128	-	136	0	---	K.CYEMASHLR.R + Oxidation (HW)
1310.7063	1309.6990	1309.5907	0.1083	127	-	136	1	---	K.KCYEMASHLR.R + Oxidation (HW)
1338.7008	1337.6935	1337.5968	0.0967	128	-	137	1	---	K.CYEMASHLRR.S + Oxidation (HW)
1354.6998	1353.6925	1353.5918	0.1008	128	-	137	1	---	K.CYEMASHLRR.S + Oxidation (M); Oxidation (HW)
1379.8292	1378.8219	1378.7092	0.1127	92	-	105	0	---	K.STGGAPTFFNVTVT.K.T
1470.8436	1469.8363	1469.7514	0.0850	57	-	70	0	75	R.SSFYVNGTLGGQK.C
1470.8436	1469.8363	1469.7514	0.0850	57	-	70	0	---	R.SSFYVNGTLGGQK.C
1641.8097	1640.8024	1640.7352	0.0673	76	-	89	0	17	R.DSLLQDGEFSMDLR.T + Oxidation (M)
1641.8097	1640.8024	1640.7352	0.0673	76	-	89	0	---	R.DSLLQDGEFSMDLR.T + Oxidation (M)
1741.9563	1740.9490	1740.8794	0.0696	55	-	70	1	---	K.DRSSFYVNGTLGGQK.C
1915.1036	1914.0963	1914.0574	0.0390	39	-	56	1	98	K.TFVNITPAEVGLVGKDR.S
1915.1036	1914.0963	1914.0574	0.0390	39	-	56	1	---	K.TFVNITPAEVGLVGKDR.S
2255.1113	2254.1040	2254.2354	-0.1314	106	-	126	2	---	K.TDKTLVLLMGKEGVHGLINK.K + Oxidation (M); Oxidation (HW)
2257.0574	2256.0501	2256.0514	-0.0013	71	-	89	1	1	K.CSVIRDSLLQDGEFSMDLR.T + Oxidation (M)
2257.0574	2256.0501	2256.0514	-0.0013	71	-	89	1	---	K.CSVIRDSLLQDGEFSMDLR.T + Oxidation (M)
2299.1658	2298.1585	2298.1360	0.0225	117	-	136	2	---	K.EGVHGGLINKKCYEMASHLR.R

No match to: 914.5476, 914.5476, 922.6635, 933.6537, 1011.7739, 1045.6943, 1066.2098, 1066.6642, 1072.2141, 1076.6603, 1082.1866, 1088.1854, 1106.6746, 1117.6753, 1126.6920, 1129.1512, 1129.6503, 1150.7201, 1165.5955, 1248.6847, 1273.8176, 1277.1991, 1320.7094, 1321.6803, 1321.6803, 1337.6744, 1453.8123, 1566.8293, 1798.8571, 1800.8695, 1826.8524, 1872.0571, 1897.1061, 1914.0070, 1923.9863, 1924.9890, 1940.9668, 1962.9539, 2011.9994, 2083.0374, 2193.0916, 2194.0903, 2208.1155, 2211.1050, 2221.1235, 2225.1221, 2233.0923, 2235.1042, 2236.1672, 2240.0742, 2240.0742, 2247.1533, 2811.2297, 3339.6401, 3353.6145

Spot 2765 [HYOU1 HUMAN](#) Mass: 111494 Score: 159 Expect: 2.6e-012 Queries matched: 28

Hypoxia up-regulated protein 1 OS=Homo sapiens GN=HYOU1 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide	
917.3814	916.3741	916.4614	-0.0873	730	-	736	1	---	R.DLEKQER.E
992.6327	991.6254	991.4909	0.1345	473	-	480	1	---	R.MGPYPQRK.V + Oxidation (M)
1005.6417	1004.6344	1004.5443	0.0901	99	-	106	0	17	R.YFQHLLGK.Q
1005.6417	1004.6344	1004.5443	0.0901	99	-	106	0	---	R.YFQHLLGK.Q
1047.6580	1046.6507	1046.5508	0.0999	283	-	291	0	27	R.LAGLFNEQR.K
1047.6580	1046.6507	1046.5508	0.0999	283	-	291	0	---	R.LAGLFNEQR.K

1134.6781	1133.6708	1133.5750	0.0958	269	-	278	0	---	R.TLGGLEMELR.L + Oxidation (M)
1150.6644	1149.6571	1149.5818	0.0753	860	-	868	0	---	K.VINETWAWK.N + kynurenin (W)
1286.7260	1285.7187	1285.6561	0.0627	298	-	308	2	---	K.DVRENPRAMAK.L
1482.8079	1481.8006	1481.7375	0.0631	107	-	119	0	52	K.QADNPHVALYQAR.F
1482.8079	1481.8006	1481.7375	0.0631	107	-	119	0	---	K.QADNPHVALYQAR.F
1515.7910	1514.7837	1514.7154	0.0684	120	-	131	0	18	R.FPEHELTFDPQR.Q
1515.7910	1514.7837	1514.7875	-0.0038	250	-	262	1	---	K.TKEAGMQPQLQIR.G + Oxidation (M)
1521.8910	1520.8837	1520.8238	0.0599	439	-	451	0	---	R.DAVVYPILVEFTR.E
1723.0687	1722.0614	1722.0113	0.0501	47	-	62	0	---	K.VAIVKPGVPMEIVLNK.E + Oxidation (M)
1756.9659	1755.9586	1755.9479	0.0107	723	-	736	2	---	K.LQDLTLRDLEKQER.E
1902.0024	1900.9951	1900.9754	0.0197	452	-	467	2	---	R.EVEEEPFIHSLKHNR.V
1922.9724	1921.9651	1921.9421	0.0230	737	-	753	1	---	R.EKAANSLEAFIFETQDK.L + Pyro-glu (N-term E)
1940.9589	1939.9516	1939.9527	-0.0010	737	-	753	1	---	R.EKAANSLEAFIFETQDK.L
2012.9928	2011.9855	2011.9673	0.0183	343	-	358	1	---	K.VTRVEFEELCADLFR.V
2095.1362	2094.1289	2094.1109	0.0180	199	-	217	0	10	K.VLQLINDNTATALSYGVFR.R
2095.1362	2094.1289	2094.1109	0.0180	199	-	217	0	---	K.VLQLINDNTATALSYGVFR.R
2211.1042	2210.0969	2210.0776	0.0193	775	-	795	0	---	K.LSAASTWLEDEGVGATTVMLK.E + Oxidation (M); Oxidation (HW)
2235.0869	2234.0796	2234.2932	-0.2136	47	-	66	2	---	K.VAIVKPGVPMEIVLNKESRR.K
2299.1697	2298.1624	2298.1011	0.0614	841	-	859	0	---	R.LIPEMDQIFTEVEMTTLEK.V + 2 Oxidation (M)
2726.2300	2725.2227	2725.2560	-0.0333	487	-	509	0	---	R.YSHDFNFHINYGDLGFLGPEDLR.V
3034.4944	3033.4871	3033.5446	-0.0575	159	-	185	1	---	R.SLAEDFAEQPIKDAVITVPVFFNQAER.R
3353.6531	3352.6458	3352.8394	-0.1936	860	-	889	2	---	K.VINETWAWKNATLAEQAKLPATEKPVLLSK.D + kynurenin (W)

No match to: 900.6008, 903.6245, 907.5855, 914.6012, 918.9532, 923.6285, 963.5696, 990.6262, 1008.6332, 1013.6597, 1044.1726, 1045.6675, 1055.5942, 1055.5942, 1066.1779, 1072.1810, 1077.2823, 1082.1498, 1088.1479, 1106.1252, 1106.6340, 1125.7017, 1277.1737, 1282.7585, 1293.1589, 1566.7920, 1713.8560, 1781.8799, 1798.8481, 1923.9673, 1944.9476, 1962.9451, 2011.9917, 2083.0193, 2193.0994, 2193.0994, 2207.1179, 2225.1223, 2233.0957, 2238.2188, 2246.1973, 2811.2778, 2811.2778, 3339.6667, 3812.7385

Spot N°	T-Test	Fold change	Mr (theor.)	pI (theor.)	Score	Queries Matched	Cov %	Protein Name	Gene name	Acc N°	Entry name	NCBI acc N°
104	0.052 0.021	B/C10 -1.91 B+M+I/C10 - 1.78	95127	5.11	151	34	33%	Heat shock 70 kDa protein 4	HSPA4	P34932	HSP74_HUMAN	GI:206729934
665	0.05 0.044 0.031	B+M/C10 1.6 B+M+I/C10 1.82 L10/C10 1.57	55454	6.30	317	39	47%	Retinal dehydrogenase 1	ALDH1A1	P00352	AL1A1_HUMAN	GI:118495
695	0.045 0.024 0.036	B/C10 1.64 B+M/C25 2.42 B+M+I/C10 1.68	61701	7.66	84	11	17%	Glutamate dehydrogenase 1, mitochondrial	GLUD1	P00367	DHE3_HUMAN	GI:118541
748	0.011 0.038 0.0018	B/B+M+I1.7 B+M/C25 -1.5 B+M+I/C25 - 2.09	48283	5.63	73	22	34%	Thioredoxin domain-containing protein 5	TXNDC5	Q8NBS9	TXND5_HUMAN	GI:29839560
761	0.027 0.032 0.048	B+M+I/C25 - 1.63 L10/C25 - 1.6 C10/C25 - 1.53	56525	5.26	180	17	25%	ATP synthase subunit beta, mitochondrial	ATP5B	P06576	ATPB_HUMAN	GI:114549
842	0.026	B+M+I/C25 - 1.74	48029	5.34	364	42	71%	Keratin type I cytoskeletal 18	K1C18	P05783	K1C18_HUMAN	GI:125083
875	0.0051 0.029 0.047	B+M/C10 1.79 B+M+I/C10 1.67 L10/C10 1.37	48846	6.57	328	34	45%	Ornithine aminotransferase mitochondrial	OAT	P04181	OAT_HUMAN	GI:129018
879	0.041 0.0035 0.03 0.050	B+M/L10 1.84 B+M/C10 2.69 B+M+I/C10 1.69 L10/C10 1.46	46915	6.53	229	30	42%	Isocitrate dehydrogenase [NADP] cytoplasmic	IDH1	O75874	IDHC_HUMAN	GI:21903432
1149	0.048 0.050 0.024 0.031	B+M/B+M+I 2.97 B+M/L10 2.77 B+M+I/C10 - 1.64 L10/C10 - 1.53	37464	8.97	222	22	52%	Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	P22626	ROA2_HUMAN	GI:133257
1156	0.047	B+M+I/C10 1.52	42052	5.29	70	12	26%	Actin, cytoplasmic 1	ACTB	P60709	ACTB_HUMAN	GI:46397333
1533	0.028 0.045 0.037	B+M/B+M+I - 2.24 B+M/L10 - 2.09 B+M+I/C10 1.95	28041	8.60	145	22	74%	Proteasome subunit alpha type-7	PSMA7	O14818	PSA7_HUMAN	GI:12643540

1580	0.014 0.0079 0.0047	B/C10 3.22 B+M/C10 2.3 B+M+I/C10 1.93 L10/C10 1.91	25672	8.91	415	24	49%	Glutathione S-transferase A1	GSTA1	P08263	GSTA1_HUMAN	GI:121730
1671	0.028	B+M+I/C10 1.48	23219	6.14	173	20	66%	Proteasome subunit beta type-3	PSMB3	P49720	PSB3_HUMAN	GI:20532411
1931	0.0004 0.035	B/L10 -1.68 B+M+I/L10 - 1.68	15216	8.44	299	18	69%	Profilin-1	PFN1	P07737	PROF1_HUMAN	GI:130979
2765	0.0038 0.0013 0.0023	B+M/C10 2.03 B+M+I/C10 1.94 L10/C10 1.63	111494	5.16	159	28	31%	Hypoxia up-regulated protein	HYOU1	Q9Y4L1	HYOU1_HUMAN	GI:10720185