Figure S1

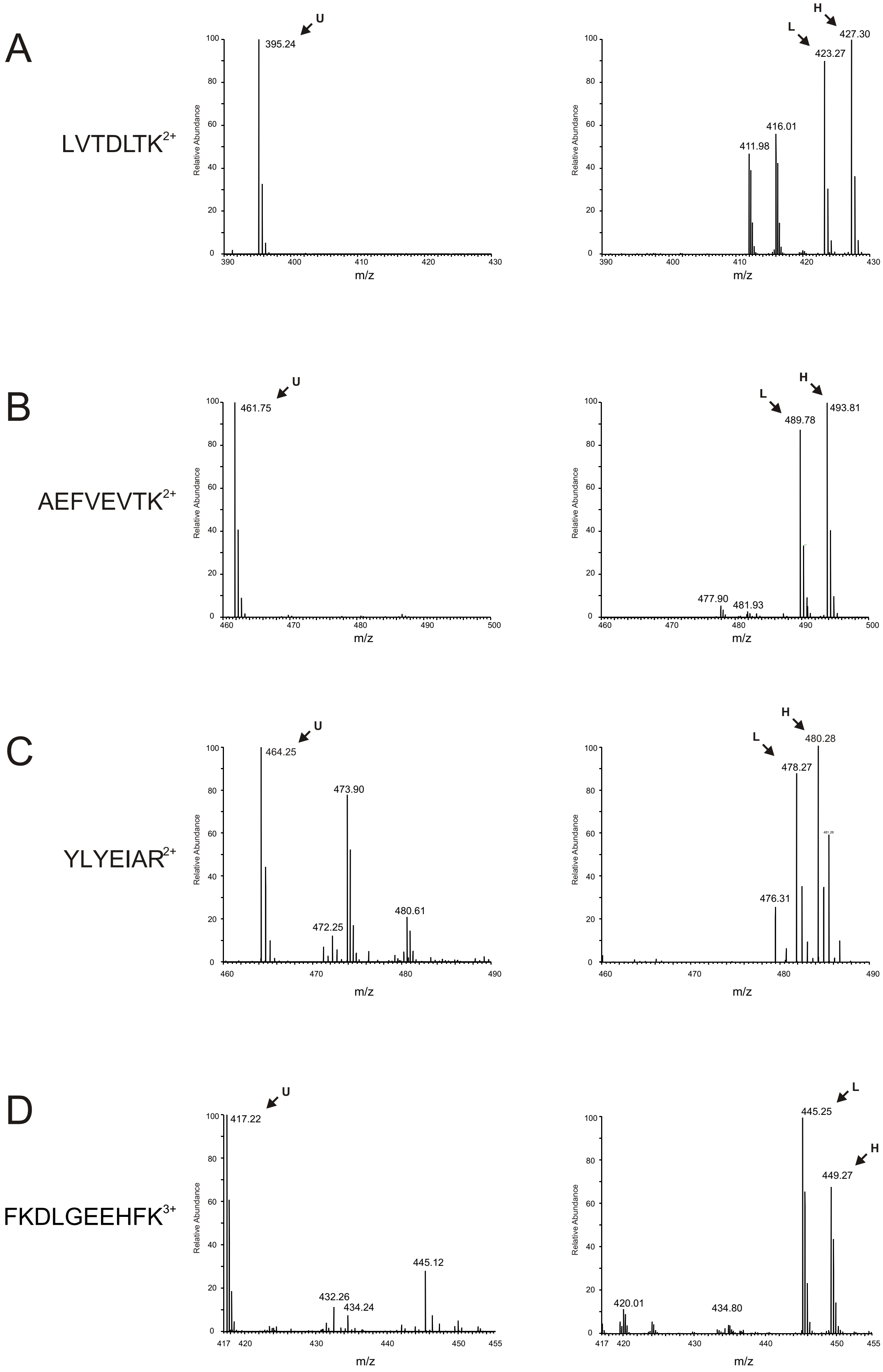
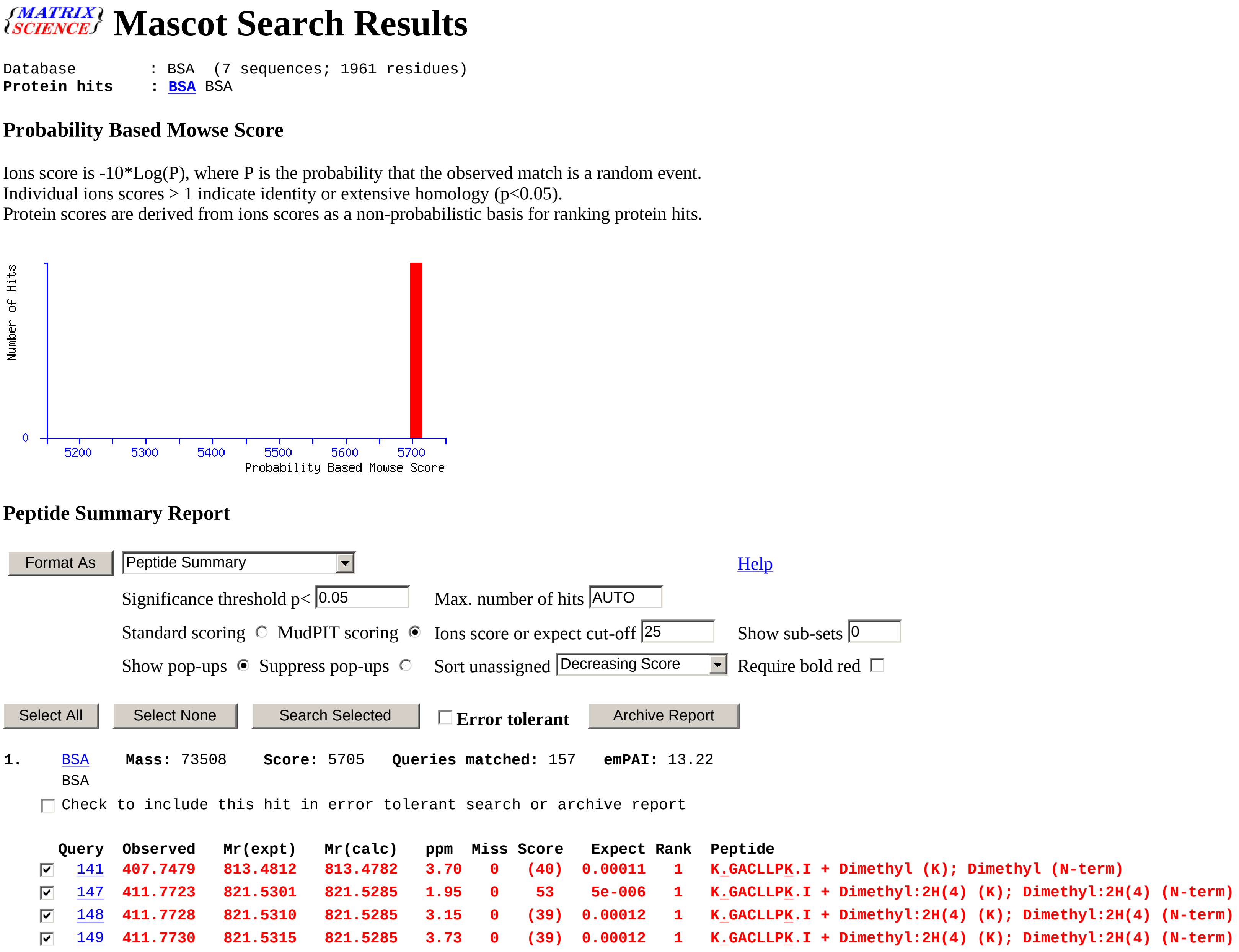

A
LVTDLTK^{2+}
U
395.24
H
L
427.30
423.27
411.98
416.01
B
AEFVEVTK^{2+}
U
461.75
H
L
489.78
493.81
477.90
481.93
C
YLYEIAR^{2+}
U
464.25
473.90
472.25
480.61
H
L
480.28
478.27
476.31
481.26
D
FKDLGEEHFK^{3+}
U
417.22
432.26
434.24
445.12
L
445.25
H
449.27
420.01
434.80
Relative Abundance
0
20
40
60
80
100
m/z
390
400
410
420
430
460
470
480
490
500
417
420
430
440
450
455

Figure S2



Mascot Search Results

```
Database        : BSA  (7 sequences; 1961 residues)
Protein hits    : BSA BSA
```

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 1 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.

Peptide Summary Report

Format As: Peptide Summary

Significance threshold p< 0.05 Max. number of hits AUTO

Standard scoring ○ MudPIT scoring ● Ions score or expect cut-off 25 Show sub-sets 0

Show pop-ups ● Suppress pop-ups ○ Sort unassigned Decreasing Score Require bold red ☐

☐ **Error tolerant**

1. BSA **Mass:** 73508 **Score:** 5705 **Queries matched:** 157 **emPAI:** 13.22
BSA

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	141	407.7479	813.4812	813.4782	3.70	0	(40)	0.00011	1	K.GACLLPK.I + Dimethyl (K); Dimethyl (N-term)
☑	147	411.7723	821.5301	821.5285	1.95	0	53	5e-006	1	K.GACLLPK.I + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	148	411.7728	821.5310	821.5285	3.15	0	(39)	0.00012	1	K.GACLLPK.I + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	149	411.7730	821.5315	821.5285	3.73	0	(39)	0.00012	1	K.GACLLPK.I + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

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☑ 173  423.2715   844.5284   844.5270  1.72  0  (40)  0.00011  1  K.LVTDLTK.V + Dimethyl (K); Dimethyl (N-term)
☑ 174  423.2715   844.5284   844.5270  1.72  0  (32)  0.00059  1  K.LVTDLTK.V + Dimethyl (K); Dimethyl (N-term)
☑ 175  423.2717   844.5288   844.5270  2.16  0  (45) 3.4e-005  1  K.LVTDLTK.V + Dimethyl (K); Dimethyl (N-term)
☑ 176  423.2719   844.5293   844.5270  2.81  0  (47) 2.2e-005  1  K.LVTDLTK.V + Dimethyl (K); Dimethyl (N-term)
☑ 177  423.2720   844.5295   844.5270  3.02  0  (47) 2.1e-005  1  K.LVTDLTK.V + Dimethyl (K); Dimethyl (N-term)
☑ 194  427.2967   852.5789   852.5772  1.99  0  (39)  0.00012  1  K.LVTDLTK.V + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑ 195  427.2968   852.5790   852.5772  2.13  0  (47) 2.1e-005  1  K.LVTDLTK.V + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑ 196  427.2968   852.5790   852.5772  2.13  0  (30)   0.0011  1  K.LVTDLTK.V + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑ 197  427.2973   852.5800   852.5772  3.28  0   47  2.1e-005  1  K.LVTDLTK.V + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑ 198  427.2976   852.5807   852.5772  4.07  0  (36)  0.00028  1  K.LVTDLTK.V + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑ 289  478.2671   954.5197   954.5174  2.41  0  (35)   0.0003  1  K.YLYEIAR.R + Dimethyl (N-term)
☑ 290  478.2676   954.5207   954.5174  3.45  0   35    0.0003  1  K.YLYEIAR.R + Dimethyl (N-term)
☑ 319  481.8016   961.5887   961.5870  1.74  0   39   0.00012  1  R.LCVLHEK.T + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑ 351  489.7799   977.5453   977.5433  2.03  0  (54) 4.1e-006  1  K.AEFVEVTK.L + Dimethyl (K); Dimethyl (N-term)
☑ 352  489.7799   977.5453   977.5433  2.03  0  (51) 7.3e-006  1  K.AEFVEVTK.L + Dimethyl (K); Dimethyl (N-term)
☑ 353  489.7801   977.5457   977.5433  2.41  0  (54) 4.4e-006  1  K.AEFVEVTK.L + Dimethyl (K); Dimethyl (N-term)
☑ 354  489.7802   977.5458   977.5433  2.47  0  (43) 5.1e-005  1  K.AEFVEVTK.L + Dimethyl (K); Dimethyl (N-term)
☑ 356  489.7807   977.5469   977.5433  3.66  0  (29)   0.0012  1  K.AEFVEVTK.L + Dimethyl (K); Dimethyl (N-term)
☑ 393  493.8046   985.5947   985.5936  1.15  0  (48) 1.7e-005  1  K.AEFVEVTK.L + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑ 395  493.8051   985.5957   985.5936  2.14  0   54  3.9e-006  1  K.AEFVEVTK.L + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑ 396  493.8052   985.5959   985.5936  2.39  0  (48) 1.5e-005  1  K.AEFVEVTK.L + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑ 397  493.8055   985.5965   985.5936  2.95  0  (51) 7.2e-006  1  K.AEFVEVTK.L + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑ 399  493.8062   985.5979   985.5936  4.37  0  (28)   0.0014  1  K.AEFVEVTK.L + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑ 500  515.7645  1029.5144  1029.5131  1.25  0   44  3.9e-005  1  K.DLGEEHFK.G + Dimethyl (K); Dimethyl (N-term)
☑ 501  344.1788  1029.5145  1029.5131  1.35  0  (27)   0.0019  1  K.DLGEEHFK.G + Dimethyl (K); Dimethyl (N-term)
☑ 555  519.7896  1037.5647  1037.5633  1.30  0  (44)   4e-005  1  K.DLGEEHFK.G + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑ 556  346.8622  1037.5647  1037.5633  1.34  0  (30)  0.00098  1  K.DLGEEHFK.G + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑ 645  539.8727  1077.7309  1077.7249  5.60  0   50  1.1e-005  1  K.QTALVELLK.H + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑ 685  569.7532  1137.4918  1137.4907  0.98  0  (47)   2e-005  1  K.CCTESLVNR.R
☑ 719  582.2941  1162.5736  1162.5692  3.74  0   61  8.3e-007  1  K.EACFAVEGPK.L + Dimethyl (K); Dimethyl (N-term)
☑ 723  583.7686  1165.5227  1165.5220  0.64  0   63  5.1e-007  1  K.CCTESLVNR.R + Dimethyl (N-term)
☑ 724  583.7700  1165.5255  1165.5220  3.01  0  (54) 3.8e-006  1  K.CCTESLVNR.R + Dimethyl (N-term)
☑ 725  583.7701  1165.5257  1165.5220  3.22  0  (46) 2.3e-005  1  K.CCTESLVNR.R + Dimethyl (N-term)
☑ 733  585.7811  1169.5477  1169.5471  0.54  0  (28)   0.0017  1  K.CCTESLVNR.R + Dimethyl:2H(4) (N-term)
☑ 734  585.7829  1169.5512  1169.5471  3.55  0  (38)  0.00017  1  K.CCTESLVNR.R + Dimethyl:2H(4) (N-term)
☑ 735  585.7851  1169.5557  1169.5471  7.38  0  (32)   0.0007  1  K.CCTESLVNR.R + Dimethyl:2H(4) (N-term)
☑ 762  598.3503  1194.6861  1194.6798  5.32  0  (26)   0.0026  1  K.LVNELTEFAK.T + Dimethyl:2H(4) (N-term)
☑ 788  610.3533  1218.6921  1218.6860  5.05  0  (40)  0.00011  1  K.LVNELTEFAK.T + Dimethyl (K); Dimethyl (N-term)
☑ 789  610.3538  1218.6930  1218.6860  5.75  0   47    2e-005  1  K.LVNELTEFAK.T + Dimethyl (K); Dimethyl (N-term)
☑ 798  409.6089  1225.8048  1225.8009  3.19  1   44  4.1e-005  1  K.KQTALVELLK.H + 2 Dimethyl (K); Dimethyl (N-term)
☑ 843  656.3776  1310.7406  1310.7347  4.52  0   46  2.5e-005  1  R.HPEYAVSVLLR.L + Dimethyl (N-term)
☑ 856  445.2433  1332.7080  1332.7078  0.20  1   62  5.8e-007  1  R.FKDLGEEHFK.G + 2 Dimethyl (K); Dimethyl (N-term)
☑ 858  334.1849  1332.7106  1332.7078  2.16  1  (33)  0.00046  1  R.FKDLGEEHFK.G + 2 Dimethyl (K); Dimethyl (N-term)
☑ 871  449.2685  1344.7837  1344.7831  0.47  1  (45) 3.1e-005  1  R.FKDLGEEHFK.G + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑ 890  681.3948  1360.7751  1360.7714  2.72  0  (49) 1.3e-005  1  K.HLVDEPQNLIK.Q + Dimethyl (K); Dimethyl (N-term)
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☑	891	681.3965	1360.7785	1360.7714	5.23	0	(30)	0.001	1	K.HLVDEPQNLIK.Q + Dimethyl (K); Dimethyl (N-term)
☑	892	681.3966	1360.7787	1360.7714	5.32	0	(33)	0.00048	1	K.HLVDEPQNLIK.Q + Dimethyl (K); Dimethyl (N-term)
☑	893	681.3976	1360.7807	1360.7714	6.84	0	49	1.3e-005	1	K.HLVDEPQNLIK.Q + Dimethyl (K); Dimethyl (N-term)
☑	901	685.4216	1368.8287	1368.8217	5.16	0	(44)	4.2e-005	1	K.HLVDEPQNLIK.Q + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	902	685.4222	1368.8299	1368.8217	6.05	0	(34)	0.0004	1	K.HLVDEPQNLIK.Q + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	903	685.4228	1368.8310	1368.8217	6.84	0	(44)	4.5e-005	1	K.HLVDEPQNLIK.Q + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	935	463.2625	1386.7658	1386.7640	1.28	0	(34)	0.00042	1	K.ECCDKPLLEK.S + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	936	463.2626	1386.7659	1386.7640	1.35	0	47	2e-005	1	K.ECCDKPLLEK.S + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	966	722.3250	1442.6354	1442.6347	0.42	0	(68)	1.7e-007	1	K.YICDNQDTISSK.L
☑	991	489.9536	1466.8390	1466.8358	2.22	1	(56)	2.6e-006	1	R.RHPEYAVSVLLR.L + Dimethyl (N-term)
☑	992	489.9539	1466.8399	1466.8358	2.84	1	(54)	4e-006	1	R.RHPEYAVSVLLR.L + Dimethyl (N-term)
☑	993	489.9539	1466.8400	1466.8358	2.90	1	73	4.8e-008	1	R.RHPEYAVSVLLR.L + Dimethyl (N-term)
☑	994	489.9546	1466.8418	1466.8358	4.15	1	(69)	1.4e-007	1	R.RHPEYAVSVLLR.L + Dimethyl (N-term)
☑	1003	736.3835	1470.7525	1470.7429	6.58	0	69	1.3e-007	1	K.TVMENFVAFVDK.C + Dimethyl (K); Dimethyl (N-term); Oxidation (M)
☑	1004	491.2952	1470.8637	1470.8609	1.94	1	(33)	0.00049	1	R.RHPEYAVSVLLR.L + Dimethyl:2H(4) (N-term)
☑	1005	491.2955	1470.8647	1470.8609	2.62	1	(41)	8.5e-005	1	R.RHPEYAVSVLLR.L + Dimethyl:2H(4) (N-term)
☑	1014	738.3531	1474.6917	1474.6912	0.39	0	(65)	2.9e-007	1	K.YICDNQDTISSK.L + Dimethyl:2H(4) (N-term)
☑	1015	492.5912	1474.7516	1474.7490	1.79	0	(42)	6.5e-005	1	K.SLHTLFGDELCK.V + Dimethyl (K); Dimethyl (N-term)
☑	1016	492.5927	1474.7562	1474.7490	4.90	0	(33)	0.00053	1	K.SLHTLFGDELCK.V + Dimethyl (K); Dimethyl (N-term)
☑	1018	738.3861	1474.7577	1474.7490	5.88	0	(59)	1.2e-006	1	K.SLHTLFGDELCK.V + Dimethyl (K); Dimethyl (N-term)
☑	1019	738.3862	1474.7578	1474.7490	5.96	0	(52)	6.3e-006	1	K.SLHTLFGDELCK.V + Dimethyl (K); Dimethyl (N-term)
☑	1030	740.4084	1478.8023	1478.7931	6.26	0	(56)	2.3e-006	1	K.TVMENFVAFVDK.C + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)
☑	1034	495.2753	1482.8042	1482.7992	3.33	0	(35)	0.00035	1	K.SLHTLFGDELCK.V + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1035	495.2760	1482.8063	1482.7992	4.75	0	(32)	0.0006	1	K.SLHTLFGDELCK.V + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1036	742.4109	1482.8073	1482.7992	5.48	0	(38)	0.00015	1	K.SLHTLFGDELCK.V + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1037	742.4119	1482.8093	1482.7992	6.80	0	65	2.9e-007	1	K.SLHTLFGDELCK.V + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1052	750.3567	1498.6988	1498.6973	0.99	0	(67)	1.9e-007	1	K.YICDNQDTISSK.L + Dimethyl (K); Dimethyl (N-term)
☑	1053	750.3571	1498.6997	1498.6973	1.59	0	(61)	8e-007	1	K.YICDNQDTISSK.L + Dimethyl (K); Dimethyl (N-term)
☑	1054	750.3579	1498.7013	1498.6973	2.62	0	(67)	2.2e-007	1	K.YICDNQDTISSK.L + Dimethyl (K); Dimethyl (N-term)
☑	1055	750.3588	1498.7031	1498.6973	3.84	0	(60)	1e-006	1	K.YICDNQDTISSK.L + Dimethyl (K); Dimethyl (N-term)
☑	1056	750.3610	1498.7075	1498.6973	6.77	0	(67)	2e-007	1	K.YICDNQDTISSK.L + Dimethyl (K); Dimethyl (N-term)
☑	1077	754.3813	1506.7481	1506.7476	0.38	0	(70)	1e-007	1	K.YICDNQDTISSK.L + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1078	754.3828	1506.7511	1506.7476	2.32	0	(71)	7.3e-008	1	K.YICDNQDTISSK.L + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1079	754.3835	1506.7525	1506.7476	3.29	0	76	2.4e-008	1	K.YICDNQDTISSK.L + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1080	754.3841	1506.7537	1506.7476	4.08	0	(46)	2.4e-005	1	K.YICDNQDTISSK.L + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1081	754.3863	1506.7580	1506.7476	6.94	0	(72)	7e-008	1	K.YICDNQDTISSK.L + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1083	754.4207	1506.8268	1506.8194	4.85	0	(45)	3.1e-005	1	K.LGEYGFQNALIVR.Y + Dimethyl (N-term)
☑	1084	754.4216	1506.8287	1506.8194	6.16	0	(74)	4.4e-008	1	K.LGEYGFQNALIVR.Y + Dimethyl (N-term)
☑	1085	754.4221	1506.8297	1506.8194	6.82	0	110	1.1e-011	1	K.LGEYGFQNALIVR.Y + Dimethyl (N-term)
☑	1100	756.4345	1510.8545	1510.8446	6.56	0	(73)	5e-008	1	K.LGEYGFQNALIVR.Y + Dimethyl:2H(4) (N-term)
☑	1101	756.4345	1510.8545	1510.8446	6.56	0	(86)	2.5e-009	1	K.LGEYGFQNALIVR.Y + Dimethyl:2H(4) (N-term)
☑	1102	756.4359	1510.8573	1510.8446	8.41	0	(68)	1.5e-007	1	K.LGEYGFQNALIVR.Y + Dimethyl:2H(4) (N-term)
☑	1122	507.2230	1518.6471	1518.6443	1.83	0	(49)	1.2e-005	1	K.TCVADESHAGCEK.S + Dimethyl (K); Dimethyl (N-term)
☑	1160	509.9051	1526.6936	1526.6945	-0.58	0	67	2.1e-007	1	K.TCVADESHAGCEK.S + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1189	767.7972	1533.5798	1533.5786	0.82	0	(31)	0.00083	1	R.ETYGDMADCCEK.Q + Dimethyl (K); Dimethyl (N-term)

☑	1190	767.7979	1533.5812	1533.5786	1.70	0	(59)	1.1e-006	1	R.ETYGDMADCCEK.Q + Dimethyl (K); Dimethyl (N-term)
☑	1191	512.2012	1533.5819	1533.5786	2.16	0	(31)	0.00071	1	R.ETYGDMADCCEK.Q + Dimethyl (K); Dimethyl (N-term)
☑	1225	770.4440	1538.8735	1538.8668	4.34	0	36	0.00024	1	K.VPQVSTPTLVEVSR.S + Dimethyl (N-term)
☑	1239	771.8224	1541.6303	1541.6288	1.01	0	(59)	1.3e-006	1	R.ETYGDMADCCEK.Q + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1240	771.8226	1541.6307	1541.6288	1.26	0	(44)	4.1e-005	1	R.ETYGDMADCCEK.Q + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1241	771.8234	1541.6322	1541.6288	2.20	0	77	2.2e-008	1	R.ETYGDMADCCEK.Q + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1271	775.7966	1549.5786	1549.5735	3.30	0	(36)	0.00023	1	R.ETYGDMADCCEK.Q + Dimethyl (K); Dimethyl (N-term); Oxidation (M)
☑	1288	779.8191	1557.6237	1557.6237	0.01	0	(56)	2.8e-006	1	R.ETYGDMADCCEK.Q + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)
☑	1289	779.8215	1557.6285	1557.6237	3.09	0	(43)	5.4e-005	1	R.ETYGDMADCCEK.Q + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)
☑	1290	779.8444	1557.6743	1557.6691	3.36	0	56	2.4e-006	1	K.EYEATLEECCAK.D + Dimethyl (K); Dimethyl (N-term)
☑	1304	783.8691	1565.7236	1565.7193	2.76	0	(54)	4.1e-006	1	K.EYEATLEECCAK.D + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1338	798.3956	1594.7767	1594.7667	6.26	0	82	5.9e-009	1	K.DAFLGSFLYEYSR.R + Dimethyl (N-term)
☑	1343	800.4080	1598.8014	1598.7919	5.95	0	(75)	3.1e-008	1	K.DAFLGSFLYEYSR.R + Dimethyl:2H(4) (N-term)
☑	1347	537.5796	1609.7169	1609.7083	5.39	0	(41)	8e-005	1	K.DDPHACYSTVFDK.L + Dimethyl (K); Dimethyl (N-term)
☑	1359	540.2629	1617.7670	1617.7585	5.25	0	46	2.7e-005	1	K.DDPHACYSTVFDK.L + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1380	411.9836	1643.9053	1643.8990	3.86	1	27	0.0022	1	K.LKECCDKPLLEK.S + 3 Dimethyl (K); Dimethyl (N-term)
☑	1463	566.0049	1694.9927	1694.9931	-0.21	1	(28)	0.0017	1	R.KVPQVSTPTLVEVSR.S + Dimethyl (K); Dimethyl (N-term)
☑	1464	566.0075	1695.0007	1694.9931	4.51	1	(36)	0.00028	1	R.KVPQVSTPTLVEVSR.S + Dimethyl (K); Dimethyl (N-term)
☑	1465	566.0080	1695.0022	1694.9931	5.36	1	54	4.2e-006	1	R.KVPQVSTPTLVEVSR.S + Dimethyl (K); Dimethyl (N-term)
☑	1485	568.6872	1703.0397	1703.0433	-2.10	1	(50)	9e-006	1	R.KVPQVSTPTLVEVSR.S + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1486	568.6914	1703.0524	1703.0433	5.34	1	(39)	0.00012	1	R.KVPQVSTPTLVEVSR.S + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1527	433.2145	1728.8288	1728.8253	2.01	1	30	0.00096	1	K.QEPERNECFLSHK.D + Dimethyl (K); Dimethyl (N-term)
☑	1585	884.9406	1767.8667	1767.8535	7.47	0	92	5.9e-010	1	R.MPCTEDYLSLILNR.L + Dimethyl (N-term); Oxidation (M)
☑	1590	593.2371	1776.6895	1776.6866	1.68	0	(57)	2.2e-006	1	K.ECCHGDLLECADDR.A + Dimethyl (N-term)
☑	1591	593.2372	1776.6897	1776.6866	1.78	0	76	2.7e-008	1	K.ECCHGDLLECADDR.A + Dimethyl (N-term)
☑	1598	594.5789	1780.7149	1780.7117	1.83	0	(42)	7e-005	1	K.ECCHGDLLECADDR.A + Dimethyl:2H(4) (N-term)
☑	1599	594.5792	1780.7157	1780.7117	2.27	0	(30)	0.0011	1	K.ECCHGDLLECADDR.A + Dimethyl:2H(4) (N-term)
☑	1615	902.3893	1802.7640	1802.7604	2.03	0	(53)	5.4e-006	1	K.YNGVFQECCQAEDK.G + Dimethyl (K); Dimethyl (N-term)
☑	1616	601.9293	1802.7660	1802.7604	3.10	0	(48)	1.5e-005	1	K.YNGVFQECCQAEDK.G + Dimethyl (K); Dimethyl (N-term)
☑	1617	601.9295	1802.7667	1802.7604	3.53	0	(50)	1.1e-005	1	K.YNGVFQECCQAEDK.G + Dimethyl (K); Dimethyl (N-term)
☑	1618	601.9297	1802.7672	1802.7604	3.81	0	(55)	3.2e-006	1	K.YNGVFQECCQAEDK.G + Dimethyl (K); Dimethyl (N-term)
☑	1619	601.9298	1802.7677	1802.7604	4.08	0	(41)	8.5e-005	1	K.YNGVFQECCQAEDK.G + Dimethyl (K); Dimethyl (N-term)
☑	1620	601.9299	1802.7680	1802.7604	4.22	0	(38)	0.00015	1	K.YNGVFQECCQAEDK.G + Dimethyl (K); Dimethyl (N-term)
☑	1621	902.3916	1802.7687	1802.7604	4.60	0	(51)	8.4e-006	1	K.YNGVFQECCQAEDK.G + Dimethyl (K); Dimethyl (N-term)
☑	1622	902.3916	1802.7687	1802.7604	4.64	0	(52)	5.6e-006	1	K.YNGVFQECCQAEDK.G + Dimethyl (K); Dimethyl (N-term)
☑	1623	902.3917	1802.7688	1802.7604	4.67	0	(59)	1.1e-006	1	K.YNGVFQECCQAEDK.G + Dimethyl (K); Dimethyl (N-term)
☑	1624	902.3921	1802.7696	1802.7604	5.10	0	79	1.3e-008	1	K.YNGVFQECCQAEDK.G + Dimethyl (K); Dimethyl (N-term)
☑	1625	902.3921	1802.7697	1802.7604	5.19	0	(59)	1.2e-006	1	K.YNGVFQECCQAEDK.G + Dimethyl (K); Dimethyl (N-term)
☑	1626	902.3921	1802.7697	1802.7604	5.19	0	(72)	5.7e-008	1	K.YNGVFQECCQAEDK.G + Dimethyl (K); Dimethyl (N-term)
☑	1646	604.6125	1810.8157	1810.8106	2.83	0	(41)	8.1e-005	1	K.YNGVFQECCQAEDK.G + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1647	604.6128	1810.8166	1810.8106	3.29	0	(47)	2.2e-005	1	K.YNGVFQECCQAEDK.G + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1648	604.6129	1810.8169	1810.8106	3.49	0	(47)	2.2e-005	1	K.YNGVFQECCQAEDK.G + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1649	604.6133	1810.8180	1810.8106	4.10	0	(45)	3e-005	1	K.YNGVFQECCQAEDK.G + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1650	906.4168	1810.8191	1810.8106	4.68	0	(63)	5.4e-007	1	K.YNGVFQECCQAEDK.G + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1651	906.4171	1810.8196	1810.8106	4.95	0	(77)	1.8e-008	1	K.YNGVFQECCQAEDK.G + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

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☑ 1652  906.4171  1810.8197  1810.8106   5.01   0   (65) 3.3e-007   1   K.YNGVFQECCQAEDK.G + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑ 1653  906.4171  1810.8197  1810.8106   5.04   0   (63) 5.5e-007   1   K.YNGVFQECCQAEDK.G + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑ 1654  906.4172  1810.8199  1810.8106   5.15   0   (63) 4.6e-007   1   K.YNGVFQECCQAEDK.G + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑ 1655  906.4176  1810.8207  1810.8106   5.59   0   (69) 1.4e-007   1   K.YNGVFQECCQAEDK.G + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑ 1711  646.3357  1935.9853  1935.9764   4.56   0   (37)   0.0002   1   R.RPCFSALTPDETYVPK.A + Dimethyl (K); Dimethyl (N-term)
☑ 1714  646.3372  1935.9898  1935.9764   6.92   0   (35)  0.00032   1   R.RPCFSALTPDETYVPK.A + Dimethyl (K); Dimethyl (N-term)
☑ 1721  649.0204  1944.0393  1944.0267   6.51   0    42  6.4e-005   1   R.RPCFSALTPDETYVPK.A + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑ 1737  655.3337  1962.9792  1962.9761   1.58   0    49  1.2e-005   1   K.LFTFHADICTLPDTEK.Q + Dimethyl (K); Dimethyl (N-term)
☑ 1738  655.3358  1962.9856  1962.9761   4.84   0   (30)    0.001   1   K.LFTFHADICTLPDTEK.Q + Dimethyl (K); Dimethyl (N-term)
☑ 1739  655.3359  1962.9858  1962.9761   4.94   0   (35)  0.00029   1   K.LFTFHADICTLPDTEK.Q + Dimethyl (K); Dimethyl (N-term)
☑ 1776  658.0196  1971.0369  1971.0263   5.38   0   (36)  0.00028   1   K.LFTFHADICTLPDTEK.Q + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑ 1843  671.3062  2010.8968  2010.8849   5.92   1    46  2.3e-005   1   K.CCAADDKEACFAVEGPK.L + 2 Dimethyl (K); Dimethyl (N-term)
☑ 1845  675.3312  2022.9719  2022.9603   5.75   1   (32)  0.00065   1   K.CCAADDKEACFAVEGPK.L + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑ 1878  533.7814  2131.0966  2131.0871   4.48   1    27    0.0019   1   K.LKPDPNTLCDEFKADEK.K + 3 Dimethyl (K); Dimethyl (N-term)
☑ 1891  543.2455  2168.9527  2168.9401   5.80   1    41  8.5e-005   1   K.VHKECCHGDLLECADDR.A + Dimethyl (K); Dimethyl (N-term)
☑ 1898  544.2455  2172.9527  2172.9653  -5.77   1   (32)  0.00065   1   K.VHKECCHGDLLECADDR.A + Dimethyl (N-term); Dimethyl:2H(4) (K)
☑ 1914  730.6315  2188.8728  2188.8711   0.76   1    44    4e-005   1   R.ETYGDMADCCEKQEPER.N + Dimethyl (K); Dimethyl (N-term); Oxidation (M)
☑ 1921  733.3138  2196.9195  2196.9213  -0.83   1   (39)  0.00013   1   R.ETYGDMADCCEKQEPER.N + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)
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Search Parameters

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Type of search         : MS/MS Ion Search
Enzyme                 : Trypsin
Fixed modifications    : Carbamidomethyl (C)
Variable modifications : Dimethyl (K),Dimethyl (N-term),Dimethyl:2H(4) (K),Dimethyl:2H(4) (N-term),Oxidation (M)
Mass values            : Monoisotopic
Protein Mass           : Unrestricted
Peptide Mass Tolerance : ± 10 ppm
Fragment Mass Tolerance: ± 0.9 Da

Instrument type        : Default
Number of queries      : 1992
```

Figure S3

Mascot Search Results

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Database        : IPI_mouse mouse_v3.36 (51326 sequences; 23682061 residues)
Protein hits    : IPI00874482 Tax_Id=10090 Gene_Symbol=Actg1 Actin, cytoplasmic 2
                  IPI00405227 Tax_Id=10090 Gene_Symbol=Vcl Vinculin
                  IPI00131695 Tax_Id=10090 Gene_Symbol=Alb Serum albumin precursor
                  IPI00131830 Tax_Id=10090 Gene_Symbol=Serpina3k Serine protease inhibitor A3K precursor
                  IPI00465786 Tax_Id=10090 Gene_Symbol=Tln1 Talin-1
                  IPI00136929 Tax_Id=10090 Gene_Symbol=Actg1 Gamma actin-like protein
                  IPI00114375 Tax_Id=10090 Gene_Symbol=Dpysl2 Dihydropyrimidinase-related protein 2
                  IPI00405058 Tax_Id=10090 Gene_Symbol=Hnrnpa2b1 Isoform 3 of Heterogeneous nuclear ribonucleoproteins A2/B1
                  IPI00128642 Tax_Id=10090 Gene_Symbol=Cbr2 Lung carbonyl reductase
                  IPI00229080 Tax_Id=10090 Gene_Symbol=Hsp90ab1 Heat shock protein 84b
                  IPI00554929 Tax_Id=10090 Gene_Symbol=Hsp90ab1 Heat shock protein HSP 90-beta
                  IPI00132722 Tax_Id=10090 Gene_Symbol=Anxa3 Annexin A3
                  IPI00323357 Tax_Id=10090 Gene_Symbol=Hspa8 Heat shock cognate 71 kDa protein
                  IPI00135284 Tax_Id=10090 Gene_Symbol=LOC100044454;LOC100039214 similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) isoform 1
                  IPI00123313 Tax_Id=10090 Gene_Symbol=Ube1y1;Ube1x Ubiquitin-activating enzyme E1 X
                  IPI00221402 Tax_Id=10090 Gene_Symbol=Aldoa Fructose-bisphosphate aldolase A
                  IPI00330804 Tax_Id=10090 Gene_Symbol=Hsp90aa1 Heat shock protein HSP 90-alpha
                  IPI00135635 Tax_Id=10090 Gene_Symbol=Serpina3m Serine protease inhibitor A3M precursor
                  IPI00317309 Tax_Id=10090 Gene_Symbol=Anxa5 Annexin A5
                  IPI00387422 Tax_Id=10090 Gene_Symbol=Zyx zyxin
                  IPI00553333 Tax_Id=10090 Gene_Symbol=Hbb-b1 Hemoglobin subunit beta-1
                  IPI00113223 Tax_Id=10090 Gene_Symbol=Fasn Fatty acid synthase
                  IPI00221528 Tax_Id=10090 Gene_Symbol=4732495G21Rik 10 days neonate skin cDNA, RIKEN full-length enriched library, clone:4732493G14 product:ACTIN, CYTOP
                  IPI00123924 Tax_Id=10090 Gene_Symbol=Serpina1d Alpha-1-antitrypsin 1-4 precursor
                  IPI00469114 Tax_Id=10090 Gene_Symbol=Hba-a1;Hba-a2 Hemoglobin subunit alpha
                  IPI00169463 Tax_Id=10090 Gene_Symbol=Tubb2c Tubulin beta-2C chain
                  IPI00169916 Tax_Id=10090 Gene_Symbol=Cltc Clathrin heavy chain
                  IPI00131138 Tax_Id=10090 Gene_Symbol=Flna Isoform 1 of Filamin-A
                  IPI00380873 Tax_Id=10090 Gene_Symbol=Sec14l3 Novel protein, ortholog of human and rat SEC14-like 3 (S. cerevisiae) SEC14L3
                  IPI00110753 Tax_Id=10090 Gene_Symbol=Tuba1a Tubulin alpha-1A chain
                  IPI00117352 Tax_Id=10090 Gene_Symbol=Tubb5 Tubulin beta-5 chain
                  IPI00624663 Tax_Id=10090 Gene_Symbol=Pzp Alpha-2-macroglobulin precursor
                  IPI00622235 Tax_Id=10090 Gene_Symbol=Vcp Transitional endoplasmic reticulum ATPase
                  IPI00230395 Tax_Id=10090 Gene_Symbol=Anxa1 Annexin A1
                  IPI00139788 Tax_Id=10090 Gene_Symbol=Trf Serotransferrin precursor
                  IPI00109073 Tax_Id=10090 Gene_Symbol=Tubb4 Tubulin beta-4 chain
                  IPI00316491 Tax_Id=10090 Gene_Symbol=Hbb-b2 Hemoglobin subunit beta-2
                  IPI00117857 Tax_Id=10090 Gene_Symbol=Spi1-6 Alpha-1-antitrypsin 1-6 precursor
                  IPI00318614 Tax_Id=10090 Gene_Symbol=Idh2 Isocitrate dehydrogenase [NADP], mitochondrial precursor
                  IPI00323816 Tax_Id=10090 Gene_Symbol=Selenbp2 Selenium-binding protein 2
                  IPI00323592 Tax_Id=10090 Gene_Symbol=Mdh2 Malate dehydrogenase, mitochondrial precursor
                  IPI00127560 Tax_Id=10090 Gene_Symbol=Ttr Transthyretin precursor
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IPI00555069 Tax_Id=10090 Gene_Symbol=Pgk1 Phosphoglycerate kinase 1
IPI00132762 Tax_Id=10090 Gene_Symbol=Trap1 Heat shock protein 75 kDa, mitochondrial precursor
IPI00128249 Tax_Id=10090 Gene_Symbol=Ahsg Alpha-2-HS-glycoprotein precursor
IPI00126248 Tax_Id=10090 Gene_Symbol=Acly Adult male testis cDNA, RIKEN full-length enriched library, clone:4922505F07 product:ATP citrate lyase, full
IPI00830223 Tax_Id=10090 Gene_Symbol=Tpm1 28 kDa protein
IPI00648086 Tax_Id=10090 Gene_Symbol=Lasp1 LIM and SH3 protein 1
IPI00121209 Tax_Id=10090 Gene_Symbol=Apoa1 Apolipoprotein A-I precursor
IPI00555059 Tax_Id=10090 Gene_Symbol=Prdx6 Peroxiredoxin-6
IPI00336324 Tax_Id=10090 Gene_Symbol=Mdh1 Malate dehydrogenase, cytoplasmic
IPI00323624 Tax_Id=10090 Gene_Symbol=C3 Isoform Long of Complement C3 precursor (Fragment)
IPI00355382 Tax_Id=10090 Gene_Symbol=Wars Isoform 2 of Tryptophanyl-tRNA synthetase, cytoplasmic
IPI00318671 Tax_Id=10090 Gene_Symbol=Ehd4 EH-domain containing 4-KJR (Fragment)
IPI00380436 Tax_Id=10090 Gene_Symbol=Actn1 Alpha-actinin-1
IPI00136906 Tax_Id=10090 Gene_Symbol=Capg Macrophage-capping protein
IPI00123223 Tax_Id=10090 Gene_Symbol=Mug1 Murinoglobulin-1 precursor
IPI00319994 Tax_Id=10090 Gene_Symbol=Ldha L-lactate dehydrogenase A chain
IPI00118899 Tax_Id=10090 Gene_Symbol=Actn4 Alpha-actinin-4
IPI00123181 Tax_Id=10090 Gene_Symbol=Myh9 Myosin-9
IPI00223757 Tax_Id=10090 Gene_Symbol=Akr1b3 Aldose reductase
IPI00137331 Tax_Id=10090 Gene_Symbol=Cap1 Adenylyl cyclase-associated protein 1
IPI00223216 Tax_Id=10090 Gene_Symbol=Tst Thiosulfate sulfurtransferase
IPI00117167 Tax_Id=10090 Gene_Symbol=Gsn Isoform 1 of Gelsolin precursor
IPI00113141 Tax_Id=10090 Gene_Symbol=Cs Citrate synthase, mitochondrial precursor
IPI00466069 Tax_Id=10090 Gene_Symbol=Eef2 Elongation factor 2
IPI00128522 Tax_Id=10090 Gene_Symbol=Hspb1 Isoform A of Heat shock protein beta-1
IPI00129526 Tax_Id=10090 Gene_Symbol=Hsp90b1 Endoplasmin precursor
IPI00269661 Tax_Id=10090 Gene_Symbol=Hnrpa3 Isoform 1 of Heterogeneous nuclear ribonucleoprotein A3
IPI00467833 Tax_Id=10090 Gene_Symbol=Tpi1 Triosephosphate isomerase
IPI00462072 Tax_Id=10090 Gene_Symbol=EG433182;Eno1;LOC100044223 Alpha-enolase
IPI00115522 Tax_Id=10090 Gene_Symbol=Fga fibrinogen, alpha polypeptide
IPI00137409 Tax_Id=10090 Gene_Symbol=Tkt Transketolase
IPI00468203 Tax_Id=10090 Gene_Symbol=Anxa2 Annexin A2
IPI00120030 Tax_Id=10090 Gene_Symbol=Crym Mu-crystallin homolog
IPI00874728 Tax_Id=10090 Gene_Symbol=Tpm2 Isoform 2 of Tropomyosin beta chain
IPI00114945 Tax_Id=10090 Gene_Symbol=Sept2 Septin-2
IPI00377592 Tax_Id=10090 Gene_Symbol=Sec31a SEC31-like 1
IPI00123494 Tax_Id=10090 Gene_Symbol=Psmd2 26S proteasome non-ATPase regulatory subunit 2
IPI00653931 Tax_Id=10090 Gene_Symbol=Fah Visual cortex cDNA, RIKEN full-length enriched library, clone:K430330E02 product:fumarylacetoacetate hydrolase
IPI00230212 Tax_Id=10090 Gene_Symbol=Gstm1 Glutathione S-transferase Mu 1
IPI00459570 Tax_Id=10090 Gene_Symbol=Tpm3 2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:C920030J24 product:tropomy
IPI00129107 Tax_Id=10090 Gene_Symbol=Gipc1 PDZ domain-containing protein GIPC1
IPI00309768 Tax_Id=10090 Gene_Symbol=Pdlim1 PDZ and LIM domain protein 1
IPI00457659 Tax_Id=10090 Gene_Symbol=Serpinb1a Leukocyte elastase inhibitor A
IPI00111265 Tax_Id=10090 Gene_Symbol=Capza2 F-actin-capping protein subunit alpha-2
IPI00133605 Tax_Id=10090 Gene_Symbol=Pklr Pyruvate kinase isozymes R/L
IPI00776343 Tax_Id=10090 Gene_Symbol=Ager RAGE
IPI00408119 Tax_Id=10090 Gene_Symbol=Mtap4 Isoform 1 of Microtubule-associated protein 4
IPI00421206 Tax_Id=10090 Gene_Symbol=Kctd12 BTB/POZ domain-containing protein KCTD12
IPI00459725 Tax_Id=10090 Gene_Symbol=Idh3a Isoform 1 of Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial precursor
IPI00467447 Tax_Id=10090 Gene_Symbol=Iqgap1 Ras GTPase-activating-like protein IQGAP1

IPI00187462 Tax_Id=10090 Gene_Symbol=Gimap4 GTPase, IMAP family member 4 isoform a
IPI00420806 Tax_Id=10090 Gene_Symbol=Dync1li2 Cytoplasmic dynein 1 light intermediate chain 2
IPI00118875 Tax_Id=10090 Gene_Symbol=Eef1d eukaryotic translation elongation factor 1 delta isoform a
IPI00229510 Tax_Id=10090 Gene_Symbol=Ldhb L-lactate dehydrogenase B chain
IPI00138342 Tax_Id=10090 Gene_Symbol=Es1 Liver carboxylesterase N precursor
IPI00119111 Tax_Id=10090 Gene_Symbol=Cnn3 Calponin-3
IPI00377351 Tax_Id=10090 Gene_Symbol=Apoa4;ENSMUSG00000074373 Apolipoprotein A-IV precursor
IPI00336362 Tax_Id=10090 Gene_Symbol=Aldh1a7 Aldehyde dehydrogenase, cytosolic 1
IPI00317710 Tax_Id=10090 Gene_Symbol=Hspa4l Isoform 1 of Heat shock 70 kDa protein 4L
IPI00116074 Tax_Id=10090 Gene_Symbol=Aco2 Aconitate hydratase, mitochondrial precursor
IPI00114017 Tax_Id=10090 Gene_Symbol=Anxa7 Annexin A7
IPI00125143 Tax_Id=10090 Gene_Symbol=Arpc1b Arpc1b protein
IPI00133903 Tax_Id=10090 Gene_Symbol=Hspa9 Stress-70 protein, mitochondrial precursor
IPI00230682 Tax_Id=10090 Gene_Symbol=Ywhab Isoform Long of 14-3-3 protein beta/alpha
IPI00115528 Tax_Id=10090 Gene_Symbol=Pls3 Plastin 3
IPI00124264 Tax_Id=10090 Gene_Symbol=Anxa11 Annexin A11
IPI00226430 Tax_Id=10090 Gene_Symbol=Acaa2 3-ketoacyl-CoA thiolase, mitochondrial
IPI00313222 Tax_Id=10090 Gene_Symbol=Rpl6 60S ribosomal protein L6
IPI00228253 Tax_Id=10090 Gene_Symbol=Acat2 Acetyl-CoA acetyltransferase, cytosolic
IPI00283862 Tax_Id=10090 Gene_Symbol=Psma1 Proteasome subunit alpha type-1
IPI00310240 Tax_Id=10090 Gene_Symbol=Anxa6 13 days embryo forelimb cDNA, RIKEN full-length enriched library, clone:5930413M14 product:annexin A6, full
IPI00116645 Tax_Id=10090 Gene_Symbol=Cnn1 Isoform Alpha of Calponin-1
IPI00221817 Tax_Id=10090 Gene_Symbol=Loh11cr2a Loss of heterozygosity 11 chromosomal region 2 gene A protein homolog
IPI00312058 Tax_Id=10090 Gene_Symbol=Cat Catalase
IPI00114894 Tax_Id=10090 Gene_Symbol=Myh11 Isoform 1 of Myosin-11
IPI00124287 Tax_Id=10090 Gene_Symbol=Pabpc1 Polyadenylate-binding protein 1
IPI00119667 Tax_Id=10090 Gene_Symbol=Eef1a2 Elongation factor 1-alpha 2
IPI00420882 Tax_Id=10090 Gene_Symbol=Ogdh Isoform 4 of 2-oxoglutarate dehydrogenase E1 component, mitochondrial precursor
IPI00129225 Tax_Id=10090 Gene_Symbol=Kng1 Isoform LMW of Kininogen-1 precursor
IPI00119114 Tax_Id=10090 Gene_Symbol=Acadl Long-chain specific acyl-CoA dehydrogenase, mitochondrial precursor
IPI00115833 Tax_Id=10090 Gene_Symbol=Mtap6 microtubule-associated protein 6 isoform 1
IPI00622946 Tax_Id=10090 Gene_Symbol=Palld Isoform 4 of Palladin
IPI00271262 Tax_Id=10090 Gene_Symbol=Mug2 Murinoglobulin-2 precursor
IPI00124692 Tax_Id=10090 Gene_Symbol=Taldo1 Transaldolase
IPI00117730 Tax_Id=10090 Gene_Symbol=Gbp3 Guanylate-binding protein 4
IPI00230706 Tax_Id=10090 Gene_Symbol=Pgam2 Phosphoglycerate mutase 2
IPI00127596 Tax_Id=10090 Gene_Symbol=Ckm Creatine kinase M-type
IPI00322312 Tax_Id=10090 Gene_Symbol=Arhgdia Rho GDP-dissociation inhibitor 1
IPI00353727 Tax_Id=10090 Gene_Symbol=Anxa4 Annexin A4
IPI00230108 Tax_Id=10090 Gene_Symbol=Pdia3 Protein disulfide-isomerase A3 precursor
IPI00462934 Tax_Id=10090 Gene_Symbol=Khsrp Far upstream element-binding protein 2
IPI00224626 Tax_Id=10090 Gene_Symbol=Sept7 cell division cycle 10 homolog
IPI00116498 Tax_Id=10090 Gene_Symbol=Ywhaz 14-3-3 protein zeta/delta
IPI00308885 Tax_Id=10090 Gene_Symbol=Hspd1 Isoform 1 of 60 kDa heat shock protein, mitochondrial precursor
IPI00314191 Tax_Id=10090 Gene_Symbol=Cbr1 Carbonyl reductase [NADPH] 1
IPI00378438 Tax_Id=10090 Gene_Symbol=Tns1 tensin 1
IPI00118678 Tax_Id=10090 Gene_Symbol=Tcp1 T-complex protein 1 subunit alpha A
IPI00223253 Tax_Id=10090 Gene_Symbol=Hnrpk Isoform 1 of Heterogeneous nuclear ribonucleoprotein K
IPI00115679 Tax_Id=10090 Gene_Symbol=Ganab Isoform 2 of Neutral alpha-glucosidase AB precursor
IPI00751017 Tax_Id=10090 Gene_Symbol=A230067G21Rik 99 kDa protein

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IPI00109600 Tax_Id=10090 Gene_Symbol=2410004A20Rik ES cells cDNA, RIKEN full-length enriched library, clone:2410004A20 product:hypothetical Alanine-ric
IPI00136703 Tax_Id=10090 Gene_Symbol=Ckb Creatine kinase B-type
IPI00154054 Tax_Id=10090 Gene_Symbol=Acat1 Acetyl-CoA acetyltransferase, mitochondrial precursor
IPI00172328 Tax_Id=10090 Gene_Symbol=Dnahc8 Isoform 1 of Ciliary dynein heavy chain 8
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IPI00348328 Tax_Id=10090 Gene_Symbol=Krt78 keratin Kb40
IPI00469952 Tax_Id=10090 Gene_Symbol=Prx Isoform 1 of Periaxin
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IPI00125971 Tax_Id=10090 Gene_Symbol=Psmc6 26S protease regulatory subunit S10B
IPI00110588 Tax_Id=10090 Gene_Symbol=Msn Moesin
IPI00116283 Tax_Id=10090 Gene_Symbol=Cct3 T-complex protein 1 subunit gamma
IPI00116281 Tax_Id=10090 Gene_Symbol=Cct6a T-complex protein 1 subunit zeta
IPI00408258 Tax_Id=10090 Gene_Symbol=Btbd12 BTB (POZ) domain containing 12
IPI00330476 Tax_Id=10090 Gene_Symbol=Cyfip1 Isoform 1 of Cytoplasmic FMR1-interacting protein 1
IPI00315948 Tax_Id=10090 Gene_Symbol=Tbcb Tubulin folding cofactor B
IPI00458583 Tax_Id=10090 Gene_Symbol=Hnrnpu Osteoclast-like cell cDNA, RIKEN full-length enriched library, clone:I420039N16 product:heterogeneous nucle
IPI00223224 Tax_Id=10090 Gene_Symbol=D130079A08Rik 12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:D130079A08 product:hy
IPI00762122 Tax_Id=10090 Gene_Symbol=- 462 kDa protein
IPI00121892 Tax_Id=10090 Gene_Symbol=Spnb2 Isoform 2 of Spectrin beta chain, brain 1
IPI00762403 Tax_Id=10090 Gene_Symbol=Usp31 ubiquitin specific protease 31
IPI00126072 Tax_Id=10090 Gene_Symbol=Vat1 Synaptic vesicle membrane protein VAT-1 homolog
IPI00402968 Tax_Id=10090 Gene_Symbol=Ehd2 13 days embryo forelimb cDNA, RIKEN full-length enriched library, clone:5930429A15 product:EH DOMAIN-CONTAINI
IPI00461360 Tax_Id=10090 Gene_Symbol=Ccdc39 Coiled-coil domain-containing protein 39
IPI00131395 Tax_Id=10090 Gene_Symbol=Znf512b MKIAA1196 protein
IPI00120274 Tax_Id=10090 Gene_Symbol=Npcd;Cbx6 Chromobox protein homolog 6
IPI00132700 Tax_Id=10090 Gene_Symbol=Mrpl35 39S ribosomal protein L35, mitochondrial precursor
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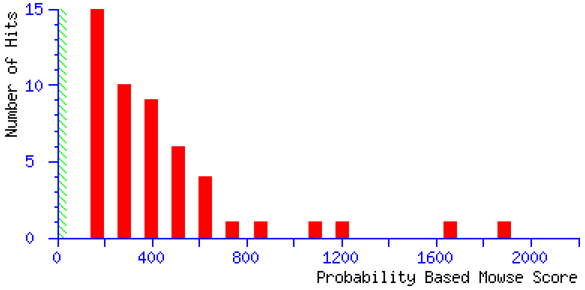
Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 34 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Peptide Summary Report

Format As | Peptide Summary ▾ | Help

Significance threshold p< 0.05 | Max. number of hits AUTO

Standard scoring ○ MudPIT scoring ● | Ions score or expect cut-off 25 | Show sub-sets 0

Show pop-ups ● Suppress pop-ups ○ | Sort unassigned Decreasing Score ▾ | Require bold red ☐

Select All | Select None | Search Selected | ☐ **Error tolerant** | Archive Report

1. IPI00874482 **Mass:** 42108 **Score:** 1889 **Queries matched:** 124 **emPAI:** 17.51
Tax_Id=10090 Gene_Symbol=Actg1 Actin, cytoplasmic 2
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	435	350.7531	699.4916	699.4894	3.02	0	(33)	0.032	1	R.GILTLK.Y + Dimethyl (K); Dimethyl (N-term)
☑	442	354.7782	707.5418	707.5397	3.07	0	(33)	0.029	1	R.GILTLK.Y + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	443	354.7784	707.5423	707.5397	3.76	0	42	0.0033	1	R.GILTLK.Y + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	642	412.2567	822.4988	822.4963	3.05	0	36	0.031	1	K.IIAPPER.K + Dimethyl (N-term)
☑	1039	504.7576	1007.5006	1007.4974	3.20	0	(51)	0.00074	1	K.AGFAGDDAPR.A + Dimethyl:2H(4) (N-term)
☑	1040	504.7577	1007.5009	1007.4974	3.45	0	57	0.00018	1	K.AGFAGDDAPR.A + Dimethyl:2H(4) (N-term)
☑	1187	527.7816	1053.5486	1053.5416	6.59	0	46	0.003	1	R.DLTDYLMK.I + Dimethyl (K); Dimethyl (N-term)
☑	1212	531.8063	1061.5981	1061.5918	5.91	0	(43)	0.0091	1	R.DLTDYLMK.I + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1437	580.7851	1159.5557	1159.5509	4.12	0	38	0.01	1	R.GYSFTTTAER.E + Dimethyl (N-term)
☑	1438	580.7855	1159.5564	1159.5509	4.68	0	(32)	0.036	1	R.GYSFTTTAER.E + Dimethyl (N-term)
☑	1446	582.7978	1163.5810	1163.5761	4.26	0	(31)	0.068	1	R.GYSFTTTAER.E + Dimethyl:2H(4) (N-term)
☑	1447	582.7985	1163.5824	1163.5761	5.42	0	(34)	0.036	1	R.GYSFTTTAER.E + Dimethyl:2H(4) (N-term)
☑	1653	609.3474	1216.6802	1216.6737	5.32	0	(42)	0.011	1	K.EITALAPSTMK.I + Dimethyl (K); Dimethyl (N-term)
☑	1654	609.3474	1216.6802	1216.6737	5.32	0	(40)	0.016	1	K.EITALAPSTMK.I + Dimethyl (K); Dimethyl (N-term)
☑	1705	613.3725	1224.7304	1224.7239	5.34	0	44	0.0071	1	K.EITALAPSTMK.I + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1706	613.3725	1224.7304	1224.7239	5.34	0	(42)	0.0098	1	K.EITALAPSTMK.I + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1712	409.5852	1225.7337	1225.7295	3.42	0	(35)	0.049	1	R.AVFPSIVGRPR.H + Dimethyl (N-term)
☑	1713	409.5852	1225.7337	1225.7295	3.42	0	(44)	0.0071	1	R.AVFPSIVGRPR.H + Dimethyl (N-term)
☑	1714	613.8741	1225.7337	1225.7295	3.43	0	67	3.3e-005	1	R.AVFPSIVGRPR.H + Dimethyl (N-term)
☑	1717	409.5854	1225.7343	1225.7295	3.92	0	(34)	0.065	1	R.AVFPSIVGRPR.H + Dimethyl (N-term)
☑	1718	409.5855	1225.7347	1225.7295	4.24	0	(43)	0.0088	1	R.AVFPSIVGRPR.H + Dimethyl (N-term)
☑	1719	613.8748	1225.7350	1225.7295	4.44	0	(52)	0.00092	1	R.AVFPSIVGRPR.H + Dimethyl (N-term)
☑	1722	409.8839	1226.6297	1226.6264	2.72	0	(43)	0.0054	1	R.HQGVMVGMGQK.D + Dimethyl (K); Dimethyl (N-term)
☑	1723	409.8839	1226.6299	1226.6264	2.86	0	(31)	0.099	1	R.HQGVMVGMGQK.D + Dimethyl (K); Dimethyl (N-term)
☑	1724	614.3229	1226.6313	1226.6264	4.02	0	48	0.0019	1	R.HQGVMVGMGQK.D + Dimethyl (K); Dimethyl (N-term)
☑	1758	410.9269	1229.7587	1229.7546	3.32	0	(36)	0.037	1	R.AVFPSIVGRPR.H + Dimethyl:2H(4) (N-term)
☑	1759	410.9271	1229.7594	1229.7546	3.84	0	(43)	0.0074	1	R.AVFPSIVGRPR.H + Dimethyl:2H(4) (N-term)
☑	1760	410.9271	1229.7595	1229.7546	3.91	0	(35)	0.041	1	R.AVFPSIVGRPR.H + Dimethyl:2H(4) (N-term)
☑	1761	410.9272	1229.7597	1229.7546	4.13	0	(37)	0.027	1	R.AVFPSIVGRPR.H + Dimethyl:2H(4) (N-term)
☑	1762	615.8871	1229.7597	1229.7546	4.13	0	(54)	0.0006	1	R.AVFPSIVGRPR.H + Dimethyl:2H(4) (N-term)
☑	1763	615.8876	1229.7607	1229.7546	4.95	0	(59)	0.00019	1	R.AVFPSIVGRPR.H + Dimethyl:2H(4) (N-term)
☑	1777	617.3446	1232.6747	1232.6686	4.91	0	(32)	0.13	1	K.EITALAPSTMK.I + Dimethyl (K); Dimethyl (N-term); Oxidation (M)

☑	1778	617.3448	1232.6751	1232.6686	5.31	0	(33)	0.089	1	K.EITALAPSTMK.I + Dimethyl (K); Dimethyl (N-term); Oxidation (M)
☑	1790	412.5673	1234.6801	1234.6766	2.84	0	(38)	0.038	1	R.HQGVMVGMGQK.D + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1791	412.5673	1234.6802	1234.6766	2.92	0	(36)	0.048	1	R.HQGVMVGMGQK.D + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1792	618.3480	1234.6814	1234.6766	3.85	0	(39)	0.025	1	R.HQGVMVGMGQK.D + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1817	621.3697	1240.7248	1240.7188	4.83	0	(30)	0.2	1	K.EITALAPSTMK.I + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)
☑	1818	621.3698	1240.7251	1240.7188	5.03	0	(30)	0.21	1	K.EITALAPSTMK.I + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)
☑	2305	473.5849	1417.7330	1417.7289	2.88	1	(25)	0.52	1	K.DSYVGDEAQSKR.G + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	2306	473.5851	1417.7335	1417.7289	3.27	1	50	0.0019	1	K.DSYVGDEAQSKR.G + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	2624	505.6606	1513.9601	1513.9543	3.86	1	42	0.004	1	K.EITALAPSTMKIK.I + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)
☑	2873	544.9758	1631.9057	1631.8990	4.09	1	(45)	0.007	1	R.MQKEITALAPSTMK.I + 2 Dimethyl (K); Dimethyl (N-term)
☑	2874	544.9761	1631.9066	1631.8990	4.65	1	(44)	0.0083	1	R.MQKEITALAPSTMK.I + 2 Dimethyl (K); Dimethyl (N-term)
☑	2907	549.0010	1643.9811	1643.9743	4.12	1	(41)	0.014	1	R.MQKEITALAPSTMK.I + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	2908	549.0011	1643.9815	1643.9743	4.34	1	51	0.0011	1	R.MQKEITALAPSTMK.I + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	2965	554.3323	1659.9752	1659.9693	3.57	1	(29)	0.2	1	R.MQKEITALAPSTMK.I + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)
☑	3301	606.9832	1817.9277	1817.9159	6.49	0	(46)	0.0048	1	K.SYELPDGQVITIGNER.F + Dimethyl (N-term)
☑	3302	909.9726	1817.9307	1817.9159	8.14	0	(90)	2e-007	1	K.SYELPDGQVITIGNER.F + Dimethyl (N-term)
☑	3303	909.9731	1817.9317	1817.9159	8.69	0	(79)	2.5e-006	1	K.SYELPDGQVITIGNER.F + Dimethyl (N-term)
☑	3323	608.3251	1821.9536	1821.9410	6.88	0	(30)	0.23	1	K.SYELPDGQVITIGNER.F + Dimethyl:2H(4) (N-term)
☑	3324	911.9853	1821.9560	1821.9410	8.22	0	92	1.6e-007	1	K.SYELPDGQVITIGNER.F + Dimethyl:2H(4) (N-term)
☑	3325	911.9858	1821.9570	1821.9410	8.76	0	(87)	5e-007	1	K.SYELPDGQVITIGNER.F + Dimethyl:2H(4) (N-term)
☑	3440	934.4482	1866.8818	1866.9005	-10.00	0	28	0.15	1	M.EEEIAALVIDNGSGMCK.A + Dimethyl:2H(4) (K)
☑	3705	670.7178	2009.1315	2009.1197	5.87	0	(40)	0.018	1	R.VAPEEHPVLLTEAPLNPK.A + Dimethyl (K); Dimethyl (N-term)
☑	3706	670.7178	2009.1315	2009.1197	5.87	0	(37)	0.038	1	R.VAPEEHPVLLTEAPLNPK.A + Dimethyl (K); Dimethyl (N-term)
☑	3707	670.7179	2009.1317	2009.1197	5.99	0	(41)	0.017	1	R.VAPEEHPVLLTEAPLNPK.A + Dimethyl (K); Dimethyl (N-term)
☑	3708	670.7179	2009.1317	2009.1197	5.99	0	(44)	0.0084	1	R.VAPEEHPVLLTEAPLNPK.A + Dimethyl (K); Dimethyl (N-term)
☑	3709	670.7180	2009.1322	2009.1197	6.24	0	(39)	0.023	1	R.VAPEEHPVLLTEAPLNPK.A + Dimethyl (K); Dimethyl (N-term)
☑	3742	673.3995	2017.1767	2017.1699	3.37	0	(31)	0.095	1	R.VAPEEHPVLLTEAPLNPK.A + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3746	673.4012	2017.1817	2017.1699	5.85	0	(44)	0.0051	1	R.VAPEEHPVLLTEAPLNPK.A + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3747	673.4013	2017.1821	2017.1699	6.03	0	(42)	0.0083	1	R.VAPEEHPVLLTEAPLNPK.A + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3748	673.4015	2017.1827	2017.1699	6.35	0	46	0.0029	1	R.VAPEEHPVLLTEAPLNPK.A + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3749	673.4017	2017.1832	2017.1699	6.57	0	(45)	0.0039	1	R.VAPEEHPVLLTEAPLNPK.A + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	4239	800.4190	2398.2352	2398.2202	6.24	1	(51)	0.002	1	R.KDLYANTVLSGGTTMYPGIADR.M + Dimethyl (K); Dimethyl (N-term)
☑	4240	800.4199	2398.2377	2398.2202	7.29	1	(71)	1.7e-005	1	R.KDLYANTVLSGGTTMYPGIADR.M + Dimethyl (K); Dimethyl (N-term)
☑	4243	803.1025	2406.2856	2406.2705	6.29	1	(55)	0.00086	1	R.KDLYANTVLSGGTTMYPGIADR.M + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	4244	803.1038	2406.2897	2406.2705	8.00	1	(32)	0.18	1	R.KDLYANTVLSGGTTMYPGIADR.M + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	4245	803.1039	2406.2898	2406.2705	8.04	1	(58)	0.00042	1	R.KDLYANTVLSGGTTMYPGIADR.M + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	4257	805.7502	2414.2289	2414.2151	5.70	1	77	4e-006	1	R.KDLYANTVLSGGTTMYPGIADR.M + Dimethyl (K); Dimethyl (N-term); Oxidation (M)
☑	4260	808.4335	2422.2788	2422.2654	5.52	1	(60)	0.00022	1	R.KDLYANTVLSGGTTMYPGIADR.M + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)
☑	4270	609.5505	2434.1727	2434.1621	4.37	1	(35)	0.046	1	R.HQGVMVGMGQKDSYVGDEAQSK.R + 2 Dimethyl (K); Dimethyl (N-term)
☑	4271	609.5505	2434.1727	2434.1621	4.37	1	(42)	0.0092	1	R.HQGVMVGMGQKDSYVGDEAQSK.R + 2 Dimethyl (K); Dimethyl (N-term)
☑	4272	609.5505	2434.1730	2434.1621	4.50	1	(39)	0.017	1	R.HQGVMVGMGQKDSYVGDEAQSK.R + 2 Dimethyl (K); Dimethyl (N-term)
☑	4273	609.5508	2434.1743	2434.1621	5.00	1	(30)	0.14	1	R.HQGVMVGMGQKDSYVGDEAQSK.R + 2 Dimethyl (K); Dimethyl (N-term)
☑	4286	612.5690	2446.2467	2446.2374	3.80	1	(27)	0.42	1	R.HQGVMVGMGQKDSYVGDEAQSK.R + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	4288	612.5695	2446.2487	2446.2374	4.62	1	(37)	0.041	1	R.HQGVMVGMGQKDSYVGDEAQSK.R + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	4289	612.5695	2446.2487	2446.2374	4.62	1	(38)	0.033	1	R.HQGVMVGMGQKDSYVGDEAQSK.R + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

☑	4291	613.5488	2450.1662	2450.1570	3.76	1	(54)	0.00046	1	R.HQGVMVGMGQKDSYVGDEAQSK.R + 2 Dimethyl (K); Dimethyl (N-term); Oxidation (M)
☑	4292	613.5492	2450.1677	2450.1570	4.38	1	(37)	0.022	1	R.HQGVMVGMGQKDSYVGDEAQSK.R + 2 Dimethyl (K); Dimethyl (N-term); Oxidation (M)
☑	4293	613.5492	2450.1677	2450.1570	4.38	1	(48)	0.0018	1	R.HQGVMVGMGQKDSYVGDEAQSK.R + 2 Dimethyl (K); Dimethyl (N-term); Oxidation (M)
☑	4294	613.5493	2450.1682	2450.1570	4.56	1	(38)	0.02	1	R.HQGVMVGMGQKDSYVGDEAQSK.R + 2 Dimethyl (K); Dimethyl (N-term); Oxidation (M)
☑	4295	613.5493	2450.1682	2450.1570	4.56	1	(30)	0.1	1	R.HQGVMVGMGQKDSYVGDEAQSK.R + 2 Dimethyl (K); Dimethyl (N-term); Oxidation (M)
☑	4296	613.5494	2450.1686	2450.1570	4.75	1	60	0.00012	1	R.HQGVMVGMGQKDSYVGDEAQSK.R + 2 Dimethyl (K); Dimethyl (N-term); Oxidation (M)
☑	4310	616.5677	2462.2416	2462.2323	3.77	1	(41)	0.019	1	R.HQGVMVGMGQKDSYVGDEAQSK.R + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)
☑	4311	616.5677	2462.2417	2462.2323	3.81	1	(35)	0.076	1	R.HQGVMVGMGQKDSYVGDEAQSK.R + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)
☑	4312	616.5679	2462.2424	2462.2323	4.07	1	(40)	0.024	1	R.HQGVMVGMGQKDSYVGDEAQSK.R + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)
☑	4313	616.5679	2462.2424	2462.2323	4.07	1	(37)	0.047	1	R.HQGVMVGMGQKDSYVGDEAQSK.R + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)
☑	4314	616.5680	2462.2427	2462.2323	4.21	1	(35)	0.067	1	R.HQGVMVGMGQKDSYVGDEAQSK.R + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)
☑	4315	616.5680	2462.2427	2462.2323	4.21	1	(31)	0.18	1	R.HQGVMVGMGQKDSYVGDEAQSK.R + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)
☑	4316	616.5680	2462.2429	2462.2323	4.27	1	(27)	0.45	1	R.HQGVMVGMGQKDSYVGDEAQSK.R + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)
☑	4320	617.5475	2466.1608	2466.1519	3.61	1	(35)	0.033	1	R.HQGVMVGMGQKDSYVGDEAQSK.R + 2 Dimethyl (K); Dimethyl (N-term); 2 Oxidation (M)
☑	4321	617.5480	2466.1627	2466.1519	4.38	1	(53)	0.00045	1	R.HQGVMVGMGQKDSYVGDEAQSK.R + 2 Dimethyl (K); Dimethyl (N-term); 2 Oxidation (M)
☑	4322	617.5482	2466.1637	2466.1519	4.79	1	(47)	0.002	1	R.HQGVMVGMGQKDSYVGDEAQSK.R + 2 Dimethyl (K); Dimethyl (N-term); 2 Oxidation (M)
☑	4323	617.5482	2466.1638	2466.1519	4.80	1	(32)	0.06	1	R.HQGVMVGMGQKDSYVGDEAQSK.R + 2 Dimethyl (K); Dimethyl (N-term); 2 Oxidation (M)
☑	4334	620.5660	2478.2347	2478.2273	3.01	1	(44)	0.0081	1	R.HQGVMVGMGQKDSYVGDEAQSK.R + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); 2 Oxidation (M)
☑	4335	620.5660	2478.2351	2478.2273	3.14	1	(50)	0.0019	1	R.HQGVMVGMGQKDSYVGDEAQSK.R + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); 2 Oxidation (M)
☑	4336	620.5665	2478.2367	2478.2273	3.82	1	(33)	0.1	1	R.HQGVMVGMGQKDSYVGDEAQSK.R + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); 2 Oxidation (M)
☑	4337	620.5665	2478.2368	2478.2273	3.83	1	(37)	0.035	1	R.HQGVMVGMGQKDSYVGDEAQSK.R + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); 2 Oxidation (M)
☑	4374	648.5753	2590.2719	2590.2632	3.37	2	(47)	0.003	1	R.HQGVMVGMGQKDSYVGDEAQSKR.G + 2 Dimethyl (K); Dimethyl (N-term)
☑	4375	648.5760	2590.2747	2590.2632	4.45	2	(60)	0.00019	1	R.HQGVMVGMGQKDSYVGDEAQSKR.G + 2 Dimethyl (K); Dimethyl (N-term)
☑	4376	648.5760	2590.2751	2590.2632	4.60	2	(58)	0.00026	1	R.HQGVMVGMGQKDSYVGDEAQSKR.G + 2 Dimethyl (K); Dimethyl (N-term)
☑	4377	648.5762	2590.2757	2590.2632	4.84	2	(49)	0.002	1	R.HQGVMVGMGQKDSYVGDEAQSKR.G + 2 Dimethyl (K); Dimethyl (N-term)
☑	4382	649.5785	2594.2847	2594.2883	-1.38	2	(29)	0.24	1	R.HQGVMVGMGQKDSYVGDEAQSKR.G + 2 Dimethyl (K); Dimethyl:2H(4) (N-term)
☑	4383	649.5792	2594.2877	2594.2883	-0.22	2	(37)	0.036	1	R.HQGVMVGMGQKDSYVGDEAQSKR.G + 2 Dimethyl (K); Dimethyl:2H(4) (N-term)
☑	4386	651.5940	2602.3467	2602.3385	3.15	2	(35)	0.074	1	R.HQGVMVGMGQKDSYVGDEAQSKR.G + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	4387	651.5942	2602.3477	2602.3385	3.53	2	(42)	0.014	1	R.HQGVMVGMGQKDSYVGDEAQSKR.G + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	4388	651.5946	2602.3493	2602.3385	4.14	2	(41)	0.018	1	R.HQGVMVGMGQKDSYVGDEAQSKR.G + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	4389	651.5947	2602.3498	2602.3385	4.33	2	(37)	0.048	1	R.HQGVMVGMGQKDSYVGDEAQSKR.G + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	4395	652.5742	2606.2677	2606.2581	3.69	2	(43)	0.0063	1	R.HQGVMVGMGQKDSYVGDEAQSKR.G + 2 Dimethyl (K); Dimethyl (N-term); Oxidation (M)
☑	4396	652.5743	2606.2683	2606.2581	3.89	2	64	5.3e-005	1	R.HQGVMVGMGQKDSYVGDEAQSKR.G + 2 Dimethyl (K); Dimethyl (N-term); Oxidation (M)
☑	4397	652.5744	2606.2685	2606.2581	3.99	2	(35)	0.042	1	R.HQGVMVGMGQKDSYVGDEAQSKR.G + 2 Dimethyl (K); Dimethyl (N-term); Oxidation (M)
☑	4398	652.5747	2606.2697	2606.2581	4.46	2	(37)	0.026	1	R.HQGVMVGMGQKDSYVGDEAQSKR.G + 2 Dimethyl (K); Dimethyl (N-term); Oxidation (M)
☑	4399	652.5747	2606.2697	2606.2581	4.46	2	(41)	0.013	1	R.HQGVMVGMGQKDSYVGDEAQSKR.G + 2 Dimethyl (K); Dimethyl (N-term); Oxidation (M)
☑	4400	652.5748	2606.2700	2606.2581	4.55	2	(51)	0.0012	1	R.HQGVMVGMGQKDSYVGDEAQSKR.G + 2 Dimethyl (K); Dimethyl (N-term); Oxidation (M)
☑	4408	655.5928	2618.3422	2618.3335	3.35	2	(49)	0.0029	1	R.HQGVMVGMGQKDSYVGDEAQSKR.G + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)
☑	4409	655.5930	2618.3427	2618.3335	3.54	2	(53)	0.0012	1	R.HQGVMVGMGQKDSYVGDEAQSKR.G + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)
☑	4410	655.5930	2618.3427	2618.3335	3.54	2	(60)	0.00023	1	R.HQGVMVGMGQKDSYVGDEAQSKR.G + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)
☑	4411	655.5932	2618.3437	2618.3335	3.92	2	(36)	0.058	1	R.HQGVMVGMGQKDSYVGDEAQSKR.G + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)
☑	4412	655.5933	2618.3439	2618.3335	4.01	2	(29)	0.28	1	R.HQGVMVGMGQKDSYVGDEAQSKR.G + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)
☑	4413	655.5933	2618.3439	2618.3335	4.01	2	(44)	0.0096	1	R.HQGVMVGMGQKDSYVGDEAQSKR.G + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)
☑	4417	656.5727	2622.2617	2622.2530	3.29	2	(27)	0.25	1	R.HQGVMVGMGQKDSYVGDEAQSKR.G + 2 Dimethyl (K); Dimethyl (N-term); 2 Oxidation (M)
☑	4420	656.5734	2622.2646	2622.2530	4.41	2	(28)	0.19	1	R.HQGVMVGMGQKDSYVGDEAQSKR.G + 2 Dimethyl (K); Dimethyl (N-term); 2 Oxidation (M)

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☑ 4421  656.5735  2622.2647  2622.2530   4.46   2  (33)    0.068   1  R.HQGVMVGMGQKDSYVGDEAQSKR.G + 2 Dimethyl (K); Dimethyl (N-term); 2 Oxidation (M)
☑ 4432  527.8740  2634.3337  2634.3284   2.04   2  (33)     0.11   1  R.HQGVMVGMGQKDSYVGDEAQSKR.G + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); 2 Oxidation (M
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2.    IPI00405227    Mass: 117215   Score: 1645   Queries matched: 81   emPAI: 3.11
      Tax_Id=10090 Gene_Symbol=Vcl Vinculin
    ☐ Check to include this hit in error tolerant search or archive report

     Query Observed  Mr(expt)  Mr(calc)   ppm  Miss Score  Expect Rank Peptide
   ☑   449 356.7715   711.5285   711.5258  3.82  0    29     0.012   1  R.ILLVAK.R + Dimethyl (K); Dimethyl (N-term)
   ☑   748 292.9004   875.6793   875.6772  2.39  1    27    0.0071   1  R.ILLVAKR.E + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
   ☑   900 483.7501   965.4857   965.4818  4.07  0    40    0.0071   1  R.DYLIDGSR.G + Dimethyl (N-term)
   ☑   904 485.7629   969.5113   969.5069  4.49  0   (39)    0.011   1  R.DYLIDGSR.G + Dimethyl:2H(4) (N-term)
   ☑   923 488.7572   975.4999   975.4964  3.59  0    30     0.092   1  K.SFLDSGYR.I + Dimethyl:2H(4) (N-term)
   ☑  1201 529.3002  1056.5859  1056.5815  4.19  0   (38)    0.022   1  K.NQGIEEALK.N + Dimethyl (K); Dimethyl (N-term)
   ☑  1217 533.3255  1064.6364  1064.6317  4.44  0    45    0.0053   1  K.NQGIEEALK.N + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
   ☑  1241 362.2218  1083.6436  1083.6400  3.30  1   (56)  0.00042   1  K.GNDIIAAAKR.M + Dimethyl (K); Dimethyl (N-term)
   ☑  1255 364.9050  1091.6932  1091.6902  2.69  1    64  3.7e-005   1  K.GNDIIAAAKR.M + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
   ☑  1382 569.3326  1136.6506  1136.6463  3.74  0    67  3.5e-005   1  R.GQGASPVAMQK.A + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
   ☑  1400 573.3455  1144.6765  1144.6703  5.40  0   (65) 5.5e-005   1  R.SLGEIAALTSK.L + Dimethyl (K); Dimethyl (N-term)
   ☑  1408 574.8097  1147.6048  1147.5981  5.88  0    47    0.0026   1  K.TISPMVMDAK.A + Dimethyl (K); Dimethyl (N-term)
   ☑  1426 577.3708  1152.7270  1152.7205  5.63  0    67  2.2e-005   1  R.SLGEIAALTSK.L + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
   ☑  1431 578.8346  1155.6546  1155.6483  5.47  0   (32)     0.14   1  K.TISPMVMDAK.A + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
   ☑  1448 582.8063  1163.5980  1163.5930  4.29  0   (32)    0.075   1  K.TISPMVMDAK.A + Dimethyl (K); Dimethyl (N-term); Oxidation (M)
   ☑  1473 586.8316  1171.6487  1171.6432  4.63  0   (31)     0.15   1  K.TISPMVMDAK.A + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)
   ☑  1474 586.8317  1171.6488  1171.6432  4.73  0   (36)    0.044   1  K.TISPMVMDAK.A + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)
   ☑  1489 587.8402  1173.6659  1173.6605  4.58  0   (61)  0.00013   1  K.STVEGIQASVK.T + Dimethyl (K); Dimethyl (N-term)
   ☑  1521 590.8011  1179.5876  1179.5814  5.31  0    48    0.0016   1  R.MALLMAEMSR.L + Dimethyl (N-term)
   ☑  1528 591.8654  1181.7162  1181.7107  4.60  0    66  3.7e-005   1  K.STVEGIQASVK.T + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
   ☑  1535 592.8136  1183.6127  1183.6065  5.28  0   (41)   0.0099   1  R.MALLMAEMSR.L + Dimethyl:2H(4) (N-term)
   ☑  1592 602.3276  1202.6407  1202.6329  6.54  0    44     0.007   1  K.MSAEINEIIR.V + Dimethyl (N-term)
   ☑  1637 606.8536  1211.6927  1211.6874  4.42  0    64  7.1e-005   1  R.ELTPQVISAAR.I + Dimethyl (N-term)
   ☑  1650 608.8666  1215.7187  1215.7125  5.14  0   (38)    0.027   1  R.ELTPQVISAAR.I + Dimethyl:2H(4) (N-term)
   ☑  1858 629.8101  1257.6057  1257.5990  5.37  0    40    0.0062   1  R.WIDNPTVDDR.G + Dimethyl (N-term)
   ☑  1866 420.8993  1259.6761  1259.6721  3.20  1    29      0.25   1  K.DIAKASDEVTR.L + Dimethyl (K); Dimethyl (N-term)
   ☑  1870 631.8226  1261.6306  1261.6241  5.15  0   (36)    0.025   1  R.WIDNPTVDDR.G + Dimethyl:2H(4) (N-term)
   ☑  1891 635.4005  1268.7864  1268.7777  6.79  0    45     0.004   1  K.ELLPVLISAMK.I + Dimethyl (K); Dimethyl (N-term)
   ☑  1913 639.4256  1276.8366  1276.8280  6.79  0   (31)    0.041   1  K.ELLPVLISAMK.I + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
   ☑  1947 647.4217  1292.8288  1292.8229  4.60  0   (41)   0.0066   1  K.ELLPVLISAMK.I + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)
   ☑  1960 650.3882  1298.7618  1298.7542  5.88  0    33      0.11   1  R.VMLVNSMNTVK.E + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
   ☑  2039 442.5871  1324.7396  1324.7350  3.40  0   (27)     0.38   1  K.AVAGNISDPGLQK.S + Dimethyl (K); Dimethyl (N-term)
   ☑  2040 663.3779  1324.7412  1324.7350  4.63  0   (57)  0.00044   1  K.AVAGNISDPGLQK.S + Dimethyl (K); Dimethyl (N-term)
   ☑  2062 444.5868  1330.7385  1330.7343  3.15  1    53   0.00089   1  R.EAVKAASDELSK.T + 2 Dimethyl (K); Dimethyl (N-term)
   ☑  2072 667.4029  1332.7912  1332.7853  4.47  0    70  1.8e-005   1  K.AVAGNISDPGLQK.S + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
   ☑  2106 448.6118  1342.8136  1342.8097  2.93  1   (51)   0.0012   1  R.EAVKAASDELSK.T + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
   ☑  2132 678.8844  1355.7542  1355.7458  6.23  0    44    0.0083   1  K.MTGLVDEAIDTK.S + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
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☑	2147	455.6034	1363.7884	1363.7846	2.78	1	38	0.031	1	R.ARGQGASPVAMQK.A + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	2156	685.9078	1369.8010	1369.7929	5.92	0	64	6.9e-005	1	K.QVATALQNLQTK.T + Dimethyl (K); Dimethyl (N-term)
☑	2196	689.9326	1377.8506	1377.8431	5.40	0	(59)	0.00012	1	K.QVATALQNLQTK.T + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	2222	463.2750	1386.8031	1386.7969	4.42	1	(40)	0.017	1	K.SLLDASEEAIKK.D + 2 Dimethyl (K); Dimethyl (N-term)
☑	2253	467.3000	1398.8781	1398.8723	4.18	1	44	0.0034	1	K.SLLDASEEAIKK.D + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	2274	469.2381	1404.6926	1404.6885	2.90	1	27	0.21	1	R.EVENSEDPKFR.E + Dimethyl (K); Dimethyl (N-term)
☑	2403	481.6259	1441.8560	1441.8504	3.90	1	31	0.13	1	R.ALASIDSKLNQAK.G + 2 Dimethyl (K); Dimethyl (N-term)
☑	2450	485.6509	1453.9310	1453.9257	3.63	1	(26)	0.15	1	R.ALASIDSKLNQAK.G + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	2591	753.3811	1504.7477	1504.7378	6.61	0	89	1.4e-007	1	K.MLGQMTDQVADLR.A + Dimethyl (N-term)
☑	2606	755.3939	1508.7732	1508.7629	6.81	0	(82)	9.2e-007	1	K.MLGQMTDQVADLR.A + Dimethyl:2H(4) (N-term)
☑	2621	757.4380	1512.8615	1512.8512	6.87	0	(103)	8.7e-009	1	K.AQQVSQGLDVLTAK.V + Dimethyl (K); Dimethyl (N-term)
☑	2645	761.4633	1520.9120	1520.9014	6.96	0	117	2.7e-010	1	K.AQQVSQGLDVLTAK.V + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	2681	769.3754	1536.7362	1536.7276	5.58	0	(74)	3e-006	1	K.MLGQMTDQVADLR.A + Dimethyl (N-term); 2 Oxidation (M)
☑	2691	771.3886	1540.7627	1540.7527	6.48	0	(53)	0.00056	1	K.MLGQMTDQVADLR.A + Dimethyl:2H(4) (N-term); 2 Oxidation (M)
☑	2712	775.8984	1549.7823	1549.7717	6.89	0	52	0.00089	1	K.AGEVINQPMMMAAR.Q + Dimethyl:2H(4) (N-term)
☑	2720	519.6401	1555.8986	1555.8933	3.39	1	(35)	0.057	1	R.LGATAEKAAAVGTANK.S + 2 Dimethyl (K); Dimethyl (N-term)
☑	2745	523.6655	1567.9746	1567.9687	3.77	1	40	0.0085	1	R.LGATAEKAAAVGTANK.S + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	2788	531.9963	1592.9672	1592.9589	5.22	1	36	0.034	1	R.ALASQLQDSLKDLK.A + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3215	591.6741	1772.0004	1771.9931	4.10	1	38	0.035	1	R.VGKETVQTTEDQILK.R + 2 Dimethyl (K); Dimethyl (N-term)
☑	3497	628.6982	1883.0727	1883.0612	6.10	1	28	0.29	1	R.LANVMMGPYRQDLLAK.C + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3557	478.0375	1908.1207	1908.1132	3.96	2	(39)	0.015	1	R.VGKETVQTTEDQILKR.D + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3558	478.0375	1908.1209	1908.1132	4.06	2	49	0.0016	1	R.VGKETVQTTEDQILKR.D + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3597	486.0515	1940.1768	1940.1696	3.74	2	(41)	0.0065	1	R.VGKETVQTTEDQILKR.D + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3632	396.3979	1976.9532	1976.9486	2.32	1	30	0.13	1	K.MIDERQQELTHQEHR.V + Dimethyl (N-term)
☑	3663	499.2447	1992.9499	1992.9435	3.19	1	(29)	0.12	1	K.MIDERQQELTHQEHR.V + Dimethyl (N-term); Oxidation (M)
☑	3728	672.3625	2014.0657	2014.0534	6.12	1	25	0.73	1	R.WIDNPTVDDRGVGQAAIR.G + Dimethyl:2H(4) (N-term)
☑	3791	680.0118	2037.0137	2037.0028	5.37	1	62	0.00011	1	K.GWLRDPNASPGDAGEQAIR.Q + Dimethyl (N-term)
☑	3801	681.3538	2041.0395	2041.0279	5.66	1	(56)	0.00048	1	K.GWLRDPNASPGDAGEQAIR.Q + Dimethyl:2H(4) (N-term)
☑	3867	690.7162	2069.1267	2069.1125	6.86	0	(31)	0.2	1	K.VAMANIQPQMLVAGATSIAR.R + Dimethyl (N-term)
☑	3880	692.0575	2073.1507	2073.1376	6.31	0	(47)	0.0039	1	K.VAMANIQPQMLVAGATSIAR.R + Dimethyl:2H(4) (N-term)
☑	3881	692.0577	2073.1512	2073.1376	6.55	0	49	0.0028	1	K.VAMANIQPQMLVAGATSIAR.R + Dimethyl:2H(4) (N-term)
☑	3957	718.7388	2153.1947	2153.1804	6.65	1	(68)	3.6e-005	1	K.AQQVSQGLDVLTAKVENAAR.K + Dimethyl (K); Dimethyl (N-term)
☑	3958	718.7389	2153.1948	2153.1804	6.70	1	78	3.9e-006	1	K.AQQVSQGLDVLTAKVENAAR.K + Dimethyl (K); Dimethyl (N-term)
☑	3969	721.4222	2161.2447	2161.2306	6.52	1	(61)	0.00011	1	K.AQQVSQGLDVLTAKVENAAR.K + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3970	721.4222	2161.2449	2161.2306	6.60	1	(67)	2.9e-005	1	K.AQQVSQGLDVLTAKVENAAR.K + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	4113	751.0674	2250.1805	2250.1644	7.14	1	58	0.00035	1	K.AVAGNISDPGLQKSFLDSGYR.I + Dimethyl (K); Dimethyl (N-term)
☑	4114	751.0679	2250.1817	2250.1644	7.69	1	(48)	0.0036	1	K.AVAGNISDPGLQKSFLDSGYR.I + Dimethyl (K); Dimethyl (N-term)
☑	4119	753.7502	2258.2287	2258.2147	6.23	1	(48)	0.0037	1	K.AVAGNISDPGLQKSFLDSGYR.I + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	4120	753.7502	2258.2287	2258.2147	6.23	1	(29)	0.3	1	K.AVAGNISDPGLQKSFLDSGYR.I + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	4248	803.7575	2408.2507	2408.2336	7.13	1	43	0.011	1	K.LLAVAATAPPDAPNREEVFDER.A + Dimethyl (N-term)
☑	4255	805.0995	2412.2767	2412.2587	7.49	1	(42)	0.016	1	K.LLAVAATAPPDAPNREEVFDER.A + Dimethyl:2H(4) (N-term)
☑	4475	669.8619	2675.4184	2675.4018	6.20	2	(38)	0.035	1	R.VLQLTSWDEDAWASKDTEAMKR.A + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	4476	669.8621	2675.4194	2675.4018	6.57	2	67	4.6e-005	1	R.VLQLTSWDEDAWASKDTEAMKR.A + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	4498	675.9139	2699.6267	2699.6124	5.28	2	29	0.031	1	R.LGATAEKAAAVGTANKSTVEGIQASVK.T + 3 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

3. IPI00131695 **Mass:** 70700 **Score:** 1179 **Queries matched:** 51 **emPAI:** 2.15

Tax_Id=10090 Gene_Symbol=Alb Serum albumin precursor

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1083	514.8236	1027.6327	1027.6277	4.81	0	(50)	0.0018	1	K.QTALAELVK.H + Dimethyl (K); Dimethyl (N-term)
☑	1084	514.8237	1027.6328	1027.6277	4.93	0	(30)	0.19	1	K.QTALAELVK.H + Dimethyl (K); Dimethyl (N-term)
☑	1085	514.8240	1027.6335	1027.6277	5.64	0	(50)	0.0018	1	K.QTALAELVK.H + Dimethyl (K); Dimethyl (N-term)
☑	1117	518.8486	1035.6827	1035.6779	4.60	0	50	0.0011	1	K.QTALAELVK.H + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1118	518.8488	1035.6831	1035.6779	4.96	0	(49)	0.0015	1	K.QTALAELVK.H + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1119	518.8491	1035.6836	1035.6779	5.42	0	(50)	0.0012	1	K.QTALAELVK.H + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1120	518.8492	1035.6838	1035.6779	5.66	0	(36)	0.027	1	K.QTALAELVK.H + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
	1228	359.2197	1074.6372	1074.6338	3.12	1	(29)	0.26	2	R.AFKAWAVAR.L + Dimethyl (K); Dimethyl (N-term)
☑	1240	361.9030	1082.6873	1082.6840	3.02	1	31	0.1	1	R.AFKAWAVAR.L + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1538	395.5932	1183.7577	1183.7540	3.14	1	51	0.00081	1	K.KQTALAELVK.H + 2 Dimethyl (K); Dimethyl (N-term)
☑	1539	592.8867	1183.7589	1183.7540	4.15	1	(26)	0.27	1	K.KQTALAELVK.H + 2 Dimethyl (K); Dimethyl (N-term)
	1543	396.2527	1185.7364	1185.7332	2.67	1	(29)	0.15	2	K.LATDLTKVNK.E + 2 Dimethyl (K); Dimethyl (N-term)
☑	1567	399.6184	1195.8333	1195.8293	3.33	1	(36)	0.0065	1	K.KQTALAELVK.H + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1568	598.9248	1195.8351	1195.8293	4.80	1	(25)	0.083	1	K.KQTALAELVK.H + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1578	400.2780	1197.8122	1197.8086	3.02	1	39	0.0054	1	K.LATDLTKVNK.E + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1600	603.3456	1204.6767	1204.6703	5.31	0	(38)	0.033	1	K.LVQEVTDFAK.T + Dimethyl (K); Dimethyl (N-term)
☑	1644	607.3706	1212.7267	1212.7206	5.08	0	56	0.00051	1	K.LVQEVTDFAK.T + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1984	436.2204	1305.6393	1305.6353	3.02	0	(38)	0.012	1	R.YNDLGEQHFK.G + Dimethyl (K); Dimethyl (N-term)
☑	2018	438.9039	1313.6898	1313.6856	3.21	0	48	0.0023	1	R.YNDLGEQHFK.G + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	2478	489.9455	1466.8147	1466.8093	3.71	0	(38)	0.035	1	K.APQVSTPTLVEAAR.N + Dimethyl (N-term)
☑	2479	734.4156	1466.8167	1466.8093	5.07	0	47	0.0036	1	K.APQVSTPTLVEAAR.N + Dimethyl (N-term)
☑	2499	491.2872	1470.8399	1470.8344	3.72	0	(26)	0.55	1	K.APQVSTPTLVEAAR.N + Dimethyl:2H(4) (N-term)
☑	2500	736.4282	1470.8419	1470.8344	5.10	0	(35)	0.064	1	K.APQVSTPTLVEAAR.N + Dimethyl:2H(4) (N-term)
☑	2524	495.2865	1482.8377	1482.8307	4.75	1	67	4.1e-005	1	R.RHPDYSVSLLLR.L + Dimethyl (N-term)
☑	2532	744.3506	1486.6866	1486.6796	4.75	0	(72)	3.1e-006	1	K.YMCENQATISSK.L + Dimethyl (K); Dimethyl (N-term)
☑	2535	496.6284	1486.8635	1486.8558	5.19	1	(64)	7.8e-005	1	R.RHPDYSVSLLLR.L + Dimethyl:2H(4) (N-term)
☑	2559	748.3759	1494.7372	1494.7298	4.92	0	78	1.9e-006	1	K.YMCENQATISSK.L + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	2598	754.4219	1506.8292	1506.8194	6.47	0	(82)	1.3e-006	1	K.LGEYGFQNAILVR.Y + Dimethyl (N-term)
☑	2599	754.4231	1506.8317	1506.8194	8.15	0	104	8.6e-009	1	K.LGEYGFQNAILVR.Y + Dimethyl (N-term)
☑	2616	756.4342	1510.8539	1510.8446	6.15	0	(77)	3.8e-006	1	K.LGEYGFQNAILVR.Y + Dimethyl:2H(4) (N-term)
☑	2617	756.4363	1510.8580	1510.8446	8.90	0	(89)	2.5e-007	1	K.LGEYGFQNAILVR.Y + Dimethyl:2H(4) (N-term)
☑	3088	857.4602	1712.9059	1712.8923	7.91	0	(81)	2e-006	1	R.LSQTFPNADFAEITK.L + Dimethyl:2H(4) (N-term)
☑	3135	579.9767	1736.9084	1736.8985	5.71	0	(52)	0.0014	1	R.LSQTFPNADFAEITK.L + Dimethyl (K); Dimethyl (N-term)
☑	3136	579.9770	1736.9093	1736.8985	6.24	0	(56)	0.00056	1	R.LSQTFPNADFAEITK.L + Dimethyl (K); Dimethyl (N-term)
☑	3137	869.4637	1736.9128	1736.8985	8.25	0	(57)	0.00044	1	R.LSQTFPNADFAEITK.L + Dimethyl (K); Dimethyl (N-term)
☑	3157	582.6603	1744.9592	1744.9487	6.00	0	(59)	0.00033	1	R.LSQTFPNADFAEITK.L + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3158	582.6604	1744.9594	1744.9487	6.11	0	82	1.6e-006	1	R.LSQTFPNADFAEITK.L + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3159	873.4886	1744.9626	1744.9487	7.97	0	(55)	0.0007	1	R.LSQTFPNADFAEITK.L + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3590	647.0078	1938.0017	1937.9921	4.97	0	31	0.16	1	R.RPCFSALTVDETYVPK.E + Dimethyl (K); Dimethyl (N-term)
☑	3729	672.7122	2015.1146	2015.1051	4.73	1	57	0.00042	1	R.YTQKAPQVSTPTLVEAAR.N + Dimethyl (K); Dimethyl (N-term)

☑	3730	672.7122	2015.1147	2015.1051	4.77	1	(53)	0.0011	1	R.YTQKAPQVSTPTLVEAAR.N + Dimethyl (K); Dimethyl (N-term)
☑	3731	672.7129	2015.1167	2015.1051	5.76	1	(49)	0.0028	1	R.YTQKAPQVSTPTLVEAAR.N + Dimethyl (K); Dimethyl (N-term)
☑	3732	672.7129	2015.1168	2015.1051	5.82	1	(49)	0.0026	1	R.YTQKAPQVSTPTLVEAAR.N + Dimethyl (K); Dimethyl (N-term)
☑	3752	674.0498	2019.1277	2019.1302	-1.24	1	(40)	0.021	1	R.YTQKAPQVSTPTLVEAAR.N + Dimethyl (K); Dimethyl:2H(4) (N-term)
☑	3764	675.3959	2023.1657	2023.1554	5.13	1	(52)	0.00094	1	R.YTQKAPQVSTPTLVEAAR.N + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3765	675.3959	2023.1660	2023.1554	5.25	1	(55)	0.00049	1	R.YTQKAPQVSTPTLVEAAR.N + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3766	675.3959	2023.1660	2023.1554	5.25	1	(41)	0.012	1	R.YTQKAPQVSTPTLVEAAR.N + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3767	675.3961	2023.1663	2023.1554	5.43	1	(45)	0.0047	1	R.YTQKAPQVSTPTLVEAAR.N + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3768	675.3961	2023.1665	2023.1554	5.52	1	(57)	0.00031	1	R.YTQKAPQVSTPTLVEAAR.N + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	4304	819.4523	2455.3352	2455.3148	8.29	1	46	0.0047	1	R.LSQTFPNADFAEITKLATDLTK.V + Dimethyl:2H(4) (N-term)
☑	4358	853.7758	2558.3056	2558.2839	8.50	1	69	2.8e-005	1	K.TNCDLYEKLGEYGFQNAILVR.Y + Dimethyl (K); Dimethyl (N-term)

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4. IPI00131830 **Mass:** 47021 **Score:** 1124 **Queries matched:** 49 **emPAI:** 2.80

Tax_Id=10090 Gene_Symbol=Serpina3k Serine protease inhibitor A3K precursor

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1060	339.2324	1014.6753	1014.6723	2.91	1	25	0.21	1	R.SVKVPMMK.M + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1174	351.5546	1051.6420	1051.6390	2.83	0	(44)	0.0062	1	K.LSVSQVVHK.A + Dimethyl (K); Dimethyl (N-term)
☑	1175	351.5548	1051.6426	1051.6390	3.45	0	55	0.00054	1	K.LSVSQVVHK.A + Dimethyl (K); Dimethyl (N-term)
☑	1210	354.2380	1059.6923	1059.6892	2.90	0	(41)	0.009	1	K.LSVSQVVHK.A + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1611	302.9493	1207.7680	1207.7652	2.31	1	(50)	0.0012	1	K.KLSVSQVVHK.A + 2 Dimethyl (K); Dimethyl (N-term)
☑	1612	403.5966	1207.7680	1207.7652	2.31	1	(36)	0.03	1	K.KLSVSQVVHK.A + 2 Dimethyl (K); Dimethyl (N-term)
☑	1613	403.5969	1207.7688	1207.7652	2.93	1	(26)	0.24	1	K.KLSVSQVVHK.A + 2 Dimethyl (K); Dimethyl (N-term)
☑	1681	305.9680	1219.8431	1219.8406	2.05	1	57	6.9e-005	1	K.KLSVSQVVHK.A + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1682	407.6218	1219.8436	1219.8406	2.44	1	(38)	0.0053	1	K.KLSVSQVVHK.A + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1683	407.6220	1219.8441	1219.8406	2.89	1	(37)	0.005	1	K.KLSVSQVVHK.A + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	2949	553.2935	1656.8587	1656.8505	4.98	0	(27)	0.37	1	R.MQQVEASLQPETLR.K + Dimethyl (N-term)
☑	2950	553.2939	1656.8597	1656.8505	5.58	0	(35)	0.055	1	R.MQQVEASLQPETLR.K + Dimethyl (N-term)
☑	2951	829.4385	1656.8624	1656.8505	7.20	0	80	2.1e-006	1	R.MQQVEASLQPETLR.K + Dimethyl (N-term)
☑	2969	831.4504	1660.8862	1660.8756	6.39	0	(70)	2e-005	1	R.MQQVEASLQPETLR.K + Dimethyl:2H(4) (N-term)
☑	3003	839.4479	1676.8813	1676.8705	6.45	0	(53)	0.0012	1	R.MQQVEASLQPETLR.K + Dimethyl:2H(4) (N-term); Oxidation (M)
☑	3020	562.3248	1683.9525	1683.9447	4.62	0	(46)	0.0051	1	K.TLFPSQIEELNLPK.F + Dimethyl (K); Dimethyl (N-term)
☑	3021	562.3256	1683.9549	1683.9447	6.04	0	(57)	0.00045	1	K.TLFPSQIEELNLPK.F + Dimethyl (K); Dimethyl (N-term)
☑	3022	842.9871	1683.9597	1683.9447	8.91	0	(99)	2.8e-008	1	K.TLFPSQIEELNLPK.F + Dimethyl (K); Dimethyl (N-term)
☑	3042	565.0081	1692.0025	1691.9949	4.49	0	(49)	0.0018	1	K.TLFPSQIEELNLPK.F + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3043	565.0088	1692.0045	1691.9949	5.68	0	(56)	0.00037	1	K.TLFPSQIEELNLPK.F + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3044	565.0090	1692.0051	1691.9949	6.01	0	(53)	0.0007	1	K.TLFPSQIEELNLPK.F + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3045	847.0112	1692.0078	1691.9949	7.60	0	112	8.6e-010	1	K.TLFPSQIEELNLPK.F + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3289	605.3359	1812.9858	1812.9767	5.00	1	(51)	0.0017	1	R.MQQVEASLQPETLRK.W + Dimethyl (K); Dimethyl (N-term)
☑	3290	605.3363	1812.9871	1812.9767	5.71	1	(60)	0.00023	1	R.MQQVEASLQPETLRK.W + Dimethyl (K); Dimethyl (N-term)
☑	3318	608.0194	1821.0364	1821.0270	5.18	1	(49)	0.0024	1	R.MQQVEASLQPETLRK.W + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3319	608.0195	1821.0366	1821.0270	5.28	1	68	3.2e-005	1	R.MQQVEASLQPETLRK.W + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3372	614.3677	1840.0814	1840.0709	5.68	1	(44)	0.0053	1	R.KTLFPSQIEELNLPK.F + 2 Dimethyl (K); Dimethyl (N-term)
☑	3373	614.3678	1840.0817	1840.0709	5.86	1	(53)	0.00073	1	R.KTLFPSQIEELNLPK.F + 2 Dimethyl (K); Dimethyl (N-term)

☑	3374	614.3682	1840.0827	1840.0709	6.40	1	(52)	0.00097	1	R.KTLFPSQIEELNLPK.F + 2 Dimethyl (K); Dimethyl (N-term)
☑	3375	614.3683	1840.0832	1840.0709	6.67	1	(54)	0.00057	1	R.KTLFPSQIEELNLPK.F + 2 Dimethyl (K); Dimethyl (N-term)
☑	3408	618.3925	1852.1557	1852.1463	5.10	1	55	0.00014	1	R.KTLFPSQIEELNLPK.F + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3409	618.3926	1852.1561	1852.1463	5.29	1	(41)	0.0034	1	R.KTLFPSQIEELNLPK.F + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3410	618.3936	1852.1588	1852.1463	6.77	1	(50)	0.00032	1	R.KTLFPSQIEELNLPK.F + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3983	724.0675	2169.1807	2169.1641	7.66	0	99	3e-008	1	K.AVLDVAETGTEAAAATGVIGGIR.K + Dimethyl (N-term)
☑	3992	725.4079	2173.2017	2173.1892	5.75	0	(44)	0.0093	1	K.AVLDVAETGTEAAAATGVIGGIR.K + Dimethyl:2H(4) (N-term)
☑	3993	725.4086	2173.2039	2173.1892	6.74	0	(39)	0.025	1	K.AVLDVAETGTEAAAATGVIGGIR.K + Dimethyl:2H(4) (N-term)
☑	3994	725.4093	2173.2061	2173.1892	7.75	0	(35)	0.07	1	K.AVLDVAETGTEAAAATGVIGGIR.K + Dimethyl:2H(4) (N-term)
☑	4003	731.0383	2190.0932	2190.0783	6.80	0	(35)	0.047	1	R.ALYQTEAFTADFQQPTEAK.N + Dimethyl:2H(4) (N-term)
☑	4046	739.0402	2214.0987	2214.0844	6.45	0	67	3.3e-005	1	R.ALYQTEAFTADFQQPTEAK.N + Dimethyl (K); Dimethyl (N-term)
☑	4047	739.0405	2214.0996	2214.0844	6.83	0	(62)	0.0001	1	R.ALYQTEAFTADFQQPTEAK.N + Dimethyl (K); Dimethyl (N-term)
☑	4048	739.0406	2214.1001	2214.0844	7.08	0	(58)	0.00029	1	R.ALYQTEAFTADFQQPTEAK.N + Dimethyl (K); Dimethyl (N-term)
☑	4049	739.0408	2214.1007	2214.0844	7.35	0	(59)	0.00024	1	R.ALYQTEAFTADFQQPTEAK.N + Dimethyl (K); Dimethyl (N-term)
☑	4074	741.7238	2222.1496	2222.1347	6.72	0	(51)	0.0019	1	R.ALYQTEAFTADFQQPTEAK.N + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	4075	741.7238	2222.1497	2222.1347	6.77	0	(34)	0.086	1	R.ALYQTEAFTADFQQPTEAK.N + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	4076	741.7238	2222.1497	2222.1347	6.77	0	(42)	0.012	1	R.ALYQTEAFTADFQQPTEAK.N + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	4077	741.7239	2222.1498	2222.1347	6.81	0	(54)	0.00091	1	R.ALYQTEAFTADFQQPTEAK.N + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	4166	776.1102	2325.3087	2325.2904	7.88	1	(66)	4.2e-005	1	K.AVLDVAETGTEAAAATGVIGGIRK.A + Dimethyl (K); Dimethyl (N-term)
☑	4167	776.1102	2325.3087	2325.2904	7.90	1	(62)	0.0001	1	K.AVLDVAETGTEAAAATGVIGGIRK.A + Dimethyl (K); Dimethyl (N-term)
☑	4174	778.7931	2333.3574	2333.3406	7.22	1	69	1.3e-005	1	K.AVLDVAETGTEAAAATGVIGGIRK.A + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

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5. IPI00465786 **Mass:** 271832 **Score:** 808 **Queries matched:** 34 **emPAI:** 0.29

Tax_Id=10090 Gene_Symbol=Tln1 Talin-1

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1248	543.3221	1084.6296	1084.6240	5.15	0	(54)	0.00077	1	K.NLGTALAELR.T + Dimethyl (N-term)
☑	1253	545.3346	1088.6547	1088.6491	5.13	0	61	0.00015	1	K.NLGTALAELR.T + Dimethyl:2H(4) (N-term)
☑	1265	548.3677	1094.7209	1094.7151	5.36	0	28	0.13	1	K.SIAAATSALVK.A + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1323	557.3376	1112.6607	1112.6553	4.86	0	(61)	0.00016	1	K.GLAGAVSELLR.S + Dimethyl (N-term)
☑	1335	559.3502	1116.6858	1116.6805	4.76	0	69	2.3e-005	1	K.GLAGAVSELLR.S + Dimethyl:2H(4) (N-term)
☑	1559	597.3780	1192.7414	1192.7341	6.17	0	45	0.0038	1	R.AAMEPIVISAK.T + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1585	601.3457	1200.6769	1200.6714	4.57	0	54	0.0008	1	K.EVANSTANLVK.T + Dimethyl (K); Dimethyl (N-term)
☑	1619	605.3707	1208.7268	1208.7216	4.28	0	(51)	0.0013	1	K.EVANSTANLVK.T + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1678	305.9428	1219.7421	1219.7401	1.71	1	34	0.063	1	K.LVQRLEHAAK.Q + Dimethyl (K); Dimethyl (N-term)
☑	1861	630.3448	1258.6751	1258.6703	3.85	0	(74)	6.4e-006	1	R.MATNAAAQNAIK.K + Dimethyl (K); Dimethyl (N-term)
☑	1884	634.3698	1266.7250	1266.7205	3.49	0	88	3e-007	1	R.MATNAAAQNAIK.K + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1888	634.9125	1267.8104	1267.8025	6.21	0	48	0.0018	1	K.VMVTNVTSLLK.T + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	2312	474.2700	1419.7880	1419.7834	3.28	1	(31)	0.17	1	K.KSTVLQQQYNR.V + Dimethyl (K); Dimethyl (N-term)
☑	2346	476.9532	1427.8378	1427.8336	2.95	1	41	0.014	1	K.KSTVLQQQYNR.V + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	2512	738.4029	1474.7912	1474.7813	6.71	0	56	0.00054	1	K.TMLESAGGLIQTAR.A + Dimethyl (N-term)
☑	3518	630.0055	1886.9947	1886.9850	5.17	0	70	2.3e-005	1	K.LLGEIAQGNENYAGIAAR.D + Dimethyl (N-term)
☑	3526	631.3476	1891.0210	1891.0101	5.75	0	(47)	0.0053	1	K.LLGEIAQGNENYAGIAAR.D + Dimethyl:2H(4) (N-term)
☑	3652	664.3527	1990.0363	1990.0258	5.27	1	48	0.004	1	K.AAAFEDQENETVVVKEK.M + 2 Dimethyl (K); Dimethyl (N-term)

☑	3692	668.3777	2002.1114	2002.1012	5.10	1	(37)	0.049	1	K.AAAFEDQENETVVVKEK.M + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3740	673.3845	2017.1317	2017.1208	5.44	1	44	0.0072	1	R.QFVQSAKEVANSTANLVK.T + 2 Dimethyl (K); Dimethyl (N-term)
☑	3741	673.3845	2017.1317	2017.1208	5.44	1	(39)	0.023	1	R.QFVQSAKEVANSTANLVK.T + 2 Dimethyl (K); Dimethyl (N-term)
☑	3756	674.3675	2020.0807	2020.0701	5.26	0	(72)	1.5e-005	1	K.QAAASATQTIAAAQHAASAPK.A + Dimethyl (K); Dimethyl (N-term)
☑	3757	674.3676	2020.0808	2020.0701	5.31	0	(79)	3e-006	1	K.QAAASATQTIAAAQHAASAPK.A + Dimethyl (K); Dimethyl (N-term)
☑	3774	677.0508	2028.1307	2028.1203	5.11	0	93	9.4e-008	1	K.QAAASATQTIAAAQHAASAPK.A + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3775	677.0508	2028.1307	2028.1203	5.12	0	(80)	1.8e-006	1	K.QAAASATQTIAAAQHAASAPK.A + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3779	677.4097	2029.2072	2029.1961	5.45	1	(39)	0.012	1	R.QFVQSAKEVANSTANLVK.T + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3841	685.7032	2054.0877	2054.0756	5.91	0	88	3.5e-007	1	R.LNEAAAGLNQAATELVQASR.G + Dimethyl (N-term)
☑	3851	687.0455	2058.1147	2058.1007	6.82	0	(44)	0.0094	1	R.LNEAAAGLNQAATELVQASR.G + Dimethyl:2H(4) (N-term)
☑	3890	696.7075	2087.1007	2087.0899	5.20	0	36	0.056	1	R.LLSDLLPPSTGTFQEAQSR.L + Dimethyl (N-term)
☑	4028	735.7631	2204.2675	2204.2528	6.68	0	(39)	0.02	1	K.LLAALLEDEGGNGRPLLQAAK.G + Dimethyl (K); Dimethyl (N-term)
☑	4038	553.0236	2208.0651	2208.0593	2.65	1	30	0.14	1	K.MVEAAKGAAAHPDSEEQQR.L + Dimethyl (K); Dimethyl (N-term)
☑	4042	738.4465	2212.3177	2212.3030	6.64	0	46	0.0017	1	K.LLAALLEDEGGNGRPLLQAAK.G + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	4189	781.4225	2341.2457	2341.2328	5.52	0	(31)	0.18	1	K.VGAIPANALDDGQWSQGLISAAR.M + Dimethyl:2H(4) (N-term)
☑	4190	781.4227	2341.2462	2341.2328	5.71	0	41	0.021	1	K.VGAIPANALDDGQWSQGLISAAR.M + Dimethyl:2H(4) (N-term)

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6. IPI00136929 **Mass:** 44029 **Score:** 797 **Queries matched:** 50 **emPAI:** 3.65

Tax_Id=10090 Gene_Symbol=Actg1 Gamma actin-like protein

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
435	350.7531	699.4916	699.4894	3.02	0	(33)	0.032	1	R.GILTLK.Y + Dimethyl (K); Dimethyl (N-term)
442	354.7782	707.5418	707.5397	3.07	0	(33)	0.029	1	R.GILTLK.Y + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
443	354.7784	707.5423	707.5397	3.76	0	42	0.0033	1	R.GILTLK.Y + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
642	412.2567	822.4988	822.4963	3.05	0	36	0.031	1	K.IIAPPER.K + Dimethyl (N-term)
1187	527.7816	1053.5486	1053.5416	6.59	0	46	0.003	1	R.DLTDYLMK.I + Dimethyl (K); Dimethyl (N-term)
1212	531.8063	1061.5981	1061.5918	5.91	0	(43)	0.0091	1	R.DLTDYLMK.I + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
1437	580.7851	1159.5557	1159.5509	4.12	0	38	0.01	1	R.GYSFTTTAER.E + Dimethyl (N-term)
1438	580.7855	1159.5564	1159.5509	4.68	0	(32)	0.036	1	R.GYSFTTTAER.E + Dimethyl (N-term)
1446	582.7978	1163.5810	1163.5761	4.26	0	(31)	0.068	1	R.GYSFTTTAER.E + Dimethyl:2H(4) (N-term)
1447	582.7985	1163.5824	1163.5761	5.42	0	(34)	0.036	1	R.GYSFTTTAER.E + Dimethyl:2H(4) (N-term)
1653	609.3474	1216.6802	1216.6737	5.32	0	(42)	0.011	1	K.EITALAPSTMK.I + Dimethyl (K); Dimethyl (N-term)
1654	609.3474	1216.6802	1216.6737	5.32	0	(40)	0.016	1	K.EITALAPSTMK.I + Dimethyl (K); Dimethyl (N-term)
1705	613.3725	1224.7304	1224.7239	5.34	0	44	0.0071	1	K.EITALAPSTMK.I + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
1706	613.3725	1224.7304	1224.7239	5.34	0	(42)	0.0098	1	K.EITALAPSTMK.I + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
1777	617.3446	1232.6747	1232.6686	4.91	0	(32)	0.13	1	K.EITALAPSTMK.I + Dimethyl (K); Dimethyl (N-term); Oxidation (M)
1778	617.3448	1232.6751	1232.6686	5.31	0	(33)	0.089	1	K.EITALAPSTMK.I + Dimethyl (K); Dimethyl (N-term); Oxidation (M)
1817	621.3697	1240.7248	1240.7188	4.83	0	(30)	0.2	1	K.EITALAPSTMK.I + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)
1818	621.3698	1240.7251	1240.7188	5.03	0	(30)	0.21	1	K.EITALAPSTMK.I + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)
2305	473.5849	1417.7330	1417.7289	2.88	1	(25)	0.52	1	K.DSYVGDEAQSKR.G + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
2306	473.5851	1417.7335	1417.7289	3.27	1	50	0.0019	1	K.DSYVGDEAQSKR.G + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
2624	505.6606	1513.9601	1513.9543	3.86	1	42	0.004	1	K.EITALAPSTMKIK.I + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)
2873	544.9758	1631.9057	1631.8990	4.09	1	(45)	0.007	1	R.MQKEITALAPSTMK.I + 2 Dimethyl (K); Dimethyl (N-term)
2874	544.9761	1631.9066	1631.8990	4.65	1	(44)	0.0083	1	R.MQKEITALAPSTMK.I + 2 Dimethyl (K); Dimethyl (N-term)
2907	549.0010	1643.9811	1643.9743	4.12	1	(41)	0.014	1	R.MQKEITALAPSTMK.I + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
2908	549.0011	1643.9815	1643.9743	4.34	1	51	0.0011	1	R.MQKEITALAPSTMK.I + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
2965	554.3323	1659.9752	1659.9693	3.57	1	(29)	0.2	1	R.MQKEITALAPSTMK.I + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)

3301	606.9832	1817.9277	1817.9159	6.49	0	(46)	0.0048	1	K.SYELPDGQVITIGNER.F + Dimethyl (N-term)
3302	909.9726	1817.9307	1817.9159	8.14	0	(90)	2e-007	1	K.SYELPDGQVITIGNER.F + Dimethyl (N-term)
3303	909.9731	1817.9317	1817.9159	8.69	0	(79)	2.5e-006	1	K.SYELPDGQVITIGNER.F + Dimethyl (N-term)
3323	608.3251	1821.9536	1821.9410	6.88	0	(30)	0.23	1	K.SYELPDGQVITIGNER.F + Dimethyl:2H(4) (N-term)
3324	911.9853	1821.9560	1821.9410	8.22	0	92	1.6e-007	1	K.SYELPDGQVITIGNER.F + Dimethyl:2H(4) (N-term)
3325	911.9858	1821.9570	1821.9410	8.76	0	(87)	5e-007	1	K.SYELPDGQVITIGNER.F + Dimethyl:2H(4) (N-term)
3440	934.4482	1866.8818	1866.9005	-10.00	0	28	0.15	1	M.EEEIAALVIDNGSGMCK.A + Dimethyl:2H(4) (K)
3705	670.7178	2009.1315	2009.1197	5.87	0	(40)	0.018	1	R.VAPEEHPVLLTEAPLNPK.R + Dimethyl (K); Dimethyl (N-term)
3706	670.7178	2009.1315	2009.1197	5.87	0	(37)	0.038	1	R.VAPEEHPVLLTEAPLNPK.R + Dimethyl (K); Dimethyl (N-term)
3707	670.7179	2009.1317	2009.1197	5.99	0	(41)	0.017	1	R.VAPEEHPVLLTEAPLNPK.R + Dimethyl (K); Dimethyl (N-term)
3708	670.7179	2009.1317	2009.1197	5.99	0	(44)	0.0084	1	R.VAPEEHPVLLTEAPLNPK.R + Dimethyl (K); Dimethyl (N-term)
3709	670.7180	2009.1322	2009.1197	6.24	0	(39)	0.023	1	R.VAPEEHPVLLTEAPLNPK.R + Dimethyl (K); Dimethyl (N-term)
3742	673.3995	2017.1767	2017.1699	3.37	0	(31)	0.095	1	R.VAPEEHPVLLTEAPLNPK.R + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
3746	673.4012	2017.1817	2017.1699	5.85	0	(44)	0.0051	1	R.VAPEEHPVLLTEAPLNPK.R + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
3747	673.4013	2017.1821	2017.1699	6.03	0	(42)	0.0083	1	R.VAPEEHPVLLTEAPLNPK.R + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
3748	673.4015	2017.1827	2017.1699	6.35	0	46	0.0029	1	R.VAPEEHPVLLTEAPLNPK.R + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
3749	673.4017	2017.1832	2017.1699	6.57	0	(45)	0.0039	1	R.VAPEEHPVLLTEAPLNPK.R + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
4239	800.4190	2398.2352	2398.2202	6.24	1	(51)	0.002	1	R.KDLYANTVLSGGTTMYPGLADR.M + Dimethyl (K); Dimethyl (N-term)
4240	800.4199	2398.2377	2398.2202	7.29	1	(71)	1.7e-005	1	R.KDLYANTVLSGGTTMYPGLADR.M + Dimethyl (K); Dimethyl (N-term)
4243	803.1025	2406.2856	2406.2705	6.29	1	(55)	0.00086	1	R.KDLYANTVLSGGTTMYPGLADR.M + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
4244	803.1038	2406.2897	2406.2705	8.00	1	(32)	0.18	1	R.KDLYANTVLSGGTTMYPGLADR.M + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
4245	803.1039	2406.2898	2406.2705	8.04	1	(58)	0.00042	1	R.KDLYANTVLSGGTTMYPGLADR.M + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
4257	805.7502	2414.2289	2414.2151	5.70	1	77	4e-006	1	R.KDLYANTVLSGGTTMYPGLADR.M + Dimethyl (K); Dimethyl (N-term); Oxidation (M)
4260	808.4335	2422.2788	2422.2654	5.52	1	(60)	0.00022	1	R.KDLYANTVLSGGTTMYPGLADR.M + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)

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7. IPI00114375 **Mass:** 62638 **Score:** 658 **Queries matched:** 30 **emPAI:** 1.53

Tax_Id=10090 Gene_Symbol=Dpysl2 Dihydropyrimidinase-related protein 2

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	828	**468.7706**	**935.5267**	**935.5229**	**4.12**	**0**	**54**	**0.00056**	**1**	**K.VFNLYPR.K + Dimethyl (N-term)**
☑	839	**470.7831**	**939.5516**	**939.5480**	**3.86**	**0**	**(50)**	**0.0013**	**1**	**K.VFNLYPR.K + Dimethyl:2H(4) (N-term)**
☑	1132	**522.2976**	**1042.5807**	**1042.5771**	**3.50**	**0**	**58**	**0.00029**	**1**	**K.SAAEVIAQAR.K + Dimethyl (N-term)**
☑	1156	**524.3103**	**1046.6061**	**1046.6022**	**3.69**	**0**	**(52)**	**0.0013**	**1**	**K.SAAEVIAQAR.K + Dimethyl:2H(4) (N-term)**
☑	1328	**372.2458**	**1113.7154**	**1113.7121**	**2.99**	**1**	**31**	**0.086**	**1**	**R.ITSDRLLIK.G + Dimethyl (K); Dimethyl (N-term)**
☑	1395	**570.8561**	**1139.6977**	**1139.6914**	**5.54**	**0**	**48**	**0.002**	**1**	**R.GSPLVVISQGK.I + Dimethyl (K); Dimethyl (N-term)**
☑	2029	**441.5809**	**1321.7207**	**1321.7177**	**2.32**	**0**	**(40)**	**0.019**	**1**	**R.MVIPGGIDVHTR.F + Dimethyl (N-term)**
☑	2044	**442.9225**	**1325.7456**	**1325.7428**	**2.15**	**0**	**(49)**	**0.0021**	**1**	**R.MVIPGGIDVHTR.F + Dimethyl:2H(4) (N-term)**
☑	2092	**446.9131**	**1337.7176**	**1337.7126**	**3.77**	**0**	**59**	**0.00024**	**1**	**R.MVIPGGIDVHTR.F + Dimethyl (N-term); Oxidation (M)**
☑	2101	**448.2549**	**1341.7429**	**1341.7377**	**3.89**	**0**	**(56)**	**0.00047**	**1**	**R.MVIPGGIDVHTR.F + Dimethyl:2H(4) (N-term); Oxidation (M)**
☑	2200	**690.4215**	**1378.8285**	**1378.8184**	**7.30**	**0**	**(59)**	**0.00019**	**1**	**K.QIGENLIVPGGVK.T + Dimethyl (K); Dimethyl (N-term)**
☑	2223	**694.4466**	**1386.8786**	**1386.8686**	**7.22**	**0**	**62**	**6.3e-005**	**1**	**K.QIGENLIVPGGVK.T + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)**
☑	3080	**570.9752**	**1709.9037**	**1709.8948**	**5.20**	**0**	**80**	**2.1e-006**	**1**	**K.IVLEDGTLHVTEGSGR.Y + Dimethyl (N-term)**
☑	3092	**572.3168**	**1713.9287**	**1713.9199**	**5.10**	**0**	**(76)**	**5.6e-006**	**1**	**K.IVLEDGTLHVTEGSGR.Y + Dimethyl:2H(4) (N-term)**
☑	3232	**597.3156**	**1788.9250**	**1788.9168**	**4.61**	**0**	**42**	**0.013**	**1**	**K.MDENQFVAVTSTNAAK.V + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)**
☑	4010	**733.0432**	**2196.1077**	**2196.0923**	**7.01**	**0**	**63**	**0.00011**	**1**	**R.NLHQSGFSLSGAQIDDNIPR.R + Dimethyl (N-term)**
☑	4015	**734.3834**	**2200.1283**	**2200.1174**	**4.91**	**0**	**(30)**	**0.22**	**1**	**R.NLHQSGFSLSGAQIDDNIPR.R + Dimethyl:2H(4) (N-term)**
☑	4016	**734.3845**	**2200.1317**	**2200.1174**	**6.49**	**0**	**(55)**	**0.00082**	**1**	**R.NLHQSGFSLSGAQIDDNIPR.R + Dimethyl:2H(4) (N-term)**

☑	4017	734.3845	2200.1317	2200.1174	6.49	0	(48)	0.0039	1	R.NLHQSGFSLSGAQIDDNIPR.R + Dimethyl:2H(4) (N-term)
☑	4018	734.3849	2200.1327	2200.1174	6.94	0	(26)	0.57	1	R.NLHQSGFSLSGAQIDDNIPR.R + Dimethyl:2H(4) (N-term)
☑	4019	734.3849	2200.1327	2200.1174	6.94	0	(30)	0.25	1	R.NLHQSGFSLSGAQIDDNIPR.R + Dimethyl:2H(4) (N-term)
☑	4024	735.3827	2203.1264	2203.1121	6.52	1	(35)	0.067	1	K.AVGKDNFTLIPEGTNGTEER.M + Dimethyl (K); Dimethyl (N-term)
☑	4029	552.3210	2205.2548	2205.2481	3.06	2	36	0.037	1	K.TVTPASSAKTSPAKQQAPPVR.N + 2 Dimethyl (K); Dimethyl (N-term)
☑	4030	736.3365	2205.9877	2205.9711	7.53	0	(46)	0.00089	1	R.FQMPDQGMTSADDFFQGTK.A + Dimethyl (K); Dimethyl (N-term)
☑	4031	736.3373	2205.9900	2205.9711	8.57	0	(56)	9.9e-005	1	R.FQMPDQGMTSADDFFQGTK.A + Dimethyl (K); Dimethyl (N-term)
☑	4041	738.0657	2211.1754	2211.1623	5.91	1	38	0.043	1	K.AVGKDNFTLIPEGTNGTEER.M + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	4045	739.0210	2214.0412	2214.0213	8.95	0	57	0.00018	1	R.FQMPDQGMTSADDFFQGTK.A + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	4554	732.8967	2927.5577	2927.5352	7.69	0	61	0.00017	1	R.ILDLGITGPEGHVLSRPEEVEAEAVNR.S + Dimethyl (N-term)
☑	4560	733.9027	2931.5817	2931.5603	7.30	0	(48)	0.0026	1	R.ILDLGITGPEGHVLSRPEEVEAEAVNR.S + Dimethyl:2H(4) (N-term)
☑	4561	733.9027	2931.5817	2931.5603	7.30	0	(55)	0.00065	1	R.ILDLGITGPEGHVLSRPEEVEAEAVNR.S + Dimethyl:2H(4) (N-term)

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8. IPI00405058 **Mass:** 32497 **Score:** 637 **Queries matched:** 27 **emPAI:** 3.27

Tax_Id=10090 Gene_Symbol=Hnrnpa2b1 Isoform 3 of Heterogeneous nuclear ribonucleoproteins A2/B1

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1128	521.2433	1040.4720	1040.4676	4.27	0	66	5.4e-006	1	R.GGNFGFGDSR.G + Dimethyl (N-term)
☑	1144	523.2556	1044.4967	1044.4927	3.86	0	(63)	1.8e-005	1	R.GGNFGFGDSR.G + Dimethyl:2H(4) (N-term)
☑	2273	703.3381	1404.6617	1404.6535	5.86	0	(75)	2.7e-006	1	R.GGGGNFGPGPGSNFR.G + Dimethyl (N-term)
☑	2285	705.3499	1408.6852	1408.6786	4.65	0	76	2.9e-006	1	R.GGGGNFGPGPGSNFR.G + Dimethyl:2H(4) (N-term)
☑	2383	360.4357	1437.7137	1437.7113	1.69	0	(40)	0.012	1	K.YHTINGHNAEVR.K + Dimethyl (N-term)
☑	2384	480.2455	1437.7145	1437.7113	2.26	0	(34)	0.043	1	K.YHTINGHNAEVR.K + Dimethyl (N-term)
☑	2401	481.5872	1441.7398	1441.7364	2.37	0	45	0.0047	1	K.YHTINGHNAEVR.K + Dimethyl:2H(4) (N-term)
☑	2997	559.6195	1675.8367	1675.8311	3.34	1	(37)	0.026	1	K.ALSRQEMQEVQSSR.S + Dimethyl (N-term)
☑	3011	560.9612	1679.8617	1679.8562	3.25	1	(38)	0.031	1	K.ALSRQEMQEVQSSR.S + Dimethyl:2H(4) (N-term)
☑	3012	560.9614	1679.8624	1679.8562	3.69	1	(41)	0.016	1	K.ALSRQEMQEVQSSR.S + Dimethyl:2H(4) (N-term)
☑	3039	564.9512	1691.8317	1691.8260	3.35	1	46	0.0027	1	K.ALSRQEMQEVQSSR.S + Dimethyl (N-term); Oxidation (M)
☑	3056	566.2930	1695.8571	1695.8512	3.48	1	(26)	0.43	1	K.ALSRQEMQEVQSSR.S + Dimethyl:2H(4) (N-term); Oxidation (M)
☑	3312	455.7663	1819.0362	1819.0316	2.55	1	26	0.56	1	R.AVAREESGKPGAHVTVK.K + 2 Dimethyl (K); Dimethyl (N-term)
☑	3352	611.6620	1831.9641	1831.9574	3.69	2	(34)	0.095	1	R.KALSRQEMQEVQSSR.S + Dimethyl (K); Dimethyl (N-term)
☑	3371	614.3457	1840.0153	1840.0076	4.17	2	(33)	0.13	1	R.KALSRQEMQEVQSSR.S + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3388	616.9935	1847.9586	1847.9523	3.39	2	(35)	0.064	1	R.KALSRQEMQEVQSSR.S + Dimethyl (K); Dimethyl (N-term); Oxidation (M)
☑	3423	619.6769	1856.0090	1856.0025	3.48	2	41	0.017	1	R.KALSRQEMQEVQSSR.S + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)
☑	3647	398.4496	1987.2114	1987.2080	1.70	2	30	0.079	1	K.RAVAREESGKPGAHVTVK.K + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3648	398.4496	1987.2117	1987.2080	1.87	2	(29)	0.077	1	K.RAVAREESGKPGAHVTVK.K + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	4071	741.3292	2220.9657	2220.9545	5.01	0	(97)	4.3e-009	1	R.NMGGPYGGGNYGPGGSGGSGGYGGR.S + Dimethyl:2H(4) (N-term)
☑	4072	741.3292	2220.9657	2220.9545	5.04	0	(78)	3.1e-007	1	R.NMGGPYGGGNYGPGGSGGSGGYGGR.S + Dimethyl:2H(4) (N-term)
☑	4089	745.3195	2232.9367	2232.9243	5.55	0	102	4.5e-010	1	R.NMGGPYGGGNYGPGGSGGSGGYGGR.S + Dimethyl (N-term); Oxidation (M)
☑	4095	746.6612	2236.9617	2236.9494	5.49	0	(50)	0.00015	1	R.NMGGPYGGGNYGPGGSGGSGGYGGR.S + Dimethyl:2H(4) (N-term); Oxidation (M)
☑	4218	591.0710	2360.2547	2360.2417	5.53	1	(45)	0.0084	1	R.GFGFVTFDDHDPVDKIVLQK.Y + 2 Dimethyl (K); Dimethyl (N-term)
☑	4219	591.0710	2360.2548	2360.2417	5.58	1	(46)	0.006	1	R.GFGFVTFDDHDPVDKIVLQK.Y + 2 Dimethyl (K); Dimethyl (N-term)
☑	4224	594.0905	2372.3327	2372.3170	6.62	1	(42)	0.011	1	R.GFGFVTFDDHDPVDKIVLQK.Y + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	4225	594.0905	2372.3327	2372.3170	6.62	1	46	0.0042	1	R.GFGFVTFDDHDPVDKIVLQK.Y + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

Proteins matching the same set of peptides:
IPI00622847 **Mass:** 36014 **Score:** 637 **Queries matched:** 27
Tax_Id=10090 Gene_Symbol=Hnrnpa2b1 Isoform 2 of Heterogeneous nuclear ribonucleoproteins A2/B1
IPI00828488 **Mass:** 37437 **Score:** 637 **Queries matched:** 27
Tax_Id=10090 Gene_Symbol=Hnrnpa2b1 Isoform 1 of Heterogeneous nuclear ribonucleoproteins A2/B1
IPI00853914 **Mass:** 87852 **Score:** 637 **Queries matched:** 27
Tax_Id=10090 Gene_Symbol=LOC100045191 similar to heterogeneous nuclear ribonucleoprotein A2/B1

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9. IPI00128642 **Mass:** 26056 **Score:** 633 **Queries matched:** 27 **emPAI:** 9.63
Tax_Id=10090 Gene_Symbol=Cbr2 Lung carbonyl reductase
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	659	417.7471	833.4796	833.4759	4.39	0	44	0.006	1	K.LNFSGLR.A + Dimethyl (N-term)
☑	662	419.7596	837.5046	837.5010	4.20	0	(28)	0.19	1	K.LNFSGLR.A + Dimethyl:2H(4) (N-term)
☑	699	425.7436	849.4727	849.4708	2.22	0	(26)	0.35	1	R.SFSVNLR.S + Dimethyl (N-term)
☑	703	427.7562	853.4978	853.4960	2.13	0	43	0.0064	1	R.SFSVNLR.S + Dimethyl:2H(4) (N-term)
☑	794	454.7523	907.4900	907.4871	3.25	0	54	0.0005	1	K.GAMTMLTK.A + Dimethyl (K); Dimethyl (N-term)
☑	1289	552.3210	1102.6274	1102.6234	3.67	0	38	0.033	1	R.TNSDLVSLAK.E + Dimethyl (K); Dimethyl (N-term)
☑	1316	556.3461	1110.6777	1110.6736	3.69	0	(35)	0.043	1	R.TNSDLVSLAK.E + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1347	374.5561	1120.6464	1120.6427	3.38	1	44	0.0083	1	-.MKLNFSGLR.A + Dimethyl (K); Dimethyl (N-term)
☑	1366	377.2397	1128.6972	1128.6929	3.84	1	(40)	0.015	1	-.MKLNFSGLR.A + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1380	379.8875	1136.6406	1136.6376	2.67	1	(41)	0.013	1	-.MKLNFSGLR.A + Dimethyl (K); Dimethyl (N-term); Oxidation (M)
☑	1393	380.8697	1139.5872	1139.5831	3.57	0	(64)	4.7e-005	1	K.AMAMELGPHK.I + Dimethyl (K); Dimethyl (N-term)
☑	1401	382.5710	1144.6912	1144.6878	2.98	1	(33)	0.082	1	-.MKLNFSGLR.A + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)
☑	1409	383.5530	1147.6372	1147.6333	3.38	0	(58)	0.00032	1	K.AMAMELGPHK.I + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1450	388.8840	1163.6303	1163.6282	1.75	0	64	6.1e-005	1	K.AMAMELGPHK.I + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)
☑	1918	640.3486	1278.6827	1278.6754	5.69	0	(69)	2.2e-005	1	R.SVFQVSQMVAR.D + Dimethyl (N-term)
☑	1926	642.3616	1282.7087	1282.7006	6.36	0	74	6.5e-006	1	R.SVFQVSQMVAR.D + Dimethyl:2H(4) (N-term)
☑	1948	648.3456	1294.6767	1294.6704	4.91	0	(40)	0.015	1	R.SVFQVSQMVAR.D + Dimethyl (N-term); Oxidation (M)
☑	1958	650.3582	1298.7019	1298.6955	4.92	0	(48)	0.0024	1	R.SVFQVSQMVAR.D + Dimethyl:2H(4) (N-term); Oxidation (M)
☑	2860	815.4538	1628.8930	1628.8808	7.54	0	98	3.6e-008	1	R.VNSVNPTVVLTDMGK.K + Dimethyl (K); Dimethyl (N-term)
☑	2894	819.4785	1636.9424	1636.9310	6.95	0	(95)	6e-008	1	R.VNSVNPTVVLTDMGK.K + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	2911	549.3015	1644.8827	1644.8757	4.28	0	(40)	0.024	1	R.VNSVNPTVVLTDMGK.K + Dimethyl (K); Dimethyl (N-term); Oxidation (M)
☑	2930	827.4266	1652.8387	1652.8257	7.86	0	78	2.6e-006	1	R.SASTSGGGILVDAGYLAS.- + Dimethyl (N-term)
☑	2934	551.9850	1652.9331	1652.9259	4.37	0	(28)	0.34	1	R.VNSVNPTVVLTDMGK.K + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)
☑	2952	829.4385	1656.8625	1656.8508	7.05	0	(43)	0.01	1	R.SASTSGGGILVDAGYLAS.- + Dimethyl:2H(4) (N-term)
☑	3542	633.6998	1898.0777	1898.0659	6.22	1	63	0.0001	1	K.IRVNSVNPTVVLTDMGK.K + Dimethyl (K); Dimethyl (N-term)
☑	3553	636.3837	1906.1292	1906.1162	6.83	1	(41)	0.0092	1	K.IRVNSVNPTVVLTDMGK.K + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	4510	695.3760	2777.4748	2777.4935	-6.74	2	42	0.015	1	R.VNSVNPTVVLTDMGKKVSADPEFAR.K + 2 Dimethyl (K); Dimethyl:2H(4) (N-term); Oxidation (M)

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10. IPI00229080 **Mass:** 83571 **Score:** 579 **Queries matched:** 19 **emPAI:** 0.73
Tax_Id=10090 Gene_Symbol=Hsp90ab1 Heat shock protein 84b
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	713	429.2858	856.5570	856.5534	4.14	0	(39)	0.017	1	**R.ALLFIPR.R + Dimethyl (N-term)**
☑	729	431.2984	860.5822	860.5786	4.22	0	42	0.009	1	**R.ALLFIPR.R + Dimethyl:2H(4) (N-term)**
☑	1690	611.8466	1221.6787	1221.6717	5.74	0	32	0.14	1	**K.IDIIPNPQER.T + Dimethyl (N-term)**
☑	1956	649.8915	1297.7685	1297.7605	6.17	0	(60)	0.00019	1	**K.ADLINNLGTIAK.S + Dimethyl (K); Dimethyl (N-term)**
☑	1988	653.9164	1305.8183	1305.8107	5.81	0	69	1.4e-005	1	**K.ADLINNLGTIAK.S + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)**
☑	2061	666.3602	1330.7058	1330.6980	5.87	0	60	0.00016	1	**R.ELISNASDALDK.I + Dimethyl (K); Dimethyl (N-term)**
☑	2276	703.4070	1404.7995	1404.7898	6.92	0	(62)	0.00014	1	**R.TLTLVDTGIGMTK.A + Dimethyl (K); Dimethyl (N-term)**
☑	2295	707.4320	1412.8495	1412.8400	6.67	0	(46)	0.0039	1	**R.TLTLVDTGIGMTK.A + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)**
☑	2318	474.6043	1420.7910	1420.7847	4.42	0	(44)	0.0086	1	**R.TLTLVDTGIGMTK.A + Dimethyl (K); Dimethyl (N-term); Oxidation (M)**
☑	2319	711.4047	1420.7949	1420.7847	7.15	0	68	3.6e-005	1	**R.TLTLVDTGIGMTK.A + Dimethyl (K); Dimethyl (N-term); Oxidation (M)**
☑	2353	477.2876	1428.8411	1428.8350	4.26	0	(44)	0.0079	1	**R.TLTLVDTGIGMTK.A + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)**
☑	2355	715.4290	1428.8434	1428.8350	5.87	0	(52)	0.0012	1	**R.TLTLVDTGIGMTK.A + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)**
☑	2692	771.4176	1540.8207	1540.8097	7.17	0	(104)	8.9e-009	1	**R.GVVDSEDLPLNISR.E + Dimethyl (N-term)**
☑	2699	773.4298	1544.8451	1544.8348	6.65	0	113	1.1e-009	1	**R.GVVDSEDLPLNISR.E + Dimethyl:2H(4) (N-term)**
☑	2812	536.9876	1607.9410	1607.9334	4.75	1	43	0.0087	1	**R.ELISNASDALDKIR.Y + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)**
☑	3279	604.3350	1809.9831	1809.9737	5.16	0	80	2.6e-006	1	**K.HLEINPDHPIVETLR.Q + Dimethyl (N-term)**
☑	3280	604.3350	1809.9832	1809.9737	5.26	0	(55)	0.00082	1	**K.HLEINPDHPIVETLR.Q + Dimethyl (N-term)**
☑	3293	605.6768	1814.0087	1813.9988	5.46	0	(39)	0.031	1	**K.HLEINPDHPIVETLR.Q + Dimethyl:2H(4) (N-term)**
☑	4026	735.6685	2203.9837	2203.9692	6.61	0	58	5.2e-005	1	**R.YHTSQSGDEMTSLSEYVSR.M + Dimethyl (N-term)**

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11. IPI00554929 **Mass:** 83615 **Score:** 565 **Queries matched:** 17 **emPAI:** 0.63

Tax_Id=10090 Gene_Symbol=Hsp90ab1 Heat shock protein HSP 90-beta

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1690	611.8466	1221.6787	1221.6717	5.74	0	32	0.14	1	K.IDILPNPQER.T + Dimethyl (N-term)
1956	649.8915	1297.7685	1297.7605	6.17	0	(60)	0.00019	1	K.ADLINNLGTIAK.S + Dimethyl (K); Dimethyl (N-term)
1988	653.9164	1305.8183	1305.8107	5.81	0	69	1.4e-005	1	K.ADLINNLGTIAK.S + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
2061	666.3602	1330.7058	1330.6980	5.87	0	60	0.00016	1	R.ELISNASDALDK.I + Dimethyl (K); Dimethyl (N-term)
2276	703.4070	1404.7995	1404.7898	6.92	0	(62)	0.00014	1	R.TLTLVDTGIGMTK.A + Dimethyl (K); Dimethyl (N-term)
2295	707.4320	1412.8495	1412.8400	6.67	0	(46)	0.0039	1	R.TLTLVDTGIGMTK.A + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
2318	474.6043	1420.7910	1420.7847	4.42	0	(44)	0.0086	1	R.TLTLVDTGIGMTK.A + Dimethyl (K); Dimethyl (N-term); Oxidation (M)
2319	711.4047	1420.7949	1420.7847	7.15	0	68	3.6e-005	1	R.TLTLVDTGIGMTK.A + Dimethyl (K); Dimethyl (N-term); Oxidation (M)
2353	477.2876	1428.8411	1428.8350	4.26	0	(44)	0.0079	1	R.TLTLVDTGIGMTK.A + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)
2355	715.4290	1428.8434	1428.8350	5.87	0	(52)	0.0012	1	R.TLTLVDTGIGMTK.A + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)
2692	771.4176	1540.8207	1540.8097	7.17	0	(104)	8.9e-009	1	R.GVVDSEDLPLNISR.E + Dimethyl (N-term)
2699	773.4298	1544.8451	1544.8348	6.65	0	113	1.1e-009	1	R.GVVDSEDLPLNISR.E + Dimethyl:2H(4) (N-term)
2812	536.9876	1607.9410	1607.9334	4.75	1	43	0.0087	1	R.ELISNASDALDKIR.Y + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
3279	604.3350	1809.9831	1809.9737	5.16	0	80	2.6e-006	1	K.HLEINPDHPIVETLR.Q + Dimethyl (N-term)
3280	604.3350	1809.9832	1809.9737	5.26	0	(55)	0.00082	1	K.HLEINPDHPIVETLR.Q + Dimethyl (N-term)
3293	605.6768	1814.0087	1813.9988	5.46	0	(39)	0.031	1	K.HLEINPDHPIVETLR.Q + Dimethyl:2H(4) (N-term)
4026	735.6685	2203.9837	2203.9692	6.61	0	58	5.2e-005	1	R.YHTSQSGDEMTSLSEYVSR.M + Dimethyl (N-term)

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12. IPI00132722 **Mass:** 36520 **Score:** 512 **Queries matched:** 17 **emPAI:** 1.79

Tax_Id=10090 Gene_Symbol=Anxa3 Annexin A3

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	885	479.2921	956.5697	956.5655	4.46	0	65	5.6e-005	1	K.ALLTLADGR.R + Dimethyl (N-term)
☑	890	481.3043	960.5941	960.5906	3.66	0	(59)	0.00023	1	K.ALLTLADGR.R + Dimethyl:2H(4) (N-term)
☑	921	488.2602	974.5059	974.5011	4.92	0	30	0.11	1	K.LTFDEYR.N + Dimethyl:2H(4) (N-term)
☑	1279	550.8402	1099.6659	1099.6601	5.26	0	(53)	0.0011	1	K.TLINILTER.S + Dimethyl (N-term)
☑	1292	552.8527	1103.6908	1103.6852	5.05	0	60	0.00015	1	K.TLINILTER.S + Dimethyl:2H(4) (N-term)
☑	1299	553.3267	1104.6388	1104.6328	5.37	0	66	5.7e-005	1	R.SEIDLLDIR.H + Dimethyl:2H(4) (N-term)
☑	2759	526.2942	1575.8607	1575.8548	3.77	1	41	0.018	1	K.EISQAYYTVYKK.S + 2 Dimethyl (K); Dimethyl (N-term)
☑	2784	530.3195	1587.9367	1587.9301	4.14	1	(40)	0.016	1	K.EISQAYYTVYKK.S + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	2816	807.3731	1612.7317	1612.7217	6.24	0	(70)	3.9e-006	1	K.SLGDDISSETSGDFR.K + Dimethyl (N-term)
☑	2824	809.3854	1616.7563	1616.7468	5.90	0	82	4.1e-007	1	K.SLGDDISSETSGDFR.K + Dimethyl:2H(4) (N-term)
☑	3884	693.7008	2078.0807	2078.0684	5.93	1	(62)	0.00015	1	R.GTIKDYPGFSPSVDAEAIR.K + Dimethyl (K); Dimethyl (N-term)
☑	3885	693.7009	2078.0808	2078.0684	5.95	1	64	9.9e-005	1	R.GTIKDYPGFSPSVDAEAIR.K + Dimethyl (K); Dimethyl (N-term)
☑	3889	696.3832	2086.1277	2086.1186	4.35	1	(48)	0.0044	1	R.GTIKDYPGFSPSVDAEAIR.K + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3932	711.0565	2130.1477	2130.1330	6.93	1	49	0.0028	1	K.SMKGTGTDEDALIEILTTR.S + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)
☑	4091	559.5584	2234.2045	2234.1947	4.42	2	73	1.2e-005	1	R.GTIKDYPGFSPSVDAEAIRK.A + 2 Dimethyl (K); Dimethyl (N-term)
☑	4092	559.5585	2234.2047	2234.1947	4.50	2	(63)	0.00012	1	R.GTIKDYPGFSPSVDAEAIRK.A + 2 Dimethyl (K); Dimethyl (N-term)
☑	4107	562.5775	2246.2807	2246.2700	4.77	2	(60)	0.00015	1	R.GTIKDYPGFSPSVDAEAIRK.A + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

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13. IPI00323357 **Mass:** 71055 **Score:** 502 **Queries matched:** 23 **emPAI:** 0.83
Tax_Id=10090 Gene_Symbol=Hspa8 Heat shock cognate 71 kDa protein

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1146	349.2020	1044.5843	1044.5815	2.65	1	26	0.46	1	R.LSKEDIER.M + Dimethyl (K); Dimethyl (N-term)
☑	1726	614.3606	1226.7067	1226.6983	6.89	0	61	0.00015	1	K.DAGTIAGLNVLR.I + Dimethyl (N-term)
☑	1766	616.3731	1230.7317	1230.7234	6.77	0	(47)	0.0036	1	K.DAGTIAGLNVLR.I + Dimethyl:2H(4) (N-term)
☑	2085	446.2580	1335.7523	1335.7471	3.82	1	40	0.018	1	K.MKEIAEAYLGK.T + 2 Dimethyl (K); Dimethyl (N-term)
☑	2122	450.2832	1347.8278	1347.8225	3.92	1	(30)	0.1	1	K.MKEIAEAYLGK.T + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	2625	758.3746	1514.7347	1514.7253	6.22	0	70	7.8e-006	1	R.TTPSYVAFTDTER.L + Dimethyl (N-term)
☑	2639	760.3879	1518.7612	1518.7504	7.10	0	(39)	0.018	1	R.TTPSYVAFTDTER.L + Dimethyl:2H(4) (N-term)
☑	3014	840.9620	1679.9094	1679.8932	9.66	0	68	4.3e-005	1	K.SFYPEEVSSMVLTK.M + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3018	561.9995	1682.9767	1682.9679	5.23	1	67	3.3e-005	1	R.QATKDAGTIAGLNVLR.I + Dimethyl (K); Dimethyl (N-term)
☑	3037	564.6832	1691.0277	1691.0181	5.67	1	(49)	0.0013	1	R.QATKDAGTIAGLNVLR.I + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3101	573.9262	1718.7567	1718.7496	4.13	0	45	0.0006	1	K.STAGDTHLGGEDFDNR.M + Dimethyl (N-term)
☑	3107	575.2679	1722.7818	1722.7747	4.11	0	(32)	0.023	1	K.STAGDTHLGGEDFDNR.M + Dimethyl:2H(4) (N-term)
☑	3444	624.7032	1871.0877	1871.0767	5.87	1	(61)	0.00012	1	R.IINEPTAAAIAYGLDKK.V + 2 Dimethyl (K); Dimethyl (N-term)
☑	3445	624.7038	1871.0897	1871.0767	6.94	1	(57)	0.00032	1	R.IINEPTAAAIAYGLDKK.V + 2 Dimethyl (K); Dimethyl (N-term)
☑	3461	626.6592	1876.9559	1876.9465	4.99	1	(33)	0.093	1	K.NQVAMNPTNTVFDAKR.L + Dimethyl (K); Dimethyl (N-term); Oxidation (M)
☑	3462	626.6593	1876.9561	1876.9465	5.09	1	36	0.053	1	K.NQVAMNPTNTVFDAKR.L + Dimethyl (K); Dimethyl (N-term); Oxidation (M)
☑	3500	628.7285	1883.1635	1883.1521	6.08	1	78	9.1e-007	1	R.IINEPTAAAIAYGLDKK.V + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3501	628.7285	1883.1637	1883.1521	6.18	1	(77)	1.3e-006	1	R.IINEPTAAAIAYGLDKK.V + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

☑ 3509	629.3427	1885.0063	1884.9968	5.07	1	(34)	0.11	1	K.NQVAMNPTNTVFDAKR.L + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)
☑ 3510	629.3430	1885.0072	1884.9968	5.56	1	(31)	0.21	1	K.NQVAMNPTNTVFDAKR.L + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)
☑ 3700	670.6862	2009.0367	2009.0218	7.42	0	40	0.021	1	K.TVTNAVVTVPAYFNDSQR.Q + Dimethyl (N-term)
☑ 3725	672.0277	2013.0613	2013.0469	7.14	0	(29)	0.3	1	K.TVTNAVVTVPAYFNDSQR.Q + Dimethyl:2H(4) (N-term)
☑ 3726	672.0278	2013.0617	2013.0469	7.35	0	(32)	0.13	1	K.TVTNAVVTVPAYFNDSQR.Q + Dimethyl:2H(4) (N-term)

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14. IPI00135284 **Mass:** 36092 **Score:** 475 **Queries matched:** 14 **emPAI:** 1.29
Tax_Id=10090 Gene_Symbol=LOC100044454;LOC100039214 similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) isoform 1
☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑ 1999	436.9481	1307.8225	1307.8176	3.74	1	48	0.0017	1	K.AVGKVIPELNGK.L + 2 Dimethyl (K); Dimethyl (N-term)
☑ 2026	440.9732	1319.8979	1319.8930	3.70	1	(47)	0.00059	1	K.AVGKVIPELNGK.L + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑ 2291	706.8668	1411.7190	1411.7091	7.00	1	(77)	2.5e-006	1	R.VVDLMAYMASKE.- + Dimethyl (K); Dimethyl (N-term)
☑ 2311	710.8921	1419.7696	1419.7593	7.27	1	(79)	2.9e-006	1	R.VVDLMAYMASKE.- + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑ 2335	713.4106	1424.8066	1424.7987	5.56	0	(56)	0.00059	1	R.GAAQNIIPASTGAAK.A + Dimethyl (K); Dimethyl (N-term)
☑ 2344	714.8636	1427.7126	1427.7040	6.04	1	(51)	0.00084	1	R.VVDLMAYMASKE.- + Dimethyl (K); Dimethyl (N-term); Oxidation (M)
☑ 2345	714.8646	1427.7147	1427.7040	7.49	1	80	1.3e-006	1	R.VVDLMAYMASKE.- + Dimethyl (K); Dimethyl (N-term); Oxidation (M)
☑ 2368	717.4359	1432.8573	1432.8489	5.83	0	62	0.00011	1	R.GAAQNIIPASTGAAK.A + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑ 2374	718.8894	1435.7643	1435.7542	6.98	1	(56)	0.0005	1	R.VVDLMAYMASKE.- + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)
☑ 2375	718.8900	1435.7654	1435.7542	7.75	1	(59)	0.00028	1	R.VVDLMAYMASKE.- + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)
☑ 2406	722.8607	1443.7069	1443.6989	5.52	1	(74)	4.3e-006	1	R.VVDLMAYMASKE.- + Dimethyl (K); Dimethyl (N-term); 2 Oxidation (M)
☑ 2442	726.8855	1451.7564	1451.7491	5.03	1	(72)	9.7e-006	1	R.VVDLMAYMASKE.- + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); 2 Oxidation (M)
☑ 3170	585.3259	1752.9560	1752.9482	4.42	1	38	0.036	1	R.DGRGAAQNIIPASTGAAK.A + Dimethyl (K); Dimethyl (N-term)
☑ 3253	603.2852	1806.8337	1806.8213	6.89	0	33	0.032	1	K.LISWYDNEYGYSNR.V + Dimethyl (N-term)

Proteins matching the same set of peptides:
IPI00273646 **Mass:** 36072 **Score:** 475 **Queries matched:** 14
Tax_Id=10090 Gene_Symbol=LOC100040053;LOC100042025;Gapdh;AK190093;ENSMUSG00000070490;ENSMUSG00000071343;LOC100048291;ENSMUSG00000068459;LOC100041325;LOC100042746;L
IPI00319731 **Mass:** 37674 **Score:** 475 **Queries matched:** 14
Tax_Id=10090 Gene_Symbol=LOC100044981 similar to Glyceraldehyde-3-phosphate dehydrogenase
IPI00462008 **Mass:** 36271 **Score:** 475 **Queries matched:** 14
Tax_Id=10090 Gene_Symbol=LOC100047352 similar to Glyceraldehyde-3-phosphate dehydrogenase
IPI00620663 **Mass:** 31288 **Score:** 475 **Queries matched:** 14
Tax_Id=10090 Gene_Symbol=LOC100042025 similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) isoform 3
IPI00622795 **Mass:** 36074 **Score:** 475 **Queries matched:** 14
Tax_Id=10090 Gene_Symbol=LOC100042427 similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) isoform 1
IPI00663957 **Mass:** 36233 **Score:** 475 **Queries matched:** 14
Tax_Id=10090 Gene_Symbol=LOC100045120 similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) isoform 1
IPI00752289 **Mass:** 36308 **Score:** 475 **Queries matched:** 14
Tax_Id=10090 Gene_Symbol=LOC100039258 similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) isoform 1
IPI00848411 **Mass:** 31260 **Score:** 475 **Queries matched:** 14
Tax_Id=10090 Gene_Symbol=LOC100039840 similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) isoform 2
IPI00848801 **Mass:** 36100 **Score:** 475 **Queries matched:** 14
Tax_Id=10090 Gene_Symbol=LOC100043724 similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) isoform 1
IPI00848807 **Mass:** 35838 **Score:** 475 **Queries matched:** 14

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     Tax_Id=10090 Gene_Symbol=LOC100048253 similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) isoform 1
     IPI00849031     Mass: 34185     Score: 475     Queries matched: 14
     Tax_Id=10090 Gene_Symbol=LOC100041342;LOC100042746;LOC100046067 similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) isoform 2
     IPI00849045     Mass: 36072     Score: 475     Queries matched: 14
     Tax_Id=10090 Gene_Symbol=LOC100039762 similar to Glyceraldehyde-3-phosphate dehydrogenase
     IPI00849049     Mass: 31348     Score: 475     Queries matched: 14
     Tax_Id=10090 Gene_Symbol=LOC100046224;LOC100040634 similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) isoform 2
     IPI00849530     Mass: 36074     Score: 475     Queries matched: 14
     Tax_Id=10090 Gene_Symbol=LOC100039229 similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) isoform 1
     IPI00850062     Mass: 31248     Score: 475     Queries matched: 14
     Tax_Id=10090 Gene_Symbol=LOC100047232 similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) isoform 3
     IPI00850243     Mass: 31122     Score: 475     Queries matched: 14
     Tax_Id=10090 Gene_Symbol=LOC100048253 similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) isoform 2
     IPI00850337     Mass: 36044     Score: 475     Queries matched: 14
     Tax_Id=10090 Gene_Symbol=LOC100048117 similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) isoform 1
     IPI00850377     Mass: 35975     Score: 475     Queries matched: 14
     Tax_Id=10090 Gene_Symbol=LOC100039840 similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) isoform 1
     IPI00850432     Mass: 31302     Score: 475     Queries matched: 14
     Tax_Id=10090 Gene_Symbol=LOC100039229 similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) isoform 3
     IPI00850434     Mass: 36149     Score: 475     Queries matched: 14
     Tax_Id=10090 Gene_Symbol=LOC100040898;LOC100045141 similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) isoform 1
     IPI00850760     Mass: 31520     Score: 475     Queries matched: 14
     Tax_Id=10090 Gene_Symbol=LOC100039258 similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) isoform 3
     IPI00851086     Mass: 36032     Score: 475     Queries matched: 14
     Tax_Id=10090 Gene_Symbol=LOC100047232 similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) isoform 1
     IPI00853668     Mass: 36136     Score: 475     Queries matched: 14
     Tax_Id=10090 Gene_Symbol=LOC100046224;LOC100040634 similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) isoform 1
     IPI00874682     Mass: 36038     Score: 475     Queries matched: 14
     Tax_Id=10090 Gene_Symbol=- 36 kDa protein
     IPI00874820     Mass: 36024     Score: 475     Queries matched: 14
     Tax_Id=10090 Gene_Symbol=- 36 kDa protein
     IPI00874964     Mass: 36512     Score: 475     Queries matched: 14
     Tax_Id=10090 Gene_Symbol=- 36 kDa protein
```

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15.  IPI00123313     Mass: 118931    Score: 470     Queries matched: 18    emPAI: 0.32
     Tax_Id=10090 Gene_Symbol=Ube1y1;Ube1x Ubiquitin-activating enzyme E1 X
   ☐ Check to include this hit in error tolerant search or archive report

    Query  Observed   Mr(expt)   Mr(calc)   ppm  Miss Score   Expect Rank  Peptide
   ☑  744  435.2964   868.5783   868.5746  4.28   0    27      0.16    1   K.NIILGGVK.A + Dimethyl (K); Dimethyl (N-term)
   ☑  750  439.3217   876.6288   876.6248  4.51   0   (26)    0.091    1   K.NIILGGVK.A + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
   ☑ 1459  389.5839  1165.7298  1165.7270  2.34   1    60   0.00013    1   K.LKSDTAAAAVR.Q + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
   ☑ 1564  399.2652  1194.7739  1194.7700  3.23   1    61  6.6e-005    1   R.GGIVSQVKVPK.K + 2 Dimethyl (K); Dimethyl (N-term)
   ☑ 1609  403.2903  1206.8489  1206.8453  2.97   1   (45)  0.00048    1   R.GGIVSQVKVPK.K + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
   ☑ 1756  615.8231  1229.6317  1229.6252  5.34   0    73  5.7e-006    1   K.QNSLDEDLIR.K + Dimethyl (N-term)
   ☑ 1783  617.8356  1233.6566  1233.6503  5.13   0   (73) 8.7e-006    1   K.QNSLDEDLIR.K + Dimethyl:2H(4) (N-term)
   ☑ 2923  551.3198  1650.9377  1650.9305  4.40   0    58    0.0003    1   R.LAGTQPLEVLEAVQR.S + Dimethyl (N-term)
   ☑ 2938  552.6617  1654.9632  1654.9556  4.62   0   (47)   0.0036    1   R.LAGTQPLEVLEAVQR.S + Dimethyl:2H(4) (N-term)
```

☑ 3152	581.9605	1742.8597	1742.8522	4.31	0	(79)	1.4e-006	1	R.QMNPYIQVTSHQNR.V + Dimethyl (N-term)
☑ 3164	583.3022	1746.8847	1746.8773	4.23	0	(50)	0.0018	1	R.QMNPYIQVTSHQNR.V + Dimethyl:2H(4) (N-term)
☑ 3184	587.2918	1758.8536	1758.8471	3.67	0	83	4.7e-007	1	R.QMNPYIQVTSHQNR.V + Dimethyl (N-term); Oxidation (M)
☑ 3194	588.6342	1762.8807	1762.8723	4.80	0	(45)	0.0048	1	R.QMNPYIQVTSHQNR.V + Dimethyl:2H(4) (N-term); Oxidation (M)
☑ 3576	643.3329	1926.9768	1926.9646	6.32	0	80	2.1e-006	1	R.NEEDATELVGLAQAVNAR.S + Dimethyl (N-term)
☑ 3577	643.3333	1926.9781	1926.9646	6.99	0	(60)	0.00023	1	R.NEEDATELVGLAQAVNAR.S + Dimethyl (N-term)
☑ 3582	644.6745	1931.0017	1930.9898	6.17	0	(33)	0.12	1	R.NEEDATELVGLAQAVNAR.S + Dimethyl:2H(4) (N-term)
☑ 3607	650.3942	1948.1607	1948.1485	6.28	0	(39)	0.012	1	R.AAVASLLQSVQVPEFTPK.S + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑ 3608	650.3943	1948.1612	1948.1485	6.53	0	41	0.0087	1	R.AAVASLLQSVQVPEFTPK.S + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

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16. IPI00221402 **Mass:** 39787 **Score:** 470 **Queries matched:** 15 **emPAI:** 1.13
Tax_Id=10090 Gene_Symbol=Aldoa Fructose-bisphosphate aldolase A
☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑ 2224	694.8886	1387.7627	1387.7558	4.93	0	(89)	2.6e-007	1	K.GILAADESTGSIAK.R + Dimethyl (K); Dimethyl (N-term)
☑ 2244	698.9139	1395.8132	1395.8061	5.12	0	93	1.1e-007	1	K.GILAADESTGSIAK.R + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑ 2646	761.8896	1521.7646	1521.7572	4.85	0	61	0.00011	1	R.LQSIGTENTEENR.R + Dimethyl:2H(4) (N-term)
☑ 2698	515.6281	1543.8625	1543.8569	3.61	1	(54)	0.00088	1	K.GILAADESTGSIAKR.L + Dimethyl (K); Dimethyl (N-term)
☑ 2716	518.3116	1551.9131	1551.9072	3.82	1	68	2.9e-005	1	K.GILAADESTGSIAKR.L + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑ 2990	558.9529	1673.8367	1673.8332	2.08	1	(38)	0.026	1	R.LQSIGTENTEENRR.F + Dimethyl (N-term)
☑ 3006	560.2955	1677.8646	1677.8584	3.71	1	44	0.0086	1	R.LQSIGTENTEENRR.F + Dimethyl:2H(4) (N-term)
☑ 3343	458.4922	1829.9398	1829.9343	2.96	2	31	0.17	1	K.RLQSIGTENTEENRR.F + Dimethyl (N-term)
☑ 3641	661.3928	1981.1567	1981.1459	5.46	1	(46)	0.004	1	R.IVAPGKGILAADESTGSIAK.R + 2 Dimethyl (K); Dimethyl (N-term)
☑ 3642	661.3929	1981.1570	1981.1459	5.60	1	(65)	4.7e-005	1	R.IVAPGKGILAADESTGSIAK.R + 2 Dimethyl (K); Dimethyl (N-term)
☑ 3669	665.4179	1993.2317	1993.2213	5.25	1	74	2e-006	1	R.IVAPGKGILAADESTGSIAK.R + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑ 3670	665.4179	1993.2319	1993.2213	5.34	1	(61)	4e-005	1	R.IVAPGKGILAADESTGSIAK.R + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑ 3942	535.3213	2137.2563	2137.2470	4.34	2	(43)	0.0051	1	R.IVAPGKGILAADESTGSIAKR.L + 2 Dimethyl (K); Dimethyl (N-term)
☑ 3948	538.3400	2149.3307	2149.3224	3.89	2	53	0.00016	1	R.IVAPGKGILAADESTGSIAKR.L + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑ 3949	538.3400	2149.3310	2149.3224	4.02	2	(40)	0.0038	1	R.IVAPGKGILAADESTGSIAKR.L + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

Proteins matching the same set of peptides:
IPI00856247 **Mass:** 20937 **Score:** 470 **Queries matched:** 15
Tax_Id=10090 Gene_Symbol=Aldoa 21 kDa protein
IPI00856379 **Mass:** 45548 **Score:** 470 **Queries matched:** 15
Tax_Id=10090 Gene_Symbol=Aldoa Fructose-bisphosphate aldolase
IPI00856415 **Mass:** 14225 **Score:** 470 **Queries matched:** 15
Tax_Id=10090 Gene_Symbol=Aldoa 14 kDa protein
IPI00858310 **Mass:** 26123 **Score:** 470 **Queries matched:** 15
Tax_Id=10090 Gene_Symbol=Aldoa 26 kDa protein
IPI00133580 **Mass:** 39802 **Score:** 470 **Queries matched:** 15
Tax_Id=10090 Gene_Symbol=- Fructose-bisphosphate aldolase

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17. IPI00330804 **Mass:** 85134 **Score:** 431 **Queries matched:** 15 **emPAI:** 0.56
Tax_Id=10090 Gene_Symbol=Hsp90aa1 Heat shock protein HSP 90-alpha

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	**626**	**406.2921**	**810.5696**	**810.5666**	**3.60**	**0**	**26**	**0.051**	**1**	**K.TLVSVTK.E + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)**
☑	**668**	**422.2776**	**842.5407**	**842.5378**	**3.48**	**0**	**(37)**	**0.032**	**1**	**R.ALLFVPR.R + Dimethyl (N-term)**
☑	**670**	**424.2906**	**846.5667**	**846.5629**	**4.50**	**0**	**52**	**0.00092**	**1**	**R.ALLFVPR.R + Dimethyl:2H(4) (N-term)**
	1956	649.8915	1297.7685	1297.7605	6.17	0	(60)	0.00019	1	K.ADLINNLGTIAK.S + Dimethyl (K); Dimethyl (N-term)
	1988	653.9164	1305.8183	1305.8107	5.81	0	69	1.4e-005	1	K.ADLINNLGTIAK.S + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
	2276	703.4070	1404.7995	1404.7898	6.92	0	(62)	0.00014	1	R.TLTIVDTGIGMTK.A + Dimethyl (K); Dimethyl (N-term)
	2295	707.4320	1412.8495	1412.8400	6.67	0	(46)	0.0039	1	R.TLTIVDTGIGMTK.A + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
	2318	474.6043	1420.7910	1420.7847	4.42	0	(44)	0.0086	1	R.TLTIVDTGIGMTK.A + Dimethyl (K); Dimethyl (N-term); Oxidation (M)
	2319	711.4047	1420.7949	1420.7847	7.15	0	68	3.6e-005	1	R.TLTIVDTGIGMTK.A + Dimethyl (K); Dimethyl (N-term); Oxidation (M)
	2353	477.2876	1428.8411	1428.8350	4.26	0	(44)	0.0079	1	R.TLTIVDTGIGMTK.A + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)
	2355	715.4290	1428.8434	1428.8350	5.87	0	(52)	0.0012	1	R.TLTIVDTGIGMTK.A + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)
	2692	771.4176	1540.8207	1540.8097	7.17	0	(104)	8.9e-009	1	R.GVVDSEDLPLNISR.E + Dimethyl (N-term)
	2699	773.4298	1544.8451	1544.8348	6.65	0	113	1.1e-009	1	R.GVVDSEDLPLNISR.E + Dimethyl:2H(4) (N-term)
☑	**3291**	**605.6665**	**1813.9777**	**1813.9686**	**5.02**	**0**	**(36)**	**0.06**	**1**	**K.HLEINPDHSIIETLR.Q + Dimethyl (N-term)**
☑	**3304**	**607.0096**	**1818.0069**	**1817.9937**	**7.25**	**0**	**37**	**0.047**	**1**	**K.HLEINPDHSIIETLR.Q + Dimethyl:2H(4) (N-term)**

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18. IPI00135635 **Mass:** 47145 **Score:** 425 **Queries matched:** 19 **emPAI:** 0.61
Tax_Id=10090 Gene_Symbol=Serpina3m Serine protease inhibitor A3M precursor

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1060	339.2324	1014.6753	1014.6723	2.91	1	25	0.21	1	R.SVKVPMMK.M + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
2949	553.2935	1656.8587	1656.8505	4.98	0	(27)	0.37	1	R.MQQVEASLQPETLR.K + Dimethyl (N-term)
2950	553.2939	1656.8597	1656.8505	5.58	0	(35)	0.055	1	R.MQQVEASLQPETLR.K + Dimethyl (N-term)
2951	829.4385	1656.8624	1656.8505	7.20	0	80	2.1e-006	1	R.MQQVEASLQPETLR.K + Dimethyl (N-term)
2969	831.4504	1660.8862	1660.8756	6.39	0	(70)	2e-005	1	R.MQQVEASLQPETLR.K + Dimethyl:2H(4) (N-term)
3003	839.4479	1676.8813	1676.8705	6.45	0	(53)	0.0012	1	R.MQQVEASLQPETLR.K + Dimethyl:2H(4) (N-term); Oxidation (M)
3289	605.3359	1812.9858	1812.9767	5.00	1	(51)	0.0017	1	R.MQQVEASLQPETLRK.W + Dimethyl (K); Dimethyl (N-term)
3290	605.3363	1812.9871	1812.9767	5.71	1	(60)	0.00023	1	R.MQQVEASLQPETLRK.W + Dimethyl (K); Dimethyl (N-term)
3318	608.0194	1821.0364	1821.0270	5.18	1	(49)	0.0024	1	R.MQQVEASLQPETLRK.W + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
3319	608.0195	1821.0366	1821.0270	5.28	1	68	3.2e-005	1	R.MQQVEASLQPETLRK.W + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
4003	731.0383	2190.0932	2190.1146	-9.81	0	(35)	0.047	1	R.ALYQTEAFTADFQKPTEAK.N + Dimethyl:2H(4) (N-term)
4046	739.0402	2214.0987	2214.1208	-9.98	0	67	3.3e-005	1	R.ALYQTEAFTADFQKPTEAK.N + Dimethyl (K); Dimethyl (N-term)
4047	739.0405	2214.0996	2214.1208	-9.60	0	(62)	0.0001	1	R.ALYQTEAFTADFQKPTEAK.N + Dimethyl (K); Dimethyl (N-term)
4048	739.0406	2214.1001	2214.1208	-9.35	0	(58)	0.00029	1	R.ALYQTEAFTADFQKPTEAK.N + Dimethyl (K); Dimethyl (N-term)
4049	739.0408	2214.1007	2214.1208	-9.08	0	(56)	0.00046	2	R.ALYQTEAFTADFQKPTEAK.N + Dimethyl (K); Dimethyl (N-term)
4074	741.7238	2222.1496	2222.1711	-9.65	0	(51)	0.0019	1	R.ALYQTEAFTADFQKPTEAK.N + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
4075	741.7238	2222.1497	2222.1711	-9.60	0	(34)	0.086	1	R.ALYQTEAFTADFQKPTEAK.N + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
4076	741.7238	2222.1497	2222.1711	-9.60	0	(42)	0.012	1	R.ALYQTEAFTADFQKPTEAK.N + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
4077	741.7239	2222.1498	2222.1711	-9.56	0	(54)	0.00091	1	R.ALYQTEAFTADFQKPTEAK.N + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

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19. IPI00317309 **Mass:** 35787 **Score:** 423 **Queries matched:** 24 **emPAI:** 3.98
Tax_Id=10090 Gene_Symbol=Anxa5 Annexin A5

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1089	515.3201	1028.6257	1028.6230	2.67	0	(57)	0.00034	1	K.VLTEIIASR.T + Dimethyl (N-term)
☑	1108	517.3333	1032.6521	1032.6481	3.86	0	61	0.00012	1	K.VLTEIIASR.T + Dimethyl:2H(4) (N-term)
☑	1133	522.3046	1042.5947	1042.5910	3.58	0	48	0.003	1	R.TPEELSAIK.Q + Dimethyl (K); Dimethyl (N-term)
☑	1160	524.7895	1047.5644	1047.5600	4.19	0	(44)	0.0068	1	R.QEIAQEFK.T + Dimethyl (K); Dimethyl (N-term)
☑	1168	526.3298	1050.6451	1050.6412	3.70	0	(33)	0.073	1	R.TPEELSAIK.Q + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1196	528.8145	1055.6144	1055.6103	3.88	0	48	0.0028	1	R.QEIAQEFK.T + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1221	535.7936	1069.5726	1069.5695	2.88	0	(41)	0.01	1	R.LYDAYELK.H + Dimethyl (K); Dimethyl (N-term)
☑	1232	539.8188	1077.6230	1077.6198	3.04	0	45	0.0067	1	R.LYDAYELK.H + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1375	567.8146	1133.6147	1133.6080	5.89	0	(44)	0.0079	1	R.SEIDLFNIR.K + Dimethyl (N-term)
☑	1385	569.8271	1137.6397	1137.6332	5.78	0	55	0.0006	1	R.SEIDLFNIR.K + Dimethyl:2H(4) (N-term)
☑	1620	403.9283	1208.7632	1208.7588	3.60	0	(31)	0.077	1	K.LIVAMMKPSR.L + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1656	406.5764	1216.7075	1216.7035	3.27	0	33	0.09	1	K.LIVAMMKPSR.L + Dimethyl (K); Dimethyl (N-term); Oxidation (M)
☑	1950	648.8188	1295.6231	1295.6147	6.55	0	46	0.0017	1	R.GTVTDFPGFDGR.A + Dimethyl (N-term)
☑	1962	650.8308	1299.6471	1299.6398	5.61	0	(45)	0.0027	1	R.GTVTDFPGFDGR.A + Dimethyl:2H(4) (N-term)
☑	2117	673.8597	1345.7049	1345.6951	7.27	0	38	0.028	1	K.NFATSLYSMIK.G + Dimethyl (K); Dimethyl (N-term); Oxidation (M)
☑	2806	535.6202	1603.8387	1603.8318	4.32	1	(35)	0.059	1	R.SNAQRQEIAQEFK.T + Dimethyl (K); Dimethyl (N-term)
☑	2815	538.3035	1611.8886	1611.8820	4.08	1	37	0.045	1	R.SNAQRQEIAQEFK.T + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3036	564.6571	1690.9495	1690.9403	5.42	1	62	0.00015	1	K.GAGTDEKVLTEIIASR.T + Dimethyl:2H(4) (N-term)
☑	3095	572.6600	1714.9583	1714.9465	6.87	1	(52)	0.0013	1	K.GAGTDEKVLTEIIASR.T + Dimethyl (K); Dimethyl (N-term)
☑	3133	868.4786	1734.9427	1734.9301	7.25	0	105	7.8e-009	1	K.GLGTDEDSILNLLTSR.S + Dimethyl:2H(4) (N-term)
☑	3830	684.3492	2050.0257	2050.0120	6.70	1	35	0.06	1	R.GTVTDFPGFDGRADAEVLR.K + Dimethyl (N-term)
☑	3840	685.6910	2054.0513	2054.0371	6.90	1	(34)	0.083	1	R.GTVTDFPGFDGRADAEVLR.K + Dimethyl:2H(4) (N-term)
☑	3920	705.3974	2113.1704	2113.1540	7.74	1	49	0.0024	1	K.AMKGLGTDEDSILNLLTSR.S + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)
☑	3921	705.3975	2113.1707	2113.1540	7.90	1	(40)	0.022	1	K.AMKGLGTDEDSILNLLTSR.S + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)

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20. IPI00387422 **Mass:** 61818 **Score:** 412 **Queries matched:** 15 **emPAI:** 0.44

Tax_Id=10090 Gene_Symbol=Zyx zyxin

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	544	393.2509	784.4873	784.4847	3.29	0	25	0.43	1	K.FAPVAPK.F + Dimethyl (K); Dimethyl (N-term)
☑	667	421.2868	840.5590	840.5561	3.47	0	26	0.23	1	K.FTPVVSK.F + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1668	610.3585	1218.7024	1218.6972	4.23	0	(66)	5.1e-005	1	R.GPLSQAPTPAPK.F + Dimethyl (K); Dimethyl (N-term)
☑	1669	610.3587	1218.7029	1218.6972	4.64	0	72	1.4e-005	1	R.GPLSQAPTPAPK.F + Dimethyl (K); Dimethyl (N-term)
☑	1733	614.3836	1226.7527	1226.7474	4.26	0	(61)	0.00013	1	R.GPLSQAPTPAPK.F + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1734	614.3837	1226.7529	1226.7474	4.45	0	(52)	0.00098	1	R.GPLSQAPTPAPK.F + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1735	614.3840	1226.7535	1226.7474	4.95	0	(71)	1.1e-005	1	R.GPLSQAPTPAPK.F + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	2838	541.2846	1620.8320	1620.8260	3.70	0	(29)	0.26	1	K.FSPGAPSGPGPQPNQK.M + Dimethyl (K); Dimethyl (N-term)
☑	2859	543.9680	1628.8820	1628.8762	3.57	0	49	0.0027	1	K.FSPGAPSGPGPQPNQK.M + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3197	589.6412	1765.9017	1765.8972	2.54	0	77	4.7e-006	1	K.QHPQPPPAQNQNQVR.S + Dimethyl (N-term)
☑	3198	589.6415	1765.9027	1765.8972	3.13	0	(71)	1.5e-005	1	K.QHPQPPPAQNQNQVR.S + Dimethyl (N-term)
☑	3199	589.6416	1765.9030	1765.8972	3.27	0	(71)	1.6e-005	1	K.QHPQPPPAQNQNQVR.S + Dimethyl (N-term)
☑	3208	590.9833	1769.9282	1769.9223	3.31	0	(62)	0.00016	1	K.QHPQPPPAQNQNQVR.S + Dimethyl:2H(4) (N-term)
☑	3209	590.9835	1769.9287	1769.9223	3.62	0	(56)	0.00054	1	K.QHPQPPPAQNQNQVR.S + Dimethyl:2H(4) (N-term)

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	3659	665.0168	1992.0287	1992.0177	5.53	0	29	0.28	1	K.VNPFRPGDSEPPVAAGAQR.A + Dimethyl (N-term)

Proteins matching the same set of peptides:
IPI00408218 **Mass:** 58244 **Score:** 412 **Queries matched:** 15
Tax_Id=10090 Gene_Symbol=Zyx Zyx protein

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21. IPI00553333 **Mass:** 15944 **Score:** 400 **Queries matched:** 20 **emPAI:** 4.23
Tax_Id=10090 Gene_Symbol=Hbb-b1 Hemoglobin subunit beta-1
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1971	651.8856	1301.7567	1301.7496	5.48	0	43	0.0096	1	R.LLVVYPWTQR.Y + Dimethyl (N-term)
☑	1972	651.8861	1301.7577	1301.7496	6.25	0	(36)	0.047	1	R.LLVVYPWTQR.Y + Dimethyl (N-term)
☑	1973	651.8861	1301.7577	1301.7496	6.25	0	(36)	0.046	1	R.LLVVYPWTQR.Y + Dimethyl (N-term)
☑	1985	653.8981	1305.7817	1305.7747	5.37	0	(39)	0.024	1	R.LLVVYPWTQR.Y + Dimethyl:2H(4) (N-term)
☑	1986	653.8984	1305.7823	1305.7747	5.84	0	(28)	0.27	1	R.LLVVYPWTQR.Y + Dimethyl:2H(4) (N-term)
☑	1987	653.8986	1305.7827	1305.7747	6.11	0	(36)	0.045	1	R.LLVVYPWTQR.Y + Dimethyl:2H(4) (N-term)
☑	2057	665.8366	1329.6587	1329.6525	4.72	0	(62)	5.8e-005	1	K.VNSDEVGGEALGR.L + Dimethyl (N-term)
☑	2074	667.8491	1333.6837	1333.6776	4.62	0	78	2.2e-006	1	K.VNSDEVGGEALGR.L + Dimethyl:2H(4) (N-term)
☑	2552	498.2946	1491.8618	1491.8562	3.79	1	51	0.0017	1	K.VVAGVATALAHKYH.- + Dimethyl (K); Dimethyl (N-term)
☑	2579	500.9779	1499.9120	1499.9064	3.71	1	(48)	0.0019	1	K.VVAGVATALAHKYH.- + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3773	676.9939	2027.9599	2027.9448	7.42	0	(29)	0.11	1	R.YFDSFGDLSSASAIMGNAK.V + Dimethyl:2H(4) (N-term); Oxidation (M)
☑	3787	679.6638	2035.9696	2035.9561	6.66	0	(46)	0.0027	1	R.YFDSFGDLSSASAIMGNAK.V + Dimethyl (K); Dimethyl (N-term)
☑	3788	679.6641	2035.9704	2035.9561	7.01	0	(53)	0.00047	1	R.YFDSFGDLSSASAIMGNAK.V + Dimethyl (K); Dimethyl (N-term)
☑	3789	679.6642	2035.9707	2035.9561	7.20	0	(42)	0.0066	1	R.YFDSFGDLSSASAIMGNAK.V + Dimethyl (K); Dimethyl (N-term)
☑	3812	682.3468	2044.0186	2044.0063	6.00	0	57	0.00037	1	R.YFDSFGDLSSASAIMGNAK.V + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3813	682.3469	2044.0187	2044.0063	6.08	0	(40)	0.016	1	R.YFDSFGDLSSASAIMGNAK.V + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3814	682.3478	2044.0215	2044.0063	7.44	0	(36)	0.041	1	R.YFDSFGDLSSASAIMGNAK.V + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3833	684.9961	2051.9665	2051.9510	7.54	0	(53)	0.00049	1	R.YFDSFGDLSSASAIMGNAK.V + Dimethyl (K); Dimethyl (N-term); Oxidation (M)
☑	3834	684.9962	2051.9667	2051.9510	7.67	0	(45)	0.0034	1	R.YFDSFGDLSSASAIMGNAK.V + Dimethyl (K); Dimethyl (N-term); Oxidation (M)
☑	3853	687.6793	2060.0161	2060.0012	7.24	0	(47)	0.0034	1	R.YFDSFGDLSSASAIMGNAK.V + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)

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22. IPI00113223 **Mass:** 274994 **Score:** 394 **Queries matched:** 29 **emPAI:** 0.19
Tax_Id=10090 Gene_Symbol=Fasn Fatty acid synthase
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	915	487.2895	972.5645	972.5604	4.27	0	(55)	0.00051	1	K.TGTVALEVR.L + Dimethyl (N-term)
☑	926	489.3022	976.5899	976.5855	4.47	0	56	0.00055	1	K.TGTVALEVR.L + Dimethyl:2H(4) (N-term)
☑	1239	542.3448	1082.6750	1082.6699	4.71	0	36	0.032	1	R.QAPLLIGSTK.S + Dimethyl (K); Dimethyl (N-term)
☑	1270	549.3005	1096.5864	1096.5815	4.50	0	30	0.14	1	K.YNGTLNLDR.A + Dimethyl:2H(4) (N-term)
☑	1739	410.2195	1227.6368	1227.6332	2.94	0	36	0.033	1	K.QAHTMDPQLR.L + Dimethyl:2H(4) (N-term)
☑	2058	665.8706	1329.7267	1329.7190	5.78	0	37	0.039	1	K.VGDPQELNGITR.S + Dimethyl:2H(4) (N-term)
☑	2235	464.6031	1390.7876	1390.7820	4.05	1	(29)	0.26	1	R.LTQGEVYKELR.L + Dimethyl (K); Dimethyl (N-term)
☑	2252	467.2866	1398.8379	1398.8322	4.09	1	48	0.0024	1	R.LTQGEVYKELR.L + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

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☑ 2568  750.4116 1498.8087 1498.7991  6.42  0   115  6.7e-010  1  R.TLEAVQDLLEQGR.Q + Dimethyl (N-term)
☑ 2588  752.4241 1502.8337 1502.8242  6.32  0  (98)  3.2e-008  1  R.TLEAVQDLLEQGR.Q + Dimethyl:2H(4) (N-term)
☑ 2893  410.2212 1636.8558 1636.8533  1.52  1    28      0.35  1  K.AVAHGDGDTQRDLVK.A + Dimethyl (K); Dimethyl (N-term)
☑ 3156  582.3013 1743.8820 1743.8726  5.37  0    31      0.15  1  K.AAMLGQEDPPQHGLPR.L + Dimethyl (N-term)
☑ 3646  663.3498 1987.0277 1987.0163  5.75  0    51    0.0021  1  R.WLSTSIPEAQWQSSLAR.T + Dimethyl (N-term)
☑ 3654  664.6915 1991.0527 1991.0414  5.68  0  (42)     0.015  1  R.WLSTSIPEAQWQSSLAR.T + Dimethyl:2H(4) (N-term)
☑ 3655  664.6916 1991.0531 1991.0414  5.88  0  (43)     0.014  1  R.WLSTSIPEAQWQSSLAR.T + Dimethyl:2H(4) (N-term)
☑ 3671  665.6720 1993.9942 1993.9878  3.21  1    45    0.0053  1  K.LQEMSSKTDSATDTTAPK.S + 2 Dimethyl (K); Dimethyl (N-term)
☑ 3710  671.0038 2009.9897 2009.9827  3.49  1  (33)     0.074  1  K.LQEMSSKTDSATDTTAPK.S + 2 Dimethyl (K); Dimethyl (N-term); Oxidation (M)
☑ 3761  675.0285 2022.0637 2022.0580  2.82  1  (44)    0.0095  1  K.LQEMSSKTDSATDTTAPK.S + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)
☑ 3762  675.0286 2022.0640 2022.0580  2.97  1  (35)     0.085  1  K.LQEMSSKTDSATDTTAPK.S + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)
☑ 3810  409.6312 2043.1197 2043.1126  3.49  0    50    0.0025  1  R.QAPAPTAHAALPHLLHASGR.T + Dimethyl (N-term)
☑ 3811  409.6312 2043.1197 2043.1126  3.50  0  (30)      0.22  1  R.QAPAPTAHAALPHLLHASGR.T + Dimethyl (N-term)
☑ 3818  410.4362 2047.1446 2047.1377  3.34  0  (32)      0.15  1  R.QAPAPTAHAALPHLLHASGR.T + Dimethyl:2H(4) (N-term)
☑ 3950  538.5377 2150.1217 2150.1140  3.58  2  (33)      0.11  1  R.KLQEMSSKTDSATDTTAPK.S + 3 Dimethyl (K); Dimethyl (N-term)
☑ 3951  538.5377 2150.1218 2150.1140  3.61  2  (34)     0.091  1  R.KLQEMSSKTDSATDTTAPK.S + 3 Dimethyl (K); Dimethyl (N-term)
☑ 3976  542.5362 2166.1157 2166.1089  3.13  2  (30)      0.21  1  R.KLQEMSSKTDSATDTTAPK.S + 3 Dimethyl (K); Dimethyl (N-term); Oxidation (M)
☑ 3977  542.5363 2166.1162 2166.1089  3.33  2  (27)      0.45  1  R.KLQEMSSKTDSATDTTAPK.S + 3 Dimethyl (K); Dimethyl (N-term); Oxidation (M)
☑ 3978  542.5626 2166.2214 2166.2145  3.19  2  (30)      0.19  1  R.KLQEMSSKTDSATDTTAPK.S + 3 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑ 3979  542.5627 2166.2217 2166.2145  3.34  2    40     0.018  1  R.KLQEMSSKTDSATDTTAPK.S + 3 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑ 4001  546.5617 2182.2177 2182.2094  3.81  2  (26)      0.55  1  R.KLQEMSSKTDSATDTTAPK.S + 3 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)
```

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23.  IPI00221528    Mass: 42319    Score: 390    Queries matched: 29    emPAI: 1.29
     Tax_Id=10090 Gene_Symbol=4732495G21Rik 10 days neonate skin cDNA, RIKEN full-length enriched library, clone:4732493G14 product:ACTIN, CYTOPLASMIC TYPE 5 homolog
   ☐ Check to include this hit in error tolerant search or archive report

   Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score   Expect Rank  Peptide
     435  350.7531  699.4916  699.4894  3.02   0   (33)     0.032   1   R.GILTLK.Y + Dimethyl (K); Dimethyl (N-term)
     442  354.7782  707.5418  707.5397  3.07   0   (33)     0.029   1   R.GILTLK.Y + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
     443  354.7784  707.5423  707.5397  3.76   0    42     0.0033   1   R.GILTLK.Y + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
     642  412.2567  822.4988  822.4963  3.05   0    36      0.031   1   K.IIAPPER.K + Dimethyl (N-term)
    1187  527.7816 1053.5486 1053.5416  6.59   0    46      0.003   1   R.DLTDYLMK.I + Dimethyl (K); Dimethyl (N-term)
    1212  531.8063 1061.5981 1061.5918  5.91   0   (43)    0.0091   1   R.DLTDYLMK.I + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
    1722  409.8839 1226.6297 1226.6264  2.72   0   (43)    0.0054   1   R.HQGVMVGMGQK.D + Dimethyl (K); Dimethyl (N-term)
    1723  409.8839 1226.6299 1226.6264  2.86   0   (31)     0.099   1   R.HQGVMVGMGQK.D + Dimethyl (K); Dimethyl (N-term)
    1724  614.3229 1226.6313 1226.6264  4.02   0    48     0.0019   1   R.HQGVMVGMGQK.D + Dimethyl (K); Dimethyl (N-term)
    1790  412.5673 1234.6801 1234.6766  2.84   0   (38)     0.038   1   R.HQGVMVGMGQK.D + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
    1791  412.5673 1234.6802 1234.6766  2.92   0   (36)     0.048   1   R.HQGVMVGMGQK.D + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
    1792  618.3480 1234.6814 1234.6766  3.85   0   (39)     0.025   1   R.HQGVMVGMGQK.D + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
    2873  544.9758 1631.9057 1631.8990  4.08   1    27       0.48   2   R.MQKEIVTLAPSTMK.I + Dimethyl (K); Dimethyl (N-term)
    3301  606.9832 1817.9277 1817.9159  6.49   0   (46)    0.0048   1   R.SYELPDGQVITIGNER.F + Dimethyl (N-term)
    3302  909.9726 1817.9307 1817.9159  8.14   0   (90)    2e-007   1   R.SYELPDGQVITIGNER.F + Dimethyl (N-term)
    3303  909.9731 1817.9317 1817.9159  8.69   0   (79)  2.5e-006   1   R.SYELPDGQVITIGNER.F + Dimethyl (N-term)
    3323  608.3251 1821.9536 1821.9410  6.88   0   (30)      0.23   1   R.SYELPDGQVITIGNER.F + Dimethyl:2H(4) (N-term)
    3324  911.9853 1821.9560 1821.9410  8.22   0    92   1.6e-007   1   R.SYELPDGQVITIGNER.F + Dimethyl:2H(4) (N-term)
    3325  911.9858 1821.9570 1821.9410  8.76   0   (87)    5e-007   1   R.SYELPDGQVITIGNER.F + Dimethyl:2H(4) (N-term)
    3705  670.7178 2009.1315 2009.1197  5.87   0   (29)      0.24   2   R.VAPDEHPILLTEAPLNPK.I + Dimethyl (K); Dimethyl (N-term)
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3706	670.7178	2009.1315	2009.1197	5.87	0	(27)	0.41	2	R.VAPDEHPILLTEAPLNPK.I + Dimethyl (K); Dimethyl (N-term)
3707	670.7179	2009.1317	2009.1197	5.99	0	(26)	0.47	2	R.VAPDEHPILLTEAPLNPK.I + Dimethyl (K); Dimethyl (N-term)
3708	670.7179	2009.1317	2009.1197	5.99	0	(32)	0.12	2	R.VAPDEHPILLTEAPLNPK.I + Dimethyl (K); Dimethyl (N-term)
3709	670.7180	2009.1322	2009.1197	6.24	0	(28)	0.27	2	R.VAPDEHPILLTEAPLNPK.I + Dimethyl (K); Dimethyl (N-term)
3742	673.3995	2017.1767	2017.1699	3.37	0	(28)	0.2	2	R.VAPDEHPILLTEAPLNPK.I + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
3746	673.4012	2017.1817	2017.1699	5.85	0	(29)	0.14	2	R.VAPDEHPILLTEAPLNPK.I + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
3747	673.4013	2017.1821	2017.1699	6.03	0	(33)	0.065	2	R.VAPDEHPILLTEAPLNPK.I + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
3748	673.4015	2017.1827	2017.1699	6.35	0	(34)	0.044	2	R.VAPDEHPILLTEAPLNPK.I + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
3749	673.4017	2017.1832	2017.1699	6.57	0	37	0.026	2	R.VAPDEHPILLTEAPLNPK.I + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

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24. IPI00123924 **Mass:** 46140 **Score:** 378 **Queries matched:** 18 **emPAI:** 0.92
Tax_Id=10090 Gene_Symbol=Serpina1d Alpha-1-antitrypsin 1-4 precursor

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1064	510.2946	1018.5746	1018.5699	4.58	0	38	0.028	1	K.VINDFVEK.G + Dimethyl (K); Dimethyl (N-term)
☑	1331	558.8291	1115.6437	1115.6373	5.80	0	44	0.0083	1	K.TLMSPLGITR.I + Dimethyl (N-term)
☑	1345	560.8419	1119.6692	1119.6624	6.07	0	(39)	0.025	1	K.TLMSPLGITR.I + Dimethyl:2H(4) (N-term)
☑	1368	566.8261	1131.6377	1131.6322	4.90	0	(37)	0.043	1	K.TLMSPLGITR.I + Dimethyl (N-term); Oxidation (M)
☑	1379	568.8386	1135.6626	1135.6573	4.65	0	(40)	0.018	1	K.TLMSPLGITR.I + Dimethyl:2H(4) (N-term); Oxidation (M)
☑	1452	582.8376	1163.6606	1163.6550	4.84	0	34	0.074	1	R.LSISGNYNLK.T + Dimethyl (K); Dimethyl (N-term)
☑	1479	586.8631	1171.7116	1171.7052	5.49	0	(26)	0.38	1	R.LSISGNYNLK.T + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	2635	506.9575	1517.8507	1517.8453	3.55	1	36	0.058	1	K.VINDFVEKGTQGK.I + 2 Dimethyl (K); Dimethyl (N-term)
☑	2661	510.9827	1529.9264	1529.9207	3.70	1	(25)	0.41	1	K.VINDFVEKGTQGK.I + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	2992	558.9998	1673.9774	1673.9716	3.49	2	(33)	0.093	1	K.KVINDFVEKGTQGK.I + 3 Dimethyl (K); Dimethyl (N-term)
☑	3035	564.3665	1690.0777	1690.0721	3.36	2	34	0.017	1	K.KVINDFVEKGTQGK.I + 3 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3849	687.0324	2058.0754	2058.0633	5.88	0	(46)	0.0057	1	R.IFNNGADLSGITEENAPLK.L + Dimethyl (K); Dimethyl (N-term)
☑	3850	687.0330	2058.0772	2058.0633	6.77	0	62	0.00017	1	R.IFNNGADLSGITEENAPLK.L + Dimethyl (K); Dimethyl (N-term)
☑	4234	799.1212	2394.3417	2394.3246	7.16	1	(82)	1.2e-006	1	R.IFNNGADLSGITEENAPLKLSK.A + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	4235	799.1212	2394.3418	2394.3246	7.20	1	93	8.3e-008	1	R.IFNNGADLSGITEENAPLKLSK.A + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	4258	805.7818	2414.3236	2414.3056	7.43	1	(86)	4.6e-007	1	R.IFNNGADLSGITEENAPLKLSK.A + 2 Dimethyl (K); Dimethyl (N-term)
☑	4537	713.3945	2849.5487	2849.5650	-5.72	2	63	7.9e-005	1	R.IFNNGADLSGITEENAPLKLSKAVHK.A + 2 Dimethyl (K); Dimethyl (N-term)
☑	4538	713.3948	2849.5500	2849.5650	-5.28	2	(53)	0.00078	1	R.IFNNGADLSGITEENAPLKLSKAVHK.A + 2 Dimethyl (K); Dimethyl (N-term)

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25. IPI00469114 **Mass:** 15133 **Score:** 355 **Queries matched:** 14 **emPAI:** 2.04
Tax_Id=10090 Gene_Symbol=Hba-a1;Hba-a2 Hemoglobin subunit alpha

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1244	543.2910	1084.5675	1084.5627	4.40	0	(37)	0.019	1	R.MFASFPTTK.T + Dimethyl (K); Dimethyl (N-term)
☑	1245	543.2912	1084.5678	1084.5627	4.74	0	56	0.00023	1	R.MFASFPTTK.T + Dimethyl (K); Dimethyl (N-term)
☑	1259	547.3163	1092.6181	1092.6129	4.76	0	(40)	0.016	1	R.MFASFPTTK.T + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1260	547.3163	1092.6181	1092.6129	4.76	0	(53)	0.00088	1	R.MFASFPTTK.T + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1934	429.2765	1284.8078	1284.8042	2.80	1	32	0.069	1	M.VLSGEDKSNIK.A + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	2721	519.9285	1556.7637	1556.7583	3.49	0	(78)	1.6e-006	1	K.IGGHGAEYGAEALER.M + Dimethyl (N-term)
	2722	519.9289	1556.7647	1556.7583	4.13	0	(70)	1.2e-005	1	K.IGGHGAEYGAEALER.M + Dimethyl (N-term)

☑										
☑	2723	519.9289	1556.7647	1556.7583	4.13	0	80	1.1e-006	1	K.IGGHGAEYGAEALER.M + Dimethyl (N-term)
☑	2733	521.2704	1560.7893	1560.7834	3.79	0	(57)	0.00029	1	K.IGGHGAEYGAEALER.M + Dimethyl:2H(4) (N-term)
☑	2734	521.2705	1560.7897	1560.7834	4.05	0	(55)	0.00048	1	K.IGGHGAEYGAEALER.M + Dimethyl:2H(4) (N-term)
☑	2735	521.2708	1560.7904	1560.7834	4.50	0	(60)	0.00015	1	K.IGGHGAEYGAEALER.M + Dimethyl:2H(4) (N-term)
☑	3451	469.7415	1874.9367	1874.9315	2.76	0	42	0.0098	1	K.TYFPHFDVSHGSAQVK.G + Dimethyl (K); Dimethyl (N-term)
☑	3495	471.7556	1882.9934	1882.9818	6.15	0	(36)	0.062	1	K.TYFPHFDVSHGSAQVK.G + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3496	471.7557	1882.9937	1882.9818	6.34	0	(34)	0.11	1	K.TYFPHFDVSHGSAQVK.G + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

Proteins matching the same set of peptides:
IPI00845802 **Mass:** 15160 **Score:** 355 **Queries matched:** 14
Tax_Id=10090 Gene_Symbol=Hba-a1;Hba-a2 hemoglobin alpha, adult chain 2

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26. IPI00169463 **Mass:** 50255 **Score:** 335 **Queries matched:** 12 **emPAI:** 0.73
Tax_Id=10090 Gene_Symbol=Tubb2c Tubulin beta-2C chain

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1218	534.3191	1066.6236	1066.6175	5.74	0	28	0.26	1	R.YLTVAAVFR.G + Dimethyl (N-term)
☑	1466	586.3401	1170.6657	1170.6583	6.32	0	(40)	0.025	1	K.LAVNMVPFPR.L + Dimethyl (N-term)
☑	1493	588.3533	1174.6921	1174.6834	7.38	0	57	0.00044	1	K.LAVNMVPFPR.L + Dimethyl:2H(4) (N-term)
☑	2216	692.8631	1383.7116	1383.7034	5.96	0	66	3.7e-005	1	R.INVYYNEATGGK.Y + Dimethyl (K); Dimethyl (N-term)
☑	2237	696.8882	1391.7618	1391.7536	5.88	0	(64)	8.1e-005	1	R.INVYYNEATGGK.Y + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	2857	815.4356	1628.8567	1628.8444	7.59	0	(76)	5.2e-006	1	R.AVLVDLEPGTMDSVR.S + Dimethyl (N-term)
☑	2877	817.4486	1632.8827	1632.8695	8.08	0	(62)	0.00015	1	R.AVLVDLEPGTMDSVR.S + Dimethyl:2H(4) (N-term)
☑	2910	823.4321	1644.8497	1644.8393	6.34	0	96	4.7e-008	1	R.AVLVDLEPGTMDSVR.S + Dimethyl (N-term); Oxidation (M)
☑	2926	551.6392	1651.8958	1651.8847	6.75	0	47	0.0044	1	R.LHFFMPGFAPLTSR.G + Dimethyl:2H(4) (N-term)
☑	3543	634.0069	1898.9989	1898.9890	5.19	1	(39)	0.026	1	R.INVYYNEATGGKYVPR.A + Dimethyl (K); Dimethyl (N-term)
☑	3554	636.6900	1907.0482	1907.0392	4.68	1	49	0.003	1	R.INVYYNEATGGKYVPR.A + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
	4269	609.3290	2433.2867	2433.2726	5.81	2	27	0.5	2	K.IREEYPDRIMNTFSVVPSPK.V + Dimethyl (K); Dimethyl (N-term)

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27. IPI00169916 **Mass:** 193202 **Score:** 308 **Queries matched:** 9 **emPAI:** 0.10
Tax_Id=10090 Gene_Symbol=Cltc Clathrin heavy chain

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	2065	666.8531	1331.6917	1331.6833	6.31	0	79	2.2e-006	1	R.NNLAGAEELFAR.K + Dimethyl (N-term)
☑	2084	668.8654	1335.7163	1335.7084	5.88	0	(62)	0.00013	1	R.NNLAGAEELFAR.K + Dimethyl:2H(4) (N-term)
☑	2141	681.8396	1361.6647	1361.6575	5.30	0	(42)	0.0053	1	K.IYIDSNNNPER.F + Dimethyl (N-term)
☑	2150	683.8522	1365.6898	1365.6826	5.26	0	52	0.00074	1	K.IYIDSNNNPER.F + Dimethyl:2H(4) (N-term)
☑	3378	614.9998	1841.9776	1841.9675	5.48	1	(42)	0.015	1	R.KFNALFAQGNYSEAAK.V + 2 Dimethyl (K); Dimethyl (N-term)
☑	3379	614.9999	1841.9777	1841.9675	5.53	1	64	8.5e-005	1	R.KFNALFAQGNYSEAAK.V + 2 Dimethyl (K); Dimethyl (N-term)
☑	3683	667.0290	1998.0653	1998.0534	5.96	0	(37)	0.043	1	R.LASTLVHLGEYQAAVDGAR.K + Dimethyl (N-term)
☑	3690	668.3709	2002.0907	2002.0785	6.09	0	76	6.4e-006	1	R.LASTLVHLGEYQAAVDGAR.K + Dimethyl:2H(4) (N-term)
☑	3691	668.3713	2002.0922	2002.0785	6.82	0	(62)	0.00015	1	R.LASTLVHLGEYQAAVDGAR.K + Dimethyl:2H(4) (N-term)

Proteins matching the same set of peptides:
IPI00648173 **Mass:** 193631 **Score:** 308 **Queries matched:** 9
Tax_Id=10090 Gene_Symbol=Cltc Clathrin, heavy polypeptide

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28. IPI00131138 **Mass:** 283869 **Score:** 297 **Queries matched:** 18 **emPAI:** 0.13
Tax_Id=10090 Gene_Symbol=Flna Isoform 1 of Filamin-A

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	837	469.8072	937.5998	937.5960	3.97	0	35	0.036	1	K.AGVAPLQVK.V + Dimethyl (K); Dimethyl (N-term)
☑	853	473.8323	945.6501	945.6463	4.01	0	(28)	0.12	1	K.AGVAPLQVK.V + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1359	564.3087	1126.6029	1126.5982	4.14	0	30	0.12	1	K.GTVEPQLEAR.G + Dimethyl (N-term)
☑	1453	388.8970	1163.6691	1163.6663	2.43	0	56	0.00045	1	R.ALTQTGGPHVK.A + Dimethyl (K); Dimethyl (N-term)
☑	1480	391.5804	1171.7193	1171.7165	2.41	0	(54)	0.00062	1	R.ALTQTGGPHVK.A + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1952	648.8732	1295.7319	1295.7238	6.28	0	45	0.0062	1	R.AWGPGLEGGIVGK.S + Dimethyl (K); Dimethyl (N-term)
☑	1979	652.8981	1303.7817	1303.7740	5.91	0	(38)	0.031	1	R.AWGPGLEGGIVGK.S + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	2233	348.4603	1389.8120	1389.8092	1.97	1	33	0.097	1	R.VNVGAGSHPNKVK.V + 2 Dimethyl (K); Dimethyl (N-term)
☑	2260	351.4792	1401.8875	1401.8846	2.11	1	(27)	0.16	1	R.VNVGAGSHPNKVK.V + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	2526	742.8882	1483.7618	1483.7532	5.82	0	77	3.3e-006	1	K.AFGPGLQGGNAGSPAR.F + Dimethyl (N-term)
☑	2547	745.9008	1489.7871	1489.7776	6.33	0	58	0.0003	1	R.ANLPQSFQVDTSK.A + Dimethyl (K); Dimethyl (N-term)
☑	2567	749.9263	1497.8381	1497.8279	6.82	0	(34)	0.085	1	R.ANLPQSFQVDTSK.A + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3422	619.6769	1856.0090	1856.0004	4.66	1	39	0.028	1	K.VAQPSITDNKDGTVTVR.Y + Dimethyl (K); Dimethyl (N-term)
☑	3433	622.3604	1864.0594	1864.0506	4.73	1	(29)	0.23	1	K.VAQPSITDNKDGTVTVR.Y + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3450	625.6731	1873.9975	1873.9898	4.09	0	(36)	0.058	1	K.VATVPQHATSGPGPADVSK.V + Dimethyl (K); Dimethyl (N-term)
☑	3489	628.3569	1882.0487	1882.0400	4.62	0	45	0.0079	1	K.VATVPQHATSGPGPADVSK.V + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	4133	758.4082	2272.2027	2272.1902	5.50	1	(42)	0.015	1	R.AGGPGLERAEAGVPAEFGIWTR.E + Dimethyl:2H(4) (N-term)
☑	4134	758.4083	2272.2031	2272.1902	5.69	1	46	0.006	1	R.AGGPGLERAEAGVPAEFGIWTR.E + Dimethyl:2H(4) (N-term)

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29. IPI00380873 **Mass:** 46510 **Score:** 288 **Queries matched:** 21 **emPAI:** 1.25
Tax_Id=10090 Gene_Symbol=Sec14l3 Novel protein, ortholog of human and rat SEC14-like 3 (S. cerevisiae) SEC14L3

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	636	410.7331	819.4516	819.4490	3.10	0	(32)	0.071	1	R.NFDLQK.S + Dimethyl (K); Dimethyl (N-term)
☑	649	414.7581	827.5017	827.4993	2.92	0	35	0.041	1	R.NFDLQK.S + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	801	460.7967	919.5788	919.5742	4.99	0	(33)	0.073	1	K.GLLFSVTK.Q + Dimethyl (K); Dimethyl (N-term)
☑	814	464.8217	927.6289	927.6245	4.81	0	33	0.03	1	K.GLLFSVTK.Q + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1150	523.7999	1045.5852	1045.5808	4.22	0	(32)	0.12	1	K.INYGGEIPK.S + Dimethyl (K); Dimethyl (N-term)
☑	1151	523.8000	1045.5855	1045.5808	4.57	0	50	0.0018	1	K.INYGGEIPK.S + Dimethyl (K); Dimethyl (N-term)
☑	1188	527.8248	1053.6351	1053.6310	3.90	0	(29)	0.21	1	K.INYGGEIPK.S + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1189	527.8253	1053.6360	1053.6310	4.71	0	(49)	0.0022	1	K.INYGGEIPK.S + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	2182	459.2382	1374.6927	1374.6892	2.59	0	(32)	0.083	1	K.TQYEHSVQISR.G + Dimethyl (N-term)
☑	2197	460.5800	1378.7181	1378.7143	2.80	0	35	0.056	1	K.TQYEHSVQISR.G + Dimethyl:2H(4) (N-term)
☑	2701	515.9947	1544.9622	1544.9541	5.24	1	37	0.017	1	K.GLLFSVTKQDLLK.T + 2 Dimethyl (K); Dimethyl (N-term)

☑	2726	520.0200	1557.0380	1557.0295	5.49	1	(34)	0.0053	1	K.GLLFSVTKQDLLK.T + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	2917	549.9648	1646.8727	1646.8661	3.99	1	(63)	0.00011	1	R.QKAGEMVEVLTSQR.Y + Dimethyl (K); Dimethyl (N-term); Oxidation (M)
☑	2937	552.6480	1654.9222	1654.9164	3.53	1	67	4.9e-005	1	R.QKAGEMVEVLTSQR.Y + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)
☑	3110	576.3569	1726.0488	1726.0393	5.52	1	(34)	0.042	1	K.IVVLGSNSWKEGLLK.L + 2 Dimethyl (K); Dimethyl (N-term)
☑	3111	576.3569	1726.0488	1726.0393	5.52	1	(33)	0.043	1	K.IVVLGSNSWKEGLLK.L + 2 Dimethyl (K); Dimethyl (N-term)
☑	3143	580.3822	1738.1248	1738.1146	5.85	1	36	0.0047	1	K.IVVLGSNSWKEGLLK.L + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	4307	616.0740	2460.2670	2460.2536	5.44	0	(28)	0.34	1	K.LISPEELPAHFGGTLTDPDGNPK.C + Dimethyl (K); Dimethyl (N-term)
☑	4308	821.0975	2460.2707	2460.2536	6.94	0	70	2.4e-005	1	K.LISPEELPAHFGGTLTDPDGNPK.C + Dimethyl (K); Dimethyl (N-term)
☑	4309	821.0975	2460.2708	2460.2536	6.96	0	(57)	0.00044	1	K.LISPEELPAHFGGTLTDPDGNPK.C + Dimethyl (K); Dimethyl (N-term)
☑	4326	823.7807	2468.3203	2468.3039	6.64	0	(51)	0.0021	1	K.LISPEELPAHFGGTLTDPDGNPK.C + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

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30. IPI00110753 **Mass:** 50788 **Score:** 282 **Queries matched:** 16 **emPAI:** 0.72
Tax_Id=10090 Gene_Symbol=Tuba1a Tubulin alpha-1A chain
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	3114	577.3208	1728.9407	1728.9298	6.31	0	(53)	0.0013	1	R.AVFVDLEPTVIDEVR.T + Dimethyl (N-term)
☑	3115	865.4796	1728.9447	1728.9298	8.62	0	(75)	7.8e-006	1	R.AVFVDLEPTVIDEVR.T + Dimethyl (N-term)
☑	3126	578.6624	1732.9654	1732.9549	6.05	0	(34)	0.08	1	R.AVFVDLEPTVIDEVR.T + Dimethyl:2H(4) (N-term)
☑	3128	867.4916	1732.9687	1732.9549	7.96	0	(81)	1.8e-006	1	R.AVFVDLEPTVIDEVR.T + Dimethyl:2H(4) (N-term)
☑	3129	867.4918	1732.9690	1732.9549	8.10	0	87	4.6e-007	1	R.AVFVDLEPTVIDEVR.T + Dimethyl:2H(4) (N-term)
☑	3285	605.0175	1812.0307	1812.0185	6.73	0	38	0.033	1	R.IHFPLATYAPVISAEK.A + Dimethyl (K); Dimethyl (N-term)
☑	3286	605.0176	1812.0311	1812.0185	6.93	0	(31)	0.16	1	R.IHFPLATYAPVISAEK.A + Dimethyl (K); Dimethyl (N-term)
☑	3317	607.7013	1820.0821	1820.0688	7.30	0	(33)	0.063	1	R.IHFPLATYAPVISAEK.A + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	4154	770.0832	2307.2277	2307.2111	7.21	1	43	0.013	1	R.AVFVDLEPTVIDEVRTGTYR.Q + Dimethyl (N-term)
☑	4155	770.0835	2307.2287	2307.2111	7.62	1	(31)	0.2	1	R.AVFVDLEPTVIDEVRTGTYR.Q + Dimethyl (N-term)
☑	4157	771.4249	2311.2530	2311.2362	7.25	1	(32)	0.14	1	R.AVFVDLEPTVIDEVRTGTYR.Q + Dimethyl:2H(4) (N-term)
☑	4331	618.5760	2470.2749	2470.2604	5.84	1	(34)	0.082	1	R.QLFHPEQLITGKEDAANNYAR.G + Dimethyl (K); Dimethyl (N-term)
☑	4332	618.5762	2470.2757	2470.2604	6.19	1	36	0.06	1	R.QLFHPEQLITGKEDAANNYAR.G + Dimethyl (K); Dimethyl (N-term)
☑	4339	620.5885	2478.3247	2478.3107	5.68	1	(35)	0.08	1	R.QLFHPEQLITGKEDAANNYAR.G + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	4340	620.5886	2478.3254	2478.3107	5.94	1	(36)	0.066	1	R.QLFHPEQLITGKEDAANNYAR.G + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	4357	639.0688	2552.2463	2552.2296	6.54	1	34	0.063	1	K.TIGGGDDSFNTFFSETGAGKHVPR.A + Dimethyl (K); Dimethyl (N-term)

Proteins matching the same set of peptides:
IPI00117348 **Mass:** 50804 **Score:** 282 **Queries matched:** 16
Tax_Id=10090 Gene_Symbol=Tuba1b Tubulin alpha-1B chain
IPI00403810 **Mass:** 50562 **Score:** 282 **Queries matched:** 16
Tax_Id=10090 Gene_Symbol=Tuba1c Tubulin alpha-1C chain

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31. IPI00117352 **Mass:** 50095 **Score:** 267 **Queries matched:** 10 **emPAI:** 0.57
Tax_Id=10090 Gene_Symbol=Tubb5 Tubulin beta-5 chain
☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1218	534.3191	1066.6236	1066.6175	5.74	0	28	0.26	1	R.YLTVAAVFR.G + Dimethyl (N-term)

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    1466  586.3401  1170.6657  1170.6583   6.32  0   (40)    0.025   1   K.LAVNMVPFPR.L + Dimethyl (N-term)
    1493  588.3533  1174.6921  1174.6834   7.38  0    57   0.00044   1   K.LAVNMVPFPR.L + Dimethyl:2H(4) (N-term)
 ☑  2901  548.6306  1642.8698  1642.8600   5.98  0   (46)   0.0061   1   R.AILVDLEPGTMDSVR.S + Dimethyl (N-term)
 ☑  2902  822.4436  1642.8727  1642.8600   7.74  0    94   1.1e-007  1   R.AILVDLEPGTMDSVR.S + Dimethyl (N-term)
 ☑  2918  824.4564  1646.8982  1646.8851   7.92  0   (70) 2.3e-005   1   R.AILVDLEPGTMDSVR.S + Dimethyl:2H(4) (N-term)
    2926  551.6392  1651.8958  1651.8847   6.75  0    47    0.0044   1   R.LHFFMPGFAPLTSR.G + Dimethyl:2H(4) (N-term)
 ☑  2960  830.4421  1658.8697  1658.8549   8.92  0   (83) 1.1e-006   1   R.AILVDLEPGTMDSVR.S + Dimethyl (N-term); Oxidation (M)
 ☑  2976  832.4550  1662.8954  1662.8800   9.22  0   (64) 8.9e-005   1   R.AILVDLEPGTMDSVR.S + Dimethyl:2H(4) (N-term); Oxidation (M)
    4269  609.3290  2433.2867  2433.2726   5.81  2    27       0.5   2   K.IREEYPDRIMNTFSVVPSPK.V + Dimethyl (K); Dimethyl (N-term)
```

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32.   IPI00624663     Mass: 168602    Score: 257     Queries matched: 10    emPAI: 0.16
      Tax_Id=10090 Gene_Symbol=Pzp Alpha-2-macroglobulin precursor
 ☐    Check to include this hit in error tolerant search or archive report

    Query  Observed   Mr(expt)   Mr(calc)   ppm  Miss Score  Expect  Rank  Peptide
 ☑  1044  505.2793  1008.5440  1008.5392   4.76  0   (45)  0.0045    1   K.ALSFYQPR.A + Dimethyl (N-term)
 ☑  1053  507.2919  1012.5693  1012.5644   4.89  0    47   0.0027    1   K.ALSFYQPR.A + Dimethyl:2H(4) (N-term)
 ☑  1138  522.8105  1043.6065  1043.6015   4.80  0   (49)  0.0025    1   K.TVSWAVTPK.S + Dimethyl (K); Dimethyl (N-term)
 ☑  1177  526.8356  1051.6567  1051.6518   4.70  0    52  0.00081    1   K.TVSWAVTPK.S + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
 ☑  1581  400.9178  1199.7315  1199.7278   3.12  1    49   0.0019    1   R.KTVSWAVTPK.S + 2 Dimethyl (K); Dimethyl (N-term)
 ☑  1641  404.9429  1211.8069  1211.8031   3.09  1   (28)   0.071    1   R.KTVSWAVTPK.S + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
 ☑  1880  633.8275  1265.6405  1265.6351   4.28  0   (61)  0.0001    1   R.DLSSSDLSTASK.I + Dimethyl (K); Dimethyl (N-term)
 ☑  1904  637.8525  1273.6905  1273.6853   4.11  0    61  0.00014    1   R.DLSSSDLSTASK.I + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
 ☑  2038  663.3686  1324.7227  1324.7139   6.66  0   (45)  0.0062    1   K.AINYLISGYQR.Q + Dimethyl (N-term)
 ☑  2055  665.3812  1328.7478  1328.7390   6.59  0    79   3e-006    1   K.AINYLISGYQR.Q + Dimethyl:2H(4) (N-term)
```

```
33.   IPI00622235     Mass: 89950     Score: 248     Queries matched: 13    emPAI: 0.40
      Tax_Id=10090 Gene_Symbol=Vcp Transitional endoplasmic reticulum ATPase
 ☐    Check to include this hit in error tolerant search or archive report

    Query  Observed   Mr(expt)   Mr(calc)   ppm  Miss Score   Expect  Rank  Peptide
 ☑  1287  552.2901  1102.5657  1102.5618   3.55  0   (53)  0.00053   1   K.LAGESESNLR.K + Dimethyl (N-term)
 ☑  1297  553.3131  1104.6117  1104.6067   4.53  0    46    0.0049   1   K.DVDLEFLAK.M + Dimethyl (K); Dimethyl (N-term)
 ☑  1304  554.3029  1106.5912  1106.5869   3.83  0    63  8.5e-005   1   K.LAGESESNLR.K + Dimethyl:2H(4) (N-term)
 ☑  1415  384.2462  1149.7166  1149.7121   3.93  0    43    0.0071   1   R.LEILQIHTK.N + Dimethyl (K); Dimethyl (N-term)
 ☑  1658  406.8622  1217.5647  1217.5611   2.96  1    30     0.036   1   R.RDHFEEAMR.F + Dimethyl (N-term)
 ☑  1688  408.2038  1221.5897  1221.5862   2.86  1   (29)    0.088   1   R.RDHFEEAMR.F + Dimethyl:2H(4) (N-term)
 ☑  1864  420.5710  1258.6910  1258.6881   2.36  1   (42)    0.011   1   K.LAGESESNLRK.A + Dimethyl (K); Dimethyl (N-term)
 ☑  1885  423.2545  1266.7417  1266.7383   2.70  1    61   0.00016   1   K.LAGESESNLRK.A + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
 ☑  2134  679.3691  1356.7237  1356.7150   6.45  0    67  3.3e-005   1   R.WALSQSNPSALR.E + Dimethyl (N-term)
 ☑  3026  562.6305  1684.8697  1684.8606   5.35  1   (47)   0.0038   1   R.KYEMFAQTLQQSR.G + Dimethyl (K); Dimethyl (N-term)
 ☑  3027  562.6305  1684.8697  1684.8606   5.39  1    54   0.00082   1   R.KYEMFAQTLQQSR.G + Dimethyl (K); Dimethyl (N-term)
 ☑  3048  565.3138  1692.9195  1692.9109   5.10  1   (39)     0.03   1   R.KYEMFAQTLQQSR.G + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
 ☑  3222  593.7088  1778.1046  1778.0939   5.98  1    32     0.036   1   R.IVSQLLTLMDGLKQR.A + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
```

Proteins matching the same set of peptides:
IPI00676914 **Mass:** 89423 **Score:** 248 **Queries matched:** 13
Tax_Id=10090 Gene_Symbol=LOC675857 similar to valosin isoform 1

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34. IPI00230395 **Mass:** 38995 **Score:** 239 **Queries matched:** 11 **emPAI:** 0.78
Tax_Id=10090 Gene_Symbol=Anxa1 Annexin A1

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	503	378.2745	754.5344	754.5316	3.68	0	(26)	0.18	1	K.ALLALAK.G + Dimethyl (K); Dimethyl (N-term)
☑	512	382.2997	762.5848	762.5818	3.89	0	40	0.0015	1	K.ALLALAK.G + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	2757	525.9831	1574.9275	1574.9181	5.92	1	(60)	0.00018	1	K.GVDEATIIDILTKR.T + Dimethyl:2H(4) (N-term)
☑	2799	533.9851	1598.9335	1598.9243	5.75	1	(56)	0.00049	1	K.GVDEATIIDILTKR.T + Dimethyl (K); Dimethyl (N-term)
☑	2810	536.6685	1606.9835	1606.9745	5.61	1	65	3.3e-005	1	K.GVDEATIIDILTKR.T + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3055	566.2870	1695.8393	1695.8315	4.58	1	66	3.4e-005	1	R.DLAKDITSDTSGDFR.K + Dimethyl (K); Dimethyl (N-term)
☑	3075	568.9707	1703.8903	1703.8818	4.99	1	(49)	0.0027	1	R.DLAKDITSDTSGDFR.K + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3224	594.3113	1779.9122	1779.9043	4.44	0	(48)	0.0028	1	R.FLENQEQEYVQAVK.S + Dimethyl (K); Dimethyl (N-term)
☑	3229	596.9949	1787.9627	1787.9545	4.59	0	51	0.0019	1	R.FLENQEQEYVQAVK.S + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3230	596.9950	1787.9632	1787.9545	4.83	0	(41)	0.019	1	R.FLENQEQEYVQAVK.S + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	4527	705.3893	2817.5283	2817.5091	6.81	1	48	0.0029	1	K.SYKGGPGSAVSPYPSFNVSSDVAALHK.A + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

Proteins matching the same set of peptides:
IPI00652811 **Mass:** 40492 **Score:** 239 **Queries matched:** 11
Tax_Id=10090 Gene_Symbol=Anxa1 16 days embryo head cDNA, RIKEN full-length enriched library, clone:C130041B04 product:annexin A1, full insert sequence

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35. IPI00139788 **Mass:** 78841 **Score:** 232 **Queries matched:** 12 **emPAI:** 0.29
Tax_Id=10090 Gene_Symbol=Trf Serotransferrin precursor

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	938	490.2842	978.5538	978.5498	4.06	0	46	0.0045	1	K.TVLPPDGPR.L + Dimethyl (N-term)
☑	944	327.8769	980.6088	980.6069	1.98	0	36	0.034	1	R.IPSHAVVAR.K + Dimethyl:2H(4) (N-term)
☑	951	492.2967	982.5789	982.5750	4.01	0	(31)	0.097	1	K.TVLPPDGPR.L + Dimethyl:2H(4) (N-term)
☑	1076	513.3072	1024.5998	1024.5957	4.02	0	(47)	0.0027	1	K.GYYAVAVVK.A + Dimethyl (K); Dimethyl (N-term)
☑	1077	513.3075	1024.6004	1024.5957	4.62	0	(56)	0.00042	1	K.GYYAVAVVK.A + Dimethyl (K); Dimethyl (N-term)
☑	1106	517.3326	1032.6506	1032.6459	4.52	0	65	5.2e-005	1	K.GYYAVAVVK.A + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1107	517.3326	1032.6506	1032.6459	4.52	0	(53)	0.00091	1	K.GYYAVAVVK.A + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	2275	703.3747	1404.7348	1404.7249	7.09	0	55	0.00062	1	K.ASDTSITWNNLK.G + Dimethyl (K); Dimethyl (N-term)
☑	2416	483.2752	1446.8037	1446.7983	3.74	0	(29)	0.24	1	R.LYLGHNYVTAIR.N + Dimethyl (N-term)
☑	2417	483.2755	1446.8047	1446.7983	4.43	0	(34)	0.08	1	R.LYLGHNYVTAIR.N + Dimethyl (N-term)
☑	2437	484.6173	1450.8300	1450.8234	4.53	0	42	0.013	1	R.LYLGHNYVTAIR.N + Dimethyl:2H(4) (N-term)
☑	2438	484.6173	1450.8302	1450.8234	4.66	0	(32)	0.13	1	R.LYLGHNYVTAIR.N + Dimethyl:2H(4) (N-term)

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36. IPI00109073 **Mass:** 50010 **Score:** 220 **Queries matched:** 8 **emPAI:** 0.42
Tax_Id=10090 Gene_Symbol=Tubb4 Tubulin beta-4 chain

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
	1218	534.3191	1066.6236	1066.6175	5.74	0	28	0.26	1	R.YLTVAAVFR.G + Dimethyl (N-term)
	1466	586.3401	1170.6657	1170.6583	6.32	0	(40)	0.025	1	K.LAVNMVPFPR.L + Dimethyl (N-term)
	1493	588.3533	1174.6921	1174.6834	7.38	0	57	0.00044	1	K.LAVNMVPFPR.L + Dimethyl:2H(4) (N-term)
	2857	815.4356	1628.8567	1628.8444	7.59	0	(76)	5.2e-006	1	R.AVLVDLEPGTMDSVR.S + Dimethyl (N-term)
	2877	817.4486	1632.8827	1632.8695	8.08	0	(62)	0.00015	1	R.AVLVDLEPGTMDSVR.S + Dimethyl:2H(4) (N-term)
	2910	823.4321	1644.8497	1644.8393	6.34	0	96	4.7e-008	1	R.AVLVDLEPGTMDSVR.S + Dimethyl (N-term); Oxidation (M)
	2926	551.6392	1651.8958	1651.8847	6.75	0	47	0.0044	1	R.LHFFMPGFAPLTSR.G + Dimethyl:2H(4) (N-term)
☑	4269	609.3290	2433.2867	2433.2726	5.80	2	28	0.4	1	K.IREEFPDRIMNTFSVVPSPK.V + Dimethyl (K); Dimethyl (N-term); Oxidation (M)

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37. IPI00316491 **Mass:** 15982 **Score:** 215 **Queries matched:** 14 **emPAI:** 2.33
Tax_Id=10090 Gene_Symbol=Hbb-b2 Hemoglobin subunit beta-2

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
	1971	651.8856	1301.7567	1301.7496	5.48	0	43	0.0096	1	R.LLVVYPWTQR.Y + Dimethyl (N-term)
	1972	651.8861	1301.7577	1301.7496	6.25	0	(36)	0.047	1	R.LLVVYPWTQR.Y + Dimethyl (N-term)
	1973	651.8861	1301.7577	1301.7496	6.25	0	(36)	0.046	1	R.LLVVYPWTQR.Y + Dimethyl (N-term)
	1985	653.8981	1305.7817	1305.7747	5.37	0	(39)	0.024	1	R.LLVVYPWTQR.Y + Dimethyl:2H(4) (N-term)
	1986	653.8984	1305.7823	1305.7747	5.84	0	(28)	0.27	1	R.LLVVYPWTQR.Y + Dimethyl:2H(4) (N-term)
	1987	653.8986	1305.7827	1305.7747	6.11	0	(36)	0.045	1	R.LLVVYPWTQR.Y + Dimethyl:2H(4) (N-term)
☑	2098	**670.8476**	**1339.6807**	**1339.6732**	**5.63**	**0**	**44**	**0.0049**	**1**	**K.VNPDEVGGEALGR.L + Dimethyl (N-term)**
☑	2108	**672.8596**	**1343.7047**	**1343.6983**	**4.75**	**0**	**(41)**	**0.012**	**1**	**K.VNPDEVGGEALGR.L + Dimethyl:2H(4) (N-term)**
	2552	498.2946	1491.8618	1491.8562	3.79	1	51	0.0017	1	K.VVAGVATALAHKYH.- + Dimethyl (K); Dimethyl (N-term)
	2579	500.9779	1499.9120	1499.9064	3.71	1	(48)	0.0019	1	K.VVAGVATALAHKYH.- + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3856	**688.3359**	**2061.9857**	**2061.9717**	**6.79**	**0**	**42**	**0.0062**	**1**	**R.YFDSFGDLSSASAIMGNPK.V + Dimethyl (K); Dimethyl (N-term)**
☑	3857	**688.3359**	**2061.9860**	**2061.9717**	**6.91**	**0**	**(33)**	**0.055**	**1**	**R.YFDSFGDLSSASAIMGNPK.V + Dimethyl (K); Dimethyl (N-term)**
☑	3870	**691.0191**	**2070.0355**	**2070.0220**	**6.53**	**0**	**(35)**	**0.056**	**1**	**R.YFDSFGDLSSASAIMGNPK.V + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)**
☑	3871	**691.0192**	**2070.0357**	**2070.0220**	**6.65**	**0**	**(33)**	**0.098**	**1**	**R.YFDSFGDLSSASAIMGNPK.V + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)**

Proteins matching the same set of peptides:
IPI00828873 **Mass:** 15851 **Score:** 215 **Queries matched:** 14
Tax_Id=10090 Gene_Symbol=Hbb Beta-2-globin (Fragment)

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38. IPI00117857 **Mass:** 45966 **Score:** 205 **Queries matched:** 14 **emPAI:** 0.73
Tax_Id=10090 Gene_Symbol=Spi1-6 Alpha-1-antitrypsin 1-6 precursor

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
	1064	510.2946	1018.5746	1018.5699	4.58	0	38	0.028	1	K.VINDFVEK.G + Dimethyl (K); Dimethyl (N-term)
	1331	558.8291	1115.6437	1115.6373	5.80	0	44	0.0083	1	K.TLMSPLGITR.I + Dimethyl (N-term)
	1345	560.8419	1119.6692	1119.6624	6.07	0	(39)	0.025	1	K.TLMSPLGITR.I + Dimethyl:2H(4) (N-term)
	1368	566.8261	1131.6377	1131.6322	4.90	0	(37)	0.043	1	K.TLMSPLGITR.I + Dimethyl (N-term); Oxidation (M)
	1379	568.8386	1135.6626	1135.6573	4.65	0	(40)	0.018	1	K.TLMSPLGITR.I + Dimethyl:2H(4) (N-term); Oxidation (M)
☑	1547	**594.3629**	**1186.7113**	**1186.7049**	**5.39**	**0**	**35**	**0.052**	**1**	**R.LSISGEYNLK.T + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)**

```
   2635  506.9575  1517.8507  1517.8453   3.55   1    36     0.058   1   K.VINDFVEKGTQGK.I + 2 Dimethyl (K); Dimethyl (N-term)
   2661  510.9827  1529.9264  1529.9207   3.70   1   (25)     0.41   1   K.VINDFVEKGTQGK.I + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
   2992  558.9998  1673.9774  1673.9716   3.49   2   (33)    0.093   1   K.KVINDFVEKGTQGK.I + 3 Dimethyl (K); Dimethyl (N-term)
   3035  564.3665  1690.0777  1690.0721   3.36   2    34     0.017   1   K.KVINDFVEKGTQGK.I + 3 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
   3849  687.0324  2058.0754  2058.0633   5.88   0   (46)   0.0057   1   R.IFNNGADLSGITEENAPLK.L + Dimethyl (K); Dimethyl (N-term)
   3850  687.0330  2058.0772  2058.0633   6.77   0    62   0.00017   1   R.IFNNGADLSGITEENAPLK.L + Dimethyl (K); Dimethyl (N-term)
   4537  713.3945  2849.5487  2849.5287   7.04   1    62  9.7e-005   2   R.IFNNGADLSGITEENAPLKLSQAVHK.A + 2 Dimethyl (K); Dimethyl (N-term)
   4538  713.3948  2849.5500  2849.5287   7.49   1   (50)   0.0018   3   R.IFNNGADLSGITEENAPLKLSQAVHK.A + 2 Dimethyl (K); Dimethyl (N-term)


      Proteins matching the same set of peptides:
      IPI00123920     Mass: 45996     Score: 205     Queries matched: 14
      Tax_Id=10090 Gene_Symbol=Serpina1c Alpha-1-antitrypsin 1-3 precursor
      IPI00406302     Mass: 46145     Score: 205     Queries matched: 14
      Tax_Id=10090 Gene_Symbol=Serpina1a Alpha-1-antitrypsin 1-1 precursor
________________________________________________________________________________________________________________________________________
39.   IPI00318614     Mass: 51330     Score: 198     Queries matched: 4    emPAI: 0.10
      Tax_Id=10090 Gene_Symbol=Idh2 Isocitrate dehydrogenase [NADP], mitochondrial precursor
    ☐ Check to include this hit in error tolerant search or archive report

     Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score   Expect Rank  Peptide
   ☑ 2212  461.9135  1382.7187  1382.7154   2.42   0   (64) 5.4e-005   1   K.TIEAEAAHGTVTR.H + Dimethyl (N-term)
   ☑ 2213  461.9139  1382.7197  1382.7154   3.14   0    86  3.7e-007   1   K.TIEAEAAHGTVTR.H + Dimethyl (N-term)
   ☑ 2219  463.2553  1386.7442  1386.7405   2.67   0   (69) 2.6e-005   1   K.TIEAEAAHGTVTR.H + Dimethyl:2H(4) (N-term)
   ☑ 2220  463.2555  1386.7447  1386.7405   3.05   0   (76) 4.6e-006   1   K.TIEAEAAHGTVTR.H + Dimethyl:2H(4) (N-term)


      Proteins matching the same set of peptides:
      IPI00875110     Mass: 52994     Score: 198     Queries matched: 4
      Tax_Id=10090 Gene_Symbol=Idh2 52 kDa protein
________________________________________________________________________________________________________________________________________
40.   IPI00323816     Mass: 53147     Score: 193     Queries matched: 6    emPAI: 0.33
      Tax_Id=10090 Gene_Symbol=Selenbp2 Selenium-binding protein 2
    ☐ Check to include this hit in error tolerant search or archive report

     Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score   Expect Rank  Peptide
   ☑ 1269  548.8611  1095.7077  1095.7016   5.63   0    59   0.00011   1   K.LILPGLISSR.I + Dimethyl (N-term)
   ☑ 1280  550.8738  1099.7331  1099.7267   5.87   0   (53)  0.00033   1   K.LILPGLISSR.I + Dimethyl:2H(4) (N-term)
   ☑ 1398  572.3370  1142.6594  1142.6546   4.15   0   (51)   0.0014   1   K.VIEASEIQAK.C + Dimethyl (K); Dimethyl (N-term)
   ☑ 1418  576.3619  1150.7093  1150.7049   3.86   0    60   0.00016   1   K.VIEASEIQAK.C + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
   ☑ 1869  631.3461  1260.6777  1260.6714   5.01   0    67  3.5e-005   1   R.IYVVDVGSEPR.A + Dimethyl (N-term)
   ☑ 1876  633.3592  1264.7038  1264.6965   5.78   0   (61)  0.00013   1   R.IYVVDVGSEPR.A + Dimethyl:2H(4) (N-term)


      Proteins matching the same set of peptides:
      IPI00623845     Mass: 53051     Score: 193     Queries matched: 6
      Tax_Id=10090 Gene_Symbol=LOC100044204;Selenbp1 Selenium-binding protein 1
________________________________________________________________________________________________________________________________________
41.   IPI00323592     Mass: 36045     Score: 188     Queries matched: 8    emPAI: 0.62
```

Tax_Id=10090 Gene_Symbol=Mdh2 Malate dehydrogenase, mitochondrial precursor

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	799	460.2621	918.5097	918.5062	3.77	0	46	0.0035	1	K.ITPFEEK.M + Dimethyl (K); Dimethyl (N-term)
☑	1197	528.8331	1055.6516	1055.6467	4.67	0	40	0.015	1	R.ANTFVAELK.G + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1365	565.3286	1128.6427	1128.6390	3.23	0	(35)	0.061	1	R.IQEAGTEVVK.A + Dimethyl (K); Dimethyl (N-term)
☑	1384	569.3539	1136.6932	1136.6893	3.48	0	51	0.0012	1	R.IQEAGTEVVK.A + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1462	585.8469	1169.6793	1169.6729	5.44	0	68	2.7e-005	1	K.MIAEAIPELK.A + Dimethyl (K); Dimethyl (N-term)
☑	1516	589.8719	1177.7293	1177.7232	5.25	0	(64)	5.2e-005	1	K.MIAEAIPELK.A + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	4262	607.0845	2424.3087	2424.2951	5.63	0	49	0.0033	1	R.LTLYDIAHTPGVAADLSHIETR.A + Dimethyl:2H(4) (N-term)
☑	4263	607.0847	2424.3095	2424.2951	5.96	0	(48)	0.0037	1	R.LTLYDIAHTPGVAADLSHIETR.A + Dimethyl:2H(4) (N-term)

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42. IPI00127560 **Mass:** 15880 **Score:** 188 **Queries matched:** 7 **emPAI:** 1.13

Tax_Id=10090 Gene_Symbol=Ttr Transthyretin precursor

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1004	499.7994	997.5843	997.5808	3.48	0	(57)	0.00032	1	R.GSPAVDVAVK.V + Dimethyl (K); Dimethyl (N-term)
☑	1005	499.7995	997.5845	997.5808	3.72	0	(57)	0.00031	1	R.GSPAVDVAVK.V + Dimethyl (K); Dimethyl (N-term)
☑	1036	503.8245	1005.6344	1005.6310	3.39	0	57	0.00027	1	R.GSPAVDVAVK.V + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1037	503.8248	1005.6351	1005.6310	4.05	0	(46)	0.0036	1	R.GSPAVDVAVK.V + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	2411	723.8761	1445.7376	1445.7278	6.79	0	73	6.8e-006	1	K.TSEGSWEPFASGK.T + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	2900	548.6112	1642.8118	1642.8050	4.14	0	35	0.035	1	K.TAESGELHGLTTDEK.F + Dimethyl (K); Dimethyl (N-term)
☑	2922	551.2947	1650.8622	1650.8552	4.24	0	(34)	0.086	1	K.TAESGELHGLTTDEK.F + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

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43. IPI00555069 **Mass:** 44921 **Score:** 184 **Queries matched:** 7 **emPAI:** 0.40

Tax_Id=10090 Gene_Symbol=Pgk1 Phosphoglycerate kinase 1

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1315	556.3246	1110.6347	1110.6285	5.62	0	(43)	0.0069	1	K.VLPGVDALSNV.- + Dimethyl (N-term)
☑	1329	558.3374	1114.6603	1114.6536	5.97	0	54	0.00073	1	K.VLPGVDALSNV.- + Dimethyl:2H(4) (N-term)
☑	2970	554.9485	1661.8237	1661.8162	4.54	0	72	8.6e-006	1	K.LGDVYVNDAFGTAHR.A + Dimethyl (N-term)
☑	2978	556.2905	1665.8497	1665.8413	5.06	0	(57)	0.00031	1	K.LGDVYVNDAFGTAHR.A + Dimethyl:2H(4) (N-term)
☑	2979	556.2906	1665.8501	1665.8413	5.29	0	(55)	0.00059	1	K.LGDVYVNDAFGTAHR.A + Dimethyl:2H(4) (N-term)
☑	3335	609.0283	1824.0631	1824.0509	6.72	0	30	0.15	1	K.ALESPERPFLAILGGAK.V + Dimethyl (K); Dimethyl (N-term)
☑	3355	611.7116	1832.1130	1832.1011	6.49	0	(26)	0.23	1	K.ALESPERPFLAILGGAK.V + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

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44. IPI00132762 **Mass:** 80501 **Score:** 181 **Queries matched:** 2 **emPAI:** 0.07

Tax_Id=10090 Gene_Symbol=Trap1 Heat shock protein 75 kDa, mitochondrial precursor

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide

2692	771.4176	1540.8207	1540.8097	7.17	0	(104)	8.9e-009	1	R.GVVDSEDIPLNLSR.E + Dimethyl (N-term)
2699	773.4298	1544.8451	1544.8348	6.65	0	113	1.1e-009	1	R.GVVDSEDIPLNLSR.E + Dimethyl:2H(4) (N-term)

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45. IPI00128249 **Mass:** 38100 **Score:** 177 **Queries matched:** 4 **emPAI:** 0.14

Tax_Id=10090 Gene_Symbol=Ahsg Alpha-2-HS-glycoprotein precursor

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	4004	732.0468	2193.1187	2193.1066	5.54	0	(58)	0.0003	1	R.HAFSPVASVESASGETLHSPK.V + Dimethyl (K); Dimethyl (N-term)
☑	4005	732.0469	2193.1190	2193.1066	5.65	0	(61)	0.00016	1	R.HAFSPVASVESASGETLHSPK.V + Dimethyl (K); Dimethyl (N-term)
☑	4020	734.7302	2201.1687	2201.1568	5.41	0	(68)	4.1e-005	1	R.HAFSPVASVESASGETLHSPK.V + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	4021	734.7303	2201.1690	2201.1568	5.55	0	73	1.1e-005	1	R.HAFSPVASVESASGETLHSPK.V + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

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46. IPI00126248 **Mass:** 121630 **Score:** 174 **Queries matched:** 7 **emPAI:** 0.11

Tax_Id=10090 Gene_Symbol=Acly Adult male testis cDNA, RIKEN full-length enriched library, clone:4922505F07 product:ATP citrate lyase, full insert sequence

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	474	366.7509	731.4872	731.4843	3.88	0	33	0.05	1	R.ELGLIR.K + Dimethyl:2H(4) (N-term)
☑	2637	760.3841	1518.7537	1518.7460	5.08	0	91	9.7e-008	1	R.SGGMSNELNNIISR.T + Dimethyl (N-term)
☑	2638	760.3842	1518.7538	1518.7460	5.10	0	(73)	6.3e-006	1	R.SGGMSNELNNIISR.T + Dimethyl (N-term)
☑	2800	800.4902	1598.9659	1598.9545	7.15	0	34	0.056	1	R.TIAIIAEGIPEALTR.K + Dimethyl:2H(4) (N-term)
☑	3463	470.2560	1876.9948	1876.9894	2.89	2	(34)	0.11	1	R.TASFSESRADEVAPAKK.A + 2 Dimethyl (K); Dimethyl (N-term)
☑	3523	473.2749	1889.0705	1889.0647	3.05	2	(37)	0.039	1	R.TASFSESRADEVAPAKK.A + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3524	473.2750	1889.0710	1889.0647	3.31	2	48	0.0037	1	R.TASFSESRADEVAPAKK.A + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

Proteins matching the same set of peptides:

IPI00762047 **Mass:** 120564 **Score:** 174 **Queries matched:** 7

Tax_Id=10090 Gene_Symbol=Acly ATP-citrate synthase

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47. IPI00830223 **Mass:** 28383 **Score:** 173 **Queries matched:** 8 **emPAI:** 0.84

Tax_Id=10090 Gene_Symbol=Tpm1 28 kDa protein

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	2179	687.8311	1373.6477	1373.6422	3.99	0	64	1.9e-005	1	R.SLQEQADAAEER.A + Dimethyl (N-term)
☑	2193	689.8439	1377.6733	1377.6674	4.32	0	(63)	4.3e-005	1	R.SLQEQADAAEER.A + Dimethyl:2H(4) (N-term)
☑	3173	585.9825	1754.9257	1754.9162	5.41	1	(38)	0.036	1	R.IQLVEEELDRAQER.L + Dimethyl (N-term)
☑	3186	587.3243	1758.9512	1758.9413	5.60	1	56	0.00069	1	R.IQLVEEELDRAQER.L + Dimethyl:2H(4) (N-term)
☑	3562	638.0165	1911.0277	1911.0173	5.44	2	31	0.21	1	R.RIQLVEEELDRAQER.L + Dimethyl (N-term)
☑	4117	565.3049	2257.1904	2257.1801	4.56	2	(34)	0.087	1	R.LATALQKLEEAEKAADESER.G + Dimethyl (K); Dimethyl (N-term)
☑	4125	567.3176	2265.2414	2265.2303	4.90	2	(32)	0.14	1	R.LATALQKLEEAEKAADESER.G + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	4126	567.3177	2265.2417	2265.2303	5.04	2	47	0.0048	1	R.LATALQKLEEAEKAADESER.G + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

Proteins matching the same set of peptides:
IPI00830333 **Mass:** 28959 **Score:** 173 **Queries matched:** 8
Tax_Id=10090 Gene_Symbol=Tpm1 29 kDa protein
IPI00831330 **Mass:** 28597 **Score:** 173 **Queries matched:** 8
Tax_Id=10090 Gene_Symbol=Tpm1 29 kDa protein
IPI00831423 **Mass:** 28651 **Score:** 173 **Queries matched:** 8
Tax_Id=10090 Gene_Symbol=Tpm1 29 kDa protein
IPI00831431 **Mass:** 28466 **Score:** 173 **Queries matched:** 8
Tax_Id=10090 Gene_Symbol=Tpm1 28 kDa protein
IPI00831626 **Mass:** 28679 **Score:** 173 **Queries matched:** 8
Tax_Id=10090 Gene_Symbol=Tpm1 29 kDa protein

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48. IPI00648086 **Mass:** 15200 **Score:** 172 **Queries matched:** 8 **emPAI:** 2.53
Tax_Id=10090 Gene_Symbol=Lasp1 LIM and SH3 protein 1

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	2412	723.8871	1445.7597	1445.7515	5.72	0	(58)	0.00034	1	K.GFSVVADTPELQR.I + Dimethyl (N-term)
☑	2430	725.9003	1449.7860	1449.7766	6.50	0	66	5.5e-005	1	K.GFSVVADTPELQR.I + Dimethyl:2H(4) (N-term)
☑	2528	495.9102	1484.7087	1484.7042	3.07	1	(39)	0.0087	1	R.MGPSGGEGVEPERR.E + Dimethyl (N-term)
☑	2540	497.2518	1488.7337	1488.7293	2.98	1	(32)	0.074	1	R.MGPSGGEGVEPERR.E + Dimethyl:2H(4) (N-term)
☑	2569	500.6250	1498.8531	1498.8467	4.25	1	52	0.0011	1	R.LKQQSELQSQVR.Y + Dimethyl (K); Dimethyl (N-term)
☑	2590	502.5834	1504.7283	1504.7242	2.72	1	48	0.0013	1	R.MGPSGGEGVEPERR.E + Dimethyl:2H(4) (N-term); Oxidation (M)
☑	2600	503.3082	1506.9028	1506.8969	3.86	1	(45)	0.0052	1	R.LKQQSELQSQVR.Y + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3914	527.0399	2104.1306	2104.1230	3.60	1	31	0.18	1	K.TQDQISNIKYHEEFEK.S + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

Proteins matching the same set of peptides:
IPI00649913 **Mass:** 21332 **Score:** 172 **Queries matched:** 8
Tax_Id=10090 Gene_Symbol=Lasp1 LIM and SH3 protein 1
IPI00125091 **Mass:** 30374 **Score:** 172 **Queries matched:** 8
Tax_Id=10090 Gene_Symbol=Lasp1 LIM and SH3 domain protein 1

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49. IPI00121209 **Mass:** 30569 **Score:** 168 **Queries matched:** 6 **emPAI:** 0.63
Tax_Id=10090 Gene_Symbol=Apoa1 Apolipoprotein A-I precursor

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	2116	449.5752	1345.7037	1345.6990	3.52	1	40	0.016	1	R.LSPVAEEFRDR.M + Dimethyl (N-term)
☑	2124	450.9172	1349.7297	1349.7241	4.16	1	(40)	0.024	1	R.LSPVAEEFRDR.M + Dimethyl:2H(4) (N-term)
☑	2138	453.8945	1358.6617	1358.6579	2.85	0	51	0.00075	1	K.SNPTLNEYHTR.A + Dimethyl (N-term)
☑	2146	455.2362	1362.6867	1362.6830	2.73	0	(47)	0.0023	1	K.SNPTLNEYHTR.A + Dimethyl:2H(4) (N-term)
☑	2153	684.8821	1367.7497	1367.7408	6.49	0	71	1.6e-005	1	K.VAPLGAELQESAR.Q + Dimethyl (N-term)
☑	2170	686.8951	1371.7756	1371.7660	7.03	0	(69)	2.6e-005	1	K.VAPLGAELQESAR.Q + Dimethyl:2H(4) (N-term)

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50. IPI00555059 **Mass:** 24969 **Score:** 168 **Queries matched:** 10 **emPAI:** 0.81
Tax_Id=10090 Gene_Symbol=Prdx6 Peroxiredoxin-6

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	823	467.7556	933.4967	933.4920	5.12	0	31	0.09	1	R.NFDEILR.V + Dimethyl (N-term)
☑	997	332.5553	994.6442	994.6415	2.67	1	29	0.14	1	K.LAPEFAKR.N + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1670	610.3591	1218.7037	1218.6972	5.35	0	(25)	0.6	1	K.LSILYPATTGR.N + Dimethyl (N-term)
☑	1696	612.3718	1222.7291	1222.7223	5.55	0	33	0.082	1	K.LSILYPATTGR.N + Dimethyl:2H(4) (N-term)
☑	1780	411.9267	1232.7582	1232.7533	3.97	1	(53)	0.00076	1	R.VVFIFGPDKK.L + 2 Dimethyl (K); Dimethyl (N-term)
☑	1832	415.9517	1244.8332	1244.8286	3.63	1	53	0.00021	1	R.VVFIFGPDKK.L + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	4097	746.7682	2237.2827	2237.2671	6.97	0	(47)	0.0027	1	R.VVDSLQLTGTKPVATPVDWK.K + 2 Dimethyl (K); Dimethyl (N-term)
☑	4098	746.7683	2237.2831	2237.2671	7.14	0	54	0.00055	1	R.VVDSLQLTGTKPVATPVDWK.K + 2 Dimethyl (K); Dimethyl (N-term)
☑	4109	750.7935	2249.3587	2249.3425	7.22	0	(43)	0.0024	1	R.VVDSLQLTGTKPVATPVDWK.K + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	4110	750.7936	2249.3589	2249.3425	7.30	0	(39)	0.0053	1	R.VVDSLQLTGTKPVATPVDWK.K + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

Proteins matching the same set of peptides:
IPI00754071 **Mass:** 22594 **Score:** 168 **Queries matched:** 10
Tax_Id=10090 Gene_Symbol=Prdx6 22 kDa protein
IPI00758024 **Mass:** 24925 **Score:** 168 **Queries matched:** 10
Tax_Id=10090 Gene_Symbol=Prdx6 Peroxiredoxin 6

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51. IPI00336324 **Mass:** 36659 **Score:** 167 **Queries matched:** 9 **emPAI:** 0.61
Tax_Id=10090 Gene_Symbol=Mdh1 Malate dehydrogenase, cytoplasmic
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	914	487.2834	972.5523	972.5492	3.21	0	48	0.0031	1	K.LGVTADDVK.N + Dimethyl (K); Dimethyl (N-term)
☑	943	491.3085	980.6025	980.5994	3.18	0	(46)	0.0038	1	K.LGVTADDVK.N + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	2315	711.3796	1420.7447	1420.7351	6.80	0	58	0.00034	1	K.FVEGLPINDFSR.E + Dimethyl (N-term)
☑	2332	713.3923	1424.7700	1424.7602	6.89	0	(57)	0.00041	1	K.FVEGLPINDFSR.E + Dimethyl:2H(4) (N-term)
☑	3514	943.9756	1885.9367	1885.9196	9.07	1	(42)	0.012	1	K.ELTEEKETAFEFLSSA.- + Dimethyl (K); Dimethyl (N-term)
☑	3536	948.0010	1893.9875	1893.9699	9.32	1	(35)	0.067	1	K.ELTEEKETAFEFLSSA.- + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3537	948.0012	1893.9879	1893.9699	9.51	1	42	0.013	1	K.ELTEEKETAFEFLSSA.- + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	4176	584.8030	2335.1827	2335.1709	5.06	0	40	0.022	1	K.NVIIWGNHSSTQYPDVNHAK.V + Dimethyl (K); Dimethyl (N-term)
☑	4177	584.8030	2335.1828	2335.1709	5.09	0	(37)	0.046	1	K.NVIIWGNHSSTQYPDVNHAK.V + Dimethyl (K); Dimethyl (N-term)

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52. IPI00323624 **Mass:** 187904 **Score:** 161 **Queries matched:** 6 **emPAI:** 0.09
Tax_Id=10090 Gene_Symbol=C3 Isoform Long of Complement C3 precursor (Fragment)
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	888	480.3149	958.6153	958.6113	4.11	0	35	0.033	1	R.QPLTITVR.T + Dimethyl:2H(4) (N-term)
☑	1086	515.2898	1028.5650	1028.5614	3.50	0	(36)	0.036	1	K.LSINTPNSR.Q + Dimethyl (N-term)
☑	1105	517.3023	1032.5901	1032.5865	3.40	0	48	0.0025	1	K.LSINTPNSR.Q + Dimethyl:2H(4) (N-term)
☑	1470	586.3583	1170.7021	1170.6972	4.19	0	(53)	0.001	1	K.VLVVTQGSNAK.A + Dimethyl (K); Dimethyl (N-term)
☑	1520	590.3837	1178.7529	1178.7475	4.62	0	71	7.9e-006	1	K.VLVVTQGSNAK.A + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

☑ 2511	737.9296	1473.8447	1473.8341	7.21	0	43	0.01	1	R.VVIEDGVGDAVLTR.K + Dimethyl:2H(4) (N-term)

Proteins matching the same set of peptides:
IPI00759878 **Mass:** 187905 **Score:** 161 **Queries matched:** 6
Tax_Id=10090 Gene_Symbol=C3 complement component 3

53. IPI00355382 **Mass:** 54063 **Score:** 161 **Queries matched:** 6 **emPAI:** 0.20
Tax_Id=10090 Gene_Symbol=Wars Isoform 2 of Tryptophanyl-tRNA synthetase, cytoplasmic
☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑ 822	467.7450	933.4754	933.4709	4.84	0	39	0.014	1	R.QLSFHFQ.- + Dimethyl (N-term)
☑ 833	469.7575	937.5005	937.4960	4.86	0	(28)	0.2	1	R.QLSFHFQ.- + Dimethyl:2H(4) (N-term)
☑ 3385	615.6958	1844.0656	1844.0520	7.38	0	(56)	0.00048	1	K.TLIDVLQPLIAEHQAR.R + Dimethyl (N-term)
☑ 3386	615.6958	1844.0657	1844.0520	7.47	0	(55)	0.00061	1	K.TLIDVLQPLIAEHQAR.R + Dimethyl (N-term)
☑ 3389	617.0375	1848.0907	1848.0771	7.39	0	63	7.1e-005	1	K.TLIDVLQPLIAEHQAR.R + Dimethyl:2H(4) (N-term)
☑ 3390	617.0375	1848.0908	1848.0771	7.42	0	(55)	0.00046	1	K.TLIDVLQPLIAEHQAR.R + Dimethyl:2H(4) (N-term)

54. IPI00318671 **Mass:** 61841 **Score:** 160 **Queries matched:** 5 **emPAI:** 0.23
Tax_Id=10090 Gene_Symbol=Ehd4 EH-domain containing 4-KJR (Fragment)
☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑ 2243	698.8561	1395.6977	1395.6857	8.65	0	47	0.0025	1	R.YLLEQDFPGMR.I + Dimethyl (N-term)
☑ 2254	700.8682	1399.7218	1399.7108	7.86	0	(44)	0.006	1	R.YLLEQDFPGMR.I + Dimethyl:2H(4) (N-term)
☑ 2562	748.8916	1495.7687	1495.7603	5.59	0	85	4.5e-007	1	R.SGGMDAVQTVTGGLR.S + Dimethyl:2H(4) (N-term); Oxidation (M)
☑ 3418	619.3577	1855.0514	1855.0414	5.34	1	(42)	0.013	1	K.SISIIDSPGILSGEKQR.I + Dimethyl (K); Dimethyl (N-term)
☑ 3430	622.0416	1863.1030	1863.0917	6.10	1	46	0.0035	1	K.SISIIDSPGILSGEKQR.I + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

55. IPI00380436 **Mass:** 103631 **Score:** 154 **Queries matched:** 6 **emPAI:** 0.16
Tax_Id=10090 Gene_Symbol=Actn1 Alpha-actinin-1
☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑ 1140	348.9126	1043.7159	1043.7132	2.54	0	33	0.031	1	K.SIVNYKPK.I + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑ 1464	391.2165	1170.6277	1170.6244	2.83	1	39	0.018	1	K.ATLPDADKER.L + Dimethyl (K); Dimethyl (N-term)
☑ 2135	453.2954	1356.8644	1356.8580	4.69	0	50	0.00075	1	R.LAILGIHNEVSK.I + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑ 2209	691.8253	1381.6361	1381.6296	4.70	0	53	0.00022	1	K.GISQEQMNEFR.A + Dimethyl (N-term); Oxidation (M)
☑ 2457	729.4056	1456.7967	1456.7885	5.63	0	(54)	0.00082	1	R.TINEVENQILTR.D + Dimethyl (N-term)
☑ 2465	731.4187	1460.8229	1460.8136	6.30	0	65	7.3e-005	1	R.TINEVENQILTR.D + Dimethyl:2H(4) (N-term)

56. IPI00136906 **Mass:** 39501 **Score:** 152 **Queries matched:** 4 **emPAI:** 0.29
Tax_Id=10090 Gene_Symbol=Capg Macrophage-capping protein
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	2024	660.8481	1319.6817	1319.6755	4.73	0	58	0.00022	1	K.VSDATGQMNLTK.V + Dimethyl (K); Dimethyl (N-term)
☑	2052	664.8730	1327.7315	1327.7257	4.38	0	(49)	0.0027	1	K.VSDATGQMNLTK.V + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	2264	702.3906	1402.7667	1402.7569	7.02	0	65	5.9e-005	1	R.QAALQVADGFISR.M + Dimethyl (N-term)
☑	2283	704.4031	1406.7917	1406.7820	6.93	0	(52)	0.0013	1	R.QAALQVADGFISR.M + Dimethyl:2H(4) (N-term)

Proteins matching the same set of peptides:

IPI00277930 **Mass:** 39030 **Score:** 152 **Queries matched:** 4
Tax_Id=10090 Gene_Symbol=Capg Capping protein
IPI00876389 **Mass:** 39158 **Score:** 152 **Queries matched:** 4
Tax_Id=10090 Gene_Symbol=Capg 10 days neonate olfactory brain cDNA, RIKEN full-length enriched library, clone:E530115O13 product:capping protein (actin filament),

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57. IPI00123223 **Mass:** 166618 **Score:** 150 **Queries matched:** 5 **emPAI:** 0.06
Tax_Id=10090 Gene_Symbol=Mug1 Murinoglobulin-1 precursor
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	438	352.7277	703.4408	703.4381	3.91	0	38	0.017	1	K.ALGFLR.A + Dimethyl (N-term)
☑	2379	719.3741	1436.7337	1436.7260	5.41	0	85	5.7e-007	1	R.FSTSQSLPASQTR.L + Dimethyl (N-term)
☑	2397	721.3866	1440.7586	1440.7511	5.26	0	(76)	4.6e-006	1	R.FSTSQSLPASQTR.L + Dimethyl:2H(4) (N-term)
☑	2868	544.6272	1630.8597	1630.8501	5.90	0	51	0.0015	1	R.AHFSVMGDILSSAIR.N + Dimethyl (N-term)
☑	2884	545.9685	1634.8837	1634.8752	5.20	0	(33)	0.11	1	R.AHFSVMGDILSSAIR.N + Dimethyl:2H(4) (N-term)

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58. IPI00319994 **Mass:** 36817 **Score:** 140 **Queries matched:** 6 **emPAI:** 0.50
Tax_Id=10090 Gene_Symbol=Ldha L-lactate dehydrogenase A chain
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1472	586.8141	1171.6137	1171.6084	4.51	0	44	0.0056	1	K.VTLTPEEEAR.L + Dimethyl (N-term)
☑	1488	587.8304	1173.6462	1173.6394	5.84	0	(66)	4.6e-005	1	K.SADTLWGIQK.E + Dimethyl (K); Dimethyl (N-term)
☑	1496	588.8265	1175.6385	1175.6336	4.22	0	(37)	0.033	1	K.VTLTPEEEAR.L + Dimethyl:2H(4) (N-term)
☑	1527	591.8557	1181.6968	1181.6896	6.06	0	67	3.3e-005	1	K.SADTLWGIQK.E + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1805	413.2544	1236.7414	1236.7376	3.09	1	(34)	0.074	1	R.RVHPISTMIK.G + Dimethyl (K); Dimethyl (N-term)
☑	1831	415.9377	1244.7912	1244.7879	2.70	1	36	0.029	1	R.RVHPISTMIK.G + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

Proteins matching the same set of peptides:

IPI00751369 **Mass:** 40075 **Score:** 140 **Queries matched:** 6
Tax_Id=10090 Gene_Symbol=Ldha L-lactate dehydrogenase

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59. IPI00118899 **Mass:** 105368 **Score:** 140 **Queries matched:** 3 **emPAI:** 0.08
Tax_Id=10090 Gene_Symbol=Actn4 Alpha-actinin-4
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide

☑	2215	692.8489	1383.6833	1383.6754	5.69	0	79	1.1e-006	1	K.GISQEQMQEFR.A + Dimethyl:2H(4) (N-term)
	2457	729.4056	1456.7967	1456.7885	5.63	0	(54)	0.00082	1	R.TINEVENQILTR.D + Dimethyl (N-term)
	2465	731.4187	1460.8229	1460.8136	6.30	0	65	7.3e-005	1	R.TINEVENQILTR.D + Dimethyl:2H(4) (N-term)

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60. IPI00123181 **Mass:** 227414 **Score:** 139 **Queries matched:** 6 **emPAI:** 0.06
Tax_Id=10090 Gene_Symbol=Myh9 Myosin-9

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	831	469.3140	936.6135	936.6095	4.26	0	59	0.00016	1	K.ASIAALEAK.I + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	2798	533.9695	1598.8867	1598.8781	5.42	0	43	0.012	1	K.VSHLLGINVTDFTR.G + Dimethyl (N-term)
☑	2805	535.3114	1602.9124	1602.9032	5.74	0	(39)	0.028	1	K.VSHLLGINVTDFTR.G + Dimethyl:2H(4) (N-term)
☑	3017	561.7184	1682.1335	1682.1248	5.18	1	57	1.7e-005	1	R.VISGVLQLGNIAFKK.E + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3233	597.6956	1790.0650	1790.0542	6.07	0	55	0.00039	1	R.QLLQANPILEAFGNAK.T + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3888	522.0145	2084.0290	2084.0208	3.95	1	25	0.43	1	K.TLEDEAKTHEAQIQEMR.Q + Dimethyl (K); Dimethyl (N-term)

Proteins matching the same set of peptides:
IPI00788324 **Mass:** 227429 **Score:** 139 **Queries matched:** 6
Tax_Id=10090 Gene_Symbol=Myh9 15 days pregnant adult female amnion cDNA, RIKEN full-length enriched library, clone:M421002E03 product:myosin heavy chain IX, full i

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61. IPI00223757 **Mass:** 36052 **Score:** 136 **Queries matched:** 3 **emPAI:** 0.15
Tax_Id=10090 Gene_Symbol=Akr1b3 Aldose reductase

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	836	469.7862	937.5578	937.5535	4.59	0	27	0.22	1	K.VAIDLGYR.H + Dimethyl:2H(4) (N-term)
☑	2821	808.4501	1614.8857	1614.8729	7.92	0	88	3.8e-007	1	K.TIGVSNFNPLQIER.I + Dimethyl (N-term)
☑	2830	810.4626	1618.9107	1618.8981	7.84	0	(76)	5.5e-006	1	K.TIGVSNFNPLQIER.I + Dimethyl:2H(4) (N-term)

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62. IPI00137331 **Mass:** 51885 **Score:** 136 **Queries matched:** 4 **emPAI:** 0.10
Tax_Id=10090 Gene_Symbol=Cap1 Adenylyl cyclase-associated protein 1

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	3434	467.0316	1864.0975	1864.0932	2.30	2	27	0.26	1	K.HVSDDMKTHKNPALK.A + 3 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)
☑	3644	662.0378	1983.0917	1983.0789	6.46	0	75	6.8e-006	1	R.SALFAQINQGESITHALK.H + Dimethyl (K); Dimethyl (N-term)
☑	3656	664.7208	1991.1406	1991.1291	5.79	0	(62)	0.00011	1	R.SALFAQINQGESITHALK.H + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3657	664.7212	1991.1417	1991.1291	6.34	0	(54)	0.00068	1	R.SALFAQINQGESITHALK.H + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

Proteins matching the same set of peptides:
IPI00869430 **Mass:** 51875 **Score:** 136 **Queries matched:** 4
Tax_Id=10090 Gene_Symbol=Cap1 Adenylyl cyclase-associated protein

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63. IPI00223216 **Mass:** 33673 **Score:** 134 **Queries matched:** 3 **emPAI:** 0.16
Tax_Id=10090 Gene_Symbol=Tst Thiosulfate sulfurtransferase

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	3901	699.0362	2094.0867	2094.0746	5.80	0	71	1.9e-005	1	R.YLGTQPEPDIVGLDSGHIR.G + Dimethyl (N-term)
☑	3906	700.3782	2098.1127	2098.0997	6.20	0	(62)	0.00017	1	R.YLGTQPEPDIVGLDSGHIR.G + Dimethyl:2H(4) (N-term)
☑	3907	700.3782	2098.1127	2098.0997	6.21	0	(66)	5.9e-005	1	R.YLGTQPEPDIVGLDSGHIR.G + Dimethyl:2H(4) (N-term)

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64. IPI00117167 **Mass:** 86287 **Score:** 122 **Queries matched:** 7 **emPAI:** 0.16
Tax_Id=10090 Gene_Symbol=Gsn Isoform 1 of Gelsolin precursor

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	630	407.2646	812.5147	812.5120	3.31	0	30	0.096	1	R.TPITVVR.Q + Dimethyl (N-term)
☑	633	409.2771	816.5397	816.5371	3.20	0	(28)	0.12	1	R.TPITVVR.Q + Dimethyl:2H(4) (N-term)
☑	2234	696.3848	1390.7550	1390.7456	6.74	0	73	1.1e-005	1	K.SGALNSNDAFVLK.T + Dimethyl (K); Dimethyl (N-term)
☑	2250	700.4101	1398.8056	1398.7958	7.00	0	(59)	0.00028	1	K.SGALNSNDAFVLK.T + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3511	629.3508	1885.0305	1885.0197	5.72	0	(30)	0.25	1	R.QTQVSVLPEGGETPLFK.Q + Dimethyl (K); Dimethyl (N-term)
☑	3512	629.3509	1885.0307	1885.0197	5.86	0	38	0.04	1	R.QTQVSVLPEGGETPLFK.Q + Dimethyl (K); Dimethyl (N-term)
☑	3534	632.0343	1893.0811	1893.0699	5.89	0	(35)	0.058	1	R.QTQVSVLPEGGETPLFK.Q + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

Proteins matching the same set of peptides:
IPI00759948 **Mass:** 80997 **Score:** 122 **Queries matched:** 7
Tax_Id=10090 Gene_Symbol=Gsn Isoform 2 of Gelsolin precursor

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65. IPI00113141 **Mass:** 51988 **Score:** 122 **Queries matched:** 4 **emPAI:** 0.16
Tax_Id=10090 Gene_Symbol=Cs Citrate synthase, mitochondrial precursor

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1337	560.2881	1118.5617	1118.5567	4.45	0	(34)	0.042	1	R.EGSSIGAIDSR.L + Dimethyl (N-term)
☑	1351	562.3006	1122.5866	1122.5819	4.26	0	52	0.00073	1	R.EGSSIGAIDSR.L + Dimethyl:2H(4) (N-term)
☑	3904	700.0475	2097.1206	2097.1044	7.72	1	(63)	0.00012	1	K.GLVYETSVLDPDEGIRFR.G + Dimethyl:2H(4) (N-term)
☑	3905	700.0475	2097.1207	2097.1044	7.77	1	67	4.5e-005	1	K.GLVYETSVLDPDEGIRFR.G + Dimethyl:2H(4) (N-term)

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66. IPI00466069 **Mass:** 96222 **Score:** 122 **Queries matched:** 8 **emPAI:** 0.20
Tax_Id=10090 Gene_Symbol=Eef2 Elongation factor 2

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	875	477.7652	953.5158	953.5120	3.96	0	33	0.053	1	K.SDPVVSYR.E + Dimethyl:2H(4) (N-term)
☑	1030	501.3076	1000.6006	1000.5967	3.82	0	42	0.013	1	R.GGGQIIPTAR.R + Dimethyl:2H(4) (N-term)
☑	1339	560.3146	1118.6147	1118.6084	5.64	0	(55)	0.00064	1	M.VNFTVDQIR.A + Dimethyl (N-term)
☑	1352	562.3271	1122.6396	1122.6335	5.43	0	58	0.00028	1	M.VNFTVDQIR.A + Dimethyl:2H(4) (N-term)
☑	2372	479.2907	1434.8503	1434.8446	3.99	1	(28)	0.27	1	R.VAVEAKNPADLPK.L + 2 Dimethyl (K); Dimethyl (N-term)
☑	2418	483.3158	1446.9257	1446.9199	3.96	1	36	0.02	1	R.VAVEAKNPADLPK.L + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

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  ☑ 3802  681.3707  2041.0904  2041.0795   5.34   0    29     0.27   1   R.GHVFEESQVAGTPMFVVK.A + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)
  ☑ 4013  550.5436  2198.1455  2198.1331   5.61   1    48   0.0035   1   K.ARPFPDGLAEDIDKGEVSAR.Q + Dimethyl (K); Dimethyl (N-term)

67.   IPI00128522    Mass: 23057    Score: 118    Queries matched: 2   emPAI: 0.24
      Tax_Id=10090 Gene_Symbol=Hspb1 Isoform A of Heat shock protein beta-1
    ☐ Check to include this hit in error tolerant search or archive report

     Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score   Expect Rank  Peptide
  ☑ 3062  566.9740  1697.9002  1697.8948   3.17   1    82  1.5e-006   1   R.AQIGGPEAGKSEQSGAK.- + 2 Dimethyl (K); Dimethyl (N-term)
  ☑ 3081  570.9990  1709.9752  1709.9701   2.99   1   (70) 2.2e-005   1   R.AQIGGPEAGKSEQSGAK.- + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)


      Proteins matching the same set of peptides:
      IPI00468068    Mass: 22004    Score: 118    Queries matched: 2
      Tax_Id=10090 Gene_Symbol=Hspb1 Isoform B of Heat shock protein beta-1
      IPI00623819    Mass: 19425    Score: 118    Queries matched: 2
      Tax_Id=10090 Gene_Symbol=Hspb1 Isoform C of Heat shock protein beta-1

68.   IPI00129526    Mass: 92703    Score: 116    Queries matched: 6   emPAI: 0.18
      Tax_Id=10090 Gene_Symbol=Hsp90b1 Endoplasmin precursor
    ☐ Check to include this hit in error tolerant search or archive report

     Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score  Expect Rank  Peptide
  ☑ 1124  519.7793  1037.5440  1037.5393   4.56   0   (29)    0.16   1   K.SGTSEFLNK.M + Dimethyl (K); Dimethyl (N-term)
  ☑ 1153  523.8042  1045.5938  1045.5895   4.12   0    42    0.011   1   K.SGTSEFLNK.M + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
  ☑ 1165  525.3004  1048.5863  1048.5804   5.56   0    44   0.0085   1   R.SGYLLPDTK.A + Dimethyl (K); Dimethyl (N-term)
  ☑ 1204  529.3252  1056.6358  1056.6307   4.88   0   (31)    0.13   1   R.SGYLLPDTK.A + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
    2061  666.3602  1330.7058  1330.6980   5.87   0    60  0.00016   1   R.ELISNASDALDK.I + Dimethyl (K); Dimethyl (N-term)
    2812  536.9876  1607.9410  1607.9334   4.75   1    43   0.0087   1   R.ELISNASDALDKIR.L + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

69.   IPI00269661    Mass: 39856    Score: 114    Queries matched: 2   emPAI: 0.06
      Tax_Id=10090 Gene_Symbol=Hnrpa3 Isoform 1 of Heterogeneous nuclear ribonucleoprotein A3
    ☐ Check to include this hit in error tolerant search or archive report

     Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score   Expect Rank  Peptide
  ☑ 3600  648.2895  1941.8466  1941.8391   3.86   0    69  2.8e-006   1   R.SSGSPYGGGYGSGGGSGGYGSR.R + Dimethyl:2H(4) (N-term)
  ☑ 3601  648.2895  1941.8467  1941.8391   3.90   0   (68) 3.9e-006   1   R.SSGSPYGGGYGSGGGSGGYGSR.R + Dimethyl:2H(4) (N-term)


      Proteins matching the same set of peptides:
      IPI00269662    Mass: 37291    Score: 114    Queries matched: 2
      Tax_Id=10090 Gene_Symbol=Hnrpa3 Isoform 2 of Heterogeneous nuclear ribonucleoprotein A3
      IPI00459722    Mass: 34683    Score: 114    Queries matched: 2
      Tax_Id=10090 Gene_Symbol=Hnrpa3 Hnrpa3 protein
      IPI00461800    Mass: 37447    Score: 114    Queries matched: 2
      Tax_Id=10090 Gene_Symbol=EG432946 similar to heterogeneous nuclear ribonucleoprotein A3, isoform 1
      IPI00466185    Mass: 33120    Score: 114    Queries matched: 2
```

Tax_Id=10090 Gene_Symbol=- 33 kDa protein
IPI00626666 **Mass:** 21719 **Score:** 114 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=- 22 kDa protein
IPI00659723 **Mass:** 37325 **Score:** 114 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=LOC630401 similar to heterogeneous nuclear ribonucleoprotein A3, isoform 5
IPI00663550 **Mass:** 32639 **Score:** 114 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=LOC630401 similar to heterogeneous nuclear ribonucleoprotein A3, isoform 1
IPI00664047 **Mass:** 32155 **Score:** 114 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=LOC633657 similar to heterogeneous nuclear ribonucleoprotein A3, isoform 5
IPI00667787 **Mass:** 36745 **Score:** 114 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=LOC545592 similar to heterogeneous nuclear ribonucleoprotein A3, isoform 16
IPI00670004 **Mass:** 36815 **Score:** 114 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=EG627828 similar to heterogeneous nuclear ribonucleoprotein A3, isoform 5
IPI00670681 **Mass:** 34383 **Score:** 114 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=EG432946 similar to heterogeneous nuclear ribonucleoprotein A3, isoform 7
IPI00674712 **Mass:** 32090 **Score:** 114 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=EG627828 similar to heterogeneous nuclear ribonucleoprotein A3, isoform 1
IPI00677689 **Mass:** 34489 **Score:** 114 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=LOC545592 similar to heterogeneous nuclear ribonucleoprotein A3, isoform 12
IPI00749630 **Mass:** 37345 **Score:** 114 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=EG668559 similar to heterogeneous nuclear ribonucleoprotein A3, isoform 4
IPI00750059 **Mass:** 35197 **Score:** 114 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=EG668559 similar to heterogeneous nuclear ribonucleoprotein A3, isoform 3
IPI00750428 **Mass:** 30660 **Score:** 114 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=LOC545592 similar to heterogeneous nuclear ribonucleoprotein A3, isoform 13
IPI00751584 **Mass:** 18456 **Score:** 114 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=Hnrpa3 Heterogeneous nuclear ribonucleoprotein A3
IPI00752179 **Mass:** 33165 **Score:** 114 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=EG668559 similar to heterogeneous nuclear ribonucleoprotein A3, isoform 1
IPI00757273 **Mass:** 33145 **Score:** 114 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=LOC630401 similar to heterogeneous nuclear ribonucleoprotein A3, isoform 6
IPI00849556 **Mass:** 33930 **Score:** 114 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=EG432946 similar to heterogeneous nuclear ribonucleoprotein A3
IPI00849731 **Mass:** 33408 **Score:** 114 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=LOC633657 similar to heterogeneous nuclear ribonucleoprotein A3

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70. IPI00467833 **Mass:** 27038 **Score:** 113 **Queries matched:** 2 **emPAI:** 0.20
Tax_Id=10090 Gene_Symbol=Tpi1 Triosephosphate isomerase

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	2647	508.2682	1521.7828	1521.7787	2.71	0	74	6.4e-006	1	K.TATPQQAQEVHEK.L + Dimethyl (K); Dimethyl (N-term)
☑	2660	510.9515	1529.8328	1529.8289	2.52	0	(69)	2.4e-005	1	K.TATPQQAQEVHEK.L + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

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71. IPI00462072 **Mass:** 47453 **Score:** 111 **Queries matched:** 8 **emPAI:** 0.37
Tax_Id=10090 Gene_Symbol=EG433182;Eno1;LOC100044223 Alpha-enolase

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	880	478.3150	954.6155	954.6113	4.37	0	28	0.22	1	K.TIAPALVSK.K + Dimethyl (K); Dimethyl (N-term)
☑	895	482.3402	962.6659	962.6616	4.52	0	(26)	0.13	1	K.TIAPALVSK.K + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	999	332.8872	995.6397	995.6367	2.97	1	26	0.33	1	R.SFRNPLAK.- + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1801	413.2357	1236.6854	1236.6826	2.26	0	(49)	0.0023	1	K.GVSQAVEHINK.T + Dimethyl (K); Dimethyl (N-term)
☑	1829	415.9194	1244.7365	1244.7328	2.91	0	61	0.00013	1	K.GVSQAVEHINK.T + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	4372	648.3453	2589.3520	2589.3398	4.71	2	36	0.061	1	R.AAVPSGASTGIYEALELRDNDKTR.F + Dimethyl (K); Dimethyl (N-term)
☑	4384	650.3584	2597.4045	2597.3900	5.56	2	(26)	0.48	1	R.AAVPSGASTGIYEALELRDNDKTR.F + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	4385	650.3585	2597.4047	2597.3900	5.66	2	(28)	0.3	1	R.AAVPSGASTGIYEALELRDNDKTR.F + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

Proteins matching the same set of peptides:
IPI00849751 **Mass:** 19464 **Score:** 111 **Queries matched:** 8
Tax_Id=10090 Gene_Symbol=LOC100047882 similar to enolase 1, alpha non-neuron

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72. IPI00115522 **Mass:** 61801 **Score:** 110 **Queries matched:** 7 **emPAI:** 0.28
Tax_Id=10090 Gene_Symbol=Fga fibrinogen, alpha polypeptide
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	989	496.3431	990.6716	990.6677	3.91	0	41	0.0047	1	K.QLQQVIAK.E + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	2381	719.4229	1436.8312	1436.8189	8.52	0	31	0.16	1	K.MSPVPDLVPGSFK.S + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	2446	727.4194	1452.8243	1452.8138	7.22	0	(27)	0.37	1	K.MSPVPDLVPGSFK.S + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)
☑	2658	510.5934	1528.7582	1528.7521	3.99	0	(54)	0.00041	1	R.EINLQDYEGHQK.Q + Dimethyl (K); Dimethyl (N-term)
☑	2683	513.2770	1536.8093	1536.8024	4.50	0	56	0.0005	1	R.EINLQDYEGHQK.Q + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3218	445.2084	1776.8045	1776.7999	2.62	1	39	0.0053	1	K.MADEAGSEAHREGETR.N + Dimethyl:2H(4) (N-term)
☑	4059	444.4196	2217.0619	2217.0571	2.12	2	26	0.25	1	K.TYKMADEAGSEAHREGETR.N + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)

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73. IPI00137409 **Mass:** 68272 **Score:** 109 **Queries matched:** 10 **emPAI:** 0.35
Tax_Id=10090 Gene_Symbol=Tkt Transketolase
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	632	408.2542	814.4939	814.4912	3.32	0	28	0.22	1	K.LILDSAR.A + Dimethyl (N-term)
☑	774	449.2811	896.5477	896.5443	3.77	0	54	0.00043	1	R.LAVSQVPR.S + Dimethyl (N-term)
☑	787	451.2935	900.5725	900.5695	3.36	0	(47)	0.0034	1	R.LAVSQVPR.S + Dimethyl:2H(4) (N-term)
☑	2025	440.9115	1319.7128	1319.7085	3.22	0	39	0.025	1	K.ISSDLDGHPVPK.Q + Dimethyl (K); Dimethyl (N-term)
☑	2516	492.9541	1475.8404	1475.8348	3.81	1	29	0.25	1	R.KISSDLDGHPVPK.Q + 2 Dimethyl (K); Dimethyl (N-term)
☑	2538	372.9859	1487.9146	1487.9101	3.03	1	(25)	0.37	1	R.KISSDLDGHPVPK.Q + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	2829	540.3158	1617.9256	1617.9164	5.67	1	42	0.012	1	K.MFGIDKDAIVQAVK.G + 2 Dimethyl (K); Dimethyl (N-term)
☑	2867	544.3411	1630.0014	1629.9917	5.91	1	(34)	0.039	1	K.MFGIDKDAIVQAVK.G + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	2882	545.6478	1633.9215	1633.9113	6.23	1	(37)	0.041	1	K.MFGIDKDAIVQAVK.G + 2 Dimethyl (K); Dimethyl (N-term); Oxidation (M)
☑	3817	683.3768	2047.1087	2047.0949	6.73	0	35	0.071	1	K.ILATPPQEDAPSVDIANIR.M + Dimethyl (N-term)

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74. IPI00468203 **Mass:** 38937 **Score:** 107 **Queries matched:** 4 **emPAI:** 0.21
Tax_Id=10090 Gene_Symbol=Anxa2 Annexin A2

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	619	405.2937	808.5729	808.5696	4.05	0	32	0.031	1	K.LMVALAK.G + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1327	372.2294	1113.6664	1113.6634	2.70	1	32	0.13	1	R.ELYDAGVKR.K + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1898	636.8333	1271.6520	1271.6469	3.94	0	69	1.5e-005	1	R.TNQELQEINR.V + Dimethyl (N-term)
☑	1907	638.8461	1275.6777	1275.6721	4.44	0	(68)	2.6e-005	1	R.TNQELQEINR.V + Dimethyl:2H(4) (N-term)

Proteins matching the same set of peptides:
IPI00605518 **Mass:** 32864 **Score:** 107 **Queries matched:** 4
Tax_Id=10090 Gene_Symbol=LOC100048867 similar to Annexin A2

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75. IPI00120030 **Mass:** 33673 **Score:** 104 **Queries matched:** 2 **emPAI:** 0.16
Tax_Id=10090 Gene_Symbol=Crym Mu-crystallin homolog

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	3079	570.9683	1709.8831	1709.8737	5.55	0	68	2.8e-005	1	R.APAFLSAEEVQDHLR.S + Dimethyl (N-term)
☑	3090	572.3100	1713.9082	1713.8988	5.48	0	(68)	3.3e-005	1	R.APAFLSAEEVQDHLR.S + Dimethyl:2H(4) (N-term)

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76. IPI00874728 **Mass:** 32995 **Score:** 103 **Queries matched:** 7 **emPAI:** 0.57
Tax_Id=10090 Gene_Symbol=Tpm2 Isoform 2 of Tropomyosin beta chain

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1465	391.2202	1170.6387	1170.6356	2.64	1	44	0.0058	1	R.ARQLEEELR.T + Dimethyl (N-term)
	3173	585.9825	1754.9257	1754.9162	5.41	1	(38)	0.036	1	R.IQLVEEELDRAQER.L + Dimethyl (N-term)
	3186	587.3243	1758.9512	1758.9413	5.60	1	56	0.00069	1	R.IQLVEEELDRAQER.L + Dimethyl:2H(4) (N-term)
	3562	638.0165	1911.0277	1911.0173	5.44	2	31	0.21	1	R.RIQLVEEELDRAQER.L + Dimethyl (N-term)
	4117	565.3049	2257.1904	2257.1801	4.56	2	(34)	0.087	1	R.LATALQKLEEAEKAADESER.G + Dimethyl (K); Dimethyl (N-term)
	4125	567.3176	2265.2414	2265.2303	4.90	2	(32)	0.14	1	R.LATALQKLEEAEKAADESER.G + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
	4126	567.3177	2265.2417	2265.2303	5.04	2	47	0.0048	1	R.LATALQKLEEAEKAADESER.G + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

Proteins matching the same set of peptides:
IPI00227918 **Mass:** 35175 **Score:** 103 **Queries matched:** 7
Tax_Id=10090 Gene_Symbol=Tpm2 Tpm2 protein

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77. IPI00114945 **Mass:** 41727 **Score:** 99 **Queries matched:** 3 **emPAI:** 0.13
Tax_Id=10090 Gene_Symbol=Sept2 Septin-2

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	3298	606.0162	1815.0267	1815.0142	6.90	0	(60)	0.0002	1	K.ASIPFSVVGSNQLIEAK.G + Dimethyl (K); Dimethyl (N-term)
☑	3299	606.0162	1815.0267	1815.0142	6.91	0	68	3.6e-005	1	K.ASIPFSVVGSNQLIEAK.G + Dimethyl (K); Dimethyl (N-term)
☑	3332	608.6996	1823.0771	1823.0644	6.96	0	(42)	0.008	1	K.ASIPFSVVGSNQLIEAK.G + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

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78.  IPI00377592    Mass: 145123    Score: 99      Queries matched: 3    emPAI: 0.05
     Tax_Id=10090 Gene_Symbol=Sec31a SEC31-like 1
   ☐ Check to include this hit in error tolerant search or archive report

     Query  Observed   Mr(expt)   Mr(calc)   ppm  Miss Score   Expect Rank  Peptide
   ☑  2545  373.4477  1489.7618  1489.7572  3.06    0    52  0.00094    1  K.GRPGPVAGHSQMPR.V + Dimethyl (N-term); Oxidation (M)
   ☑  2558  374.4540  1493.7867  1493.7823  2.94    0   (36)    0.041    1  K.GRPGPVAGHSQMPR.V + Dimethyl:2H(4) (N-term); Oxidation (M)
   ☑  4369  646.8604  2583.4125  2583.4046  3.08    1    70  1.9e-005    1  K.AQGKPVSGQESSQSPYERQPLSK.G + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)


     Proteins matching the same set of peptides:
     IPI00807797    Mass: 38332     Score: 99      Queries matched: 3
     Tax_Id=10090 Gene_Symbol=Sec31a Sec31a protein
     IPI00853859    Mass: 130509    Score: 99      Queries matched: 3
     Tax_Id=10090 Gene_Symbol=Sec31a Isoform 2 of Protein transport protein Sec31A
```

```
79.  IPI00123494    Mass: 100937    Score: 99      Queries matched: 2    emPAI: 0.05
     Tax_Id=10090 Gene_Symbol=Psmd2 26S proteasome non-ATPase regulatory subunit 2
   ☐ Check to include this hit in error tolerant search or archive report

     Query  Observed   Mr(expt)   Mr(calc)   ppm  Miss Score   Expect Rank  Peptide
   ☑  2679  512.9770  1535.9091  1535.9035  3.65    0    68  2.5e-005    1  R.VGQAVDVVGQAGKPK.T + 2 Dimethyl (K); Dimethyl (N-term)
   ☑  2708  517.0018  1547.9837  1547.9789  3.09    0   (61) 5.9e-005    1  R.VGQAVDVVGQAGKPK.T + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
```

```
80.  IPI00653931    Mass: 46488     Score: 99      Queries matched: 1    emPAI: 0.06
     Tax_Id=10090 Gene_Symbol=Fah Visual cortex cDNA, RIKEN full-length enriched library, clone:K430330E02 product:fumarylacetoacetate hydrolase, full insert sequence
   ☐ Check to include this hit in error tolerant search or archive report

     Query  Observed   Mr(expt)   Mr(calc)   ppm  Miss Score   Expect Rank  Peptide
   ☑  2218  693.8935  1385.7724  1385.7626  7.07    0    99  2.8e-008    1  R.ASLQNLLSASQAR.L + Dimethyl (N-term)


     Proteins matching the same set of peptides:
     IPI00856685    Mass: 15678     Score: 99      Queries matched: 1
     Tax_Id=10090 Gene_Symbol=Fah 16 kDa protein
     IPI00310035    Mass: 46416     Score: 99      Queries matched: 1
     Tax_Id=10090 Gene_Symbol=Fah Fumarylacetoacetase
```

```
81.  IPI00230212    Mass: 26067     Score: 97      Queries matched: 6    emPAI: 0.46
     Tax_Id=10090 Gene_Symbol=Gstm1 Glutathione S-transferase Mu 1
   ☐ Check to include this hit in error tolerant search or archive report

     Query  Observed   Mr(expt)   Mr(calc)   ppm  Miss Score Expect  Rank  Peptide
   ☑  1158  524.3284  1046.6423  1046.6386  3.56    0    32    0.11    1  K.ITQSNAILR.Y + Dimethyl:2H(4) (N-term)
   ☑  1264  548.3287  1094.6429  1094.6376  4.89    0   (28)   0.29    1  R.YIATPIFSK.M + Dimethyl (K); Dimethyl (N-term)
   ☑  1290  552.3539  1102.6932  1102.6878  4.92    0    33    0.11    1  R.YIATPIFSK.M + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
   ☑  2321  711.8669  1421.7192  1421.7122  4.91    0    63  7e-005    1  R.ADIVENQVMDTR.M + Dimethyl:2H(4) (N-term)
```

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  ☑ 3619  655.0475  1962.1207  1962.1066   7.19   0   (45) 0.0067    1   K.LGLDFPNLPYLIDGSHK.I + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
  ☑ 3620  655.0476  1962.1210  1962.1066   7.33   0    49  0.0024    1   K.LGLDFPNLPYLIDGSHK.I + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)


     Proteins matching the same set of peptides:
     IPI00649135    Mass: 28709    Score: 97     Queries matched: 6
     Tax_Id=10090 Gene_Symbol=Gstm1 Glutathione S-transferase, mu 1
________________________________________________________________________________________________________________________________
82.  IPI00459570    Mass: 28993    Score: 95     Queries matched: 7   emPAI: 0.67
     Tax_Id=10090 Gene_Symbol=Tpm3 2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:C920030J24 product:tropomyosin 3, gamma, full inse
  ☐ Check to include this hit in error tolerant search or archive report

    Query  Observed   Mr(expt)   Mr(calc)   ppm  Miss Score  Expect Rank  Peptide
  ☑ 2748  524.6113  1570.8120  1570.8063  3.63    1    27     0.34    1   R.AREQAEAEVASLNR.R + Dimethyl (N-term)
    3173  585.9825  1754.9257  1754.9162  5.41    1   (38)   0.036    1   R.IQLVEEELDRAQER.L + Dimethyl (N-term)
    3186  587.3243  1758.9512  1758.9413  5.60    1    56  0.00069    1   R.IQLVEEELDRAQER.L + Dimethyl:2H(4) (N-term)
    3562  638.0165  1911.0277  1911.0173  5.44    2    31     0.21    1   R.RIQLVEEELDRAQER.L + Dimethyl (N-term)
    4117  565.3049  2257.1904  2257.1801  4.56    2   (34)   0.087    1   R.LATALQKLEEAEKAADESER.G + Dimethyl (K); Dimethyl (N-term)
    4125  567.3176  2265.2414  2265.2303  4.90    2   (32)    0.14    1   R.LATALQKLEEAEKAADESER.G + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
    4126  567.3177  2265.2417  2265.2303  5.04    2    47   0.0048    1   R.LATALQKLEEAEKAADESER.G + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)


     Proteins matching the same set of peptides:
     IPI00230044    Mass: 29231    Score: 95     Queries matched: 7
     Tax_Id=10090 Gene_Symbol=Tpm3 Isoform 2 of Tropomyosin alpha-3 chain
________________________________________________________________________________________________________________________________
83.  IPI00129107    Mass: 36221    Score: 91     Queries matched: 2   emPAI: 0.15
     Tax_Id=10090 Gene_Symbol=Gipc1 PDZ domain-containing protein GIPC1
  ☐ Check to include this hit in error tolerant search or archive report

    Query  Observed   Mr(expt)   Mr(calc)   ppm  Miss Score  Expect Rank  Peptide
  ☑ 2471  488.5845  1462.7316  1462.7277  2.65    0    60  0.00013    1   R.SAGGHPGSGPQLGTGR.G + Dimethyl (N-term)
  ☑ 2477  489.9262  1466.7567  1466.7528  2.66    0   (57) 0.00029    1   R.SAGGHPGSGPQLGTGR.G + Dimethyl:2H(4) (N-term)

________________________________________________________________________________________________________________________________
84.  IPI00309768    Mass: 36208    Score: 89     Queries matched: 2   emPAI: 0.15
     Tax_Id=10090 Gene_Symbol=Pdlim1 PDZ and LIM domain protein 1
  ☐ Check to include this hit in error tolerant search or archive report

    Query  Observed   Mr(expt)   Mr(calc)   ppm  Miss Score   Expect Rank  Peptide
  ☑ 2420  724.8666  1447.7187  1447.7129  4.00    0    71  8.9e-006    1   R.SAMPFTASPAPSTR.V + Dimethyl (N-term)
  ☑ 3029  562.6599  1684.9577  1684.9512  3.88    1    44    0.0091    1   R.LVGGKDFEQPLAISR.V + Dimethyl (K); Dimethyl (N-term)

________________________________________________________________________________________________________________________________
85.  IPI00457659    Mass: 42719    Score: 88     Queries matched: 2   emPAI: 0.12
     Tax_Id=10090 Gene_Symbol=Serpinb1a Leukocyte elastase inhibitor A
  ☐ Check to include this hit in error tolerant search or archive report

    Query  Observed   Mr(expt)   Mr(calc)   ppm  Miss Score   Expect Rank  Peptide
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☑ 1827	622.8746	1243.7347	1243.7264	6.70	0	71	1.5e-005	1	R.LGVQDLFSSSK.A + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑ 2075	445.5872	1333.7399	1333.7354	3.42	1	49	0.0028	1	R.FQSLNAEVSKR.G + Dimethyl (K); Dimethyl (N-term)

Proteins matching the same set of peptides:
IPI00515459 **Mass:** 39195 **Score:** 88 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=Serpinb1a 39 kDa protein

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86. IPI00111265 **Mass:** 33118 **Score:** 88 **Queries matched:** 4 **emPAI:** 0.25
Tax_Id=10090 Gene_Symbol=Capza2 F-actin-capping protein subunit alpha-2
☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑ 1704	613.3706	1224.7267	1224.7190	6.32	0	47	0.0033	1	R.LLLNNDNLLR.E + Dimethyl (N-term)
☑ 1752	615.3832	1228.7518	1228.7441	6.27	0	(33)	0.064	1	R.LLLNNDNLLR.E + Dimethyl:2H(4) (N-term)
☑ 3933	711.7128	2132.1165	2132.0993	8.06	0	53	0.0011	1	K.FIIHAPPGEFNEVFNDVR.L + Dimethyl:2H(4) (N-term)
☑ 3934	711.7129	2132.1167	2132.0993	8.18	0	(43)	0.011	1	K.FIIHAPPGEFNEVFNDVR.L + Dimethyl:2H(4) (N-term)

Proteins matching the same set of peptides:
IPI00857651 **Mass:** 19660 **Score:** 88 **Queries matched:** 4
Tax_Id=10090 Gene_Symbol=Capza2 20 kDa protein

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87. IPI00133605 **Mass:** 62612 **Score:** 87 **Queries matched:** 2 **emPAI:** 0.08
Tax_Id=10090 Gene_Symbol=Pklr Pyruvate kinase isozymes R/L
☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑ 1570	599.3438	1196.6731	1196.6652	6.56	0	61	0.00015	1	R.GDLGIEIPAEK.V + Dimethyl (K); Dimethyl (N-term)
☑ 1602	603.3688	1204.7230	1204.7155	6.26	0	(55)	0.00059	1	R.GDLGIEIPAEK.V + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

Proteins matching the same set of peptides:
IPI00407130 **Mass:** 58378 **Score:** 87 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=Pkm2 Isoform M2 of Pyruvate kinase isozymes M1/M2
IPI00775829 **Mass:** 59126 **Score:** 87 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=Pklr pyruvate kinase liver and red blood cell isoform 2
IPI00845840 **Mass:** 58461 **Score:** 87 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=Pkm2 Isoform M1 of Pyruvate kinase isozymes M1/M2

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88. IPI00776343 **Mass:** 42969 **Score:** 86 **Queries matched:** 6 **emPAI:** 0.34
Tax_Id=10090 Gene_Symbol=Ager RAGE
☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑ 1803	413.2496	1236.7270	1236.7230	3.21	0	33	0.081	1	K.KPPQQLEWK.L + 2 Dimethyl (K); Dimethyl (N-term)
☑ 1837	417.2748	1248.8027	1248.7984	3.47	0	(32)	0.056	1	K.KPPQQLEWK.L + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑ 2470	488.3052	1461.8937	1461.8892	3.11	1	37	0.026	1	R.RRPLNTAPIQLR.V + Dimethyl (N-term)
☑ 2475	489.6470	1465.9193	1465.9143	3.40	1	(27)	0.18	1	R.RRPLNTAPIQLR.V + Dimethyl:2H(4) (N-term)

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  ☑ 2563  748.9008 1495.7871 1495.7783  5.85   0  (51)  0.0014   1   K.VLSPQGGPWDSVAR.I + Dimethyl (N-term)
  ☑ 2575  750.9150 1499.8154 1499.8035  7.97   0    58 0.00033   1   K.VLSPQGGPWDSVAR.I + Dimethyl:2H(4) (N-term)
```

```
89.    IPI00408119     Mass: 117927    Score: 85      Queries matched: 7    emPAI: 0.14
       Tax_Id=10090 Gene_Symbol=Mtap4 Isoform 1 of Microtubule-associated protein 4
     ☐ Check to include this hit in error tolerant search or archive report

     Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score Expect Rank  Peptide
     ☑ 1116  346.2198 1035.6374 1035.6350  2.32   0    47 0.0031   1   R.VKPMSAPSR.S + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
     ☑ 1469  586.3530 1170.6914 1170.6860  4.62   0  (42)   0.01   1   R.LATTVSAPDLK.S + Dimethyl (K); Dimethyl (N-term)
     ☑ 1519  590.3781 1178.7416 1178.7362  4.54   0    48 0.0016   1   R.LATTVSAPDLK.S + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
     ☑ 3219  445.2937 1777.1458 1777.1404  3.03   0    28  0.046   1   R.TSPSKPSSAPALKPGPK.T + 3 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
     ☑ 3572  482.2796 1925.0892 1925.0833  3.06   1  (32)   0.12   1   K.KTEAATTAGKPEPNAVTK.A + 3 Dimethyl (K); Dimethyl (N-term)
     ☑ 3598  486.3044 1941.1883 1941.1838  2.34   1  (28)  0.095   1   K.KTEAATTAGKPEPNAVTK.A + 3 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
     ☑ 3599  486.3045 1941.1887 1941.1838  2.55   1    33  0.032   1   K.KTEAATTAGKPEPNAVTK.A + 3 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)


       Proteins matching the same set of peptides:
       IPI00848818     Mass: 117940    Score: 85      Queries matched: 7
       Tax_Id=10090 Gene_Symbol=Mtap4 microtubule-associated protein 4
```

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90.    IPI00421206     Mass: 36155     Score: 85      Queries matched: 2    emPAI: 0.15
       Tax_Id=10090 Gene_Symbol=Kctd12 BTB/POZ domain-containing protein KCTD12
     ☐ Check to include this hit in error tolerant search or archive report

     Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score  Expect Rank  Peptide
     ☑ 3098  573.3112 1716.9117 1716.9060  3.34   0    61 0.00019   1   R.LGAPQQPGPGPPPPHSR.R + Dimethyl (N-term)
     ☑ 3105  574.6531 1720.9374 1720.9311  3.66   0  (56) 0.00055   1   R.LGAPQQPGPGPPPPHSR.R + Dimethyl:2H(4) (N-term)
```

```
91.    IPI00459725     Mass: 40069     Score: 84      Queries matched: 2    emPAI: 0.13
       Tax_Id=10090 Gene_Symbol=Idh3a Isoform 1 of Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial precursor
     ☐ Check to include this hit in error tolerant search or archive report

     Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score  Expect Rank  Peptide
     ☑ 1271  549.3213 1096.6281 1096.6241  3.73   0  (55) 0.00057   1   R.NVTAIQGPGGK.W + Dimethyl (K); Dimethyl (N-term)
     ☑ 1300  553.3464 1104.6782 1104.6743  3.54   0    57 0.00037   1   R.NVTAIQGPGGK.W + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
```

```
92.    IPI00467447     Mass: 189437    Score: 84      Queries matched: 6    emPAI: 0.07
       Tax_Id=10090 Gene_Symbol=Iqgap1 Ras GTPase-activating-like protein IQGAP1
     ☐ Check to include this hit in error tolerant search or archive report

     Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score   Expect Rank  Peptide
     ☑  716  430.3011  858.5877  858.5840  4.31   0    42   0.0056   1   R.LIVDVIR.F + Dimethyl:2H(4) (N-term)
     ☑  898  483.2787  964.5428  964.5382  4.80   0    32    0.085   1   K.LGNFFSPK.V + Dimethyl (K); Dimethyl (N-term)
     ☑  918  487.3038  972.5931  972.5884  4.82   0  (27)     0.32   1   K.LGNFFSPK.V + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
```

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   ☑ 1959  433.9186  1298.7340  1298.7306   2.60   1   (32)     0.12   1   K.QLQSDLQQKR.Q + Dimethyl (K); Dimethyl (N-term)
   ☑ 1990  436.6021  1306.7845  1306.7809   2.79   1    33     0.092   1   K.QLQSDLQQKR.Q + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
   ☑ 3568  641.6793  1922.0161  1922.0047   5.94   0    67  4.6e-005   1   R.FALGISAINEAVDSGDVGR.T + Dimethyl:2H(4) (N-term)

93.    IPI00187462     Mass: 38362     Score: 83     Queries matched: 4   emPAI: 0.22
       Tax_Id=10090 Gene_Symbol=Gimap4 GTPase, IMAP family member 4 isoform a
   ☐ Check to include this hit in error tolerant search or archive report

      Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score   Expect Rank  Peptide
   ☑ 3246  602.9778  1805.9117  1805.9020   5.38   0    41    0.014   1   R.SSHELGNQDQGIPQLR.I + Dimethyl (N-term)
   ☑ 3278  604.3193  1809.9362  1809.9271   5.00   0   (29)    0.25   1   R.SSHELGNQDQGIPQLR.I + Dimethyl:2H(4) (N-term)
   ☑ 3915  702.4355  2104.2846  2104.2710   6.45   0    48  0.00086   1   R.YVALTSPGPHALLLVVPLGR.Y + Dimethyl:2H(4) (N-term)
   ☑ 3916  702.4355  2104.2847  2104.2710   6.50   0   (43)  0.0024   1   R.YVALTSPGPHALLLVVPLGR.Y + Dimethyl:2H(4) (N-term)


       Proteins matching the same set of peptides:
       IPI00754464     Mass: 24767     Score: 83     Queries matched: 4
       Tax_Id=10090 Gene_Symbol=Gimap4 GTPase IMAP family member 4

94.    IPI00420806     Mass: 54469     Score: 83     Queries matched: 2   emPAI: 0.10
       Tax_Id=10090 Gene_Symbol=Dync1li2 Cytoplasmic dynein 1 light intermediate chain 2
   ☐ Check to include this hit in error tolerant search or archive report

      Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score    Expect Rank  Peptide
   ☑ 3069  567.6460  1699.9162  1699.9105   3.35   1   (47)    0.0046   1   K.KTGSPGSPSAGGVQSTAK.K + 2 Dimethyl (K); Dimethyl (N-term)
   ☑ 3086  571.6711  1711.9914  1711.9858   3.27   1    68  2.6e-005   1   K.KTGSPGSPSAGGVQSTAK.K + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

95.    IPI00118875     Mass: 73513     Score: 81     Queries matched: 3   emPAI: 0.11
       Tax_Id=10090 Gene_Symbol=Eef1d eukaryotic translation elongation factor 1 delta isoform a
   ☐ Check to include this hit in error tolerant search or archive report

      Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score   Expect Rank  Peptide
   ☑ 2452  485.9286  1454.7640  1454.7602   2.63   0   (40)    0.017   1   R.ATAPQTQHVSPMR.Q + Dimethyl:2H(4) (N-term)
   ☑ 2476  489.9185  1466.7337  1466.7300   2.54   0    52  0.00073   1   R.ATAPQTQHVSPMR.Q + Dimethyl (N-term); Oxidation (M)
   ☑ 2497  491.2603  1470.7591  1470.7551   2.72   0   (43)  0.0086   1   R.ATAPQTQHVSPMR.Q + Dimethyl:2H(4) (N-term); Oxidation (M)


       Proteins matching the same set of peptides:
       IPI00468771     Mass: 30730     Score: 81     Queries matched: 3
       Tax_Id=10090 Gene_Symbol=Eef1d Eef1d protein
       IPI00515654     Mass: 31387     Score: 81     Queries matched: 3
       Tax_Id=10090 Gene_Symbol=Eef1d eukaryotic translation elongation factor 1 delta isoform b
       IPI00620302     Mass: 28826     Score: 81     Queries matched: 3
       Tax_Id=10090 Gene_Symbol=Eef1d Isoform 2 of Elongation factor 1-delta
       IPI00831082     Mass: 23158     Score: 81     Queries matched: 3
       Tax_Id=10090 Gene_Symbol=Eef1d 23 kDa protein
       IPI00831202     Mass: 15722     Score: 81     Queries matched: 3
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Tax_Id=10090 Gene_Symbol=Eef1d 16 kDa protein
IPI00831299 **Mass:** 13160 **Score:** 81 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=Eef1d 13 kDa protein

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96. IPI00229510 **Mass:** 36834 **Score:** 81 **Queries matched:** 2 **emPAI:** 0.15
Tax_Id=10090 Gene_Symbol=Ldhb L-lactate dehydrogenase B chain
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1059	508.3129	1014.6112	1014.6073	3.80	0	(57)	0.00036	1	R.GLTSVINQK.L + Dimethyl (K); Dimethyl (N-term)
☑	1072	512.3378	1022.6610	1022.6576	3.35	0	58	0.00022	1	R.GLTSVINQK.L + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

Proteins matching the same set of peptides:
IPI00280156 **Mass:** 36959 **Score:** 81 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=EG433229 hypothetical protein isoform 7

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97. IPI00138342 **Mass:** 61418 **Score:** 74 **Queries matched:** 2 **emPAI:** 0.09
Tax_Id=10090 Gene_Symbol=Es1 Liver carboxylesterase N precursor
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	4668	939.2121	3752.8193	3752.7819	9.97	1	57	0.00031	1	R.NGNPNGEGLPHWPEYDEKEGYLQIGATTQQAQR.L + Dimethyl (K); Dimethyl (N-term)
☑	4672	941.2208	3760.8542	3760.8321	5.87	1	(50)	0.0017	1	R.NGNPNGEGLPHWPEYDEKEGYLQIGATTQQAQR.L + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

Proteins matching the same set of peptides:
IPI00831484 **Mass:** 62500 **Score:** 74 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=LOC382044 liver carboxylesterase N-like

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98. IPI00119111 **Mass:** 36577 **Score:** 74 **Queries matched:** 4 **emPAI:** 0.23
Tax_Id=10090 Gene_Symbol=Cnn3 Calponin-3
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1442	582.3228	1162.6310	1162.6234	6.52	0	40	0.018	1	K.GPSYGLSAEVK.N + Dimethyl (K); Dimethyl (N-term)
☑	1467	586.3474	1170.6803	1170.6736	5.70	0	(26)	0.48	1	K.GPSYGLSAEVK.N + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	2299	472.9185	1415.7337	1415.7303	2.41	1	(39)	0.02	1	K.GASQAGMLAPGTRR.D + Dimethyl (N-term); Oxidation (M)
☑	2310	474.2603	1419.7592	1419.7554	2.65	1	53	0.00097	1	K.GASQAGMLAPGTRR.D + Dimethyl:2H(4) (N-term); Oxidation (M)

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99. IPI00377351 **Mass:** 45001 **Score:** 74 **Queries matched:** 6 **emPAI:** 0.25
Tax_Id=10090 Gene_Symbol=Apoa4;ENSMUSG00000074373 Apolipoprotein A-IV precursor
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1435	580.3486	1158.6827	1158.6761	5.74	0	32	0.11	1	K.LQLTPYIQR.M + Dimethyl (N-term)
☑	1865	630.3636	1258.7127	1258.7034	7.46	0	60	0.00017	1	K.ALVQQLEQFR.Q + Dimethyl (N-term)
☑	2498	491.2687	1470.7844	1470.7790	3.65	1	(35)	0.066	1	K.ATIDQNLEDLRR.S + Dimethyl (N-term)

☑	2513	492.6105	1474.8097	1474.8041	3.76	1	39	0.029	1	K.ATIDQNLEDLRR.S + Dimethyl:2H(4) (N-term)
☑	2541	497.2655	1488.7746	1488.7685	4.11	1	29	0.21	1	R.QLEQQVEEFRR.T + Dimethyl (N-term)
☑	2553	498.6071	1492.7996	1492.7936	4.04	1	(28)	0.35	1	R.QLEQQVEEFRR.T + Dimethyl:2H(4) (N-term)

Proteins matching the same set of peptides:
IPI00775913 **Mass:** 45001 **Score:** 74 **Queries matched:** 6
Tax_Id=10090 Gene_Symbol=Apoa4;ENSMUSG00000074373 apolipoprotein A-IV

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100. IPI00336362 **Mass:** 55009 **Score:** 74 **Queries matched:** 3 **emPAI:** 0.15
Tax_Id=10090 Gene_Symbol=Aldh1a7 Aldehyde dehydrogenase, cytosolic 1
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1651	609.3281	1216.6417	1216.6353	5.29	0	38	0.028	1	R.QAFQIGSPWR.T + Dimethyl (N-term)
☑	1684	611.3406	1220.6667	1220.6604	5.18	0	(33)	0.089	1	R.QAFQIGSPWR.T + Dimethyl:2H(4) (N-term)
☑	3694	669.3423	2005.0050	2004.9917	6.62	0	53	0.00079	1	K.GFFVQPTVFSNVTDEMR.I + Dimethyl:2H(4) (N-term)

Proteins matching the same set of peptides:
IPI00626662 **Mass:** 55060 **Score:** 74 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=Aldh1a1 Retinal dehydrogenase 1

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101. IPI00317710 **Mass:** 95178 **Score:** 72 **Queries matched:** 1 **emPAI:** 0.03
Tax_Id=10090 Gene_Symbol=Hspa4l Isoform 1 of Heat shock 70 kDa protein 4L
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	2328	712.4122	1422.8098	1422.8020	5.46	0	72	1.3e-005	1	K.SIDLPIQSSLYR.Q + Dimethyl:2H(4) (N-term)

Proteins matching the same set of peptides:
IPI00317711 **Mass:** 92935 **Score:** 72 **Queries matched:** 1
Tax_Id=10090 Gene_Symbol=Hspa4l Isoform 2 of Heat shock 70 kDa protein 4L
IPI00856856 **Mass:** 13575 **Score:** 72 **Queries matched:** 1
Tax_Id=10090 Gene_Symbol=Hspa4l Protein

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102. IPI00116074 **Mass:** 86151 **Score:** 71 **Queries matched:** 6 **emPAI:** 0.13
Tax_Id=10090 Gene_Symbol=Aco2 Aconitate hydratase, mitochondrial precursor
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	508	380.7537	759.4929	759.4905	3.20	0	26	0.32	1	K.NINIVR.K + Dimethyl:2H(4) (N-term)
☑	1277	550.3081	1098.6017	1098.5971	4.19	0	27	0.25	1	K.NTIVTSYNR.N + Dimethyl:2H(4) (N-term)
☑	2560	748.4111	1494.8077	1494.7980	6.49	0	25	0.63	1	K.SQFTITPGSEQIR.A + Dimethyl:2H(4) (N-term)
☑	3545	634.3319	1899.9737	1899.9628	5.73	0	37	0.042	1	K.IVYGHLDDPANQEIER.G + Dimethyl:2H(4) (N-term)
☑	3822	683.7342	2048.1807	2048.1695	5.46	1	(31)	0.12	1	R.AKDINQEVYNFLATAGAK.Y + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3823	683.7343	2048.1809	2048.1695	5.56	1	57	0.00034	1	R.AKDINQEVYNFLATAGAK.Y + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

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103. IPI00114017 **Mass:** 50192 **Score:** 71 **Queries matched:** 2 **emPAI:** 0.11
Tax_Id=10090 Gene_Symbol=Anxa7 Annexin A7
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	2981	557.2635	1668.7687	1668.7638	2.95	0	(42)	0.0029	1	R.QSVNHQMAQEDAQR.L + Dimethyl (N-term)
☑	2985	558.6052	1672.7937	1672.7889	2.88	0	51	0.00057	1	R.QSVNHQMAQEDAQR.L + Dimethyl:2H(4) (N-term)

Proteins matching the same set of peptides:
IPI00461322 **Mass:** 44896 **Score:** 71 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=Anxa7 Adult male medulla oblongata cDNA, RIKEN full-length enriched library, clone:6330545A10 product:annexin A7, full insert sequence
IPI00653636 **Mass:** 52503 **Score:** 71 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=Anxa7 Adult male medulla oblongata cDNA, RIKEN full-length enriched library, clone:6330438J06 product:annexin A7, full insert sequence

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104. IPI00125143 **Mass:** 42270 **Score:** 70 **Queries matched:** 1 **emPAI:** 0.06
Tax_Id=10090 Gene_Symbol=Arpc1b Arpc1b protein
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	3040	564.9735	1691.8987	1691.8930	3.38	0	70	2e-005	1	K.ASSEGGAATGAGLDSLHK.N + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

Proteins matching the same set of peptides:
IPI00462975 **Mass:** 41757 **Score:** 70 **Queries matched:** 1
Tax_Id=10090 Gene_Symbol=EG434782 hypothetical protein
IPI00857408 **Mass:** 11306 **Score:** 70 **Queries matched:** 1
Tax_Id=10090 Gene_Symbol=Arpc1b Protein
IPI00874737 **Mass:** 41921 **Score:** 70 **Queries matched:** 1
Tax_Id=10090 Gene_Symbol=Arpc1b Actin-related protein 2/3 complex subunit 1B

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105. IPI00133903 **Mass:** 73768 **Score:** 70 **Queries matched:** 2 **emPAI:** 0.07
Tax_Id=10090 Gene_Symbol=Hspa9 Stress-70 protein, mitochondrial precursor
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	3225	594.3187	1779.9342	1779.9268	4.16	1	(48)	0.0041	1	R.QAVTNPNNTFYATKR.L + Dimethyl (K); Dimethyl (N-term)
☑	3231	597.0021	1787.9846	1787.9770	4.25	1	53	0.0013	1	R.QAVTNPNNTFYATKR.L + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

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106. IPI00230682 **Mass:** 28183 **Score:** 68 **Queries matched:** 3 **emPAI:** 0.30
Tax_Id=10090 Gene_Symbol=Ywhab Isoform Long of 14-3-3 protein beta/alpha
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	910	486.3246	970.6347	970.6303	4.62	0	32	0.063	1	R.NLLSVAYK.N + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	2853	542.9305	1625.7697	1625.7645	3.22	0	(47)	0.0016	1	K.AVTEQGHELSNEER.N + Dimethyl (N-term)
☑	2862	544.2721	1629.7945	1629.7896	2.97	0	53	0.00056	1	K.AVTEQGHELSNEER.N + Dimethyl:2H(4) (N-term)

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         Proteins matching the same set of peptides:
         IPI00750790     Mass: 18394     Score: 68      Queries matched: 3
         Tax_Id=10090 Gene_Symbol=Ywhab Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta
         IPI00760000     Mass: 27951     Score: 68      Queries matched: 3
         Tax_Id=10090 Gene_Symbol=Ywhab Isoform Short of 14-3-3 protein beta/alpha
```

```
107.     IPI00115528     Mass: 71210     Score: 68      Queries matched: 2    emPAI: 0.07
         Tax_Id=10090 Gene_Symbol=Pls3 Plastin 3
       ☐ Check to include this hit in error tolerant search or archive report

        Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score Expect Rank  Peptide
      ☑  2659  765.9017  1529.7889  1529.7759   8.49    0   (42)   0.01    1  K.MINLSVPDTIDER.A + Dimethyl (N-term)
      ☑  2676  767.9132  1533.8119  1533.8010   7.06    0    52  0.0013    1  K.MINLSVPDTIDER.A + Dimethyl:2H(4) (N-term)


         Proteins matching the same set of peptides:
         IPI00118892     Mass: 70732     Score: 68      Queries matched: 2
         Tax_Id=10090 Gene_Symbol=Lcp1 Plastin-2
         IPI00776023     Mass: 72214     Score: 68      Queries matched: 2
         Tax_Id=10090 Gene_Symbol=Pls3 Plastin 3
         IPI00874762     Mass: 71732     Score: 68      Queries matched: 2
         Tax_Id=10090 Gene_Symbol=Pls3 13 days embryo liver cDNA, RIKEN full-length enriched library, clone:I920006B08 product:plastin 3 (T-isoform), full insert sequence
```

```
108.     IPI00124264     Score: 66      Queries matched: 1
         Tax_Id=10090 Gene_Symbol=Anxa11 Annexin A11
       ☐ Check to include this hit in error tolerant search or archive report

        Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score    Expect Rank  Peptide
         1299  553.3267  1104.6388  1104.6328   5.37    0    66  5.7e-005    1  R.SELDLLDIR.A + Dimethyl:2H(4) (N-term)


         Proteins matching the same set of peptides:
         IPI00848382     Score: 66      Queries matched: 1
         IPI00849293     Score: 66      Queries matched: 1
```

```
109.     IPI00226430     Mass: 42288     Score: 64      Queries matched: 4    emPAI: 0.19
         Tax_Id=10090 Gene_Symbol=Acaa2 3-ketoacyl-CoA thiolase, mitochondrial
       ☐ Check to include this hit in error tolerant search or archive report

        Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score Expect Rank  Peptide
      ☑   739  434.8108   867.6070   867.6033   4.17    0    43  0.0026    1  R.GVFIVAAK.R + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
      ☑  4278  610.0705  2436.2527  2436.2431   3.95    0   (30)   0.23    1  K.QTMQVDEHARPQTTLEQLQK.L + Dimethyl (K); Dimethyl (N-term)
      ☑  4279  610.0709  2436.2546  2436.2431   4.72    0    38   0.038    1  K.QTMQVDEHARPQTTLEQLQK.L + Dimethyl (K); Dimethyl (N-term)
      ☑  4499  676.6194  2702.4484  2702.4351   4.92    1    28    0.36    1  K.ALDLDPSKTNVSGGAIALGHPLGGSGSR.I + Dimethyl (K); Dimethyl (N-term)


         Proteins matching the same set of peptides:
         IPI00653158     Mass: 42260     Score: 64      Queries matched: 4
```

```
      Tax_Id=10090 Gene_Symbol=Acaa2 14 days embryo liver cDNA, RIKEN full-length enriched library, clone:I530029G20 product:acetyl-Coenzyme A acyltransferase 2
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110.  IPI00313222     Mass: 33546     Score: 64      Queries matched: 2    emPAI: 0.16
      Tax_Id=10090 Gene_Symbol=Rpl6 60S ribosomal protein L6
    ☐ Check to include this hit in error tolerant search or archive report

      Query  Observed    Mr(expt)    Mr(calc)    ppm  Miss Score Expect Rank  Peptide
    ☑  1475  586.8456  1171.6767  1171.6713   4.62    0   (39)  0.023    1   K.AVPQLQGYLR.S + Dimethyl (N-term)
    ☑  1499  588.8591  1175.7036  1175.6964   6.07    0    50  0.0019    1   K.AVPQLQGYLR.S + Dimethyl:2H(4) (N-term)


      Proteins matching the same set of peptides:
      IPI00378933     Mass: 13643     Score: 64      Queries matched: 2
      Tax_Id=10090 Gene_Symbol=EG383462 similar to ribosomal protein L6
      IPI00457852     Mass: 34930     Score: 64      Queries matched: 2
      Tax_Id=10090 Gene_Symbol=EG432502 similar to ribosomal protein L6
      IPI00626312     Mass: 33518     Score: 64      Queries matched: 2
      Tax_Id=10090 Gene_Symbol=EG620213 similar to ribosomal protein L6
      IPI00750333     Mass: 33429     Score: 64      Queries matched: 2
      Tax_Id=10090 Gene_Symbol=EG627889 similar to ribosomal protein L6 isoform 1
      IPI00848644     Mass: 32313     Score: 64      Queries matched: 2
      Tax_Id=10090 Gene_Symbol=EG627889 similar to ribosomal protein L6 isoform 2
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111.  IPI00228253     Mass: 41727     Score: 64      Queries matched: 2    emPAI: 0.06
      Tax_Id=10090 Gene_Symbol=Acat2 Acetyl-CoA acetyltransferase, cytosolic
    ☐ Check to include this hit in error tolerant search or archive report

      Query  Observed    Mr(expt)    Mr(calc)    ppm  Miss Score   Expect Rank  Peptide
    ☑  2644  507.9676  1520.8811  1520.8762   3.23    1    64  8.1e-005    1   R.EAQDKVAVLSQNR.A + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
    ☑  4060  444.4610  2217.2686  2217.2619   3.04    2    32     0.094    1   R.EAQDKVAVLSQNRAEHAQK.A + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)


      Proteins matching the same set of peptides:
      IPI00330685     Mass: 41895     Score: 64      Queries matched: 2
      Tax_Id=10090 Gene_Symbol=Acat3 Acetyl CoA transferase-like protein
      IPI00776358     Mass: 41900     Score: 64      Queries matched: 2
      Tax_Id=10090 Gene_Symbol=Acat3 acetyl-Coenzyme A acetyltransferase 3
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112.  IPI00283862     Mass: 29813     Score: 63      Queries matched: 2    emPAI: 0.18
      Tax_Id=10090 Gene_Symbol=Psma1 Proteasome subunit alpha type-1
    ☐ Check to include this hit in error tolerant search or archive report

      Query  Observed    Mr(expt)    Mr(calc)    ppm  Miss Score  Expect Rank  Peptide
    ☑  4232  599.0397  2392.1296  2392.1216   3.34    2   (42)  0.0061    1   R.KAQPSQAAAEEPAEKADEPMEH.- + 2 Dimethyl (K); Dimethyl (N-term); Oxidation (M)
    ☑  4242  602.0583  2404.2040  2404.1969   2.96    2    54  0.00071    1   R.KAQPSQAAAEEPAEKADEPMEH.- + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term); Oxidation (M)

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113.  IPI00310240     Mass: 75697     Score: 63      Queries matched: 1    emPAI: 0.03
      Tax_Id=10090 Gene_Symbol=Anxa6 13 days embryo forelimb cDNA, RIKEN full-length enriched library, clone:5930413M14 product:annexin A6, full insert sequence
```

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	3149	581.6619	1741.9638	1741.9512	7.19	0	63	0.00012	1	K.GIGTDEATIIDIVTHR.S + Dimethyl:2H(4) (N-term)

Proteins matching the same set of peptides:
IPI00554894 **Mass:** 76295 **Score:** 63 **Queries matched:** 1
Tax_Id=10090 Gene_Symbol=Anxa6 Annexin A6
IPI00649152 **Mass:** 76294 **Score:** 63 **Queries matched:** 1
Tax_Id=10090 Gene_Symbol=Anxa6 Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:G530123A09 product:annexin A6, full insert sequence
IPI00875218 **Mass:** 76208 **Score:** 63 **Queries matched:** 1
Tax_Id=10090 Gene_Symbol=Anxa6 76 kDa protein

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114. IPI00116645 **Mass:** 33506 **Score:** 62 **Queries matched:** 2 **emPAI:** 0.16
Tax_Id=10090 Gene_Symbol=Cnn1 Isoform Alpha of Calponin-1

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1826	622.8587	1243.7029	1243.6958	5.66	0	(42)	0.013	1	R.NIIGLQMGTNK.F + Dimethyl (K); Dimethyl (N-term)
☑	1848	626.8844	1251.7542	1251.7460	6.55	0	44	0.0072	1	R.NIIGLQMGTNK.F + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

Proteins matching the same set of peptides:
IPI00228258 **Mass:** 29250 **Score:** 62 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=Cnn1 Isoform Beta of Calponin-1

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115. IPI00221817 **Mass:** 87829 **Score:** 62 **Queries matched:** 2 **emPAI:** 0.06
Tax_Id=10090 Gene_Symbol=Loh11cr2a Loss of heterozygosity 11 chromosomal region 2 gene A protein homolog

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1572	599.3749	1196.7353	1196.7281	6.04	0	54	0.00058	1	R.YLLPAILNPR.Y + Dimethyl (N-term)
☑	1586	601.3872	1200.7599	1200.7532	5.55	0	(32)	0.062	1	R.YLLPAILNPR.Y + Dimethyl:2H(4) (N-term)

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116. IPI00312058 **Mass:** 60013 **Score:** 61 **Queries matched:** 3 **emPAI:** 0.13
Tax_Id=10090 Gene_Symbol=Cat Catalase

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	3015	561.2923	1680.8551	1680.8481	4.12	1	42	0.011	1	K.RFNSANEDNVTQVR.T + Dimethyl:2H(4) (N-term)
☑	4548	721.3897	2881.5297	2881.5080	7.55	1	47	0.0039	1	R.ASQRPDVLTTGGGNPIGDKLNIMTAGSR.G + Dimethyl (K); Dimethyl (N-term)
☑	4550	723.4017	2889.5778	2889.5582	6.79	1	(26)	0.37	1	R.ASQRPDVLTTGGGNPIGDKLNIMTAGSR.G + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

Proteins matching the same set of peptides:
IPI00869393 **Mass:** 60043 **Score:** 61 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=Cat catalase

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117. IPI00114894 **Mass:** 227743 **Score:** 60 **Queries matched:** 2 **emPAI:** 0.02
Tax_Id=10090 Gene_Symbol=Myh11 Isoform 1 of Myosin-11
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	874	477.3112	952.6078	952.6044	3.48	0	32	0.081	1	K.STVAALEAK.I + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
	3233	597.6956	1790.0650	1790.0542	6.07	0	55	0.00039	1	K.QLLQANPILEAFGNAK.T + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

Proteins matching the same set of peptides:
IPI00227865 **Mass:** 223983 **Score:** 60 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=Myh11 Isoform 2 of Myosin-11
IPI00876408 **Mass:** 227864 **Score:** 60 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=Myh11 Myh11 protein

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118. IPI00124287 **Mass:** 70826 **Score:** 59 **Queries matched:** 1 **emPAI:** 0.04
Tax_Id=10090 Gene_Symbol=Pabpc1 Polyadenylate-binding protein 1
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	2314	474.5816	1420.7230	1420.7183	3.29	0	59	0.00021	1	R.QAHLTNQYMQR.M + Dimethyl:2H(4) (N-term)

Proteins matching the same set of peptides:
IPI00331552 **Mass:** 70854 **Score:** 59 **Queries matched:** 1
Tax_Id=10090 Gene_Symbol=Pabpc1 Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:I830046M23 product:poly A binding protein, cytoplasmic 1, fu

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119. IPI00119667 **Mass:** 50764 **Score:** 58 **Queries matched:** 7 **emPAI:** 0.16
Tax_Id=10090 Gene_Symbol=Eef1a2 Elongation factor 1-alpha 2
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	906	485.8203	969.6261	969.6223	3.92	0	(31)	0.091	1	R.QTVAVGVIK.N + Dimethyl (K); Dimethyl (N-term)
☑	907	485.8205	969.6265	969.6223	4.37	0	(27)	0.25	1	R.QTVAVGVIK.N + Dimethyl (K); Dimethyl (N-term)
☑	930	489.8456	977.6766	977.6725	4.20	0	35	0.025	1	R.QTVAVGVIK.N + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	931	489.8456	977.6766	977.6725	4.20	0	(28)	0.13	1	R.QTVAVGVIK.N + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	1183	527.3262	1052.6379	1052.6342	3.48	0	(32)	0.1	1	K.IGGIGTVPVGR.V + Dimethyl (N-term)
☑	1184	527.3266	1052.6387	1052.6342	4.25	0	38	0.02	1	K.IGGIGTVPVGR.V + Dimethyl (N-term)
☑	1206	529.3393	1056.6640	1056.6594	4.42	0	(33)	0.083	1	K.IGGIGTVPVGR.V + Dimethyl:2H(4) (N-term)

Proteins matching the same set of peptides:
IPI00307837 **Mass:** 50424 **Score:** 58 **Queries matched:** 7
Tax_Id=10090 Gene_Symbol=Eef1a1 Elongation factor 1-alpha 1

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120. IPI00420882 **Mass:** 118937 **Score:** 57 **Queries matched:** 3 **emPAI:** 0.07
Tax_Id=10090 Gene_Symbol=Ogdh Isoform 4 of 2-oxoglutarate dehydrogenase E1 component, mitochondrial precursor
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1342	560.7875	1119.5605	1119.5560	4.01	0	39	0.012	1	R.SSPYPTDVAR.V + Dimethyl (N-term)
☑	1353	562.8001	1123.5857	1123.5811	4.07	0	(38)	0.017	1	R.SSPYPTDVAR.V + Dimethyl:2H(4) (N-term)
☑	3087	571.9473	1712.8202	1712.8130	4.16	0	29	0.11	1	R.TSFDEMLPGTHFQR.V + Dimethyl:2H(4) (N-term); Oxidation (M)

Proteins matching the same set of peptides:
IPI00626237 **Mass:** 117572 **Score:** 57 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=Ogdh Isoform 1 of 2-oxoglutarate dehydrogenase E1 component, mitochondrial precursor
IPI00719841 **Mass:** 117208 **Score:** 57 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=Ogdh Isoform 2 of 2-oxoglutarate dehydrogenase E1 component, mitochondrial precursor
IPI00845652 **Mass:** 119301 **Score:** 57 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=Ogdh Isoform 3 of 2-oxoglutarate dehydrogenase E1 component, mitochondrial precursor

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121. IPI00129225 **Mass:** 48951 **Score:** 57 **Queries matched:** 3 **emPAI:** 0.11
Tax_Id=10090 Gene_Symbol=Kng1 Isoform LMW of Kininogen-1 precursor
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	3589	647.0034	1937.9882	1937.9806	3.93	2	47	0.004	1	K.AGAEPAPERQAESSQVKQ.- + Dimethyl (K); Dimethyl (N-term)
☑	3604	649.6862	1946.0367	1946.0309	3.02	2	(32)	0.13	1	K.AGAEPAPERQAESSQVKQ.- + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑	3605	649.6863	1946.0372	1946.0309	3.26	2	(35)	0.073	1	K.AGAEPAPERQAESSQVKQ.- + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

Proteins matching the same set of peptides:
IPI00857103 **Mass:** 48940 **Score:** 57 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=Kng2 kininogen 2 isoform 2

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122. IPI00119114 **Mass:** 48277 **Score:** 57 **Queries matched:** 2 **emPAI:** 0.11
Tax_Id=10090 Gene_Symbol=Acadl Long-chain specific acyl-CoA dehydrogenase, mitochondrial precursor
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1635	606.3754	1210.7363	1210.7285	6.46	0	(36)	0.044	1	K.QGLLGINIAEK.H + Dimethyl (K); Dimethyl (N-term)
☑	1672	610.4009	1218.7872	1218.7787	6.96	0	47	0.0015	1	K.QGLLGINIAEK.H + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

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123. IPI00115833 **Mass:** 96676 **Score:** 57 **Queries matched:** 2 **emPAI:** 0.03
Tax_Id=10090 Gene_Symbol=Mtap6 microtubule-associated protein 6 isoform 1
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	3980	543.0380	2168.1227	2168.1073	7.10	1	27	0.42	1	K.NQGLAGPELVKDTGTDTTAPR.Y + Dimethyl (K)
☑	4330	495.0500	2470.2135	2470.2061	3.00	2	57	0.00032	1	R.RSEGHEQTPAAHAQGTGPEGGKGR.A + Dimethyl (K); Dimethyl (N-term)

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124. IPI00622946 **Mass:** 109360 **Score:** 57 **Queries matched:** 3 **emPAI:** 0.02
Tax_Id=10090 Gene_Symbol=Palld Isoform 4 of Palladin

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑ 2123	675.3737	1348.7328	1348.7238	6.65	0	26	0.44	1	R.YAALSDQGLDIK.A + Dimethyl (K); Dimethyl (N-term)
☑ 4147	765.4199	2293.2377	2293.2253	5.43	1	(38)	0.034	1	R.IASDEEIQGTKDAVIQDLER.K + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑ 4148	765.4199	2293.2379	2293.2253	5.52	1	50	0.0025	1	R.IASDEEIQGTKDAVIQDLER.K + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

Proteins matching the same set of peptides:
IPI00756702 **Mass:** 73567 **Score:** 57 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=Palld Isoform 5 of Palladin
IPI00856302 **Mass:** 151999 **Score:** 57 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=Palld Isoform 6 of Palladin
IPI00856926 **Mass:** 72950 **Score:** 57 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=Palld Isoform 3 of Palladin
IPI00858000 **Mass:** 153576 **Score:** 57 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=Palld Isoform 1 of Palladin

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125. IPI00271262 **Mass:** 163691 **Score:** 55 **Queries matched:** 2 **emPAI:** 0.03
Tax_Id=10090 Gene_Symbol=Mug2 Murinoglobulin-2 precursor
☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
438	352.7277	703.4408	703.4381	3.91	0	38	0.017	1	K.ALGFLR.A + Dimethyl (N-term)
2868	544.6272	1630.8597	1630.8752	-9.52	0	51	0.0015	1	R.AHFSVMGDILSSAIK.N + Dimethyl (K); Dimethyl (N-term)

Proteins matching the same set of peptides:
IPI00420891 **Mass:** 163807 **Score:** 55 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=Mug4 Murinoglubulin-4 precursor

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126. IPI00124692 **Mass:** 37534 **Score:** 54 **Queries matched:** 5 **emPAI:** 0.39
Tax_Id=10090 Gene_Symbol=Taldo1 Transaldolase
☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑ 704	427.7906	853.5666	853.5637	3.47	0	34	0.038	1	K.LAPALSVK.A + Dimethyl (K); Dimethyl (N-term)
☑ 731	431.8156	861.6166	861.6139	3.09	0	(32)	0.023	1	K.LAPALSVK.A + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑ 2011	656.8497	1311.6849	1311.6798	3.89	0	27	0.27	1	K.SYEPQEDPGVK.S + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑ 2113	449.2796	1344.8170	1344.8129	3.05	2	40	0.016	1	R.KFAADAIKLER.M + 2 Dimethyl (K); Dimethyl (N-term)
☑ 2136	453.3047	1356.8923	1356.8882	3.03	2	(29)	0.064	1	R.KFAADAIKLER.M + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

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127. IPI00117730 **Mass:** 71270 **Score:** 54 **Queries matched:** 1 **emPAI:** 0.04
Tax_Id=10090 Gene_Symbol=Gbp3 Guanylate-binding protein 4
☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑ 2382	480.2291	1437.6655	1437.6608	3.27	0	54	0.00019	1	K.AADHYSEQMAQR.M + Dimethyl:2H(4) (N-term)

```
      Proteins matching the same set of peptides:
      IPI00225190    Mass: 72046    Score: 54     Queries matched: 1
      Tax_Id=10090 Gene_Symbol=BC057170 CDNA sequence BC057170
      IPI00454028    Mass: 73188    Score: 54     Queries matched: 1
      Tax_Id=10090 Gene_Symbol=Gbp6 guanylate binding protein 7
      IPI00660746    Mass: 70997    Score: 54     Queries matched: 1
      Tax_Id=10090 Gene_Symbol=EG634650 70 kDa protein
      IPI00675360    Mass: 71694    Score: 54     Queries matched: 1
      Tax_Id=10090 Gene_Symbol=EG634650 Predicted
      IPI00751212    Mass: 70977    Score: 54     Queries matched: 1
      Tax_Id=10090 Gene_Symbol=Mpa2l Mpa2l protein
      IPI00853773    Mass: 70926    Score: 54     Queries matched: 1
      Tax_Id=10090 Gene_Symbol=EG634650 Guanylate-binding protein 10
      IPI00875535    Mass: 71048    Score: 54     Queries matched: 1
      Tax_Id=10090 Gene_Symbol=Mpa2l 71 kDa protein
```

```
128.  IPI00230706    Mass: 28980    Score: 54     Queries matched: 2   emPAI: 0.19
      Tax_Id=10090 Gene_Symbol=Pgam2 Phosphoglycerate mutase 2
    ☐ Check to include this hit in error tolerant search or archive report

      Query  Observed    Mr(expt)   Mr(calc)    ppm  Miss Score Expect Rank  Peptide
    ☑  1515  393.5729  1177.6967  1177.6931  3.06    0   (44) 0.0082   1   R.VLIAAHGNSLR.G + Dimethyl (N-term)
    ☑  1529  394.9146  1181.7218  1181.7182  3.04    0    44  0.0062   1   R.VLIAAHGNSLR.G + Dimethyl:2H(4) (N-term)


      Proteins matching the same set of peptides:
      IPI00457898    Mass: 28928    Score: 54     Queries matched: 2
      Tax_Id=10090 Gene_Symbol=Pgam1 Phosphoglycerate mutase 1
```

```
129.  IPI00127596    Mass: 43246    Score: 53     Queries matched: 4   emPAI: 0.19
      Tax_Id=10090 Gene_Symbol=Ckm Creatine kinase M-type
    ☐ Check to include this hit in error tolerant search or archive report

      Query  Observed    Mr(expt)   Mr(calc)    ppm  Miss Score Expect Rank  Peptide
    ☑   847  472.2775   942.5404   942.5370  3.64    0    39   0.025   1   K.LMVEMEK.K + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
    ☑  1358  563.8547  1125.6948  1125.6885  5.57    0    30    0.18   1   K.VLTPDLYNK.L + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
    ☑  3255  603.3235  1806.9486  1806.9403  4.61    0    40   0.026   1   K.LNYKPQEEYPDLSK.H + 2 Dimethyl (K); Dimethyl (N-term)
    ☑  3309  607.3486  1819.0241  1819.0157  4.63    0   (28)   0.38   1   K.LNYKPQEEYPDLSK.H + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
```

```
130.  IPI00322312    Mass: 23450    Score: 53     Queries matched: 2   emPAI: 0.23
      Tax_Id=10090 Gene_Symbol=Arhgdia Rho GDP-dissociation inhibitor 1
    ☐ Check to include this hit in error tolerant search or archive report

      Query  Observed    Mr(expt)   Mr(calc)    ppm  Miss Score Expect Rank  Peptide
    ☑  3628  658.6758  1973.0057  1972.9953  5.28    1    44  0.0082   1   K.SIQEIQELDKDDESLR.K + Dimethyl (K); Dimethyl (N-term)
    ☑  3640  661.3589  1981.0550  1981.0455  4.80    1   (34)  0.099   1   K.SIQEIQELDKDDESLR.K + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
```

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131. IPI00353727 **Mass:** 36252 **Score:** 53 **Queries matched:** 2 **emPAI:** 0.15
Tax_Id=10090 Gene_Symbol=Anxa4 Annexin A4
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	2772	528.2760	1581.8062	1581.8012	3.17	1	53	0.00086	1	R.RINQTYQQQYGR.S + Dimethyl (N-term)
☑	2778	529.6175	1585.8307	1585.8263	2.80	1	(31)	0.14	1	R.RINQTYQQQYGR.S + Dimethyl:2H(4) (N-term)

Proteins matching the same set of peptides:
IPI00473555 **Mass:** 22028 **Score:** 53 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=Anxa4 Truncated annexin IV
IPI00830586 **Mass:** 28755 **Score:** 53 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=Anxa4 29 kDa protein

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132. IPI00230108 **Mass:** 57099 **Score:** 52 **Queries matched:** 1 **emPAI:** 0.05
Tax_Id=10090 Gene_Symbol=Pdia3 Protein disulfide-isomerase A3 precursor
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1924	427.9443	1280.8112	1280.8067	3.47	1	52	0.00052	1	K.LSKDPNIVIAK.M + 2 Dimethyl (K); Dimethyl (N-term)

---

133. IPI00462934 **Mass:** 77218 **Score:** 52 **Queries matched:** 3 **emPAI:** 0.10
Tax_Id=10090 Gene_Symbol=Khsrp Far upstream element-binding protein 2
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	872	476.2921	950.5697	950.5662	3.75	0	(37)	0.033	1	R.HSVGVVIGR.S + Dimethyl (N-term)
☑	879	478.3047	954.5948	954.5913	3.71	0	37	0.029	1	R.HSVGVVIGR.S + Dimethyl:2H(4) (N-term)
☑	1272	549.3371	1096.6596	1096.6543	4.89	0	32	0.1	1	R.VGGGIDVPVPR.H + Dimethyl:2H(4) (N-term)

Proteins matching the same set of peptides:
IPI00876559 **Mass:** 68960 **Score:** 52 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=Khsrp KH type splicing regulatory protein KSRP

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134. IPI00224626 **Mass:** 50959 **Score:** 52 **Queries matched:** 2 **emPAI:** 0.10
Tax_Id=10090 Gene_Symbol=Sept7 cell division cycle 10 homolog
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1825	415.5676	1243.6809	1243.6772	2.97	1	(42)	0.014	1	K.LKDSEAELQR.R + Dimethyl (K); Dimethyl (N-term)
☑	1845	418.2509	1251.7308	1251.7274	2.73	1	43	0.0088	1	K.LKDSEAELQR.R + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

Proteins matching the same set of peptides:

```
      IPI00874440    Mass: 50860    Score: 52     Queries matched: 2
      Tax_Id=10090 Gene_Symbol=Sept7 Septin-7

135.  IPI00116498    Mass: 27925    Score: 51     Queries matched: 2   emPAI: 0.19
      Tax_Id=10090 Gene_Symbol=Ywhaz 14-3-3 protein zeta/delta
    ☐ Check to include this hit in error tolerant search or archive report

      Query  Observed   Mr(expt)   Mr(calc)   ppm  Miss Score Expect Rank  Peptide
        910  486.3246   970.6347   970.6303  4.62   0     32   0.063   1   R.NLLSVAYK.N + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
    ☑  2188  459.2805  1374.8195  1374.8148  3.46   1     51  0.0014   1   R.YLAEVAAGDDKK.G + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)


      Proteins matching the same set of peptides:
      IPI00853851    Mass: 24370    Score: 51     Queries matched: 2
      Tax_Id=10090 Gene_Symbol=LOC100047236 similar to 14-3-3 zeta

136.  IPI00308885    Mass: 61088    Score: 50     Queries matched: 2   emPAI: 0.04
      Tax_Id=10090 Gene_Symbol=Hspd1 Isoform 1 of 60 kDa heat shock protein, mitochondrial precursor
    ☐ Check to include this hit in error tolerant search or archive report

      Query  Observed   Mr(expt)   Mr(calc)   ppm  Miss Score Expect Rank  Peptide
    ☑   886  479.3046   956.5946   956.5906  4.20   0     33   0.084   1   K.LSDGVAVLK.V + Dimethyl (K); Dimethyl (N-term)
    ☑  2408  482.6011  1444.7814  1444.7773  2.82   1     50  0.0023   1   K.VGGTSDVEVNEKK.D + 2 Dimethyl (K); Dimethyl (N-term)


      Proteins matching the same set of peptides:
      IPI00461249    Mass: 61188    Score: 50     Queries matched: 2
      Tax_Id=10090 Gene_Symbol=Hspd1 similar to Heat shock protein 1
      IPI00845678    Mass: 27112    Score: 50     Queries matched: 2
      Tax_Id=10090 Gene_Symbol=Hspd1 Isoform 2 of 60 kDa heat shock protein, mitochondrial precursor

137.  IPI00314191    Mass: 30907    Score: 46     Queries matched: 2   emPAI: 0.08
      Tax_Id=10090 Gene_Symbol=Cbr1 Carbonyl reductase [NADPH] 1
    ☐ Check to include this hit in error tolerant search or archive report

      Query  Observed   Mr(expt)   Mr(calc)   ppm  Miss Score Expect Rank  Peptide
    ☑  1003  499.7871   997.5597   997.5556  4.11   0     46  0.0031   1   K.LQAEGLSPR.F + Dimethyl (N-term)
    ☑  1032  501.7994  1001.5843  1001.5807  3.58   0    (34)  0.084   1   K.LQAEGLSPR.F + Dimethyl:2H(4) (N-term)


138.  IPI00378438    Mass: 202911   Score: 45     Queries matched: 2   emPAI: 0.03
      Tax_Id=10090 Gene_Symbol=Tns1 tensin 1
    ☐ Check to include this hit in error tolerant search or archive report

      Query  Observed   Mr(expt)   Mr(calc)   ppm  Miss Score Expect Rank  Peptide
    ☑   843  471.7650   941.5154   941.5120  3.57   0     38   0.018   1   R.SYVESVAR.T + Dimethyl:2H(4) (N-term)
    ☑  4184  585.5518  2338.1782  2338.1679  4.40   1     37   0.038   1   R.GLNSWQQQQPHPPPRQQER.S + Dimethyl (N-term)
```

139. IPI00118678 **Mass:** 60930 **Score:** 45 **Queries matched:** 2 **emPAI:** 0.09
Tax_Id=10090 Gene_Symbol=Tcp1 T-complex protein 1 subunit alpha A
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	2792	399.7137	1594.8259	1594.8215	2.71	1	(40)	0.016	1	R.AFHNEAQVNPERK.N + Dimethyl (K); Dimethyl (N-term)
☑	2804	401.7263	1602.8763	1602.8718	2.81	1	41	0.02	1	R.AFHNEAQVNPERK.N + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

Proteins matching the same set of peptides:
IPI00459493 **Mass:** 60867 **Score:** 45 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=Tcp1 Isoform 1 of T-complex protein 1 subunit alpha B
IPI00845611 **Mass:** 55880 **Score:** 45 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=Tcp1 Isoform 2 of T-complex protein 1 subunit alpha B

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140. IPI00223253 **Mass:** 51230 **Score:** 45 **Queries matched:** 2 **emPAI:** 0.10
Tax_Id=10090 Gene_Symbol=Hnrpk Isoform 1 of Heterogeneous nuclear ribonucleoprotein K
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	817	465.2894	928.5642	928.5593	5.25	0	39	0.025	1	K.DLAGSIIGK.G + Dimethyl (K); Dimethyl (N-term)
☑	832	469.3146	936.6147	936.6095	5.53	0	(32)	0.097	1	K.DLAGSIIGK.G + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

Proteins matching the same set of peptides:
IPI00224575 **Mass:** 51281 **Score:** 45 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=Hnrpk Isoform 2 of Heterogeneous nuclear ribonucleoprotein K
IPI00465574 **Mass:** 51259 **Score:** 45 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=Hnrpk Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:I830091E20 product:heterogeneous nuclear ribonucleoprotein K,
IPI00761237 **Mass:** 51186 **Score:** 45 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=- 51 kDa protein
IPI00875420 **Mass:** 48664 **Score:** 45 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=- 48 kDa protein

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141. IPI00115679 **Mass:** 109791 **Score:** 45 **Queries matched:** 3 **emPAI:** 0.02
Tax_Id=10090 Gene_Symbol=Ganab Isoform 2 of Neutral alpha-glucosidase AB precursor
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1009	500.8139	999.6132	999.6077	5.55	0	45	0.006	1	R.SLLLSVNAR.G + Dimethyl (N-term)
☑	3057	566.3208	1695.9406	1695.9308	5.76	1	30	0.24	1	R.YRVPDVLVADPPTAR.L + Dimethyl (N-term)
☑	3070	567.6622	1699.9647	1699.9559	5.18	1	(25)	0.61	1	R.YRVPDVLVADPPTAR.L + Dimethyl:2H(4) (N-term)

Proteins matching the same set of peptides:
IPI00403058 **Mass:** 107300 **Score:** 45 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=Ganab Isoform 1 of Neutral alpha-glucosidase AB precursor

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142. IPI00751017 **Score:** 43 **Queries matched:** 3

```
       Tax_Id=10090 Gene_Symbol=A230067G21Rik 99 kDa protein
     ☐ Check to include this hit in error tolerant search or archive report

       Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score Expect Rank  Peptide
        1245  543.2912  1084.5678  1084.5779  -9.31   0     40   0.011   2   -.MFASWLFK.A + Dimethyl (K); Dimethyl (N-term)
        1259  547.3163  1092.6181  1092.6282  -9.19   0    (26)   0.43   2   -.MFASWLFK.A + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
        1260  547.3163  1092.6181  1092.6282  -9.19   0    (37)  0.033   2   -.MFASWLFK.A + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)


       Proteins matching the same set of peptides:
       IPI00756343     Score: 43     Queries matched: 3
       IPI00845657     Score: 43     Queries matched: 3

143.   IPI00109600     Mass: 48308     Score: 43      Queries matched: 2    emPAI: 0.05
       Tax_Id=10090 Gene_Symbol=2410004A20Rik ES cells cDNA, RIKEN full-length enriched library, clone:2410004A20 product:hypothetical Alanine-rich region containing prot
     ☐ Check to include this hit in error tolerant search or archive report

       Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score Expect Rank  Peptide
     ☑  3160  582.9787  1745.9143  1745.9055   5.01   1    (28)   0.36   1   R.MKLMEIEALEAGVER.R + Dimethyl (K)
     ☑  3161  873.9658  1745.9171  1745.9055   6.62   1     43  0.0099   1   R.MKLMEIEALEAGVER.R + Dimethyl (N-term)


       Proteins matching the same set of peptides:
       IPI00874395     Mass: 45827     Score: 43      Queries matched: 2
       Tax_Id=10090 Gene_Symbol=- OEEP48 variant

144.   IPI00136703     Mass: 42971     Score: 43      Queries matched: 2    emPAI: 0.12
       Tax_Id=10090 Gene_Symbol=Ckb Creatine kinase B-type
     ☐ Check to include this hit in error tolerant search or archive report

       Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score Expect Rank  Peptide
     ☑  2064  666.3866  1330.7587  1330.7496   6.84   0    (32)   0.13   1   K.VLTPELYAELR.A + Dimethyl (N-term)
     ☑  2082  668.3992  1334.7839  1334.7747   6.88   0     39   0.026   1   K.VLTPELYAELR.A + Dimethyl:2H(4) (N-term)

145.   IPI00154054     Mass: 45129     Score: 43      Queries matched: 3    emPAI: 0.06
       Tax_Id=10090 Gene_Symbol=Acat1 Acetyl-CoA acetyltransferase, mitochondrial precursor
     ☐ Check to include this hit in error tolerant search or archive report

       Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score Expect Rank  Peptide
     ☑  3120  577.6645  1729.9717  1729.9614   5.95   0     40   0.023   1   R.TPIGSFLGSLASQPATK.L + Dimethyl (K); Dimethyl (N-term)
     ☑  3121  577.6645  1729.9718  1729.9614   6.01   0    (36)  0.053   1   R.TPIGSFLGSLASQPATK.L + Dimethyl (K); Dimethyl (N-term)
     ☑  3141  580.3477  1738.0211  1738.0117   5.46   0    (33)   0.08   1   R.TPIGSFLGSLASQPATK.L + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

146.   IPI00172328     Mass: 544766    Score: 43      Queries matched: 1    emPAI: 0.00
       Tax_Id=10090 Gene_Symbol=Dnahc8 Isoform 1 of Ciliary dynein heavy chain 8
     ☐ Check to include this hit in error tolerant search or archive report
```

```
  Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score Expect Rank  Peptide
   2868  544.6272  1630.8597  1630.8712  -7.05    1     43   0.011    3  R.RSMTGIPNLQETLK.E + Dimethyl (K); Oxidation (M)
```

Proteins matching the same set of peptides:
IPI00652480 **Score:** 43 **Queries matched:** 1
IPI00750189 **Mass:** 483380 **Score:** 43 **Queries matched:** 1
Tax_Id=10090 Gene_Symbol=Dnahc8 Isoform 2 of Ciliary dynein heavy chain 8

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147. IPI00229988 **Mass:** 98458 **Score:** 42 **Queries matched:** 2 **emPAI:** 0.05
Tax_Id=10090 Gene_Symbol=Eif2c2 Eukaryotic translation initiation factor 2C 2
☐ Check to include this hit in error tolerant search or archive report

```
  Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score Expect Rank  Peptide
☑  1560  398.8922  1193.6547  1193.6517   2.55    0   (34)  0.067    1  K.AVQVHQDTLR.T + Dimethyl (N-term)
☑  1577  400.2339  1197.6800  1197.6768   2.69    0    38   0.028    1  K.AVQVHQDTLR.T + Dimethyl:2H(4) (N-term)
```

Proteins matching the same set of peptides:
IPI00229989 **Mass:** 98236 **Score:** 42 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=Eif2c1 Eukaryotic translation initiation factor 2C 1

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148. IPI00553798 **Mass:** 604664 **Score:** 42 **Queries matched:** 2 **emPAI:** 0.01
Tax_Id=10090 Gene_Symbol=Ahnak AHNAK nucleoprotein isoform 1
☐ Check to include this hit in error tolerant search or archive report

```
  Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score Expect Rank  Peptide
☑  2850  542.3188  1623.9347  1623.9269   4.80    1    37    0.04    1  K.ISMPDIDLNLKGPK.V + 2 Dimethyl (K); Dimethyl (N-term)
☑  2892  546.3442  1636.0109  1636.0023   5.26    1   (35)  0.029    1  K.ISMPDIDLNLKGPK.V + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
```

---

149. IPI00348328 **Mass:** 114018 **Score:** 42 **Queries matched:** 1 **emPAI:** 0.02
Tax_Id=10090 Gene_Symbol=Krt78 keratin Kb40
☐ Check to include this hit in error tolerant search or archive report

```
  Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score Expect Rank  Peptide
☑  3052  565.6494  1693.9264  1693.9151   6.66    1    42   0.015    1  R.SLNNQFASFIDKVR.F + Dimethyl (K); Dimethyl (N-term)
```

---

150. IPI00469952 **Mass:** 147823 **Score:** 42 **Queries matched:** 5 **emPAI:** 0.04
Tax_Id=10090 Gene_Symbol=Prx Isoform 1 of Periaxin
☐ Check to include this hit in error tolerant search or archive report

```
  Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score Expect Rank  Peptide
☑   745  435.3030   868.5915   868.5874   4.80    0    26     0.2    1  K.FTISLPK.A + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)
☑  1317  371.2336  1110.6791  1110.6761   2.72    1    29    0.17    1  K.LSKVPEVQR.K + Dimethyl (K); Dimethyl (N-term)
☑  1802  413.2462  1236.7168  1236.7118   4.06    1    30    0.18    1  K.GTEFSFKLPK.M + 2 Dimethyl (K); Dimethyl (N-term)
☑  2217  462.2575  1383.7507  1383.7470   2.69    1    44  0.0074    1  R.VREVAEEAQVAR.M + Dimethyl (N-term)
☑  2225  463.5994  1387.7764  1387.7721   3.06    1   (33)  0.096    1  R.VREVAEEAQVAR.M + Dimethyl:2H(4) (N-term)
```

```
      Proteins matching the same set of peptides:
      IPI00762284     Mass: 147780    Score: 42      Queries matched: 5
      Tax_Id=10090 Gene_Symbol=Prx Prx protein

151.  IPI00119818     Mass: 100375    Score: 41      Queries matched: 1   emPAI: 0.03
      Tax_Id=10090 Gene_Symbol=Itih4 Adult male liver cDNA, RIKEN full-length enriched library, clone:1300004A21 product:inter alpha-trypsin inhibitor, heavy chain 4, fu
    ☐ Check to include this hit in error tolerant search or archive report

      Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score Expect Rank  Peptide
    ☑ 1967  434.2854  1299.8344  1299.8304   3.06   0     41  0.0064   1   R.FKPTLSQQQK.S + 2 Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

      Proteins matching the same set of peptides:
      IPI00312711     Mass: 104774    Score: 41      Queries matched: 1
      Tax_Id=10090 Gene_Symbol=Itih4 PK-120

152.  IPI00125971     Mass: 44430     Score: 41      Queries matched: 1   emPAI: 0.06
      Tax_Id=10090 Gene_Symbol=Psmc6 26S protease regulatory subunit S10B
    ☐ Check to include this hit in error tolerant search or archive report

      Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score Expect Rank  Peptide
    ☑ 2657  509.9301  1526.7686  1526.7627   3.88   1     41  0.0095   1   R.FSEGTSADREIQR.T + Dimethyl:2H(4) (N-term)

153.  IPI00110588     Mass: 67839     Score: 41      Queries matched: 3   emPAI: 0.04
      Tax_Id=10090 Gene_Symbol=Msn Moesin
    ☐ Check to include this hit in error tolerant search or archive report

      Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score Expect Rank  Peptide
    ☑ 1056  508.2765  1014.5385  1014.5345   3.90   0     41    0.01   1   R.ALELEQER.K + Dimethyl (N-term)
    ☑ 1063  510.2891  1018.5637  1018.5596   4.00   0    (31)   0.13   1   R.ALELEQER.K + Dimethyl:2H(4) (N-term)
    ☑ 2767  395.7314  1578.8964  1578.8929   2.24   2     32     0.12   1   K.KAQQELEEQTRR.A + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

154.  IPI00116283     Mass: 61162     Score: 41      Queries matched: 1   emPAI: 0.04
      Tax_Id=10090 Gene_Symbol=Cct3 T-complex protein 1 subunit gamma
    ☐ Check to include this hit in error tolerant search or archive report

      Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score Expect Rank  Peptide
    ☑ 1537  395.5806  1183.7200  1183.7165   2.96   0     41   0.017   1   R.EIQVQHPAAK.S + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

155.  IPI00116281     Mass: 58424     Score: 40      Queries matched: 1   emPAI: 0.04
      Tax_Id=10090 Gene_Symbol=Cct6a T-complex protein 1 subunit zeta
    ☐ Check to include this hit in error tolerant search or archive report

      Query  Observed  Mr(expt)  Mr(calc)    ppm  Miss Score Expect Rank  Peptide
```

```
   ☑  653  416.7648  831.5151  831.5116   4.14   0    40   0.012   1   R.GLQDVLR.T + Dimethyl:2H(4) (N-term)

156.  IPI00408258    Mass: 174129    Score: 40     Queries matched: 1    emPAI: 0.01
      Tax_Id=10090 Gene_Symbol=Btbd12 BTB (POZ) domain containing 12
   ☐  Check to include this hit in error tolerant search or archive report

     Query  Observed    Mr(expt)   Mr(calc)    ppm  Miss Score Expect Rank  Peptide
      2600  503.3082  1506.9028  1506.8894   8.87   1     40   0.015   2    K.NLPPKVPITPMPR.Y + Dimethyl:2H(4) (K); Oxidation (M)

157.  IPI00330476    Mass: 146801    Score: 40     Queries matched: 1    emPAI: 0.02
      Tax_Id=10090 Gene_Symbol=Cyfip1 Isoform 1 of Cytoplasmic FMR1-interacting protein 1
   ☐  Check to include this hit in error tolerant search or archive report

     Query  Observed    Mr(expt)   Mr(calc)    ppm  Miss Score Expect Rank  Peptide
   ☑  2198  690.3730  1378.7314  1378.7245   5.02   0     40   0.019   1    R.TVLPFSQEFQR.D + Dimethyl (N-term)


      Proteins matching the same set of peptides:
      IPI00831544    Mass: 146537    Score: 40     Queries matched: 1
      Tax_Id=10090 Gene_Symbol=Cyfip1 Isoform 2 of Cytoplasmic FMR1-interacting protein 1

158.  IPI00315948    Mass: 27654     Score: 40     Queries matched: 1    emPAI: 0.09
      Tax_Id=10090 Gene_Symbol=Tbcb Tubulin folding cofactor B
   ☐  Check to include this hit in error tolerant search or archive report

     Query  Observed    Mr(expt)   Mr(calc)    ppm  Miss Score Expect Rank  Peptide
   ☑  3058  566.3300  1695.9682  1695.9606   4.47   1     40   0.022   1    R.LSEEKAQASAISVGSR.C + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)

159.  IPI00458583    Mass: 88661     Score: 39     Queries matched: 1    emPAI: 0.03
      Tax_Id=10090 Gene_Symbol=Hnrnpu Osteoclast-like cell cDNA, RIKEN full-length enriched library, clone:I420039N16 product:heterogeneous nuclear ribonucleoprotein U,
   ☐  Check to include this hit in error tolerant search or archive report

     Query  Observed    Mr(expt)   Mr(calc)    ppm  Miss Score Expect Rank  Peptide
   ☑  3148  581.6559  1741.9458  1741.9363   5.47   0     39   0.029   1    K.SSGPTSLFAVTVAPPGAR.Q + Dimethyl (N-term)

160.  IPI00223224    Mass: 14508     Score: 38     Queries matched: 1    emPAI: 0.18
      Tax_Id=10090 Gene_Symbol=D130079A08Rik 12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:D130079A08 product:hypothetical protein, full
   ☐  Check to include this hit in error tolerant search or archive report

     Query  Observed  Mr(expt)  Mr(calc)    ppm  Miss Score Expect Rank  Peptide
   ☑   816  465.2616  928.5087  928.5090  -0.30   0     38   0.017   1   R.SSEVARPR.R + Dimethyl (N-term)

161.  IPI00762122    Mass: 464816    Score: 38     Queries matched: 1    emPAI: 0.01
      Tax_Id=10090 Gene_Symbol=- 462 kDa protein
```

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
2868	544.6272	1630.8597	1630.8575	1.37	1	38	0.036	4	K.MPARFLPQLPMDK.L + Dimethyl (K); Dimethyl (N-term); 2 Oxidation (M)

---

162. IPI00121892 **Mass:** 251741 **Score:** 37 **Queries matched:** 2 **emPAI:** 0.02
Tax_Id=10090 Gene_Symbol=Spnb2 Isoform 2 of Spectrin beta chain, brain 1

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑ 1002	**499.3134**	**996.6123**	**996.6080**	**4.29**	**0**	**(29)**	**0.14**	**1**	**R.VAVVNQIAR.Q + Dimethyl (N-term)**
☑ 1031	**501.3258**	**1000.6371**	**1000.6331**	**3.93**	**0**	**36**	**0.034**	**1**	**R.VAVVNQIAR.Q + Dimethyl:2H(4) (N-term)**

Proteins matching the same set of peptides:

IPI00319830 **Mass:** 274908 **Score:** 37 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=Spnb2 Isoform 1 of Spectrin beta chain, brain 1
IPI00831369 **Mass:** 244840 **Score:** 37 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=Spnb2 MKIAA4049 protein

---

163. IPI00762403 **Mass:** 147882 **Score:** 36 **Queries matched:** 1 **emPAI:** 0.02
Tax_Id=10090 Gene_Symbol=Usp31 ubiquitin specific protease 31

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
3105	574.6531	1720.9374	1720.9546	-9.98	1	36	0.049	2	-.MSKVTAPGPGPPVAAGGK.E + 2 Dimethyl (K); Dimethyl (N-term); Oxidation (M)

---

164. IPI00126072 **Mass:** 43297 **Score:** 36 **Queries matched:** 1 **emPAI:** 0.06
Tax_Id=10090 Gene_Symbol=Vat1 Synaptic vesicle membrane protein VAT-1 homolog

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑ 1830	**623.4023**	**1244.7901**	**1244.7832**	**5.60**	**1**	**36**	**0.026**	**1**	**K.VLLVPGPEKET.- + Dimethyl:2H(4) (K); Dimethyl:2H(4) (N-term)**

---

165. IPI00402968 **Mass:** 61307 **Score:** 35 **Queries matched:** 1 **emPAI:** 0.04
Tax_Id=10090 Gene_Symbol=Ehd2 13 days embryo forelimb cDNA, RIKEN full-length enriched library, clone:5930429A15 product:EH DOMAIN-CONTAINING PROTEIN-2 homolog

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑ 2063	**444.5876**	**1330.7411**	**1330.7357**	**4.05**	**0**	**35**	**0.059**	**1**	**K.LEGHGLPTNLPR.R + Dimethyl (N-term)**

---

166. IPI00461360 **Mass:** 110460 **Score:** 35 **Queries matched:** 1 **emPAI:** 0.02
Tax_Id=10090 Gene_Symbol=Ccdc39 Coiled-coil domain-containing protein 39

☐ Check to include this hit in error tolerant search or archive report

```
     Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score Expect Rank  Peptide
  ☑  1228  359.2197  1074.6372  1074.6284   8.14   2     35   0.059   1   R.SEKELSKAK.A + 2 Dimethyl (K)
```

```
167.   IPI00131395     Mass: 96752     Score: 35      Queries matched: 2    emPAI: 0.03
       Tax_Id=10090 Gene_Symbol=Znf512b MKIAA1196 protein
    ☐  Check to include this hit in error tolerant search or archive report

     Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score Expect Rank  Peptide
  ☑   717  430.7651  859.5157  859.5239  -9.54   2     35   0.041   1   K.SLSGGKKR.G + Dimethyl (N-term)
  ☑   733  432.7777  863.5409  863.5490  -9.47   2    (28)   0.21   1   K.SLSGGKKR.G + Dimethyl:2H(4) (N-term)


       Proteins matching the same set of peptides:
       IPI00756808     Mass: 121307    Score: 35      Queries matched: 2
       Tax_Id=10090 Gene_Symbol=Znf512b similar to mKIAA1196 protein
```

```
168.   IPI00120274     Mass: 44661     Score: 34      Queries matched: 1    emPAI: 0.06
       Tax_Id=10090 Gene_Symbol=Npcd;Cbx6 Chromobox protein homolog 6
    ☐  Check to include this hit in error tolerant search or archive report

     Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score Expect Rank  Peptide
  ☑  2822  539.3262  1614.9567  1614.9569  -0.12   2     34   0.056   1   K.TFLLKARAQAEALR.I + Dimethyl (N-term)


       Proteins matching the same set of peptides:
       IPI00420763     Mass: 73456     Score: 34      Queries matched: 1
       Tax_Id=10090 Gene_Symbol=Cbx6 Neuronal pentraxin with chromo domain
       IPI00464339     Mass: 52546     Score: 34      Queries matched: 1
       Tax_Id=10090 Gene_Symbol=Cbx6 Neuronal pentraxin 1.4 kb variant
       IPI00751159     Mass: 73521     Score: 34      Queries matched: 1
       Tax_Id=10090 Gene_Symbol=Npcd 73 kDa protein
       IPI00757836     Mass: 52483     Score: 34      Queries matched: 1
       Tax_Id=10090 Gene_Symbol=Npcd neuronal pentraxin with chromo domain isoform 2
       IPI00776097     Mass: 15514     Score: 34      Queries matched: 1
       Tax_Id=10090 Gene_Symbol=Cbx6;Npcd 15 kDa protein
```

```
169.   IPI00132700     Mass: 21773     Score: 34      Queries matched: 1    emPAI: 0.12
       Tax_Id=10090 Gene_Symbol=Mrpl35 39S ribosomal protein L35, mitochondrial precursor
    ☐  Check to include this hit in error tolerant search or archive report

     Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score Expect Rank  Peptide
  ☑  1185  351.8892  1052.6457  1052.6455   0.25   2     34   0.046   1   R.KTVKSVVHR.F
```

Search Parameters

```
Type of search         : MS/MS Ion Search
Enzyme                 : Trypsin
Fixed modifications    : Carbamidomethyl (C)
Variable modifications : Dimethyl (K),Dimethyl (N-term),Dimethyl:2H(4) (K),Dimethyl:2H(4) (N-term),Oxidation (M)
Mass values            : Monoisotopic
Protein Mass           : Unrestricted
Peptide Mass Tolerance : ± 10 ppm
Fragment Mass Tolerance: ± 0.9 Da
Instrument type        : Default
Number of queries      : 4680
```

Figure S4, Raijmakers et al.

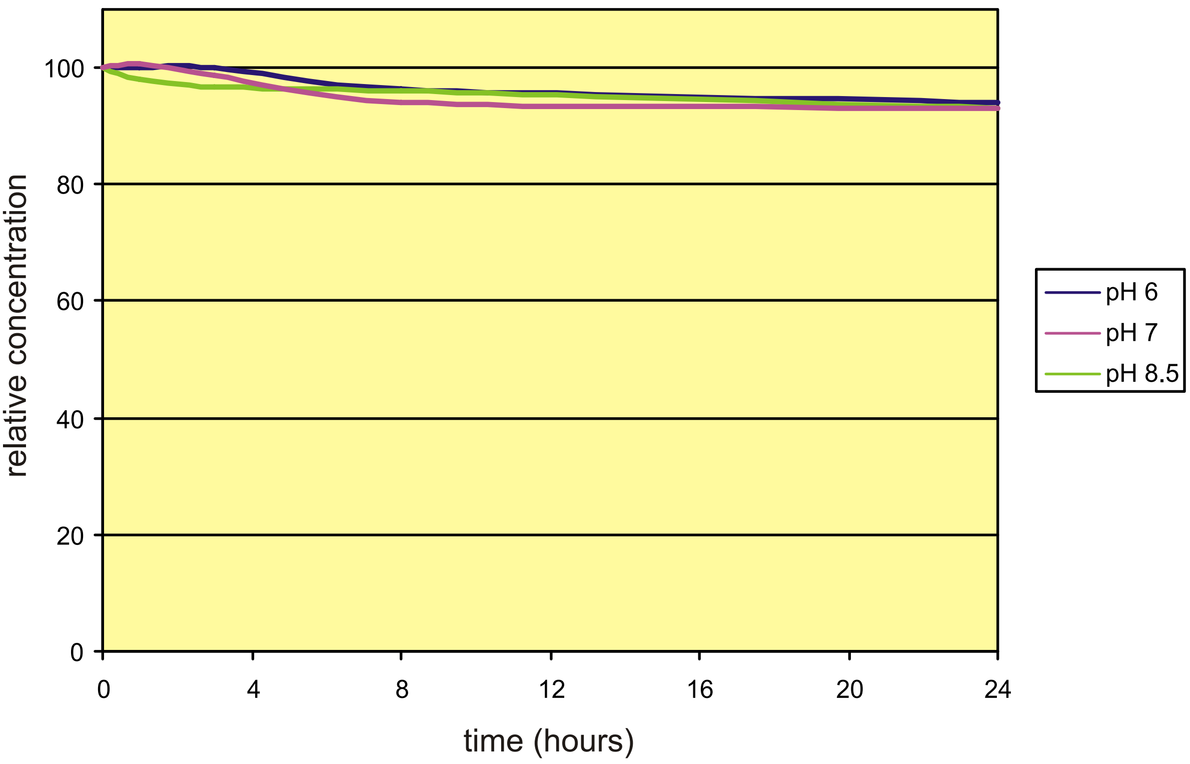

Figure S5, Raijmakers et al.

PSME2, peptide **ALVHERDEAVYGDLR**

Monoisotopic mass of neutral peptide Mr(calc): 1773.9311
Variable modifications: N-term : Dimethyl:2H(4) (N-term)
Ions Score: 48 **Expect:** 0.00031
Matches (Bold Red): 39/146 fragment ions using 84 most intense peaks