Mascot Search Results

```
User          : Dominic
Email         : dominic.kurian@bbsrc.ac.uk
Search title  : IPI Mouse_15-02-2010
MS data file  : D:\Peaklist\Dominic Kurian\QTofDK20010806 GATC P 0010884.pkl
Database      : IPI_mouse MOUSE_v3_79 (54943 sequences; 24917557 residues)
Timestamp     : 15 Feb 2011 at 15:26:16 GMT
Protein hits  : IPI00420725 Tax_Id=10090 Gene_Symbol=Camk2a Uncharacterized protein
                IPI00875723 Tax_Id=10090 Gene_Symbol=Camk2b 68 kDa protein
                IPI00112584 Tax_Id=10090 Gene_Symbol=Camk2d Isoform 1 of Calcium/calmodulin-dependent protein kinase type II subunit
                IPI00608020 Tax_Id=10090 Gene_Symbol=Ftl1 ferritin light chain 1
                IPI00347110 Tax_Id=10090 Gene_Symbol=Krt73 Keratin, type II cytoskeletal 73
                IPI00625729 Tax_Id=10090 Gene_Symbol=Krt1 Keratin, type II cytoskeletal 1
                IPI00222228 Tax_Id=10090 Gene_Symbol=4732456N10Rik hypothetical protein LOC239673
                IPI00138892 Tax_Id=10090 Gene_Symbol=Uba52 Ubiquitin-60S ribosomal protein L40
                IPI00874682 Tax_Id=10090 Gene_Symbol=- 36 kDa protein
                IPI00223714 Tax_Id=10090 Gene_Symbol=Hist1h1e Histone H1.4
```

	IPI_mouse	**Decoy**	**False discovery rate**
Peptide matches above identity threshold	65	0	0.00 %
Peptide matches above homology or identity threshold	75	0	0.00 %

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 > 37 indicate identity or extensive homology (p<0.01).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.

Score Distribution

Peptide Summary Report

Format As | Peptide Summary | Help

Significance threshold p< 0.01 | Max. number of hits AUTO

Standard scoring ○ MudPIT scoring ● | Ions score or expect cut-off 0 | 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. IPI00420725 **Mass:** 55882 **Score:** 1043 **Queries matched:** 83 **emPAI:** 0.33
Tax_Id=10090 Gene_Symbol=Camk2a Uncharacterized 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
☑	105	**463.2481**	**924.4816**	**924.4777**	**4.26**	**1**	**2**	**39**	**1**	**R.DHQKLER.E**
	183	**574.3185**	**1146.6224**	**1146.6431**	**-17.98**	**0**	**(0)**	**75**	**3**	**K.GAILTTMLATR.N**
☑	184	**574.3212**	**1146.6278**	**1146.6431**	**-13.27**	**0**	**(39)**	**0.0084**	**1**	**K.GAILTTMLATR.N**
☑	190	**574.3264**	**1146.6382**	**1146.6431**	**-4.20**	**0**	**(35)**	**0.022**	**1**	**K.GAILTTMLATR.N**
☑	191	**574.3266**	**1146.6386**	**1146.6431**	**-3.85**	**0**	**(36)**	**0.016**	**1**	**K.GAILTTMLATR.N**
☑	192	**574.3272**	**1146.6398**	**1146.6431**	**-2.81**	**0**	**(42)**	**0.0034**	**1**	**K.GAILTTMLATR.N**
☑	193	**574.3276**	**1146.6406**	**1146.6431**	**-2.11**	**0**	**(51)**	**0.00041**	**1**	**K.GAILTTMLATR.N**
☑	195	**574.3278**	**1146.6410**	**1146.6431**	**-1.76**	**0**	**(47)**	**0.0012**	**1**	**K.GAILTTMLATR.N**
☑	197	**574.3286**	**1146.6426**	**1146.6431**	**-0.36**	**0**	**(12)**	**3.8**	**1**	**K.GAILTTMLATR.N**
☑	198	**574.3288**	**1146.6430**	**1146.6431**	**-0.02**	**0**	**(42)**	**0.0031**	**1**	**K.GAILTTMLATR.N**
☑	199	**574.3290**	**1146.6434**	**1146.6431**	**0.33**	**0**	**(54)**	**0.0002**	**1**	**K.GAILTTMLATR.N**
☑	200	**574.3296**	**1146.6446**	**1146.6431**	**1.38**	**0**	**64**	**2.3e-005**	**1**	**K.GAILTTMLATR.N**
☑	201	**574.3298**	**1146.6450**	**1146.6431**	**1.73**	**0**	**(45)**	**0.0018**	**1**	**K.GAILTTMLATR.N**
☑	202	**574.3300**	**1146.6454**	**1146.6431**	**2.08**	**0**	**(64)**	**2.2e-005**	**1**	**K.GAILTTMLATR.N**
☑	203	**574.3303**	**1146.6460**	**1146.6431**	**2.60**	**0**	**(45)**	**0.0017**	**1**	**K.GAILTTMLATR.N**
☑	204	**574.3303**	**1146.6460**	**1146.6431**	**2.60**	**0**	**(25)**	**0.18**	**1**	**K.GAILTTMLATR.N**
☑	205	**574.3306**	**1146.6466**	**1146.6431**	**3.12**	**0**	**(39)**	**0.0056**	**1**	**K.GAILTTMLATR.N**
☑	207	**574.3308**	**1146.6470**	**1146.6431**	**3.47**	**0**	**(48)**	**0.00072**	**1**	**K.GAILTTMLATR.N**
☑	208	**574.3308**	**1146.6470**	**1146.6431**	**3.47**	**0**	**(50)**	**0.00047**	**1**	**K.GAILTTMLATR.N**
☑	209	**574.3309**	**1146.6472**	**1146.6431**	**3.65**	**0**	**(42)**	**0.0033**	**1**	**K.GAILTTMLATR.N**
☑	212	**574.3314**	**1146.6482**	**1146.6431**	**4.52**	**0**	**(35)**	**0.014**	**1**	**K.GAILTTMLATR.N**
☑	213	**574.3317**	**1146.6488**	**1146.6431**	**5.04**	**0**	**(31)**	**0.035**	**1**	**K.GAILTTMLATR.N**
☑	214	**574.3324**	**1146.6502**	**1146.6431**	**6.26**	**0**	**(26)**	**0.12**	**1**	**K.GAILTTMLATR.N**
☑	242	**631.2996**	**1260.5846**	**1260.5927**	**-6.42**	**0**	**(46)**	**0.0014**	**1**	**R.FYFENLWSR.N**
☑	243	**631.3040**	**1260.5934**	**1260.5927**	**0.56**	**0**	**(48)**	**0.001**	**1**	**R.FYFENLWSR.N**
☑	244	**631.3043**	**1260.5940**	**1260.5927**	**1.04**	**0**	**57**	**0.00013**	**1**	**R.FYFENLWSR.N**

☑	246	631.3052	1260.5958	1260.5927	2.46	0	(23)	0.31	1	R.FYFENLWSR.N
☑	247	631.3057	1260.5968	1260.5927	3.26	0	(42)	0.0042	1	R.FYFENLWSR.N
☑	248	631.3059	1260.5972	1260.5927	3.57	0	(48)	0.001	1	R.FYFENLWSR.N
☑	249	631.3065	1260.5984	1260.5927	4.53	0	(4)	31	1	R.FYFENLWSR.N
☑	250	631.3067	1260.5988	1260.5927	4.84	0	(44)	0.0027	1	R.FYFENLWSR.N
☑	273	652.3435	1302.6724	1302.6932	-15.92	0	(8)	12	1	R.ITQYLDAGGIPR.T
☑	274	652.3566	1302.6986	1302.6932	4.19	0	(53)	0.00039	1	R.ITQYLDAGGIPR.T
☑	275	652.3569	1302.6992	1302.6932	4.65	0	(39)	0.0089	1	R.ITQYLDAGGIPR.T
☑	276	652.3579	1302.7012	1302.6932	6.18	0	59	8e-005	1	R.ITQYLDAGGIPR.T
☑	277	652.3600	1302.7054	1302.6932	9.41	0	(55)	0.0002	1	R.ITQYLDAGGIPR.T
	297	670.8989	1339.7832	1339.7711	9.09	0	2	19	6	R.DLKPENLLLASK.L
☑	491	816.8908	1631.7670	1631.7719	-2.96	0	(36)	0.014	1	R.FTEEYQLFEELGK.G
☑	492	816.8912	1631.7678	1631.7719	-2.47	0	(47)	0.0011	1	R.FTEEYQLFEELGK.G
☑	494	816.8917	1631.7688	1631.7719	-1.86	0	(52)	0.00042	1	R.FTEEYQLFEELGK.G
☑	495	816.8923	1631.7700	1631.7719	-1.12	0	(31)	0.046	1	R.FTEEYQLFEELGK.G
☑	496	816.8926	1631.7706	1631.7719	-0.76	0	(44)	0.0028	1	R.FTEEYQLFEELGK.G
☑	497	816.8933	1631.7720	1631.7719	0.10	0	(54)	0.00023	1	R.FTEEYQLFEELGK.G
☑	498	816.8933	1631.7720	1631.7719	0.10	0	(37)	0.011	1	R.FTEEYQLFEELGK.G
☑	499	816.8934	1631.7722	1631.7719	0.22	0	(54)	0.00027	1	R.FTEEYQLFEELGK.G
☑	500	816.8934	1631.7722	1631.7719	0.22	0	(27)	0.13	1	R.FTEEYQLFEELGK.G
☑	502	816.8936	1631.7726	1631.7719	0.47	0	(70)	5.6e-006	1	R.FTEEYQLFEELGK.G
☑	503	816.8936	1631.7726	1631.7719	0.47	0	(55)	0.00021	1	R.FTEEYQLFEELGK.G
☑	504	816.8936	1631.7726	1631.7719	0.47	0	(27)	0.12	1	R.FTEEYQLFEELGK.G
☑	505	816.8938	1631.7730	1631.7719	0.72	0	(73)	2.8e-006	1	R.FTEEYQLFEELGK.G
☑	506	816.8939	1631.7732	1631.7719	0.84	0	74	2.8e-006	1	R.FTEEYQLFEELGK.G
☑	507	816.8943	1631.7740	1631.7719	1.33	0	(59)	8.2e-005	1	R.FTEEYQLFEELGK.G
☑	509	816.8944	1631.7742	1631.7719	1.45	0	(54)	0.00027	1	R.FTEEYQLFEELGK.G
☑	510	816.8944	1631.7742	1631.7719	1.45	0	(56)	0.00014	1	R.FTEEYQLFEELGK.G
☑	511	816.8944	1631.7742	1631.7719	1.45	0	(63)	3.2e-005	1	R.FTEEYQLFEELGK.G
☑	512	816.8945	1631.7744	1631.7719	1.57	0	(62)	4.3e-005	1	R.FTEEYQLFEELGK.G
☑	513	816.8946	1631.7746	1631.7719	1.70	0	(63)	3.1e-005	1	R.FTEEYQLFEELGK.G
☑	515	816.8948	1631.7750	1631.7719	1.94	0	(51)	0.00047	1	R.FTEEYQLFEELGK.G
☑	516	816.8951	1631.7756	1631.7719	2.31	0	(48)	0.00096	1	R.FTEEYQLFEELGK.G
☑	517	816.8954	1631.7762	1631.7719	2.68	0	(71)	5.3e-006	1	R.FTEEYQLFEELGK.G
☑	518	816.8955	1631.7764	1631.7719	2.80	0	(37)	0.014	1	R.FTEEYQLFEELGK.G
☑	519	816.8956	1631.7766	1631.7719	2.92	0	(9)	8	1	R.FTEEYQLFEELGK.G
☑	520	816.8956	1631.7766	1631.7719	2.92	0	(22)	0.43	1	R.FTEEYQLFEELGK.G
☑	523	816.8964	1631.7782	1631.7719	3.90	0	(20)	0.61	1	R.FTEEYQLFEELGK.G
☑	524	816.8965	1631.7784	1631.7719	4.02	0	(48)	0.00099	1	R.FTEEYQLFEELGK.G
☑	525	816.8968	1631.7790	1631.7719	4.39	0	(50)	0.00064	1	R.FTEEYQLFEELGK.G
☑	526	816.8972	1631.7798	1631.7719	4.88	0	(3)	35	1	R.FTEEYQLFEELGK.G
☑	527	816.8974	1631.7802	1631.7719	5.13	0	(57)	0.00014	1	R.FTEEYQLFEELGK.G
☑	528	816.8977	1631.7808	1631.7719	5.50	0	(2)	44	1	R.FTEEYQLFEELGK.G
☑	529	816.8980	1631.7814	1631.7719	5.86	0	(41)	0.005	1	R.FTEEYQLFEELGK.G
☑	530	816.8983	1631.7820	1631.7719	6.23	0	(20)	0.63	1	R.FTEEYQLFEELGK.G
☑	531	816.8991	1631.7836	1631.7719	7.21	0	(63)	3.1e-005	1	R.FTEEYQLFEELGK.G
	532	816.8991	1631.7836	1631.7719	7.21	0	(1)	57	4	R.FTEEYQLFEELGK.G
☑	533	816.8996	1631.7846	1631.7719	7.82	0	(52)	0.00037	1	R.FTEEYQLFEELGK.G
☑	534	816.9014	1631.7882	1631.7719	10.0	0	(41)	0.0058	1	R.FTEEYQLFEELGK.G
☑	535	816.9016	1631.7886	1631.7719	10.3	0	(38)	0.011	1	R.FTEEYQLFEELGK.G
☑	598	1040.9820	2079.9494	2079.9426	3.32	0	32	0.027	1	K.AGAYDFPSPEWDTVTPEAK.D
☑	599	1040.9830	2079.9514	2079.9426	4.28	0	(9)	6	1	K.AGAYDFPSPEWDTVTPEAK.D
☑	602	1040.9895	2079.9644	2079.9426	10.5	0	(17)	1.1	1	K.AGAYDFPSPEWDTVTPEAK.D
☑	623	715.3424	2143.0054	2143.0321	-12.46	0	(14)	1.7	1	K.VTEQLIEAISNGDFESYTK.M
☑	625	715.3448	2143.0126	2143.0321	-9.10	0	(43)	0.0023	1	K.VTEQLIEAISNGDFESYTK.M
☑	626	715.3478	2143.0216	2143.0321	-4.90	0	63	2.4e-005	1	K.VTEQLIEAISNGDFESYTK.M
☑	629	1072.5308	2143.0470	2143.0321	6.99	0	(22)	0.35	1	K.VTEQLIEAISNGDFESYTK.M

Proteins matching the same set of peptides:
IPI00621806 **Mass:** 54651 **Score:** 1043 **Queries matched:** 83
Tax_Id=10090 Gene_Symbol=Camk2a Isoform Alpha CaMKII of Calcium/calmodulin-dependent protein kinase type II subunit alpha

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2. IPI00875723 **Mass:** 68686 **Score:** 313 **Queries matched:** 44 **emPAI:** 0.32
Tax_Id=10090 Gene_Symbol=Camk2b 68 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
105	463.2481	924.4816	924.4777	4.26	1	2	39	1	R.DHQKLER.E
183	574.3185	1146.6224	1146.6431	-17.98	0	(0)	75	3	K.GAILTTMLATR.N
184	574.3212	1146.6278	1146.6431	-13.27	0	(39)	0.0084	1	K.GAILTTMLATR.N
190	574.3264	1146.6382	1146.6431	-4.20	0	(35)	0.022	1	K.GAILTTMLATR.N
191	574.3266	1146.6386	1146.6431	-3.85	0	(36)	0.016	1	K.GAILTTMLATR.N
192	574.3272	1146.6398	1146.6431	-2.81	0	(42)	0.0034	1	K.GAILTTMLATR.N
193	574.3276	1146.6406	1146.6431	-2.11	0	(51)	0.00041	1	K.GAILTTMLATR.N
195	574.3278	1146.6410	1146.6431	-1.76	0	(47)	0.0012	1	K.GAILTTMLATR.N
197	574.3286	1146.6426	1146.6431	-0.36	0	(12)	3.8	1	K.GAILTTMLATR.N
198	574.3288	1146.6430	1146.6431	-0.02	0	(42)	0.0031	1	K.GAILTTMLATR.N
199	574.3290	1146.6434	1146.6431	0.33	0	(54)	0.0002	1	K.GAILTTMLATR.N
200	574.3296	1146.6446	1146.6431	1.38	0	64	2.3e-005	1	K.GAILTTMLATR.N
201	574.3298	1146.6450	1146.6431	1.73	0	(45)	0.0018	1	K.GAILTTMLATR.N
202	574.3300	1146.6454	1146.6431	2.08	0	(64)	2.2e-005	1	K.GAILTTMLATR.N
203	574.3303	1146.6460	1146.6431	2.60	0	(45)	0.0017	1	K.GAILTTMLATR.N
204	574.3303	1146.6460	1146.6431	2.60	0	(25)	0.18	1	K.GAILTTMLATR.N

	205	574.3306	1146.6466	1146.6431	3.12	0	(39)	0.0056	1	K.GAILTTMLATR.N
	207	574.3308	1146.6470	1146.6431	3.47	0	(48)	0.00072	1	K.GAILTTMLATR.N
	208	574.3308	1146.6470	1146.6431	3.47	0	(50)	0.00047	1	K.GAILTTMLATR.N
	209	574.3309	1146.6472	1146.6431	3.65	0	(42)	0.0033	1	K.GAILTTMLATR.N
	212	574.3314	1146.6482	1146.6431	4.52	0	(35)	0.014	1	K.GAILTTMLATR.N
	213	574.3317	1146.6488	1146.6431	5.04	0	(31)	0.035	1	K.GAILTTMLATR.N
	214	574.3324	1146.6502	1146.6431	6.26	0	(26)	0.12	1	K.GAILTTMLATR.N
☑	217	579.2984	1156.5822	1156.6313	-42.37	1	14	3.3	1	R.VAAVPASGSRSR.R
	297	670.8989	1339.7832	1339.7711	9.09	0	2	19	6	R.DLKPENLLLASK.C
☑	309	458.5792	1372.7158	1372.7310	-11.12	1	38	0.011	1	K.KADGVKPQTNSTK.N
☑	310	458.5814	1372.7224	1372.7310	-6.31	1	(25)	0.25	1	K.KADGVKPQTNSTK.N
☑	481	810.8718	1619.7290	1619.7355	-3.99	0	(18)	0.69	1	R.FTDEYQLYEDIGK.G
☑	482	810.8729	1619.7312	1619.7355	-2.63	0	(41)	0.0039	1	R.FTDEYQLYEDIGK.G
☑	483	810.8740	1619.7334	1619.7355	-1.27	0	52	0.00033	1	R.FTDEYQLYEDIGK.G
☑	485	810.8782	1619.7418	1619.7355	3.92	0	(3)	24	1	R.FTDEYQLYEDIGK.G
☑	487	810.8815	1619.7484	1619.7355	7.99	0	(7)	10	1	R.FTDEYQLYEDIGK.G
	571	897.9096	1793.8046	1793.8652	-33.75	0	0	42	10	R.TPSPIATAMATTVTCTR.F + Oxidation (M)
	598	1040.9820	2079.9494	2079.9426	3.32	0	32	0.027	1	K.AGAYDFPSPEWDTVTPEAK.N
	599	1040.9830	2079.9514	2079.9426	4.28	0	(9)	6	1	K.AGAYDFPSPEWDTVTPEAK.N
	602	1040.9895	2079.9644	2079.9426	10.5	0	(17)	1.1	1	K.AGAYDFPSPEWDTVTPEAK.N
☑	604	704.9893	2111.9461	2112.0011	-26.05	0	(14)	1.4	1	K.TTEQLIEAVNNGDFEAYAK.I
☑	607	705.0047	2111.9923	2112.0011	-4.18	0	29	0.061	1	K.TTEQLIEAVNNGDFEAYAK.I
	609	1057.0087	2112.0028	2112.0011	0.83	0	(3)	22	3	K.TTEQLIEAVNNGDFEAYAK.I
☑	674	785.0440	2352.1102	2352.1301	-8.48	0	(66)	9.2e-006	1	R.QTTAPATMSTAASGTTMGLVEQAK.S
☑	675	785.0443	2352.1111	2352.1301	-8.09	0	85	1.4e-007	1	R.QTTAPATMSTAASGTTMGLVEQAK.S
☑	677	1177.0797	2352.1448	2352.1301	6.26	0	(30)	0.045	1	R.QTTAPATMSTAASGTTMGLVEQAK.S
☑	678	1177.0834	2352.1522	2352.1301	9.41	0	(45)	0.0013	1	R.QTTAPATMSTAASGTTMGLVEQAK.S
	680	1177.0856	2352.1566	2352.1301	11.3	0	(2)	28	3	R.QTTAPATMSTAASGTTMGLVEQAK.S

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3. IPI00112584 **Mass:** 56961 **Score:** 198 **Queries matched:** 30 **emPAI:** 0.12
Tax_Id=10090 Gene_Symbol=Camk2d Isoform 1 of Calcium/calmodulin-dependent protein kinase type II subunit 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
	105	463.2481	924.4816	924.4777	4.26	1	2	39	1	R.DHQKLER.E
	183	574.3185	1146.6224	1146.6431	-17.98	0	(0)	75	3	K.GAILTTMLATR.N
	184	574.3212	1146.6278	1146.6431	-13.27	0	(39)	0.0084	1	K.GAILTTMLATR.N
	190	574.3264	1146.6382	1146.6431	-4.20	0	(35)	0.022	1	K.GAILTTMLATR.N
	191	574.3266	1146.6386	1146.6431	-3.85	0	(36)	0.016	1	K.GAILTTMLATR.N
	192	574.3272	1146.6398	1146.6431	-2.81	0	(42)	0.0034	1	K.GAILTTMLATR.N
	193	574.3276	1146.6406	1146.6431	-2.11	0	(51)	0.00041	1	K.GAILTTMLATR.N
	195	574.3278	1146.6410	1146.6431	-1.76	0	(47)	0.0012	1	K.GAILTTMLATR.N
	197	574.3286	1146.6426	1146.6431	-0.36	0	(12)	3.8	1	K.GAILTTMLATR.N
	198	574.3288	1146.6430	1146.6431	-0.02	0	(42)	0.0031	1	K.GAILTTMLATR.N
	199	574.3290	1146.6434	1146.6431	0.33	0	(54)	0.0002	1	K.GAILTTMLATR.N
	200	574.3296	1146.6446	1146.6431	1.38	0	64	2.3e-005	1	K.GAILTTMLATR.N
	201	574.3298	1146.6450	1146.6431	1.73	0	(45)	0.0018	1	K.GAILTTMLATR.N
	202	574.3300	1146.6454	1146.6431	2.08	0	(64)	2.2e-005	1	K.GAILTTMLATR.N
	203	574.3303	1146.6460	1146.6431	2.60	0	(45)	0.0017	1	K.GAILTTMLATR.N
	204	574.3303	1146.6460	1146.6431	2.60	0	(25)	0.18	1	K.GAILTTMLATR.N
	205	574.3306	1146.6466	1146.6431	3.12	0	(39)	0.0056	1	K.GAILTTMLATR.N
	207	574.3308	1146.6470	1146.6431	3.47	0	(48)	0.00072	1	K.GAILTTMLATR.N
	208	574.3308	1146.6470	1146.6431	3.47	0	(50)	0.00047	1	K.GAILTTMLATR.N
	209	574.3309	1146.6472	1146.6431	3.65	0	(42)	0.0033	1	K.GAILTTMLATR.N
	212	574.3314	1146.6482	1146.6431	4.52	0	(35)	0.014	1	K.GAILTTMLATR.N
	213	574.3317	1146.6488	1146.6431	5.04	0	(31)	0.035	1	K.GAILTTMLATR.N
	214	574.3324	1146.6502	1146.6431	6.26	0	(26)	0.12	1	K.GAILTTMLATR.N
	297	670.8989	1339.7832	1339.7711	9.09	0	2	19	6	R.DLKPENLLLASK.S
☑	472	809.8823	1617.7500	1617.7562	-3.83	0	(2)	34	1	R.FTDEYQLFEELGK.G
☑	473	809.8842	1617.7538	1617.7562	-1.48	0	37	0.0098	1	R.FTDEYQLFEELGK.G
☑	475	809.8906	1617.7666	1617.7562	6.43	0	(35)	0.021	1	R.FTDEYQLFEELGK.G
	598	1040.9820	2079.9494	2079.9426	3.32	0	32	0.027	1	K.AGAYDFPSPEWDTVTPEAK.D
	599	1040.9830	2079.9514	2079.9426	4.28	0	(9)	6	1	K.AGAYDFPSPEWDTVTPEAK.D
	602	1040.9895	2079.9644	2079.9426	10.5	0	(17)	1.1	1	K.AGAYDFPSPEWDTVTPEAK.D

Proteins matching the same set of peptides:
IPI00406790 **Mass:** 60593 **Score:** 198 **Queries matched:** 30
Tax_Id=10090 Gene_Symbol=Camk2d Isoform 4 of Calcium/calmodulin-dependent protein kinase type II subunit delta
IPI00475044 **Mass:** 55899 **Score:** 198 **Queries matched:** 30
Tax_Id=10090 Gene_Symbol=Camk2d Isoform 2 of Calcium/calmodulin-dependent protein kinase type II subunit delta
IPI00828919 **Mass:** 58492 **Score:** 198 **Queries matched:** 30
Tax_Id=10090 Gene_Symbol=Camk2d Isoform 3 of Calcium/calmodulin-dependent protein kinase type II subunit delta
IPI00857865 **Mass:** 54664 **Score:** 198 **Queries matched:** 30
Tax_Id=10090 Gene_Symbol=Camk2d Putative uncharacterized protein
IPI00858128 **Mass:** 58283 **Score:** 198 **Queries matched:** 30
Tax_Id=10090 Gene_Symbol=Camk2d calcium/calmodulin-dependent protein kinase type II subunit delta isoform 1
IPI00858144 **Mass:** 55828 **Score:** 198 **Queries matched:** 30
Tax_Id=10090 Gene_Symbol=Camk2d 55 kDa protein

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4. IPI00608020 **Mass:** 20817 **Score:** 71 **Queries matched:** 5 **emPAI:** 0.16
Tax_Id=10090 Gene_Symbol=Ftl1 ferritin light chain 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
☑	133	517.7672	1033.5198	1033.5192	0.59	0	(6)	24	1	R.LLEFQNDR.G
☑	134	517.7681	1033.5216	1033.5192	2.33	0	17	2.1	1	R.LLEFQNDR.G

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	135	517.7722	1033.5298	1033.5192	10.3	0	(9)	11	1	R.LLEFQNDR.G
☑	682	791.7310	2372.1712	2372.1761	-2.07	0	(40)	0.0043	1	R.VAGPQPAQTGAPQGSLGEYLFER.L
☑	683	791.7352	2372.1838	2372.1761	3.25	0	54	0.00015	1	R.VAGPQPAQTGAPQGSLGEYLFER.L

Proteins matching the same set of peptides:
IPI00625129 **Mass:** 20783 **Score:** 71 **Queries matched:** 5
Tax_Id=10090 Gene_Symbol=Ftl2 ferritin light chain 2
IPI00762203 **Mass:** 20847 **Score:** 71 **Queries matched:** 5
Tax_Id=10090 Gene_Symbol=Ftl1 Ferritin light chain 1

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5. IPI00347110 **Mass:** 59502 **Score:** 69 **Queries matched:** 4 **emPAI:** 0.11
Tax_Id=10090 Gene_Symbol=Krt73 Keratin, type II cytoskeletal 73
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	263	639.3532	1276.6918	1276.7027	-8.47	0	(33)	0.036	1	K.LALDIEIATYR.K
☑	264	639.3586	1276.7026	1276.7027	-0.01	0	40	0.0068	1	K.LALDIEIATYR.K
☑	354	738.3995	1474.7844	1474.7780	4.38	0	(22)	0.4	1	R.FLEQQNQVLQTK.W
☑	355	738.4022	1474.7898	1474.7780	8.04	0	55	0.0002	1	R.FLEQQNQVLQTK.W

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6. IPI00625729 **Mass:** 66079 **Score:** 55 **Queries matched:** 3 **emPAI:** 0.05
Tax_Id=10090 Gene_Symbol=Krt1 Keratin, type II cytoskeletal 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
☑	258	633.3261	1264.6376	1264.6299	6.12	0	11	5.7	1	R.TNAENEFVTIK.K
	354	738.3995	1474.7844	1474.7780	4.38	0	(22)	0.4	1	R.FLEQQNQVLQTK.W
	355	738.4022	1474.7898	1474.7780	8.04	0	55	0.0002	1	R.FLEQQNQVLQTK.W

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7. IPI00222228 **Mass:** 58587 **Score:** 45 **Queries matched:** 3 **emPAI:** 0.06
Tax_Id=10090 Gene_Symbol=4732456N10Rik hypothetical protein LOC239673
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
	263	639.3532	1276.6918	1276.7027	-8.47	0	(33)	0.036	1	K.LALDIEIATYR.K
	264	639.3586	1276.7026	1276.7027	-0.01	0	40	0.0068	1	K.LALDIEIATYR.K
☑	577	906.4692	1810.9238	1810.8923	17.4	0	9	7.3	1	R.TNLEPMFEAYITNLR.R

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8. IPI00138892 **Mass:** 15004 **Score:** 43 **Queries matched:** 3 **emPAI:** 0.23
Tax_Id=10090 Gene_Symbol=Uba52 Ubiquitin-60S ribosomal protein L40
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	564	894.4686	1786.9226	1786.9200	1.47	0	(35)	0.019	1	K.TITLEVEPSDTIENVK.A
☑	566	894.4698	1786.9250	1786.9200	2.82	0	37	0.011	1	K.TITLEVEPSDTIENVK.A
☑	567	894.4714	1786.9282	1786.9200	4.61	0	(21)	0.48	1	K.TITLEVEPSDTIENVK.A

Proteins matching the same set of peptides:
IPI00470152 **Mass:** 18282 **Score:** 43 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=Rps27a Ubiquitin-40S ribosomal protein S27a
IPI00895319 **Mass:** 22277 **Score:** 43 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=2810422J05Rik 22 kDa protein
IPI00895479 **Mass:** 27181 **Score:** 43 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=2810422J05Rik 27 kDa protein
IPI00918763 **Mass:** 11021 **Score:** 43 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=Uba52 Ubiqutin subunit 1
IPI00750889 **Mass:** 22822 **Score:** 43 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=Ubc Ubc protein
IPI00923013 **Mass:** 26603 **Score:** 43 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=Ubb Ubiquitin B
IPI00923037 **Mass:** 22578 **Score:** 43 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=Ubc Putative uncharacterized protein
IPI00139518 **Mass:** 34348 **Score:** 43 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=Ubb Polyubiquitin-B
IPI00755916 **Mass:** 82614 **Score:** 43 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=Ubc ubiquitin
IPI00969323 **Mass:** 82603 **Score:** 43 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=Ubc Polyubiquitin-C

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9. IPI00874682 **Mass:** 36038 **Score:** 38 **Queries matched:** 3 **emPAI:** 0.09
Tax_Id=10090 Gene_Symbol=- 36 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
☑	306	685.3730	1368.7314	1368.7361	-3.40	0	38	0.011	1	R.GAAQNIIPASTGAAK.A
☑	307	685.3763	1368.7380	1368.7361	1.42	0	(6)	15	1	R.GAAQNIIPASTGAAK.A
	648	737.6991	2210.0755	2210.1075	-14.50	0	1	38	2	R.VIISAPSADAPMIVMGVNHEK.Y + 2 Oxidation (M)

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10. IPI00223714 **Mass:** 21964 **Score:** 38 **Queries matched:** 2 **emPAI:** 0.15
Tax_Id=10090 Gene_Symbol=Hist1h1e Histone H1.4
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	230	614.8427	1227.6708	1227.6711	-0.18	0	38	0.012	1	K.TSGPPVSELITK.A
☑	231	614.8442	1227.6738	1227.6711	2.27	0	(4)	28	1	K.TSGPPVSELITK.A

Peptide matches not assigned to protein hits: (no details means no match)

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	138	523.2836	1044.5526	1044.5564	-3.55	0	30	0.084	1	INDITLNSR
☑	141	523.2860	1044.5574	1044.5564	1.05	0	30	0.089	1	INDITLNSR
☑	140	523.2858	1044.5570	1044.5564	0.67	0	30	0.09	1	INDITLNSR
☑	550	851.4625	1700.9104	1700.8985	7.02	0	29	0.065	1	AVFVDLEPTVIDEVR
☑	756	1188.2642	3561.7708	3561.7951	-6.83	0	27	0.042	1	TAGAQVVLTDQELQLWPSDLDKPSASEGLPPGSR
☑	82	423.2244	844.4342	844.4515	-20.40	1	26	0.29	1	AIRENSR
☑	234	615.3033	1228.5920	1228.6088	-13.63	0	21	0.5	1	DAVLEPFPADR
☑	93	435.7734	869.5322	869.5123	22.9	0	21	0.32	1	VSLWLPR
☑	25	325.1812	648.3478	648.3595	-17.97	0	21	0.69	1	AFNAVK
☑	137	523.2833	1044.5520	1044.5564	-4.12	0	20	1	1	INDITLNSR
☑	542	851.4489	1700.8832	1700.8985	-8.98	0	19	0.8	1	AVFVDLEPTVIDEVR
☑	78	421.7591	841.5036	841.4658	45.0	0	18	0.78	1	ATHTVSVK
☑	270	651.8633	1301.7120	1301.7078	3.24	0	18	0.83	1	SLDLDSIIAEVK
☑	159	556.3107	1110.6068	1110.5777	26.2	1	17	0.98	1	LMKTVQTMK + 2 Oxidation (M)
☑	420	785.8442	1569.6738	1569.7466	-46.32	1	17	0.51	1	KWTMILMMNNTR + 2 Oxidation (M)
☑	285	657.8660	1313.7174	1313.7092	6.30	0	17	1.3	1	LATVGELQAAWR
☑	251	631.3092	1260.6038	1260.5656	30.3	0	17	1.5	1	SDLEAHVESMK + Oxidation (M)
☑	132	517.2679	1032.5212	1032.4771	42.8	1	16	2.1	1	NAMRDPSSR
☑	91	435.7730	869.5314	869.4971	39.6	0	15	1.4	1	AVVESLPR
☑	235	615.3042	1228.5938	1228.6200	-21.31	0	14	2.3	1	IGGLNWAIDDR
☑	68	412.7538	823.4930	823.5028	-11.85	1	14	1	1	VPSRLPR
☑	145	525.2818	1048.5490	1048.5553	-5.93	0	14	3.3	1	AAAGEIIYNK
☑	288	657.8696	1313.7246	1313.7092	11.8	0	14	2.3	1	LATVGELQAAWR
☑	67	412.7532	823.4918	823.4664	30.9	0	14	1.1	1	ALSIHQR
☑	50	379.7120	757.4094	757.3719	49.6	0	14	4.4	1	SSPAGSPR
☑	552	851.4630	1700.9114	1700.8985	7.60	0	14	2	1	AVFVDLEPTVIDEVR
☑	90	435.7719	869.5292	869.4858	49.9	0	14	1.7	1	VSGVEVPLA
☑	348	738.3803	1474.7460	1474.8065	-40.98	1	14	3.2	1	VESLLENMGIKVK + Oxidation (M)
☑	64	412.7518	823.4890	823.4916	-3.07	0	14	1.2	1	TVAPALPR
☑	269	651.8616	1301.7086	1301.6649	33.6	0	14	2.6	1	ATIATMPVPETR + Oxidation (M)
☑	549	851.4609	1700.9072	1700.8985	5.13	0	13	2.4	1	AVFVDLEPTVIDEVR
☑	142	523.2862	1044.5578	1044.5829	-23.94	1	13	4.3	1	AVGRRPFDK
☑	75	421.7574	841.5002	841.4810	22.9	0	13	2.6	1	AVLTWPR
☑	168	565.3207	1128.6268	1128.6291	-2.01	0	13	3.6	1	IGSGLAHAYIK
☑	86	428.7643	855.5140	855.4814	38.2	0	13	2.5	1	LGAETLPR
☑	638	1073.0280	2144.0414	2144.0055	16.7	1	13	2.6	1	TPKPGNPSSEESSKEVPSCK
☑	681	791.7297	2372.1673	2372.2059	-16.28	1	13	2.2	1	DPLARLSNPLCANASYWAVVR
☑	759	1188.2699	3561.7879	3561.6931	26.6	1	13	1.1	1	TGWAMVSLCIVFAMTSGQMWNHIRGPPYAHK + Oxidation (M)
☑	259	634.3560	1266.6974	1266.6720	20.1	1	13	2.6	1	RNIIGYFEQK
☑	670	1168.5640	2335.1134	2335.0751	16.4	1	13	2.4	1	TPWRMDTSGTPQTTADSATSPK
☑	352	738.3887	1474.7628	1474.7741	-7.66	0	12	4.1	1	LMVEFPLDPALSK + Oxidation (M)
☑	117	496.2275	990.4404	990.4804	-40.33	1	12	2.8	1	AKMDLEER
☑	76	421.7582	841.5018	841.4658	42.9	0	12	3.3	1	ATHTVSVK
☑	74	421.7559	841.4972	841.4810	19.3	0	12	3.6	1	AVLTWPR
☑	130	516.2977	1030.5808	1030.6036	-22.07	1	12	5.2	1	GLVGLNFRR
☑	139	523.2856	1044.5566	1044.5564	0.28	0	12	6.6	1	INDITLNSR
☑	271	651.8643	1301.7140	1301.7078	4.78	0	11	4.1	1	SLDLDSIIAEVK
☑	37	692.3918	691.3845	691.3765	11.5	1	11	5.8	1	KFAGNR
☑	94	435.7735	869.5324	869.5698	-42.96	1	11	3.1	1	VLKILER
☑	553	851.4633	1700.9120	1700.8985	7.96	0	11	4	1	AVFVDLEPTVIDEVR
☑	298	672.8471	1343.6796	1343.7157	-26.84	1	11	5.7	1	GSVGRSSAPAASLGK
☑	331	717.8047	1433.5948	1433.6535	-40.92	1	11	1.7	1	ALQRDDWSGSDGK
☑	51	379.7136	757.4126	757.4334	-27.39	0	11	9.4	1	GLNEVVK
☑	462	801.9191	1601.8236	1601.7443	49.6	0	11	5.7	1	FHTMPACAATNLPR + Oxidation (M)
☑	129	515.7794	1029.5442	1029.5931	-47.43	1	11	8	1	AQVKLSTQR
☑	312	691.3352	1380.6558	1380.6741	-13.21	1	11	5.2	1	KNVIMELSEMR + 2 Oxidation (M)
☑	467	802.8889	1603.7632	1603.7512	7.53	0	10	5.8	1	AEVMNPTRPVSSSET
☑	654	737.7070	2210.0992	2210.0967	1.11	0	10	5.3	1	LGEHNINVLEGNEQFIDAAK
☑	398	785.8391	1569.6636	1569.6960	-20.62	0	10	2.4	1	ESWEAAQEAWAHR
☑	762	1188.2935	3561.8587	3561.9534	-26.60	1	10	2	1	ELLTGTDLWPVAIFTVIFILLVDLMHRHQR + Oxidation (M)
☑	96	435.7746	869.5346	869.5698	-40.43	1	10	4.3	1	VLKEILR
☑	713	958.1292	2871.3658	2871.4477	-28.53	1	10	4	1	WDVCLTLSEKGFQQISFVNSIATTK
☑	350	738.3823	1474.7500	1474.6787	48.4	1	9	8.4	1	VDTEPKAEEASGDK
☑	73	414.2264	826.4382	826.4773	-47.26	1	9	6.3	1	AALPRGSR
☑	340	738.3669	1474.7192	1474.7602	-27.80	1	9	8.6	1	GDGLAFQMRTGLLP
☑	543	851.4530	1700.8914	1700.8985	-4.15	0	9	7	1	AVFVDLEPTVIDEVR
☑	95	435.7746	869.5346	869.4971	43.2	0	9	4.7	1	AVVESLPR
☑	345	738.3784	1474.7422	1474.7932	-34.58	0	9	9.1	1	LHHTSLPDFPAIK
☑	71	414.2235	826.4324	826.4297	3.32	0	9	6.4	1	DVLPNNR
☑	371	760.8850	1519.7554	1519.6833	47.5	1	9	9.1	1	VLEMSMKSTCFR + 2 Oxidation (M)
☑	77	421.7587	841.5028	841.4810	25.9	0	9	7.1	1	AVLTWPR
☑	176	565.3246	1128.6346	1128.5928	37.1	0	9	9.3	1	TDVNPFLAPR
☑	729	772.4192	3085.6477	3085.5989	15.8	0	8	2.7	1	MILGIILSMMVVSIFVFSCLLHHEHK + 2 Oxidation (M)

☑	489	810.8901	1619.7656	1619.7865	-12.89	0	8	9.1	1	GLYDGPVCEVSVTPK
☑	128	514.2868	1026.5590	1026.5458	12.9	0	8	10	1	GPLVQGVDSR
☑	460	801.4333	1600.8520	1600.8429	5.71	0	8	9	1	SMIISATIHMQVVR + Oxidation (M)
☑	614	1057.5195	2113.0244	2112.9687	26.4	1	8	9.3	1	KCFQTAHFYLEDNTSPR
☑	646	737.3643	2209.0711	2209.1491	-35.32	1	8	8.3	1	LGEHNIKVLEGNEQFVNAAK
☑	282	657.8612	1313.7078	1313.7415	-25.63	1	8	12	1	AALEASVLRATGR
☑	314	691.3487	1380.6828	1380.7150	-23.26	0	8	12	1	EHLGLSWAELAR
☑	69	412.7543	823.4940	823.4817	15.0	0	8	4.8	1	RPWLPR
☑	92	435.7733	869.5320	869.5334	-1.61	1	8	7	1	VTPKQGIK
☑	643	732.0196	2193.0370	2193.0452	-3.76	1	7	8.9	1	FGSDPATYNGFLEIMKEFK
☑	422	785.8444	1569.6742	1569.6399	21.9	1	7	5.4	1	MKTECDSEQGETR
☑	279	652.3647	1302.7148	1302.6608	41.5	1	7	13	1	KWQPPVFSSDI
☑	233	615.3006	1228.5866	1228.5989	-9.97	0	7	13	1	GEWPWQASLR
☑	72	414.2238	826.4330	826.4198	16.0	1	7	12	1	HHYSKR
☑	508	816.8943	1631.7740	1631.8460	-44.10	0	7	14	1	LVFAAYGNVFSAFAR
☑	663	763.3481	2287.0225	2287.1154	-40.63	1	7	6.9	1	EMKAEVNAGFSAIYESIGSLR + Oxidation (M)
☑	546	851.4565	1700.8984	1700.8985	-0.04	0	7	12	1	AVFVDLEPTVIDEVR
☑	297	670.8989	1339.7832	1339.7282	41.1	1	6	7.2	1	KMPVGLEPAVGSR
☑	761	1188.2787	3561.8143	3561.7859	7.96	1	6	5.3	1	QQQQTGNHPITVHCSAGAGRTGTFIALSNILER
☑	695	888.7545	2663.2417	2663.3009	-22.24	1	6	11	1	WMGVSDKSVIVCSTGSSLLLFSMK + 2 Oxidation (M)
☑	622	709.6712	2125.9918	2125.9747	8.01	1	5	13	1	ITCAQTFNFTRGLCMYK + Oxidation (M)
☑	113	485.7493	969.4840	969.4563	28.6	1	5	17	1	HCRDQVR
☑	636	1073.0161	2144.0176	2143.9740	20.3	1	5	15	1	KWMEQFEMAMSNIKPDK + 2 Oxidation (M)
☑	605	704.9991	2111.9755	2112.0773	-48.20	1	5	13	1	AFIATSTEGTDKGIMLNTVK + Oxidation (M)
☑	649	737.6996	2210.0770	2210.0967	-8.94	0	5	16	1	LGEHNINVLEGNEQFIDAAK
☑	754	891.4431	3561.7433	3561.6393	29.2	1	5	7	1	MVKDSSLVACAFSPDGGLFVTGSSGGDLTVWDDR + Oxidation (M)
☑	89	435.7656	869.5166	869.5083	9.60	1	5	15	1	VGQPVRSK
☑	640	1073.0392	2144.0638	2144.1399	-35.45	1	5	19	1	IGPISDTSSPELMGVGSLLKK + Oxidation (M)
☑	299	672.8474	1343.6802	1343.6616	13.9	1	5	24	1	CASKQAAVEPGAR
☑	680	1177.0856	2352.1566	2352.1518	2.04	0	5	16	1	ETEAEAQEVSLPALLMEHLDK
☑	589	976.4807	1950.9468	1950.9543	-3.84	0	5	20	1	DEIQCVVATVAFGMGINK
☑	36	692.3890	691.3817	691.3574	35.1	0	5	28	1	TALMEK
☑	570	897.8961	1793.7776	1793.7699	4.32	1	4	12	1	MSYLKTTMEDEESSK + Oxidation (M)
☑	688	819.4637	2455.3693	2455.2642	42.8	1	4	5.7	1	VREVEVVPSNMWGGQGLLGASVR + Oxidation (M)
☑	210	574.3311	1146.6476	1146.6318	13.8	0	4	18	1	TAMIVAEVLGK + Oxidation (M)
☑	571	897.9096	1793.8046	1793.8764	-40.00	1	4	16	1	NTMLSTPCVATKQSTR
☑	709	929.7959	2786.3659	2786.5001	-48.16	1	4	15	1	GLDLLQTCFVVSGGSLNLPRLQSLSL
☑	609	1057.0087	2112.0028	2112.0487	-21.71	1	4	19	1	EKWLLQGVPAGTAEEEEAR
☑	734	801.4522	3201.7797	3201.8601	-25.11	1	4	4.6	1	PPPPGPAAALGTALLLLLLASESSHTVLLRAR
☑	255	631.8049	1261.5952	1261.5537	33.0	0	4	26	1	MDFSDYDLLK + Oxidation (M)
☑	396	785.8381	1569.6616	1569.7059	-28.22	0	4	8.8	1	TEGASPEGEGTPWPR
☑	114	485.7534	969.4922	969.4992	-7.16	0	4	23	1	SQQPGGQLR
☑	711	933.4422	2797.3048	2797.2450	21.4	1	4	14	1	GARSVAGAGGGGCPAGGNDFQWCFSQVK
☑	522	816.8959	1631.7772	1631.8195	-25.90	1	4	26	1	TEFTFLDYVKQNK
☑	87	428.7668	855.5190	855.4814	44.0	1	4	20	1	IDRLPDK
☑	573	897.9128	1793.8110	1793.7699	22.9	1	4	20	1	MSYLKTTMEDEESSK + Oxidation (M)
☑	178	565.3273	1128.6400	1128.5961	38.9	0	4	28	1	AVMQSQKPPK + Oxidation (M)
☑	70	414.2226	826.4306	826.4259	5.80	0	4	24	1	YLVMSAK + Oxidation (M)
☑	760	1188.2722	3561.7948	3561.7951	-0.09	0	4	9.6	1	TAGAQVVLTDQELQLWPSDLDKPSASEGLPPGSR
☑	671	1168.5660	2335.1174	2335.2019	-36.17	0	4	20	1	LISATDIQYSASLLNSLNEQR
☑	131	517.2668	1032.5190	1032.5352	-15.68	1	3	39	1	RGLQYPDGK
☑	148	530.7909	1059.5672	1059.6077	-38.14	1	3	48	1	VATHTLKYK
☑	49	379.7111	757.4076	757.4195	-15.60	1	3	55	1	DALRQR
☑	618	707.3326	2118.9760	2118.9826	-3.14	1	3	21	1	LKNTSEQDQPMGGWEMIR
☑	697	903.1155	2706.3247	2706.2570	25.0	1	3	20	1	KDVLFGNMAEIYEFHNNIFMSR + 2 Oxidation (M)
☑	281	657.8579	1313.7012	1313.6438	43.7	0	3	37	1	LGTLGYPSYGMR
☑	490	816.8853	1631.7560	1631.7474	5.28	1	3	28	1	SMVNGGSWSGEPPRR + Oxidation (M)
☑	532	816.8991	1631.7836	1631.8460	-38.21	0	3	33	1	LVFAAYGNVFSAFAR
☑	478	810.4119	1618.8092	1618.8501	-25.23	1	3	37	1	SACREVFTQLPALK
☑	647	737.6964	2210.0674	2210.0929	-11.54	1	3	26	1	ELGEHGLYEYTELKTVAMK
☑	346	738.3788	1474.7430	1474.7528	-6.64	1	3	40	1	ADGLYRGSPLVGDR
☑	126	514.2750	1026.5354	1026.5094	25.4	0	3	35	1	NVEGPEGLGR
☑	110	476.7457	951.4768	951.4331	46.0	1	2	42	1	MTKGEENK + Oxidation (M)
☑	764	905.7182	3618.8437	3618.6866	43.4	1	2	13	1	VAVVSVDGCDTGVALRFGAMLGNYSCAAQGTQGGSK + Oxidation (M)
☑	740	851.2089	3400.8065	3400.7409	19.3	1	2	11	1	QLISVFSSPQELGASLAQLVAQRAASCLEGDR
☑	456	795.8763	1589.7380	1589.7113	16.8	1	2	33	1	TQMQQMHGRMVPV + 3 Oxidation (M)
☑	252	631.3129	1260.6112	1260.6172	-4.76	0	2	47	1	GLLSYVMSGYR + Oxidation (M)
☑	776	1019.7321	4074.8993	4074.8525	11.5	1	2	11	1	LFATEECFAICNQALQMHGGYGYLKDYAVQQYMR
☑	648	737.6991	2210.0755	2210.0500	11.5	0	2	34	1	VMQNFSFQPCQETQIPLK + Oxidation (M)
☑	27	325.1888	648.3630	648.3629	0.28	1	2	39	1	GLGMKK + Oxidation (M)
☑	574	897.9168	1793.8190	1793.9029	-46.73	1	2	35	1	NRNLSGGVLMGFMLNR + Oxidation (M)
☑	501	816.8934	1631.7722	1631.7951	-13.98	1	2	44	1	AAGCPTGPGHKAQQPR
☑	339	736.8575	1471.7004	1471.6990	0.97	0	2	44	1	MNLGNTWIHNTR + Oxidation (M)
☑	590	656.9555	1967.8447	1967.8274	8.76	0	2	17	1	ATQADLMELDMAMEPDR + 2 Oxidation (M)
☑	627	1072.5190	2143.0234	2143.0521	-13.35	1	1	36	1	IMGGVDAEEGKWPWQVSVR
☑	150	533.2669	1064.5192	1064.4743	42.2	0	1	55	1	IQACAMESR
☑	344	738.3780	1474.7414	1474.8065	-44.10	1	1	57	1	VESLLENMGIKVK + Oxidation (M)
☑	746	863.4315	3449.6969	3449.7368	-11.57	0	1	18	1	IGVPQASDLAAEAVVLHYTDWLHPEDPTHLR
☑	26	325.1886	648.3626	648.3595	4.86	0	1	45	1	AFNAVK
☑	741	851.4378	3401.7221	3401.6532	20.3	0	1	19	1	MGIPLTWMLLVMMVTSWFTLAEASNSTEAR + Oxidation (M)
☑	668	779.0337	2334.0793	2334.1196	-17.26	1	1	28	1	AGRVCEGDMVIPTGDELSVTTK

☑	639	1073.0326	2144.0506	2143.9844	30.9	0	1	48	1	EMFAQDHPEVNSLEEVVR + Oxidation (M)
☑	617	707.3309	2118.9709	2119.0599	-42.02	1	0	37	1	FREFVYQEAAGPHQTLAR
☑	488	810.8825	1619.7504	1619.7209	18.2	0	0	52	1	LEASADANIQDNMGR + Oxidation (M)
☑	632	715.6734	2143.9984	2144.0498	-23.98	1	0	41	1	KLQNSIQESTQNFDDHLK
☑	183	574.3185	1146.6224	1146.6145	6.89	1	0	70	1	AGSAWVSKVSR
☑	120	505.7470	1009.4794	1009.5127	-32.96	1	0	59	1	VRQMFASR + Oxidation (M)
☑	470	805.9015	1609.7884	1609.8538	-40.57	1	0	61	1	EISNGKWLLYLMK + Oxidation (M)
☑	1	355.0797	354.0724							
☑	2	361.1398	360.1325							
☑	3	361.1489	360.1416							
☑	4	424.3160	423.3087							
☑	5	429.1035	428.0962							
☑	6	445.1225	444.1152							
☑	7	445.1355	444.1282							
☑	8	453.1935	452.1862							
☑	9	472.2896	471.2823							
☑	10	484.8884	483.8811							
☑	11	503.1200	502.1127							
☑	12	503.3114	502.3041							
☑	13	517.2617	516.2544							
☑	14	517.7728	516.7655							
☑	15	519.1511	518.1438							
☑	16	519.2682	518.2609							
☑	17	582.3313	581.3240							
☑	18	591.3353	590.3280							
☑	19	591.3372	590.3299							
☑	20	591.3375	590.3302							
☑	21	615.7893	614.7820							
☑	22	616.3849	615.3776							
☑	23	618.2722	617.2649							
☑	24	632.3665	631.3592							
☑	28	327.6999	653.3852							
☑	29	327.7017	653.3888							
☑	30	332.5570	663.0994							
☑	31	670.8994	669.8921							
☑	32	688.3806	687.3733							
☑	33	692.3674	691.3601							
☑	34	692.3825	691.3752							
☑	35	692.3873	691.3800							
☑	38	714.7493	713.7420							
☑	39	718.3547	717.3474							
☑	40	722.3738	721.3665							
☑	41	729.8591	728.8518							
☑	42	729.8614	728.8541							
☑	43	736.8525	735.8452							
☑	44	742.7342	741.7269							
☑	45	743.8713	742.8640							
☑	46	744.4328	743.4255							
☑	47	747.8560	746.8487							
☑	48	755.4680	754.4607							
☑	52	761.3905	760.3832							
☑	53	763.4495	762.4422							
☑	54	772.7581	771.7508							
☑	55	793.4175	792.4102							
☑	56	793.4280	792.4207							
☑	57	793.4313	792.4240							
☑	58	793.4393	792.4320							
☑	59	797.3967	796.3894							
☑	60	797.6718	796.6645							
☑	61	802.7986	801.7913							
☑	62	808.3721	807.3648							
☑	63	810.4214	809.4141							
☑	65	412.7524	823.4902							
☑	66	412.7527	823.4908							
☑	79	421.7620	841.5094							
☑	80	842.5316	841.5243							
☑	81	423.2233	844.4320							
☑	83	423.2282	844.4418							
☑	84	846.4227	845.4154							
☑	85	846.4623	845.4550							
☑	88	863.7095	862.7022							
☑	97	872.5276	871.5203							
☑	98	874.5309	873.5236							
☑	99	438.7576	875.5006							
☑	100	894.7733	893.7660							
☑	101	906.5190	905.5117							
☑	102	906.5303	905.5230							
☑	103	906.5461	905.5388							
☑	104	920.4861	919.4788							
☑	106	932.4200	931.4127							
☑	107	470.8339	939.6532							

☑	108	951.4979	950.4906
☑	109	951.8571	950.8498
☑	111	478.1041	954.1936
☑	112	963.6493	962.6420
☑	115	977.7725	976.7652
☑	116	982.6216	981.6143
☑	118	999.6141	998.6068
☑	119	505.2855	1008.5564
☑	121	510.2983	1018.5820
☑	122	510.2990	1018.5834
☑	123	510.3012	1018.5878
☑	124	1021.6116	1020.6043
☑	125	1021.8164	1020.8091
☑	127	514.2797	1026.5448
☑	136	520.2693	1038.5240
☑	143	524.7946	1047.5746
☑	144	525.2810	1048.5474
☑	146	525.2917	1048.5688
☑	147	530.7836	1059.5526
☑	149	533.2592	1064.5038
☑	151	538.1253	1074.2360
☑	152	542.7958	1083.5770
☑	153	545.7363	1089.4580
☑	154	545.7634	1089.5122
☑	155	545.7640	1089.5134
☑	156	545.7656	1089.5166
☑	157	546.7594	1091.5042
☑	158	554.2649	1106.5152
☑	160	556.3140	1110.6134
☑	161	556.3168	1110.6190
☑	162	562.2876	1122.5606
☑	163	563.8179	1125.6212
☑	164	565.3137	1128.6128
☑	165	565.3169	1128.6192
☑	166	565.3170	1128.6194
☑	167	565.3181	1128.6216
☑	169	565.3208	1128.6270
☑	170	565.3210	1128.6274
☑	171	565.3214	1128.6282
☑	172	565.3215	1128.6284
☑	173	565.3229	1128.6312
☑	174	565.3243	1128.6340
☑	175	565.3245	1128.6344
☑	177	565.3268	1128.6390
☑	179	565.3289	1128.6432
☑	180	565.3292	1128.6438
☑	181	572.3431	1142.6716
☑	182	574.3153	1146.6160
☑	185	574.3215	1146.6284
☑	186	574.3222	1146.6298
☑	187	574.3236	1146.6326
☑	188	574.3245	1146.6344
☑	189	574.3263	1146.6380
☑	194	574.3277	1146.6408
☑	196	574.3279	1146.6412
☑	206	574.3306	1146.6466
☑	211	574.3311	1146.6476
☑	215	1148.7328	1147.7255
☑	216	579.2955	1156.5764
☑	218	1162.4799	1161.4726
☑	219	582.3195	1162.6244
☑	220	582.3254	1162.6362
☑	221	582.3277	1162.6408
☑	222	582.3297	1162.6448
☑	223	583.2960	1164.5774
☑	224	584.8265	1167.6384
☑	225	588.3420	1174.6694
☑	226	590.2976	1178.5806
☑	227	590.3051	1178.5956
☑	228	606.8477	1211.6808
☑	229	614.8415	1227.6684
☑	232	615.2973	1228.5800
☑	236	615.3125	1228.6104
☑	237	615.3173	1228.6200
☑	238	616.8066	1231.5986
☑	239	618.2707	1234.5268
☑	240	626.3076	1250.6006
☑	241	629.9429	1257.8712
☑	245	631.3045	1260.5944
☑	253	631.3146	1260.6146
☑	254	631.8029	1261.5912

☑	256	631.8098	1261.6050
☑	257	632.3793	1262.7440
☑	260	1276.0366	1275.0293
☑	261	639.3495	1276.6844
☑	262	639.3512	1276.6878
☑	265	639.3650	1276.7154
☑	266	641.3467	1280.6788
☑	267	428.7611	1283.2615
☑	268	648.3688	1294.7230
☑	272	651.8669	1301.7192
☑	278	652.3638	1302.7130
☑	280	657.8510	1313.6874
☑	283	657.8622	1313.7098
☑	284	657.8630	1313.7114
☑	286	657.8670	1313.7194
☑	287	657.8687	1313.7228
☑	289	664.8458	1327.6770
☑	290	665.3529	1328.6912
☑	291	665.3602	1328.7058
☑	292	667.9150	1333.8154
☑	293	670.8458	1339.6770
☑	294	670.8692	1339.7238
☑	295	670.8762	1339.7378
☑	296	670.8839	1339.7532
☑	300	675.8537	1349.6928
☑	301	676.9324	1351.8502
☑	302	677.7803	1353.5460
☑	303	678.8408	1355.6670
☑	304	679.3489	1356.6832
☑	305	341.0215	1360.0569
☑	308	685.3792	1368.7438
☑	311	688.3701	1374.7256
☑	313	691.3355	1380.6564
☑	315	692.3530	1382.6914
☑	316	692.3760	1382.7374
☑	317	692.3795	1382.7444
☑	318	693.8282	1385.6418
☑	319	693.8896	1385.7646
☑	320	694.3635	1386.7124
☑	321	696.3606	1390.7066
☑	322	705.9033	1409.7920
☑	323	355.0473	1416.1601
☑	324	711.3118	1420.6090
☑	325	711.3287	1420.6428
☑	326	711.3327	1420.6508
☑	327	711.8225	1421.6304
☑	328	711.8459	1421.6772
☑	329	716.3568	1430.6990
☑	330	717.3319	1432.6492
☑	332	720.8417	1439.6688
☑	333	720.8440	1439.6734
☑	334	728.3522	1454.6898
☑	335	730.9031	1459.7916
☑	336	731.3462	1460.6778
☑	337	732.3721	1462.7296
☑	338	736.8455	1471.6764
☑	341	738.3699	1474.7252
☑	342	738.3713	1474.7280
☑	343	738.3729	1474.7312
☑	347	738.3795	1474.7444
☑	349	738.3814	1474.7482
☑	351	738.3840	1474.7534
☑	353	738.3912	1474.7678
☑	356	740.3666	1478.7186
☑	357	740.3692	1478.7238
☑	358	742.4603	1482.9060
☑	359	742.8790	1483.7434
☑	360	745.8330	1489.6514
☑	361	748.8511	1495.6876
☑	362	748.8543	1495.6940
☑	363	753.3779	1504.7412
☑	364	756.8419	1511.6692
☑	365	757.3382	1512.6618
☑	366	757.8568	1513.6990
☑	367	757.8580	1513.7014
☑	368	757.8599	1513.7052
☑	369	757.8612	1513.7078
☑	370	758.4351	1514.8556
☑	372	762.8272	1523.6398
☑	373	762.9028	1523.7910
☑	374	766.8405	1531.6664

☑	375	*766.8597*	*1531.7048*
☑	376	*766.8657*	*1531.7168*
☑	377	*766.8687*	*1531.7228*
☑	378	*774.8998*	*1547.7850*
☑	379	*775.8703*	*1549.7260*
☑	380	*775.8704*	*1549.7262*
☑	381	*775.8705*	*1549.7264*
☑	382	*1550.7377*	*1549.7304*
☑	383	*775.8734*	*1549.7322*
☑	384	*775.8805*	*1549.7464*
☑	385	*785.3551*	*1568.6956*
☑	386	*785.8297*	*1569.6448*
☑	387	*785.8307*	*1569.6468*
☑	388	*785.8309*	*1569.6472*
☑	389	*785.8321*	*1569.6496*
☑	390	*785.8323*	*1569.6500*
☑	391	*785.8363*	*1569.6580*
☑	392	*785.8364*	*1569.6582*
☑	393	*785.8367*	*1569.6588*
☑	394	*785.8369*	*1569.6592*
☑	395	*785.8376*	*1569.6606*
☑	397	*785.8386*	*1569.6626*
☑	399	*785.8392*	*1569.6638*
☑	400	*785.8399*	*1569.6652*
☑	401	*785.8403*	*1569.6660*
☑	402	*785.8403*	*1569.6660*
☑	403	*785.8405*	*1569.6664*
☑	404	*785.8408*	*1569.6670*
☑	405	*785.8409*	*1569.6672*
☑	406	*785.8413*	*1569.6680*
☑	407	*785.8414*	*1569.6682*
☑	408	*785.8416*	*1569.6686*
☑	409	*785.8417*	*1569.6688*
☑	410	*785.8417*	*1569.6688*
☑	411	*785.8420*	*1569.6694*
☑	412	*785.8422*	*1569.6698*
☑	413	*785.8422*	*1569.6698*
☑	414	*785.8422*	*1569.6698*
☑	415	*785.8427*	*1569.6708*
☑	416	*785.8431*	*1569.6716*
☑	417	*785.8435*	*1569.6724*
☑	418	*785.8436*	*1569.6726*
☑	419	*785.8437*	*1569.6728*
☑	421	*785.8442*	*1569.6738*
☑	423	*785.8444*	*1569.6742*
☑	424	*785.8445*	*1569.6744*
☑	425	*785.8447*	*1569.6748*
☑	426	*785.8448*	*1569.6750*
☑	427	*785.8455*	*1569.6764*
☑	428	*785.8459*	*1569.6772*
☑	429	*785.8461*	*1569.6776*
☑	430	*785.8463*	*1569.6780*
☑	431	*785.8463*	*1569.6780*
☑	432	*785.8471*	*1569.6796*
☑	433	*785.8471*	*1569.6796*
☑	434	*785.8474*	*1569.6802*
☑	435	*785.8475*	*1569.6804*
☑	436	*785.8475*	*1569.6804*
☑	437	*785.8478*	*1569.6810*
☑	438	*785.8478*	*1569.6810*
☑	439	*785.8479*	*1569.6812*
☑	440	*785.8482*	*1569.6818*
☑	441	*785.8482*	*1569.6818*
☑	442	*785.8493*	*1569.6840*
☑	443	*785.8496*	*1569.6846*
☑	444	*785.8521*	*1569.6896*
☑	445	*785.8522*	*1569.6898*
☑	446	*785.8557*	*1569.6968*
☑	447	*786.8522*	*1571.6898*
☑	448	*786.8541*	*1571.6936*
☑	449	*786.8574*	*1571.7002*
☑	450	*788.7875*	*1575.5604*
☑	451	*794.8399*	*1587.6652*
☑	452	*794.8420*	*1587.6694*
☑	453	*794.8519*	*1587.6892*
☑	454	*794.8831*	*1587.7516*
☑	455	*795.8742*	*1589.7338*
☑	457	*795.8964*	*1589.7782*
☑	458	*796.3791*	*1590.7436*
☑	459	*801.4287*	*1600.8428*
☑	461	*801.4580*	*1600.9014*

☑	463	*801.9247*	*1601.8348*
☑	464	*801.9269*	*1601.8392*
☑	465	*801.9270*	*1601.8394*
☑	466	*802.8834*	*1603.7522*
☑	468	*802.8927*	*1603.7708*
☑	469	*805.8164*	*1609.6182*
☑	471	*808.3991*	*1614.7836*
☑	474	*809.8861*	*1617.7576*
☑	476	*809.8953*	*1617.7760*
☑	477	*809.8990*	*1617.7834*
☑	479	*810.8393*	*1619.6640*
☑	480	*810.8716*	*1619.7286*
☑	484	*810.8779*	*1619.7412*
☑	486	*810.8810*	*1619.7474*
☑	493	*816.8915*	*1631.7684*
☑	514	*816.8947*	*1631.7748*
☑	521	*816.8958*	*1631.7770*
☑	536	*832.6773*	*1663.3400*
☑	537	*834.4014*	*1666.7882*
☑	538	*844.8012*	*1687.5878*
☑	539	*850.9382*	*1699.8618*
☑	540	*851.4467*	*1700.8788*
☑	541	*851.4474*	*1700.8802*
☑	544	*851.4534*	*1700.8922*
☑	545	*851.4555*	*1700.8964*
☑	547	*851.4571*	*1700.8996*
☑	548	*851.4595*	*1700.9044*
☑	551	*851.4625*	*1700.9104*
☑	554	*851.4734*	*1700.9322*
☑	555	*852.4055*	*1702.7964*
☑	556	*854.3867*	*1706.7588*
☑	557	*854.4058*	*1706.7970*
☑	558	*428.8021*	*1711.1793*
☑	559	*858.4742*	*1714.9338*
☑	560	*890.4050*	*1778.7954*
☑	561	*890.4119*	*1778.8092*
☑	562	*890.4155*	*1778.8164*
☑	563	*892.7701*	*1783.5256*
☑	565	*894.4686*	*1786.9226*
☑	568	*896.3610*	*1790.7074*
☑	569	*896.3789*	*1790.7432*
☑	572	*897.9101*	*1793.8056*
☑	575	*905.9919*	*1809.9692*
☑	576	*906.0045*	*1809.9944*
☑	578	*906.5100*	*1811.0054*
☑	579	*908.4478*	*1814.8810*
☑	580	*914.9546*	*1827.8946*
☑	581	*915.4625*	*1828.9104*
☑	582	*915.4660*	*1828.9174*
☑	583	*915.4718*	*1828.9290*
☑	584	*616.3306*	*1845.9700*
☑	585	*924.9957*	*1847.9768*
☑	586	*954.7288*	*1907.4430*
☑	587	*956.0098*	*1910.0050*
☑	588	*973.5104*	*1945.0062*
☑	591	*671.3910*	*2011.1512*
☑	592	*1011.4334*	*2020.8522*
☑	593	*1024.5026*	*2046.9906*
☑	594	*1030.4009*	*2058.7872*
☑	595	*1040.9728*	*2079.9310*
☑	596	*694.3204*	*2079.9394*
☑	597	*1040.9795*	*2079.9444*
☑	600	*1040.9845*	*2079.9544*
☑	601	*1040.9870*	*2079.9594*
☑	603	*699.3636*	*2095.0690*
☑	606	*1056.9989*	*2111.9832*
☑	608	*1057.0073*	*2112.0000*
☑	610	*705.0086*	*2112.0040*
☑	611	*705.3356*	*2112.9850*
☑	612	*705.3407*	*2113.0003*
☑	613	*1057.5079*	*2113.0012*
☑	615	*706.3426*	*2116.0060*
☑	616	*707.0169*	*2118.0289*
☑	619	*707.3403*	*2118.9991*
☑	620	*709.3424*	*2125.0054*
☑	621	*709.3670*	*2125.0792*
☑	624	*715.3429*	*2143.0069*
☑	628	*1072.5261*	*2143.0376*
☑	630	*1072.5365*	*2143.0584*
☑	631	*1072.5383*	*2143.0620*
☑	633	*1073.0101*	*2144.0056*

☑	634	*715.6771*	*2144.0095*
☑	635	*715.6795*	*2144.0167*
☑	637	*1073.0237*	*2144.0328*
☑	641	*720.3670*	*2158.0792*
☑	642	*722.6668*	*2164.9786*
☑	644	*732.0351*	*2193.0835*
☑	645	*735.3560*	*2203.0462*
☑	650	*737.6997*	*2210.0773*
☑	651	*737.7006*	*2210.0800*
☑	652	*737.7010*	*2210.0812*
☑	653	*737.7034*	*2210.0884*
☑	655	*737.7103*	*2210.1091*
☑	656	*738.0344*	*2211.0814*
☑	657	*1108.0321*	*2214.0496*
☑	658	*744.0340*	*2229.0802*
☑	659	*761.3887*	*2281.1443*
☑	660	*761.7104*	*2282.1094*
☑	661	*762.0528*	*2283.1366*
☑	662	*762.0620*	*2283.1642*
☑	664	*767.3689*	*2299.0849*
☑	665	*767.3712*	*2299.0918*
☑	666	*767.3818*	*2299.1236*
☑	667	*768.0377*	*2301.0913*
☑	669	*779.0370*	*2334.0892*
☑	672	*779.7130*	*2336.1172*
☑	673	*780.0542*	*2337.1408*
☑	676	*1177.0771*	*2352.1396*
☑	679	*1177.0840*	*2352.1534*
☑	684	*792.3639*	*2374.0699*
☑	685	*792.7459*	*2375.2159*
☑	686	*800.3902*	*2398.1488*
☑	687	*803.7632*	*2408.2678*
☑	689	*821.3797*	*2461.1173*
☑	690	*834.4104*	*2500.2094*
☑	691	*834.4430*	*2500.3072*
☑	692	*838.4274*	*2512.2604*
☑	693	*858.4812*	*2572.4218*
☑	694	*888.7502*	*2663.2288*
☑	696	*888.7626*	*2663.2660*
☑	698	*1372.7352*	*2743.4558*
☑	699	*916.4213*	*2746.2421*
☑	700	*917.0810*	*2748.2212*
☑	701	*917.0811*	*2748.2215*
☑	702	*919.0511*	*2754.1315*
☑	703	*919.7774*	*2756.3104*
☑	704	*929.1258*	*2784.3556*
☑	705	*929.4644*	*2785.3714*
☑	706	*929.7783*	*2786.3131*
☑	707	*929.7839*	*2786.3299*
☑	708	*929.7928*	*2786.3566*
☑	710	*933.4380*	*2797.2922*
☑	712	*958.1219*	*2871.3439*
☑	714	*958.1293*	*2871.3661*
☑	715	*958.1404*	*2871.3994*
☑	716	*958.1454*	*2871.4144*
☑	717	*958.1537*	*2871.4393*
☑	718	*964.1164*	*2889.3274*
☑	719	*972.9012*	*2915.6818*
☑	720	*973.4361*	*2917.2865*
☑	721	*731.1655*	*2920.6329*
☑	722	*979.8508*	*2936.5306*
☑	723	*738.4187*	*2949.6457*
☑	724	*738.4551*	*2949.7913*
☑	725	*1005.4928*	*3013.4566*
☑	726	*1015.8009*	*3044.3809*
☑	727	*766.3745*	*3061.4689*
☑	728	*1026.1361*	*3075.3865*
☑	730	*793.2418*	*3168.9381*
☑	731	*1065.4698*	*3193.3876*
☑	732	*801.2135*	*3200.8249*
☑	733	*801.4345*	*3201.7089*
☑	735	*802.1821*	*3204.6993*
☑	736	*802.4299*	*3205.6905*
☑	737	*812.4256*	*3245.6733*
☑	738	*1087.5117*	*3259.5133*
☑	739	*838.3743*	*3349.4681*
☑	742	*851.4606*	*3401.8133*
☑	743	*854.1410*	*3412.5349*
☑	744	*1139.8470*	*3416.5192*
☑	745	*859.4880*	*3433.9229*
☑	747	*872.0906*	*3484.3333*

☑	748	872.4459	3485.7545
☑	749	877.3615	3505.4169
☑	750	1172.2100	3513.6082
☑	751	882.1300	3524.4909
☑	752	888.2696	3549.0493
☑	753	891.4270	3561.6789
☑	755	1188.2625	3561.7657
☑	757	891.4513	3561.7761
☑	758	1188.2662	3561.7768
☑	763	896.4558	3581.7941
☑	765	906.2194	3620.8485
☑	766	911.6751	3642.6713
☑	767	915.6857	3658.7137
☑	768	929.2371	3712.9193
☑	769	933.8598	3731.4101
☑	770	939.4158	3753.6341
☑	771	943.0184	3768.0445
☑	772	958.7573	3831.0001
☑	773	967.6097	3866.4097
☑	774	1004.0294	4012.0885
☑	775	1011.5858	4042.3141
☑	777	1081.1510	4320.5749
☑	778	1085.1560	4336.5949
☑	779	1140.0453	4556.1521
☑	780	1143.4764	4569.8765
☑	781	1151.2518	4600.9781
☑	782	1192.8083	4767.2041
☑	783	1223.8950	4891.5509
☑	784	1262.2261	5044.8753
☑	785	1280.1780	5116.6829
☑	786	1385.7402	5538.9317

Search Parameters

```
Type of search         : MS/MS Ion Search
Enzyme                 : Trypsin
Fixed modifications    : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values            : Monoisotopic
Protein Mass           : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages   : 1
Instrument type        : ESI-QUAD-TOF
Number of queries      : 786
```

Mascot: http://www.matrixscience.com/

Mascot Search Results

User : **Dominic**
Email : **dominic.kurian@bbsrc.ac.uk**
Search title : **IPI Mouse_15-02-2010**
MS data file : **D:\Peaklist\Dominic Kurian\QTofDK20010807 GATC P 0010885.pkl**
Database : **IPI_mouse MOUSE_v3_79 (54943 sequences; 24917557 residues)**
Timestamp : **15 Feb 2011 at 16:07:35 GMT**
Protein hits : **IPI00420725** Tax_Id=10090 Gene_Symbol=Camk2a Uncharacterized protein
IPI00755181 Tax_Id=10090 Gene_Symbol=Krt10 keratin, type I cytoskeletal 10
IPI00131366 Tax_Id=10090 Gene_Symbol=Krt6b Keratin, type II cytoskeletal 6B
IPI00348328 Tax_Id=10090 Gene_Symbol=Krt78 keratin Kb40
IPI00322209 Tax_Id=10090 Gene_Symbol=Krt8 Keratin, type II cytoskeletal 8
IPI00347110 Tax_Id=10090 Gene_Symbol=Krt73 Keratin, type II cytoskeletal 73

	IPI_mouse	**Decoy**	**False discovery rate**
Peptide matches above identity threshold	18	0	0.00 %
Peptide matches above homology or identity threshold	22	0	0.00 %

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 > 37 indicate identity or extensive homology (p<0.01).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.

Score Distribution

Peptide Summary Report

Format As | Peptide Summary | Help

Significance threshold p< 0.01 | Max. number of hits AUTO

Standard scoring ○ MudPIT scoring ● | Ions score or expect cut-off 0 | 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. IPI00420725 **Mass:** 55882 **Score:** 276 **Queries matched:** 24 **emPAI:** 0.12
Tax_Id=10090 Gene_Symbol=Camk2a Uncharacterized 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**
☑	196	**574.3283**	**1146.6420**	**1146.6431**	**-0.89**	**0**	**(1)**	**44**	**1**	**K.GAILTTMLATR.N**
☑	197	**574.3286**	**1146.6426**	**1146.6431**	**-0.36**	**0**	**23**	**0.26**	**1**	**K.GAILTTMLATR.N**
	198	**574.3295**	**1146.6444**	**1146.6431**	**1.21**	**0**	**(2)**	**35**	**3**	**K.GAILTTMLATR.N**
☑	268	**631.3032**	**1260.5918**	**1260.5927**	**-0.71**	**0**	**(8)**	**10**	**1**	**R.FYFENLWSR.N**
☑	270	**631.3068**	**1260.5990**	**1260.5927**	**5.00**	**0**	**38**	**0.01**	**1**	**R.FYFENLWSR.N**
☑	301	**652.3496**	**1302.6846**	**1302.6932**	**-6.56**	**0**	**(12)**	**4.6**	**1**	**R.ITQYLDAGGIPR.T**
☑	302	**652.3525**	**1302.6904**	**1302.6932**	**-2.11**	**0**	**18**	**1.3**	**1**	**R.ITQYLDAGGIPR.T**
☑	493	**816.8842**	**1631.7538**	**1631.7719**	**-11.05**	**0**	**(55)**	**0.00019**	**1**	**R.FTEEYQLFEELGK.G**
☑	496	**816.8906**	**1631.7666**	**1631.7719**	**-3.21**	**0**	**(16)**	**1.5**	**1**	**R.FTEEYQLFEELGK.G**
☑	497	**816.8911**	**1631.7676**	**1631.7719**	**-2.59**	**0**	**(56)**	**0.00014**	**1**	**R.FTEEYQLFEELGK.G**
☑	498	**816.8913**	**1631.7680**	**1631.7719**	**-2.35**	**0**	**(51)**	**0.00053**	**1**	**R.FTEEYQLFEELGK.G**
☑	500	**816.8914**	**1631.7682**	**1631.7719**	**-2.23**	**0**	**(55)**	**0.00019**	**1**	**R.FTEEYQLFEELGK.G**
☑	501	**816.8923**	**1631.7700**	**1631.7719**	**-1.12**	**0**	**72**	**4e-006**	**1**	**R.FTEEYQLFEELGK.G**
☑	502	**816.8925**	**1631.7704**	**1631.7719**	**-0.88**	**0**	**(39)**	**0.0085**	**1**	**R.FTEEYQLFEELGK.G**
☑	503	**816.8937**	**1631.7728**	**1631.7719**	**0.59**	**0**	**(30)**	**0.069**	**1**	**R.FTEEYQLFEELGK.G**
☑	505	**816.8957**	**1631.7768**	**1631.7719**	**3.04**	**0**	**(57)**	**0.00013**	**1**	**R.FTEEYQLFEELGK.G**
☑	507	**816.8961**	**1631.7776**	**1631.7719**	**3.53**	**0**	**(26)**	**0.16**	**1**	**R.FTEEYQLFEELGK.G**
☑	508	**816.8961**	**1631.7776**	**1631.7719**	**3.53**	**0**	**(11)**	**5**	**1**	**R.FTEEYQLFEELGK.G**
☑	511	**816.8971**	**1631.7796**	**1631.7719**	**4.76**	**0**	**(57)**	**0.00013**	**1**	**R.FTEEYQLFEELGK.G**
☑	514	**816.8975**	**1631.7804**	**1631.7719**	**5.25**	**0**	**(26)**	**0.15**	**1**	**R.FTEEYQLFEELGK.G**
☑	515	**816.8981**	**1631.7816**	**1631.7719**	**5.99**	**0**	**(48)**	**0.0011**	**1**	**R.FTEEYQLFEELGK.G**
☑	518	**816.8998**	**1631.7850**	**1631.7719**	**8.07**	**0**	**(14)**	**2.9**	**1**	**R.FTEEYQLFEELGK.G**
☑	519	**816.9008**	**1631.7870**	**1631.7719**	**9.29**	**0**	**(65)**	**1.9e-005**	**1**	**R.FTEEYQLFEELGK.G**
☑	521	**816.9054**	**1631.7962**	**1631.7719**	**14.9**	**0**	**(10)**	**6.2**	**1**	**R.FTEEYQLFEELGK.G**

Proteins matching the same set of peptides:

```
          IPI00621806     Mass: 54651     Score: 276     Queries matched: 24
          Tax_Id=10090 Gene_Symbol=Camk2a Isoform Alpha CaMKII of Calcium/calmodulin-dependent protein kinase type II subunit alpha
```

```
2.        IPI00755181     Mass: 57178     Score: 79      Queries matched: 3    emPAI: 0.12
          Tax_Id=10090 Gene_Symbol=Krt10 keratin, type I cytoskeletal 10
       ☐  Check to include this hit in error tolerant search or archive report

         Query  Observed   Mr(expt)   Mr(calc)   ppm  Miss Score   Expect Rank   Peptide
       ☑  173   545.7680  1089.5214  1089.5237  -2.05   0    68  1.2e-005   1   K.VTMQNLNDR.L
       ☑  344   691.3235  1380.6324  1380.6408  -6.08   0   (28)    0.083   1   R.ALEESNYELEGK.I
       ☑  345   691.3331  1380.6516  1380.6408   7.83   0    49   0.00069   1   R.ALEESNYELEGK.I


          Proteins matching the same set of peptides:
          IPI00798492     Mass: 57906     Score: 79      Queries matched: 3
          Tax_Id=10090 Gene_Symbol=Krt10 Isoform 1 of Keratin, type I cytoskeletal 10
          IPI00828744     Mass: 57197     Score: 79      Queries matched: 3
          Tax_Id=10090 Gene_Symbol=Krt10 Isoform 2 of Keratin, type I cytoskeletal 10
```

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3.        IPI00131366     Mass: 60627     Score: 70      Queries matched: 3    emPAI: 0.05
          Tax_Id=10090 Gene_Symbol=Krt6b Keratin, type II cytoskeletal 6B
       ☐  Check to include this hit in error tolerant search or archive report

         Query  Observed   Mr(expt)   Mr(calc)   ppm  Miss Score  Expect Rank  Peptide
       ☑  298   651.8590  1301.7034  1301.7078  -3.36   0    54  0.00027    1  R.SLDLDSIIAEVK.A
       ☑  299   651.8593  1301.7040  1301.7078  -2.90   0   (38)  0.0097    1  R.SLDLDSIIAEVK.A
       ☑  300   651.8599  1301.7052  1301.7078  -1.98   0   (39)  0.0084    1  R.SLDLDSIIAEVK.A


          Proteins matching the same set of peptides:
          IPI00131368     Mass: 59641     Score: 70      Queries matched: 3
          Tax_Id=10090 Gene_Symbol=Krt6a Keratin, type II cytoskeletal 6A
          IPI00139301     Mass: 61957     Score: 70      Queries matched: 3
          Tax_Id=10090 Gene_Symbol=Krt5 Keratin, type II cytoskeletal 5
          IPI00221797     Mass: 59932     Score: 70      Queries matched: 3
          Tax_Id=10090 Gene_Symbol=Krt75 Keratin, type II cytoskeletal 75
          IPI00330480     Mass: 35315     Score: 70      Queries matched: 3
          Tax_Id=10090 Gene_Symbol=- 35 kDa protein
          IPI00470126     Mass: 60553     Score: 70      Queries matched: 3
          Tax_Id=10090 Gene_Symbol=Krt5 Uncharacterized protein
          IPI00762364     Mass: 50641     Score: 70      Queries matched: 3
          Tax_Id=10090 Gene_Symbol=Krt6a Uncharacterized protein
          IPI00785403     Mass: 59832     Score: 70      Queries matched: 3
          Tax_Id=10090 Gene_Symbol=Krt6b keratin, type II cytoskeletal 6B
```

```
4.        IPI00348328     Mass: 114018    Score: 52      Queries matched: 2    emPAI: 0.03
          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
          160   523.7686  1045.5226  1045.4975  24.1   0    14      4.1    2  R.GSGGQVTMPGR.G
       ☑  348   692.3519  1382.6892  1382.6830  4.51   0    52  0.00046    1  R.SLNNQFASFIDK.V
```

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5.        IPI00322209     Mass: 54531     Score: 52      Queries matched: 1    emPAI: 0.06
          Tax_Id=10090 Gene_Symbol=Krt8 Keratin, type II cytoskeletal 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
          348   692.3519  1382.6892  1382.7194  -21.80   1    52  0.00046    1  K.SLNNKFASFIDK.V
```

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6.        IPI00347110     Mass: 59502     Score: 46      Queries matched: 4    emPAI: 0.06
          Tax_Id=10090 Gene_Symbol=Krt73 Keratin, type II cytoskeletal 73
       ☐  Check to include this hit in error tolerant search or archive report

         Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score Expect Rank  Peptide
       ☑  281   639.3522  1276.6898  1276.7027  -10.04   0   (18)     1.1   1  K.LALDIEIATYR.K
       ☑  282   639.3556  1276.6966  1276.7027   -4.71   0    20     0.72   1  K.LALDIEIATYR.K
       ☑  284   639.3583  1276.7020  1276.7027   -0.48   0   (19)    0.73   1  K.LALDIEIATYR.K
       ☑  401   738.3970  1474.7794  1474.7780    0.99   0    46   0.0016   1  R.FLEQQNQVLQTK.W
```

```
Peptide matches not assigned to protein hits: (no details means no match)

         Query    Observed    Mr(expt)   Mr(calc)     ppm  Miss Score Expect Rank  Peptide
       ☑  240   614.8435   1227.6724  1227.6711    1.13   0    36   0.019    1  TSGPPVSELITK
       ☑  157   523.2830   1044.5514  1044.5564   -4.69   0    32   0.058    1  INDITLNSR
       ☑  156   523.2830   1044.5514  1044.5564   -4.69   0    30   0.098    1  INDITLNSR
       ☑  155   523.2829   1044.5512  1044.5564   -4.89   0    30     0.1    1  INDITLNSR
       ☑  103   421.7574    841.5002   841.4810    22.9   0    27    0.11    1  LGTWLPR
       ☑  109   428.7642    855.5138   855.4814    37.9   0    24    0.22    1  LGAETLPR
       ☑  102   421.7571    841.4996   841.4810    22.1   0    20     0.5    1  LGTWLPR
```

☑	170	533.2635	1064.5124	1064.5138	-1.28	0	20	0.68	1	AQYEDIAQK
☑	534	851.4528	1700.8910	1700.8985	-4.39	0	20	0.64	1	AVFVDLEPTVIDEVR
☑	104	423.2249	844.4352	844.4515	-19.22	1	19	1.7	1	AIRENSR
☑	67	741.4396	740.4323	740.4657	-45.07	1	19	0.54	1	RLVTPR
☑	245	616.3294	1230.6442	1230.6456	-1.06	0	18	1.4	1	ASQEVQEILSK
☑	248	616.7965	1231.5784	1231.5621	13.2	0	18	0.95	1	IANEWEEWR
☑	100	421.7558	841.4970	841.4810	19.0	0	18	0.9	1	LGTWLPR
☑	391	738.3775	1474.7404	1474.6731	45.7	0	18	1.3	1	MIHTGEKPCVCK + Oxidation (M)
☑	229	601.8072	1201.5998	1201.6302	-25.30	1	17	1.6	1	LGSEGVEEVKR
☑	91	412.7550	823.4954	823.5028	-8.94	1	17	0.55	1	VPSRLPR
☑	378	730.8994	1459.7842	1459.7592	17.2	1	17	1.3	1	DVLEKMELLDQK
☑	86	407.2395	812.4644	812.4756	-13.69	1	17	1.1	1	AGPKALEK
☑	243	615.3023	1228.5900	1228.6241	-27.69	0	16	1.4	1	AVPPHETFGFK
☑	160	523.7686	1045.5226	1045.5597	-35.42	1	16	2.4	1	SGKFVFSFK
☑	436	785.8358	1569.6570	1569.7245	-43.00	0	16	0.52	1	MSLAESYAQYVHR + Oxidation (M)
☑	130	485.7459	969.4772	969.4563	21.6	1	16	1.5	1	HCRDQVR
☑	376	730.8926	1459.7706	1459.7453	17.4	1	16	1.9	1	VDILENRVMDTR
☑	566	894.4688	1786.9230	1786.9070	9.00	0	15	1.9	1	LVCSSEPITCKPQLR
☑	373	728.8590	1455.7034	1455.7569	-36.71	0	15	2.1	1	ALALLEDEEQAVR
☑	99	421.7558	841.4970	841.4810	19.0	0	14	2.1	1	AVLTWPR
☑	110	428.7671	855.5196	855.5112	9.82	1	14	1.8	1	ALRMLPR
☑	158	523.2841	1044.5536	1044.5564	-2.59	0	14	3.7	1	INDITLNSR
☑	79	785.3552	784.3479	784.3868	-49.54	1	14	1.1	1	KDYGFR
☑	149	517.7773	1033.5400	1033.5192	20.1	0	14	3.9	1	LLEFQNDR
☑	175	546.7536	1091.4926	1091.5393	-42.77	1	14	2.2	1	RDMQVNTTK
☑	601	705.0020	2111.9842	2112.0011	-8.01	0	14	1.9	1	TTEQLIEAVNNGDFEAYAK
☑	223	594.3091	1186.6036	1186.6492	-38.39	1	14	3.7	1	MSRAPEILVR + Oxidation (M)
☑	241	614.8456	1227.6766	1227.6711	4.55	0	14	3	1	TSGPPVSELITK
☑	63	363.2190	724.4234	724.4344	-15.10	0	13	1.5	1	RPLSPR
☑	88	412.7511	823.4876	823.4817	7.25	0	13	1.3	1	RPWLPR
☑	254	618.2742	1234.5338	1234.5401	-5.04	0	13	1.8	1	NMSGNVHFEGK + Oxidation (M)
☑	286	639.8024	1277.5902	1277.6265	-28.39	0	13	2.9	1	GTSDHWIGLHR
☑	313	665.3237	1328.6328	1328.5992	25.3	0	13	3.1	1	GLMTIYEDEMK
☑	316	665.3463	1328.6780	1328.6547	17.6	0	13	3.7	1	CLPAGPSPEVFR
☑	327	670.8930	1339.7714	1339.7096	46.2	1	13	1.8	1	LSVGGDSDPPLKR
☑	258	624.8118	1247.6090	1247.6180	-7.15	1	13	4	1	KLDSTAGMPNSK
☑	154	523.2826	1044.5506	1044.5564	-5.46	0	13	5	1	INDITLNSR
☑	105	423.2271	844.4396	844.4654	-30.50	1	13	6.6	1	SPASKLDK
☑	115	435.7732	869.5318	869.5123	22.5	0	12	2.3	1	VSLWLPR
☑	90	412.7530	823.4914	823.4664	30.4	1	12	1.6	1	RDIPPAR
☑	148	517.7643	1033.5140	1033.5040	9.72	0	12	5.8	1	AVDLSSGETR
☑	224	595.3015	1188.5884	1188.6251	-30.83	1	12	5.2	1	EVPKQQAAYR
☑	320	665.3650	1328.7154	1328.6684	35.4	1	12	4.3	1	IAVDQEGKDQAR
☑	535	851.4545	1700.8944	1700.8985	-2.39	0	12	3.7	1	AVFVDLEPTVIDEVR
☑	352	696.3466	1390.6786	1390.7279	-35.39	0	12	4.9	1	QFCLELNGLAVK
☑	47	632.3531	631.3458	631.3289	26.8	0	12	14	1	ETNLR
☑	393	738.3797	1474.7448	1474.7528	-5.41	0	12	5.2	1	SGAGSHATHELPAIK
☑	128	476.7454	951.4762	951.4960	-20.78	1	11	5.5	1	MVGQAFRK + Oxidation (M)
☑	392	738.3784	1474.7422	1474.8065	-43.56	1	11	5.6	1	VESLLENMGIKVK + Oxidation (M)
☑	72	379.7110	757.4074	757.3719	47.0	0	11	8.4	1	SSPAGSPR
☑	159	523.3225	1044.6304	1044.5828	45.6	1	11	2.4	1	AARLGSPFAR
☑	321	665.3677	1328.7208	1328.7187	1.60	0	11	4.9	1	NLDLDSIIAEVK
☑	417	768.4241	1534.8336	1534.9096	-49.51	1	11	3.9	1	HFLGGLVPVRVSVR
☑	267	630.8173	1259.6200	1259.6357	-12.44	0	11	6.6	1	AVEESITNLER
☑	73	763.4373	762.4300	762.4276	3.20	0	11	6.8	1	LGAFDLK
☑	120	437.7486	873.4826	873.4807	2.18	0	11	8.5	1	ATEDVLVK
☑	165	530.7841	1059.5536	1059.5383	14.5	1	11	8.9	1	AQKMDPSGVK
☑	491	815.3732	1628.7318	1628.7214	6.39	0	11	3.3	1	MGAPEAGMAEYLFDK
☑	172	545.2977	1088.5808	1088.5714	8.71	0	10	8.6	1	VTDLQGDLTK
☑	118	435.7745	869.5344	869.5123	25.5	0	10	3.7	1	VSLWLPR
☑	234	605.8242	1209.6338	1209.6466	-10.52	1	10	7.1	1	EPVEQPRVTR
☑	504	816.8955	1631.7764	1631.8242	-29.27	0	10	6.2	1	MHAINGFLFSNLPR + Oxidation (M)
☑	309	659.3605	1316.7064	1316.7010	4.17	0	10	7.1	1	IEMEVEVALLR + Oxidation (M)
☑	198	574.3295	1146.6444	1146.6649	-17.80	0	10	5.7	1	AVALDGTLFLK
☑	145	517.2630	1032.5114	1032.5273	-15.40	1	10	9	1	KEQEQMLK
☑	127	475.2524	948.4902	948.5280	-39.80	0	10	9	1	NYLELVAK
☑	98	421.7497	841.4848	841.4844	0.58	0	9	6.4	1	AAPMLIAR
☑	388	738.3769	1474.7392	1474.6949	30.1	1	9	9.3	1	QMNSFQVAFLKM + 2 Oxidation (M)
☑	418	772.8556	1543.6966	1543.6395	37.0	0	9	5.1	1	CSNSADMTGPSFVR + Oxidation (M)
☑	577	901.4461	1800.8776	1800.8328	24.9	0	9	8.5	1	LYGWTMEPVFVCQR + Oxidation (M)
☑	150	519.2672	1036.5198	1036.5077	11.7	0	9	10	1	EFDGTEVLK
☑	565	894.4647	1786.9148	1786.9764	-34.43	1	9	9	1	IAFPNLKVVMVVDGNR + Oxidation (M)
☑	274	632.3272	1262.6398	1262.6441	-3.40	1	9	11	1	NVTIECPFKR
☑	57	692.3731	691.3658	691.3905	-35.63	0	8	13	1	ATYLPK
☑	89	412.7522	823.4898	823.5280	-46.27	1	8	4	1	TKILPPR
☑	557	883.9029	1765.7912	1765.7789	7.02	1	8	5.5	1	KADSGEDSLGCLNGDTK
☑	554	879.9472	1757.8798	1757.9060	-14.89	1	8	9.3	1	TEHAPSGKLSEIQHPK

☑	528	832.3854	1662.7562	1662.8366	-48.31	0	8	7.8	1	FVTLQIWDTAGQER
☑	179	554.2792	1106.5438	1106.5940	-45.33	1	8	13	1	ALCMTLVKR + Oxidation (M)
☑	580	913.9105	1825.8064	1825.8298	-12.82	0	8	5.5	1	EGSVGGSQVAALMMSSQR + 2 Oxidation (M)
☑	375	730.8780	1459.7414	1459.7042	25.5	0	8	12	1	GVSEPLLETDTGDK
☑	424	776.8488	1551.6830	1551.7199	-23.73	1	8	6.3	1	CKQLESTQTESNK
☑	632	758.4205	2272.2397	2272.1311	47.8	1	8	4.3	1	GFGFVTFMDQAGVDKVLAQSR
☑	371	727.8940	1453.7734	1453.7776	-2.89	0	8	10	1	ISDAVAALDPVDLR
☑	53	327.7028	653.3910	653.3609	46.2	0	8	5.1	1	SAIAHR
☑	399	738.3895	1474.7644	1474.6948	47.2	1	7	12	1	WMVAGKADPEMPK + Oxidation (M)
☑	146	517.2634	1032.5122	1032.4724	38.6	0	7	16	1	VLDEEGSER
☑	273	631.8104	1261.6062	1261.6150	-6.91	1	7	14	1	EASESQNLEKK
☑	453	785.8453	1569.6760	1569.7497	-46.93	1	7	5.7	1	GEMFVLEKGEYPR + Oxidation (M)
☑	676	753.4116	3009.6173	3009.6136	1.21	1	7	4.3	1	YLEYLFDVELAPPTLVLTQMEKILR + Oxidation (M)
☑	215	590.7988	1179.5830	1179.6111	-23.74	0	7	16	1	TYVCHIIFK
☑	361	714.3387	1426.6628	1426.7173	-38.19	1	7	10	1	CAPCRGNGVPVLK
☑	147	517.2635	1032.5124	1032.4724	38.8	0	7	18	1	VLDEEGSER
☑	307	659.3557	1316.6968	1316.6473	37.6	1	7	16	1	DAREAGFALDPR
☑	247	616.3654	1230.7162	1230.7006	12.7	0	7	7.4	1	QSVVVLMGSLAK
☑	484	801.9233	1601.8320	1601.8534	-13.34	1	7	14	1	MPLVHMSFLSIRR + Oxidation (M)
☑	624	737.7004	2210.0794	2210.0585	9.43	1	7	11	1	IITQNALHRAPHYNSCCR
☑	117	435.7735	869.5324	869.4971	40.7	0	7	8.7	1	AVVESLPR
☑	595	693.9965	2078.9677	2078.9700	-1.11	1	6	10	1	MQQHCDELMNLLKTFR + Oxidation (M)
☑	526	824.3863	1646.7580	1646.7747	-10.12	1	6	13	1	ARLGEASDSELADADK
☑	71	379.7092	757.4038	757.4082	-5.81	1	6	21	1	DKGVPSR
☑	45	619.2937	618.2864	618.2973	-17.57	0	6	19	1	IEDSR
☑	555	879.9559	1757.8972	1757.8916	3.19	1	6	16	1	QPCILLMDSLRGPSR + Oxidation (M)
☑	385	738.3738	1474.7330	1474.7780	-30.45	0	6	19	1	SYLRPITEAPSNK
☑	354	701.8492	1401.6838	1401.6783	3.97	1	6	17	1	TRPPKEQSSGCR
☑	116	435.7733	869.5320	869.5222	11.3	0	6	11	1	VTLEALPK
☑	397	738.3874	1474.7602	1474.7524	5.34	0	6	20	1	LPAAGVGDMVMATVK + Oxidation (M)
☑	261	625.3146	1248.6146	1248.5809	27.1	0	6	23	1	EGEWQTMIQK
☑	607	707.3361	2118.9865	2119.0629	-36.04	1	6	13	1	CMGPVMVGLRLPLTDVSQF
☑	144	516.3068	1030.5990	1030.5811	17.4	1	5	15	1	AKWLSVAEK
☑	477	795.8834	1589.7522	1589.8096	-36.08	1	5	17	1	SAAGLSMARAVSWQR
☑	279	639.3420	1276.6694	1276.6598	7.55	0	5	24	1	VVVQNNLCFGK
☑	294	647.3664	1292.7182	1292.6976	16.0	0	5	14	1	ISYEPITTTLR
☑	444	785.8418	1569.6690	1569.6399	18.6	1	5	7.8	1	MKTECDSEQGETR
☑	364	719.3223	1436.6300	1436.6783	-33.60	0	5	12	1	DNDSYINVQEIK
☑	571	897.9120	1793.8094	1793.8189	-5.28	1	5	14	1	MSGGGGDDVVCTGWLRK
☑	351	692.3663	1382.7180	1382.7194	-0.98	1	5	21	1	RDIVFAASLYTQ
☑	479	795.8920	1589.7694	1589.8096	-25.27	1	5	21	1	SAAGLSMARAVSWQR
☑	135	505.2794	1008.5442	1008.5716	-27.11	1	5	20	1	AKAHILNDK
☑	239	614.8431	1227.6716	1227.6625	7.43	1	5	24	1	RWGHTVFVAR
☑	510	816.8969	1631.7792	1631.7205	36.0	0	5	23	1	MMTTATSGNIMTTEK + Oxidation (M)
☑	277	633.3164	1264.6182	1264.6187	-0.33	1	5	26	1	DELEFEKEVK
☑	330	672.3507	1342.6868	1342.6915	-3.46	0	5	27	1	MPTGTTVNPAGIGK
☑	271	631.8051	1261.5956	1261.5826	10.3	0	4	24	1	EALEVDWSGEK
☑	226	599.8269	1197.6392	1197.6183	17.5	0	4	23	1	FLFTTGFHTK
☑	142	516.3029	1030.5912	1030.5519	38.2	1	4	25	1	SARAAEAVTR
☑	169	533.2592	1064.5038	1064.4774	24.8	0	4	26	1	DDVAQENFK
☑	360	711.3236	1420.6326	1420.6318	0.63	0	4	16	1	LTGASSDVEEEER
☑	591	1011.4652	2020.9158	2020.9459	-14.85	0	4	13	1	SMSQIYCIENAHGQLVR + Oxidation (M)
☑	342	688.3369	1374.6592	1374.6449	10.4	0	4	26	1	EPGETIVEAMQR + Oxidation (M)
☑	694	855.1420	3416.5389	3416.6612	-35.79	1	4	8.7	1	TTNEGLLYPNPAAQMLVGDSFARHYYFLGR + Oxidation (M)
☑	94	414.2219	826.4292	826.4661	-44.57	0	4	22	1	VAAPNLSR
☑	262	625.3168	1248.6190	1248.5809	30.6	0	4	32	1	DDGMQIWGAIK + Oxidation (M)
☑	572	897.9121	1793.8096	1793.7699	22.2	1	4	19	1	MSYLKTTMEDEESSK + Oxidation (M)
☑	573	897.9143	1793.8140	1793.7699	24.6	1	4	20	1	MSYLKTTMEDEESSK + Oxidation (M)
☑	466	785.8697	1569.7248	1569.7132	7.44	0	4	22	1	EVQESQTQGSQGHR
☑	400	738.3921	1474.7696	1474.7991	-19.95	1	4	29	1	AIEAASSLKSQAATK
☑	516	816.8981	1631.7816	1631.8301	-29.68	1	4	29	1	KVASGSAAAAAGPSCSLK
☑	517	816.8984	1631.7822	1631.7205	37.9	0	3	30	1	MMTTATSGNIMTTEK + Oxidation (M)
☑	394	738.3853	1474.7560	1474.7528	2.19	0	3	34	1	SGAGSHATHELPAIK
☑	626	738.0252	2211.0538	2211.0379	7.20	0	3	23	1	GITSFIQHPASTPCEEANPR
☑	167	530.7861	1059.5576	1059.5358	20.7	0	3	50	1	WPMLLNMR
☑	384	738.3727	1474.7308	1474.6737	38.7	0	3	36	1	MFWNLMPFTTR + 2 Oxidation (M)
☑	638	786.3861	2356.1365	2356.0868	21.1	0	3	21	1	EGQLYAMELQGFWMDIGQPK + Oxidation (M)
☑	570	897.9114	1793.8082	1793.7699	21.4	1	3	22	1	MSYLKTTMEDEESSK + Oxidation (M)
☑	512	816.8972	1631.7798	1631.7865	-4.07	1	3	32	1	CNKEIYVVTESYK
☑	138	513.7487	1025.4828	1025.5142	-30.53	0	3	31	1	QPDTPAELR
☑	675	752.1354	3004.5125	3004.5943	-27.24	1	3	16	1	TFQTALFLDRLLDGSPLPQEVVMSLSK
☑	134	505.2752	1008.5358	1008.5127	22.9	0	3	34	1	EYLESLQK
☑	21	517.2652	516.2579	516.2656	-14.89	0	3	45	1	AGDVR
☑	644	801.7284	2402.1634	2402.1570	2.67	1	3	27	1	SGLCIEANSRIMELDPNDGALK
☑	576	901.4456	1800.8766	1800.8469	16.5	0	3	37	1	LMPMFLMVMPGMISR + 3 Oxidation (M)
☑	119	435.7748	869.5350	869.5123	26.1	0	2	22	1	VSLWLPR
☑	199	574.3331	1146.6516	1146.6649	-11.52	0	2	27	1	VSATFLPTAIK

☑	218	590.8070	1179.5994	1179.5554	37.4	1	2	45	1	AVTKENSEMR + Oxidation (M)
☑	569	897.9113	1793.8080	1793.7672	22.8	1	2	26	1	CDLNMQQQEEEKAR + Oxidation (M)
☑	525	824.3836	1646.7526	1646.8055	-32.08	1	2	32	1	GLRTLCCCLPIER
☑	276	632.3409	1262.6672	1262.7095	-33.45	0	2	44	1	SRPPALEPGALR
☑	292	644.8557	1287.6968	1287.6459	39.6	1	2	42	1	AVTVEFKHDDK
☑	210	587.3012	1172.5878	1172.6149	-23.09	0	2	56	1	LNQEVSQLSR
☑	405	747.8829	1493.7512	1493.6966	36.6	1	2	40	1	NANNINMLKDGMK + 2 Oxidation (M)
☑	356	707.3298	1412.6450	1412.7129	-48.02	1	2	31	1	CRPPRCDLLAR
☑	408	757.8497	1513.6848	1513.7307	-30.29	1	2	30	1	THEAQIQEMRQK + Oxidation (M)
☑	471	1572.7390	1571.7317	1571.7171	9.30	1	2	38	1	KMGEMQLSSVTDSK + 2 Oxidation (M)
☑	415	766.8577	1531.7008	1531.7743	-47.95	0	2	35	1	EVQQHALVHQESK
☑	140	514.2820	1026.5494	1026.5757	-25.53	1	2	45	1	RLMTLTHR
☑	153	523.2803	1044.5460	1044.5638	-16.95	0	2	68	1	VLEAPMTIR + Oxidation (M)
☑	617	715.3487	2143.0243	2143.0831	-27.44	1	1	36	1	CPKVSVATPDVSLEASEGAVK
☑	168	533.2479	1064.4812	1064.5219	-38.18	1	1	37	1	MAAQMVRSR + Oxidation (M)
☑	93	414.2217	826.4288	826.4661	-45.05	0	1	40	1	VAAPNLSR
☑	478	795.8888	1589.7630	1589.7475	9.81	0	1	47	1	SGPLFSFDVHDDVR
☑	143	516.3063	1030.5980	1030.5546	42.1	0	1	40	1	VDILDIDTK
☑	275	632.3361	1262.6576	1262.6579	-0.17	1	1	54	1	LSSTPTATSRSR
☑	372	727.8994	1453.7842	1453.8252	-28.19	1	1	42	1	ALELENDRLLLR
☑	544	859.4189	1716.8232	1716.8519	-16.67	0	1	49	1	CVVPGQAHAQVTWHK
☑	428	781.3944	1560.7742	1560.7330	26.4	1	1	54	1	VYSMRFCPFAQR
☑	410	757.8604	1513.7062	1513.6323	48.8	1	1	42	1	MNSVGEACTDMKR + Oxidation (M)
☑	64	725.4449	724.4376	724.4020	49.1	1	1	23	1	KQFFR
☑	166	530.7843	1059.5540	1059.5673	-12.47	1	1	91	1	KQEGIVGSSR
☑	256	618.3239	1234.6332	1234.5942	31.6	1	1	68	1	QNGDRFIEEK
☑	139	514.2798	1026.5450	1026.5393	5.64	1	1	56	1	VALRHMER + Oxidation (M)
☑	152	519.2725	1036.5304	1036.5777	-45.63	1	0	69	1	QAAPREPLR
☑	666	958.1300	2871.3682	2871.3536	5.07	1	0	33	1	DVFQRNQQDGQLEESPGSWPGAGTIR
☑	568	897.9097	1793.8048	1793.8651	-33.60	0	0	43	1	LMAEALAMIESTQQAR + 2 Oxidation (M)
☑	1	341.0242	340.0169							
☑	2	341.0275	340.0202							
☑	3	342.2688	341.2615							
☑	4	360.9891	359.9818							
☑	5	416.2400	415.2327							
☑	6	424.3148	423.3075							
☑	7	429.0965	428.0892							
☑	8	429.0978	428.0905							
☑	9	430.2511	429.2438							
☑	10	445.1122	444.1049							
☑	11	445.1232	444.1159							
☑	12	445.1351	444.1278							
☑	13	451.1725	450.1652							
☑	14	459.2731	458.2658							
☑	15	469.1872	468.1799							
☑	16	469.1905	468.1832							
☑	17	470.2026	469.1953							
☑	18	492.2361	491.2288							
☑	19	503.0361	502.0288							
☑	20	503.3152	502.3079							
☑	22	521.0000	519.9927							
☑	23	522.9882	521.9809							
☑	24	533.2681	532.2608							
☑	25	545.3068	544.2995							
☑	26	549.0557	548.0484							
☑	27	553.0099	552.0026							
☑	28	558.7847	557.7774							
☑	29	562.2796	561.2723							
☑	30	565.0400	564.0327							
☑	31	565.3137	564.3064							
☑	32	572.3085	571.3012							
☑	33	579.0262	578.0189							
☑	34	579.2961	578.2888							
☑	35	585.0348	584.0275							
☑	36	585.0372	584.0299							
☑	37	587.0353	586.0280							
☑	38	590.3307	589.3234							
☑	39	595.0097	594.0024							
☑	40	595.2759	594.2686							
☑	41	616.3271	615.3198							
☑	42	616.3747	615.3674							
☑	43	617.2840	616.2767							
☑	44	617.3132	616.3059							
☑	46	620.7597	619.7524							
☑	48	632.3674	631.3601							
☑	49	634.9940	633.9867							
☑	50	638.3274	637.3201							

☑	51	643.4092	642.4019
☑	52	327.6973	653.3800
☑	54	665.3381	664.3308
☑	55	665.3527	664.3454
☑	56	668.9276	667.9203
☑	58	694.3491	693.3418
☑	59	350.1557	698.2968
☑	60	707.3477	706.3404
☑	61	723.3727	722.3654
☑	62	363.2188	724.4230
☑	65	729.7198	728.7125
☑	66	729.8578	728.8505
☑	68	743.4255	742.4182
☑	69	745.9082	744.9009
☑	70	757.3588	756.3515
☑	74	766.4128	765.4055
☑	75	766.6998	765.6925
☑	76	774.3881	773.3808
☑	77	775.8660	774.8587
☑	78	391.2271	780.4396
☑	80	787.7332	786.7259
☑	81	793.4234	792.4161
☑	82	793.4310	792.4237
☑	83	794.3906	793.3833
☑	84	802.3954	801.3881
☑	85	804.7424	803.7351
☑	87	819.4597	818.4524
☑	92	826.5800	825.5727
☑	95	414.2317	826.4488
☑	96	828.1093	827.1020
☑	97	839.7756	838.7683
☑	101	421.7563	841.4980
☑	106	846.4387	845.4314
☑	107	847.7014	846.6941
☑	108	855.3943	854.3870
☑	111	861.4664	860.4591
☑	112	431.7305	861.4464
☑	113	431.7315	861.4484
☑	114	435.7690	869.5234
☑	121	449.2104	896.4062
☑	122	899.4448	898.4375
☑	123	908.7192	907.7119
☑	124	924.6996	923.6923
☑	125	935.0483	934.0410
☑	126	470.7675	939.5204
☑	129	958.4771	957.4698
☑	131	487.2795	972.5444
☑	132	493.2934	984.5722
☑	133	505.2740	1008.5334
☑	136	505.7445	1009.4744
☑	137	1021.3894	1020.3821
☑	141	515.3065	1028.5984
☑	151	519.2700	1036.5254
☑	161	1053.5415	1052.5342
☑	162	528.3117	1054.6088
☑	163	530.7632	1059.5118
☑	164	530.7643	1059.5140
☑	171	537.2878	1072.5610
☑	174	545.7690	1089.5234
☑	176	546.7556	1091.4966
☑	177	546.7605	1091.5064
☑	178	553.2914	1104.5682
☑	180	554.2919	1106.5692
☑	181	556.7847	1111.5548
☑	182	564.8070	1127.5994
☑	183	565.3002	1128.5858
☑	184	565.3081	1128.6016
☑	185	565.3114	1128.6082
☑	186	1135.5474	1134.5401
☑	187	1137.5103	1136.5030
☑	188	572.3028	1142.5910
☑	189	572.3290	1142.6434
☑	190	574.3148	1146.6150
☑	191	574.3186	1146.6226
☑	192	574.3219	1146.6292
☑	193	574.3220	1146.6294
☑	194	574.3242	1146.6338

☑	195	*574.3255*	*1146.6364*
☑	200	*574.3392*	*1146.6638*
☑	201	*574.3395*	*1146.6644*
☑	202	*574.8029*	*1147.5912*
☑	203	*578.8290*	*1155.6434*
☑	204	*579.3042*	*1156.5938*
☑	205	*579.3061*	*1156.5976*
☑	206	*1158.7262*	*1157.7189*
☑	207	*580.3287*	*1158.6428*
☑	208	*582.3223*	*1162.6300*
☑	209	*582.3409*	*1162.6672*
☑	211	*587.3020*	*1172.5894*
☑	212	*588.3432*	*1174.6718*
☑	213	*589.8100*	*1177.6054*
☑	214	*590.2994*	*1178.5842*
☑	216	*590.7989*	*1179.5832*
☑	217	*590.8007*	*1179.5868*
☑	219	*590.8085*	*1179.6024*
☑	220	*592.2846*	*1182.5546*
☑	221	*1186.3834*	*1185.3761*
☑	222	*593.8180*	*1185.6214*
☑	225	*596.7852*	*1191.5558*
☑	227	*599.8465*	*1197.6784*
☑	228	*599.8491*	*1197.6836*
☑	230	*602.3141*	*1202.6136*
☑	231	*602.3174*	*1202.6202*
☑	232	*1204.8134*	*1203.8061*
☑	233	*604.8074*	*1207.6002*
☑	235	*606.8433*	*1211.6720*
☑	236	*606.8468*	*1211.6790*
☑	237	*608.3107*	*1214.6068*
☑	238	*612.7756*	*1223.5366*
☑	242	*615.3013*	*1228.5880*
☑	244	*615.3051*	*1228.5956*
☑	246	*616.3533*	*1230.6920*
☑	249	*616.7987*	*1231.5828*
☑	250	*616.8149*	*1231.6152*
☑	251	*616.8370*	*1231.6594*
☑	252	*617.8182*	*1233.6218*
☑	253	*618.2675*	*1234.5204*
☑	255	*618.3215*	*1234.6284*
☑	257	*624.2947*	*1246.5748*
☑	259	*625.3065*	*1248.5984*
☑	260	*625.3119*	*1248.6092*
☑	263	*625.3206*	*1248.6266*
☑	264	*626.3072*	*1250.5998*
☑	265	*627.7880*	*1253.5614*
☑	266	*629.9380*	*1257.8614*
☑	269	*631.3054*	*1260.5962*
☑	272	*631.8072*	*1261.5998*
☑	278	*636.3246*	*1270.6346*
☑	280	*639.3491*	*1276.6836*
☑	283	*639.3563*	*1276.6980*
☑	285	*639.3596*	*1276.7046*
☑	287	*639.8105*	*1277.6064*
☑	288	*428.7632*	*1283.2678*
☑	289	*643.8198*	*1285.6250*
☑	290	*644.7901*	*1287.5656*
☑	291	*644.8137*	*1287.6128*
☑	293	*646.3283*	*1290.6420*
☑	295	*648.3762*	*1294.7378*
☑	296	*651.8530*	*1301.6914*
☑	297	*651.8588*	*1301.7030*
☑	303	*653.7860*	*1305.5574*
☑	304	*657.3508*	*1312.6870*
☑	305	*657.8543*	*1313.6940*
☑	306	*659.3350*	*1316.6554*
☑	308	*659.3590*	*1316.7034*
☑	310	*662.8101*	*1323.6056*
☑	311	*662.8180*	*1323.6214*
☑	312	*664.8234*	*1327.6322*
☑	314	*665.3420*	*1328.6694*
☑	315	*665.3454*	*1328.6762*
☑	317	*665.3479*	*1328.6812*
☑	318	*665.3576*	*1328.7006*
☑	319	*665.3637*	*1328.7128*
☑	322	*668.3506*	*1334.6866*

☑	323	669.8050	1337.5954
☑	324	670.3049	1338.5952
☑	325	670.3211	1338.6276
☑	326	670.8461	1339.6776
☑	328	671.3350	1340.6554
☑	329	671.3575	1340.7004
☑	331	672.3639	1342.7132
☑	332	672.8434	1343.6722
☑	333	674.8414	1347.6682
☑	334	675.3286	1348.6426
☑	335	676.9155	1351.8164
☑	336	677.8329	1353.6512
☑	337	680.3687	1358.7228
☑	338	681.3326	1360.6506
☑	339	682.3409	1362.6672
☑	340	685.3844	1368.7542
☑	341	687.3656	1372.7166
☑	343	688.3516	1374.6886
☑	346	691.3408	1380.6670
☑	347	692.3462	1382.6778
☑	349	692.3532	1382.6918
☑	350	692.3560	1382.6974
☑	353	698.8453	1395.6760
☑	355	702.8401	1403.6656
☑	357	708.9245	1415.8344
☑	358	710.8427	1419.6708
☑	359	711.3199	1420.6252
☑	362	714.7645	1427.5144
☑	363	715.8468	1429.6790
☑	365	719.3273	1436.6400
☑	366	720.3449	1438.6752
☑	367	720.8420	1439.6694
☑	368	722.8765	1443.7384
☑	369	722.8981	1443.7816
☑	370	723.3694	1444.7242
☑	374	730.8651	1459.7156
☑	377	730.8934	1459.7722
☑	379	730.8994	1459.7842
☑	380	730.9032	1459.7918
☑	381	733.3936	1464.7726
☑	382	735.8239	1469.6332
☑	383	737.8687	1473.7228
☑	386	738.3757	1474.7368
☑	387	738.3763	1474.7380
☑	389	738.3772	1474.7398
☑	390	738.3773	1474.7400
☑	395	738.3854	1474.7562
☑	396	738.3863	1474.7580
☑	398	738.3889	1474.7632
☑	402	740.3651	1478.7156
☑	403	746.8673	1491.7200
☑	404	747.8588	1493.7030
☑	406	748.8496	1495.6846
☑	407	748.8518	1495.6890
☑	409	757.8577	1513.7008
☑	411	758.4211	1514.8276
☑	412	759.4084	1516.8022
☑	413	759.4500	1516.8854
☑	414	766.8566	1531.6986
☑	416	766.8604	1531.7062
☑	419	773.8304	1545.6462
☑	420	774.8945	1547.7744
☑	421	775.3884	1548.7622
☑	422	775.8660	1549.7174
☑	423	775.8663	1549.7180
☑	425	1552.7470	1551.7397
☑	426	778.8869	1555.7592
☑	427	778.9056	1555.7966
☑	429	783.8977	1565.7808
☑	430	784.8284	1567.6422
☑	431	785.3452	1568.6758
☑	432	785.3531	1568.6916
☑	433	785.8189	1569.6232
☑	434	785.8344	1569.6542
☑	435	785.8349	1569.6552
☑	437	785.8361	1569.6576
☑	438	785.8381	1569.6616

☑	439	*785.8392*	*1569.6638*
☑	440	*785.8394*	*1569.6642*
☑	441	*785.8402*	*1569.6658*
☑	442	*785.8404*	*1569.6662*
☑	443	*785.8405*	*1569.6664*
☑	445	*785.8419*	*1569.6692*
☑	446	*785.8422*	*1569.6698*
☑	447	*785.8422*	*1569.6698*
☑	448	*785.8430*	*1569.6714*
☑	449	*785.8434*	*1569.6722*
☑	450	*785.8450*	*1569.6754*
☑	451	*785.8452*	*1569.6758*
☑	452	*785.8452*	*1569.6758*
☑	454	*785.8458*	*1569.6770*
☑	455	*785.8459*	*1569.6772*
☑	456	*785.8461*	*1569.6776*
☑	457	*785.8469*	*1569.6792*
☑	458	*785.8471*	*1569.6796*
☑	459	*785.8486*	*1569.6826*
☑	460	*785.8491*	*1569.6836*
☑	461	*785.8521*	*1569.6896*
☑	462	*785.8521*	*1569.6896*
☑	463	*785.8529*	*1569.6912*
☑	464	*785.8530*	*1569.6914*
☑	465	*785.8535*	*1569.6924*
☑	467	*786.3513*	*1570.6880*
☑	468	*786.3592*	*1570.7038*
☑	469	*786.8524*	*1571.6902*
☑	470	*786.8537*	*1571.6928*
☑	472	*793.4410*	*1584.8674*
☑	473	*794.8373*	*1587.6600*
☑	474	*794.8431*	*1587.6716*
☑	475	*794.8470*	*1587.6794*
☑	476	*795.8804*	*1589.7462*
☑	480	*801.9072*	*1601.7998*
☑	481	*801.9081*	*1601.8016*
☑	482	*801.9114*	*1601.8082*
☑	483	*801.9171*	*1601.8196*
☑	485	*803.8721*	*1605.7296*
☑	486	*803.8863*	*1605.7580*
☑	487	*809.8927*	*1617.7708*
☑	488	*809.9073*	*1617.8000*
☑	489	*810.8683*	*1619.7220*
☑	490	*810.8767*	*1619.7388*
☑	492	*816.3729*	*1630.7312*
☑	494	*816.8885*	*1631.7624*
☑	495	*816.8889*	*1631.7632*
☑	499	*816.8913*	*1631.7680*
☑	506	*816.8958*	*1631.7770*
☑	509	*816.8964*	*1631.7782*
☑	513	*816.8972*	*1631.7798*
☑	520	*816.9018*	*1631.7890*
☑	522	*816.9097*	*1631.8048*
☑	523	*818.8920*	*1635.7694*
☑	524	*824.3835*	*1646.7524*
☑	527	*827.7864*	*1653.5582*
☑	529	*834.9656*	*1667.9166*
☑	530	*839.8098*	*1677.6050*
☑	531	*843.3881*	*1684.7616*
☑	532	*849.9309*	*1697.8472*
☑	533	*851.3857*	*1700.7568*
☑	536	*851.4559*	*1700.8972*
☑	537	*851.4569*	*1700.8992*
☑	538	*851.4605*	*1700.9064*
☑	539	*851.4640*	*1700.9134*
☑	540	*854.3861*	*1706.7576*
☑	541	*854.3962*	*1706.7778*
☑	542	*854.4028*	*1706.7910*
☑	543	*428.7939*	*1711.1465*
☑	545	*859.4514*	*1716.8882*
☑	546	*864.9410*	*1727.8674*
☑	547	*864.9565*	*1727.8984*
☑	548	*870.4334*	*1738.8522*
☑	549	*870.8630*	*1739.7114*
☑	550	*872.4373*	*1742.8600*
☑	551	*878.4237*	*1754.8328*
☑	552	*878.9592*	*1755.9038*

☑	553	*879.9443*	*1757.8740*
☑	556	*883.8915*	*1765.7684*
☑	558	*883.9031*	*1765.7916*
☑	559	*886.4130*	*1770.8114*
☑	560	*888.4164*	*1774.8182*
☑	561	*445.0783*	*1776.2841*
☑	562	*595.3426*	*1783.0060*
☑	563	*892.8724*	*1783.7302*
☑	564	*892.8902*	*1783.7658*
☑	567	*896.3662*	*1790.7178*
☑	574	*898.4035*	*1794.7924*
☑	575	*900.1204*	*1798.2262*
☑	578	*913.4081*	*1824.8016*
☑	579	*913.9026*	*1825.7906*
☑	581	*913.9164*	*1825.8182*
☑	582	*914.4834*	*1826.9522*
☑	583	*917.4860*	*1832.9574*
☑	584	*917.4905*	*1832.9664*
☑	585	*918.5268*	*1835.0390*
☑	586	*929.0120*	*1856.0094*
☑	587	*937.9552*	*1873.8958*
☑	588	*959.0217*	*1916.0288*
☑	589	*973.5071*	*1944.9996*
☑	590	*979.4918*	*1956.9690*
☑	592	*678.8873*	*2033.6401*
☑	593	*688.3813*	*2062.1221*
☑	594	*1039.0304*	*2076.0462*
☑	596	*1040.9813*	*2079.9480*
☑	597	*1040.9854*	*2079.9562*
☑	598	*697.7272*	*2090.1598*
☑	599	*704.9998*	*2111.9776*
☑	600	*705.0000*	*2111.9782*
☑	602	*705.0046*	*2111.9920*
☑	603	*1057.0109*	*2112.0072*
☑	604	*705.3431*	*2113.0075*
☑	605	*707.3242*	*2118.9508*
☑	606	*707.3287*	*2118.9643*
☑	608	*707.3390*	*2118.9952*
☑	609	*707.3412*	*2119.0018*
☑	610	*707.9768*	*2120.9086*
☑	611	*708.3425*	*2122.0057*
☑	612	*712.6883*	*2135.0431*
☑	613	*715.3429*	*2143.0069*
☑	614	*715.3459*	*2143.0159*
☑	615	*1072.5183*	*2143.0220*
☑	616	*1072.5190*	*2143.0234*
☑	618	*1072.5215*	*2143.0284*
☑	619	*1072.5273*	*2143.0400*
☑	620	*1072.5293*	*2143.0440*
☑	621	*1074.9668*	*2147.9190*
☑	622	*723.3387*	*2166.9943*
☑	623	*737.6983*	*2210.0731*
☑	625	*737.7109*	*2210.1109*
☑	627	*743.4150*	*2227.2232*
☑	628	*745.4305*	*2233.2697*
☑	629	*748.0370*	*2241.0892*
☑	630	*752.6371*	*2254.8895*
☑	631	*757.3587*	*2269.0543*
☑	633	*762.0526*	*2283.1360*
☑	634	*769.3136*	*2304.9190*
☑	635	*773.5890*	*2317.7452*
☑	636	*776.3817*	*2326.1233*
☑	637	*776.3966*	*2326.1680*
☑	639	*1186.5781*	*2371.1416*
☑	640	*1187.2501*	*2372.4856*
☑	641	*795.3820*	*2383.1242*
☑	642	*1193.6521*	*2385.2896*
☑	643	*801.3739*	*2401.0999*
☑	645	*1204.4891*	*2406.9636*
☑	646	*1206.2017*	*2410.3888*
☑	647	*813.3870*	*2437.1392*
☑	648	*1233.2035*	*2464.3924*
☑	649	*828.0746*	*2481.2020*
☑	650	*843.8010*	*2528.3812*
☑	651	*857.3363*	*2568.9871*
☑	652	*859.6450*	*2575.9132*
☑	653	*875.4052*	*2623.1938*

☑	654	670.4191	2677.6473
☑	655	896.6437	2686.9093
☑	656	899.5475	2695.6207
☑	657	900.0706	2697.1900
☑	658	915.8900	2744.6482
☑	659	918.9715	2753.8927
☑	660	929.7820	2786.3242
☑	661	930.1228	2787.3466
☑	662	706.6091	2822.4073
☑	663	958.1210	2871.3412
☑	664	958.1260	2871.3562
☑	665	958.1278	2871.3616
☑	667	961.4618	2881.3636
☑	668	973.1750	2916.5032
☑	669	732.3851	2925.5113
☑	670	737.3884	2945.5245
☑	671	742.2606	2965.0133
☑	672	748.3859	2989.5145
☑	673	748.4033	2989.5841
☑	674	749.1548	2992.5901
☑	677	758.6400	3030.5309
☑	678	1016.1148	3045.3226
☑	679	1022.4659	3064.3759
☑	680	1031.4298	3091.2676
☑	681	774.1323	3092.5001
☑	682	776.1229	3100.4625
☑	683	785.6156	3138.4333
☑	684	786.3461	3141.3553
☑	685	789.1204	3152.4525
☑	686	797.1930	3184.7429
☑	687	810.3776	3237.4813
☑	688	810.3818	3237.4981
☑	689	1085.5421	3253.6045
☑	690	816.9273	3263.6801
☑	691	823.1737	3288.6657
☑	692	829.1945	3312.7489
☑	693	1119.1757	3354.5053
☑	695	858.6205	3430.4529
☑	696	869.3155	3473.2329
☑	697	870.4107	3477.6137
☑	698	873.2922	3489.1397
☑	699	1176.4674	3526.3804
☑	700	886.1975	3540.7609
☑	701	889.4472	3553.7597
☑	702	908.3743	3629.4681
☑	703	914.8817	3655.4977
☑	704	930.3966	3717.5573
☑	705	932.3429	3725.3425
☑	706	944.9282	3775.6837
☑	707	959.3601	3833.4113
☑	708	962.2110	3844.8149
☑	709	968.3356	3869.3133
☑	710	969.9287	3875.6857
☑	711	982.5540	3926.1869
☑	712	1342.2548	4023.7426
☑	713	1011.4422	4041.7397
☑	714	1015.4938	4057.9461
☑	715	1078.9778	4311.8821
☑	716	1094.4548	4373.7901
☑	717	1133.5477	4530.1617
☑	718	1134.9469	4535.7585
☑	719	1135.4979	4537.9625
☑	720	1139.0413	4552.1361
☑	721	1169.6051	4674.3913
☑	722	1210.4652	4837.8317
☑	723	1225.5979	4898.3625
☑	724	1309.0933	5232.3441
☑	725	1359.3607	5433.4137

Search Parameters

```
Type of search         : MS/MS Ion Search
Enzyme                 : Trypsin
Fixed modifications    : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values            : Monoisotopic
Protein Mass           : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
```

```
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages   : 1
Instrument type        : ESI-QUAD-TOF
Number of queries      : 725
```

Mascot: http://www.matrixscience.com/

Mascot Search Results

```
User           : Dominic
Email          : dominic.kurian@bbsrc.ac.uk
Search title   : IPI Mouse_15-02-2010
MS data file   : C:\Program Files\Matrix Science\Mascot Daemon\mgf\33 10753\mascot_daemon_merge.mgf
Database       : IPI_mouse MOUSE_v3_79 (54943 sequences; 24917557 residues)
Timestamp      : 15 Feb 2011 at 12:03:54 GMT
Protein hits   : IPI00420725 Tax_Id=10090 Gene_Symbol=Camk2a Uncharacterized protein
                 IPI00474502 Tax_Id=10090 Gene_Symbol=Camk2b Calcium/calmodulin-dependent protein kinase type II subunit beta
                 IPI00117352 Tax_Id=10090 Gene_Symbol=Tubb5 Tubulin beta-5 chain
                 IPI00112584 Tax_Id=10090 Gene_Symbol=Camk2d Isoform 1 of Calcium/calmodulin-dependent protein kinase type II subunit
                 IPI00608020 Tax_Id=10090 Gene_Symbol=Ftl1 ferritin light chain 1
                 IPI00109061 Tax_Id=10090 Gene_Symbol=Tubb2b Tubulin beta-2B chain
                 IPI00169463 Tax_Id=10090 Gene_Symbol=Tubb2c Tubulin beta-2C chain
                 IPI00124695 Tax_Id=10090 Gene_Symbol=Camk2g Isoform 1 of Calcium/calmodulin-dependent protein kinase type II subunit
                 IPI00117348 Tax_Id=10090 Gene_Symbol=Tuba1b Tubulin alpha-1B chain
                 IPI00230145 Tax_Id=10090 Gene_Symbol=Fth1 Ferritin heavy chain
                 IPI00112251 Tax_Id=10090 Gene_Symbol=Tubb3 Tubulin beta-3 chain
                 IPI00115546 Tax_Id=10090 Gene_Symbol=Gnao1 Isoform Alpha-2 of Guanine nucleotide-binding protein G(o) subunit alpha
                 IPI00138892 Tax_Id=10090 Gene_Symbol=Uba52 Ubiquitin-60S ribosomal protein L40
                 IPI00122048 Tax_Id=10090 Gene_Symbol=Atp1a3 Sodium/potassium-transporting ATPase subunit alpha-3
                 IPI00121038 Tax_Id=10090 Gene_Symbol=Vcan Isoform V0 of Versican core protein
                 IPI00621468 Tax_Id=10090 Gene_Symbol=Gm7866 similar to ubiquitin A-52 residue ribosomal protein fusion product 1
                 IPI00110850 Tax_Id=10090 Gene_Symbol=Actb Actin, cytoplasmic 1
                 IPI00136929 Tax_Id=10090 Gene_Symbol=Actg1 Gamma actin-like protein
                 IPI00123176 Tax_Id=10090 Gene_Symbol=Gm6316 Glyceraldehyde-3-phosphate dehydrogenase
                 IPI00114642 Tax_Id=10090 Gene_Symbol=Hist1h2bn;Hist1h2bl;Hist1h2bj;Hist1h2bf Histone H2B type 1-F/J/L
                 IPI00380227 Tax_Id=10090 Gene_Symbol=Nrgn Neurogranin
                 IPI00135106 Tax_Id=10090 Gene_Symbol=Mobp Isoform 1 of Myelin-associated oligodendrocyte basic protein
                 IPI00221528 Tax_Id=10090 Gene_Symbol=Actbl2 Beta-actin-like protein 2
                 IPI00136703 Tax_Id=10090 Gene_Symbol=Ckb Creatine kinase B-type
                 IPI00404590 Tax_Id=10090 Gene_Symbol=H1f0 Putative uncharacterized protein
                 IPI00131366 Tax_Id=10090 Gene_Symbol=Krt6b Keratin, type II cytoskeletal 6B
                 IPI00348094 Tax_Id=10090 Gene_Symbol=Tubb1 Tubulin, beta 1
                 IPI00229525 Tax_Id=10090 Gene_Symbol=Gnal Guanine nucleotide-binding protein G(olf) subunit alpha
                 IPI00118569 Tax_Id=10090 Gene_Symbol=Gna13 Guanine nucleotide-binding protein subunit alpha-13
                 IPI00119067 Tax_Id=10090 Gene_Symbol=Tppp Tubulin polymerization-promoting protein
```

	IPI_mouse	Decoy	False discovery rate
Peptide matches above identity threshold	111	2	1.80 %
Peptide matches above homology or identity threshold	121	3	2.48 %

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 > 37 indicate identity or extensive homology (p<0.01).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.

Score Distribution

Peptide Summary Report

Format As | Peptide Summary | Help

Significance threshold p< 0.01 | Max. number of hits AUTO

Standard scoring ○ MudPIT scoring ● | Ions score or expect cut-off 0 | 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. IPI00420725 **Mass:** 55882 **Score:** 921 **Queries matched:** 37 **emPAI:** 1.23
Tax_Id=10090 Gene_Symbol=Camk2a Uncharacterized 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
☑	155	445.2853	444.2780	444.2696	18.9	0	5	23	1	K.GAAVK.L
☑	414	432.7276	863.4406	863.4501	-10.97	0	20	1.1	1	R.SGAPSVLPH.-
	424	446.2583	890.5020	890.5086	-7.40	1	8	12	2	K.GAFSVVRR.C
	441	452.2508	902.4870	902.4895	-2.74	0	4	41	2	K.MLTINPSK.R
☑	502	525.2626	1048.5106	1048.5553	-42.57	0	53	0.0004	1	K.VLAGQEYAAK.I
	503	525.2869	1048.5592	1048.5553	3.78	0	(3)	38	3	K.VLAGQEYAAK.I
☑	510	530.2837	1058.5528	1058.5906	-35.68	1	(40)	0.0088	1	K.MLTINPSKR.I
☑	511	530.2865	1058.5584	1058.5906	-30.39	1	(47)	0.002	1	K.MLTINPSKR.I

☑	512	530.2960	1058.5774	1058.5906	-12.44	1	(42)	0.0056	1	K.MLTINPSKR.I
☑	513	530.3043	1058.5940	1058.5906	3.24	1	47	0.0014	1	K.MLTINPSKR.I
☑	529	538.2988	1074.5830	1074.5855	-2.32	1	(43)	0.0044	1	K.MLTINPSKR.I + Oxidation (M)
☑	530	538.3007	1074.5868	1074.5855	1.22	1	(43)	0.0046	1	K.MLTINPSKR.I + Oxidation (M)
☑	531	538.3033	1074.5920	1074.5855	6.06	1	(44)	0.0033	1	K.MLTINPSKR.I + Oxidation (M)
☑	554	574.3305	1146.6464	1146.6431	2.95	0	(46)	0.0012	1	K.GAILTTMLATR.N
☑	563	582.3281	1162.6416	1162.6380	3.15	0	83	2.8e-007	1	K.GAILTTMLATR.N + Oxidation (M)
☑	564	582.3326	1162.6506	1162.6380	10.9	0	(10)	5	1	K.GAILTTMLATR.N + Oxidation (M)
☑	601	631.2774	1260.5402	1260.5927	-41.64	0	(42)	0.0017	1	R.FYFENLWSR.N
☑	602	631.2971	1260.5796	1260.5927	-10.39	0	54	0.00022	1	R.FYFENLWSR.N
☑	603	631.2980	1260.5814	1260.5927	-8.96	0	(8)	9.1	1	R.FYFENLWSR.N
☑	630	652.3443	1302.6740	1302.6932	-14.70	0	(49)	0.0011	1	R.ITQYLDAGGIPR.T
☑	631	652.3544	1302.6942	1302.6932	0.81	0	(61)	5.6e-005	1	R.ITQYLDAGGIPR.T
☑	632	652.3555	1302.6964	1302.6932	2.50	0	105	2.4e-009	1	R.ITQYLDAGGIPR.T
☑	656	670.8677	1339.7208	1339.7711	-37.49	0	(77)	1.1e-006	1	R.DLKPENLLLASK.L
☑	657	670.8842	1339.7538	1339.7711	-12.86	0	78	7.5e-007	1	R.DLKPENLLLASK.L
☑	658	447.5925	1339.7557	1339.7711	-11.49	0	(59)	6e-005	1	R.DLKPENLLLASK.L
☑	799	816.8861	1631.7576	1631.7719	-8.72	0	66	1.5e-005	1	R.FTEEYQLFEELGK.G
☑	800	816.8922	1631.7698	1631.7719	-1.25	0	(64)	2.3e-005	1	R.FTEEYQLFEELGK.G
☑	801	816.8947	1631.7748	1631.7719	1.82	0	(7)	12	1	R.FTEEYQLFEELGK.G
☑	802	816.8953	1631.7760	1631.7719	2.55	0	(63)	3.3e-005	1	R.FTEEYQLFEELGK.G
☑	883	1040.9640	2079.9134	2079.9426	-13.99	0	78	5.2e-007	1	K.AGAYDFPSPEWDTVTPEAK.D
☑	908	783.7256	2348.1550	2348.1689	-5.91	1	(26)	0.13	1	R.FTEEYQLFEELGKGAFSVVR.R
☑	909	783.7288	2348.1646	2348.1689	-1.82	1	125	1.7e-011	1	R.FTEEYQLFEELGKGAFSVVR.R
☑	910	783.7297	2348.1673	2348.1689	-0.67	1	(52)	0.00031	1	R.FTEEYQLFEELGKGAFSVVR.R
☑	928	888.7346	2663.1820	2663.2755	-35.12	1	(94)	1.1e-008	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
☑	929	1332.6436	2663.2726	2663.2755	-1.07	1	(59)	5.1e-005	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
☑	930	888.7660	2663.2762	2663.2755	0.25	1	100	4.3e-009	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
☑	931	888.7662	2663.2768	2663.2755	0.48	1	(95)	1.3e-008	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M

Proteins matching the same set of peptides:
IPI00621806 **Mass:** 54651 **Score:** 921 **Queries matched:** 37
Tax_Id=10090 Gene_Symbol=Camk2a Isoform Alpha CaMKII of Calcium/calmodulin-dependent protein kinase type II subunit alpha

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2. IPI00474502 **Mass:** 61164 **Score:** 816 **Queries matched:** 31 **emPAI:** 1.57
Tax_Id=10090 Gene_Symbol=Camk2b Calcium/calmodulin-dependent protein kinase type II subunit 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
	155	445.2853	444.2780	444.2696	18.9	0	5	23	1	K.GAAVK.L
	424	446.2583	890.5020	890.5086	-7.40	1	8	12	2	K.GAFSVVRR.C
☑	489	510.2411	1018.4676	1018.4688	-1.14	0	37	0.011	1	R.STVASMMHR.Q
☑	495	518.2553	1034.4960	1034.4637	31.2	0	(28)	0.13	1	R.STVASMMHR.Q + Oxidation (M)
☑	552	572.8067	1143.5988	1143.5964	2.12	0	(22)	0.54	1	R.FYFENLLAK.N
☑	553	572.8070	1143.5994	1143.5964	2.65	0	23	0.44	1	R.FYFENLLAK.N
	554	574.3305	1146.6464	1146.6431	2.95	0	(46)	0.0012	1	K.GAILTTMLATR.N
	563	582.3281	1162.6416	1162.6380	3.15	0	83	2.8e-007	1	K.GAILTTMLATR.N + Oxidation (M)
	564	582.3326	1162.6506	1162.6380	10.9	0	(10)	5	1	K.GAILTTMLATR.N + Oxidation (M)
☑	596	623.3240	1244.6334	1244.6361	-2.11	0	63	4e-005	1	K.ADGVKPQTNSTK.N
	656	670.8677	1339.7208	1339.7711	-37.49	0	(77)	1.1e-006	1	R.DLKPENLLLASK.C
	657	670.8842	1339.7538	1339.7711	-12.86	0	78	7.5e-007	1	R.DLKPENLLLASK.C
	658	447.5925	1339.7557	1339.7711	-11.49	0	(59)	6e-005	1	R.DLKPENLLLASK.C
	680	458.5831	1372.7275	1372.7310	-2.59	1	(2)	51	7	K.KADGVKPQTNSTK.N
☑	681	687.3759	1372.7372	1372.7310	4.53	1	41	0.0061	1	K.KADGVKPQTNSTK.N
☑	688	468.5813	1402.7221	1402.7317	-6.87	0	(26)	0.16	1	R.LTQYIDGQGRPR.T
☑	689	468.5816	1402.7230	1402.7317	-6.23	0	(40)	0.0067	1	R.LTQYIDGQGRPR.T
☑	690	702.3738	1402.7330	1402.7317	0.96	0	(37)	0.015	1	R.LTQYIDGQGRPR.T
☑	691	702.3776	1402.7406	1402.7317	6.38	0	51	0.00048	1	R.LTQYIDGQGRPR.T
☑	707	743.4136	1484.8126	1484.8021	7.13	0	75	1.7e-006	1	K.NLINQMLTINPAK.R + Oxidation (M)
☑	786	810.8771	1619.7396	1619.7355	2.56	0	66	1.4e-005	1	R.FTDEYQLYEDIGK.G
☑	787	810.8881	1619.7616	1619.7355	16.1	0	(29)	0.068	1	R.FTDEYQLYEDIGK.G
☑	794	542.6372	1624.8898	1624.9082	-11.37	1	89	5.7e-008	1	K.NLINQMLTINPAKR.I
☑	795	813.4636	1624.9126	1624.9082	2.71	1	(55)	9.8e-005	1	K.NLINQMLTINPAKR.I
	883	1040.9640	2079.9134	2079.9426	-13.99	0	78	5.2e-007	1	K.AGAYDFPSPEWDTVTPEAK.N
☑	890	1056.9772	2111.9398	2112.0011	-29.00	0	(1)	25	1	K.TTEQLIEAVNNGDFEAYAK.I
☑	891	1057.0093	2112.0040	2112.0011	1.40	0	95	1.6e-008	1	K.TTEQLIEAVNNGDFEAYAK.I
☑	906	779.7075	2336.1007	2336.1325	-13.61	1	(59)	5.7e-005	1	R.FTDEYQLYEDIGKGAFSVVR.R
☑	907	779.7144	2336.1214	2336.1325	-4.75	1	124	1.7e-011	1	R.FTDEYQLYEDIGKGAFSVVR.R
☑	911	1177.0757	2352.1368	2352.1301	2.86	0	128	7.5e-012	1	R.QTTAPATMSTAASGTTMGLVEQAK.S
☑	912	1185.0782	2368.1418	2368.1250	7.10	0	(118)	6.1e-011	1	R.QTTAPATMSTAASGTTMGLVEQAK.S + Oxidation (M)

Proteins matching the same set of peptides:
IPI00649778 **Mass:** 73827 **Score:** 816 **Queries matched:** 31
Tax_Id=10090 Gene_Symbol=Camk2b Calcium/calmodulin-dependent protein kinase II, beta, isoform CRA_b
IPI00875723 **Mass:** 68686 **Score:** 816 **Queries matched:** 31
Tax_Id=10090 Gene_Symbol=Camk2b 68 kDa protein

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3. IPI00117352 **Mass:** 50095 **Score:** 504 **Queries matched:** 18 **emPAI:** 1.15
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

☑	557	580.3218	1158.6290	1158.6219	6.13	0	48	0.0012	1	K.LAVNMVPFPR.L + Oxidation (M)
☑	643	660.3592	1318.7038	1318.6955	6.32	0	63	3.3e-005	1	R.IMNTFSVVPSPK.V
☑	653	668.3525	1334.6904	1334.6904	0.01	0	(8)	12	1	R.IMNTFSVVPSPK.V + Oxidation (M)
	654	668.3532	1334.6918	1334.6904	1.06	0	(4)	28	4	R.IMNTFSVVPSPK.V + Oxidation (M)
☑	783	808.4200	1614.8254	1614.8287	-2.02	0	(49)	0.00091	1	R.AILVDLEPGTMDSVR.S
☑	788	540.9453	1619.8141	1619.8283	-8.76	0	(53)	0.00031	1	R.LHFFMPGFAPLTSR.G
☑	789	810.9224	1619.8302	1619.8283	1.23	0	57	0.00013	1	R.LHFFMPGFAPLTSR.G
☑	790	810.9226	1619.8306	1619.8283	1.47	0	(45)	0.0019	1	R.LHFFMPGFAPLTSR.G
☑	797	816.4169	1630.8192	1630.8236	-2.68	0	59	0.0001	1	R.AILVDLEPGTMDSVR.S + Oxidation (M)
☑	808	830.4500	1658.8854	1658.8879	-1.50	0	62	3.2e-005	1	R.ALTVPELTQQVFDAK.N
☑	819	848.9158	1695.8170	1695.8257	-5.07	0	64	2.6e-005	1	K.NSSYFVEWIPNNVK.T
☑	820	848.9227	1695.8308	1695.8257	3.06	0	(47)	0.0013	1	K.NSSYFVEWIPNNVK.T
☑	877	653.6544	1957.9414	1957.9745	-16.94	0	(41)	0.0039	1	K.GHYTEGAELVDSVLDVVR.K
☑	878	980.0190	1958.0234	1957.9745	25.0	0	101	4.2e-009	1	K.GHYTEGAELVDSVLDVVR.K
☑	936	933.4480	2797.3222	2797.3361	-4.99	0	(89)	4.3e-008	1	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
☑	937	933.4524	2797.3354	2797.3361	-0.27	0	99	5.2e-009	1	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
☑	938	1399.6794	2797.3442	2797.3361	2.91	0	(71)	2.9e-006	1	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
☑	939	933.4583	2797.3531	2797.3361	6.06	0	(34)	0.016	1	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G

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4. IPI00112584 **Mass:** 56961 **Score:** 475 **Queries matched:** 21 **emPAI:** 0.66
Tax_Id=10090 Gene_Symbol=Camk2d Isoform 1 of Calcium/calmodulin-dependent protein kinase type II subunit 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
	155	445.2853	444.2780	444.2696	18.9	0	5	23	1	K.GAAVK.L
	424	446.2583	890.5020	890.5086	-7.40	1	8	12	2	K.GAFSVVRR.C
	489	510.2411	1018.4676	1018.4688	-1.14	0	37	0.011	1	R.STVASMMHR.Q
	495	518.2553	1034.4960	1034.4637	31.2	0	(28)	0.13	1	R.STVASMMHR.Q + Oxidation (M)
	510	530.2837	1058.5528	1058.5906	-35.68	1	6	24	3	K.MLTINPAKR.I + Oxidation (M)
	513	530.3043	1058.5940	1058.5906	3.24	1	(5)	20	8	K.MLTINPAKR.I + Oxidation (M)
☑	547	559.7811	1117.5476	1117.5444	2.92	0	20	0.77	1	R.FYFENALSK.S
☑	548	559.7846	1117.5546	1117.5444	9.18	0	(17)	1.8	1	R.FYFENALSK.S
	554	574.3305	1146.6464	1146.6431	2.95	0	(46)	0.0012	1	K.GAILTTMLATR.N
	563	582.3281	1162.6416	1162.6380	3.15	0	83	2.8e-007	1	K.GAILTTMLATR.N + Oxidation (M)
	564	582.3326	1162.6506	1162.6380	10.9	0	(10)	5	1	K.GAILTTMLATR.N + Oxidation (M)
	656	670.8677	1339.7208	1339.7711	-37.49	0	(77)	1.1e-006	1	R.DLKPENLLLASK.S
	657	670.8842	1339.7538	1339.7711	-12.86	0	78	7.5e-007	1	R.DLKPENLLLASK.S
	658	447.5925	1339.7557	1339.7711	-11.49	0	(59)	6e-005	1	R.DLKPENLLLASK.S
☑	785	809.8809	1617.7472	1617.7562	-5.56	0	52	0.00035	1	R.FTDEYQLFEELGK.G
	883	1040.9640	2079.9134	2079.9426	-13.99	0	78	5.2e-007	1	K.AGAYDFPSPEWDTVTPEAK.D
☑	905	779.0534	2334.1384	2334.1532	-6.36	1	26	0.11	1	R.FTDEYQLFEELGKGAFSVVR.R
	928	888.7346	2663.1820	2663.2755	-35.12	1	(94)	1.1e-008	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
	929	1332.6436	2663.2726	2663.2755	-1.07	1	(59)	5.1e-005	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
	930	888.7660	2663.2762	2663.2755	0.25	1	100	4.3e-009	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
	931	888.7662	2663.2768	2663.2755	0.48	1	(95)	1.3e-008	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M

Proteins matching the same set of peptides:
IPI00406790 **Mass:** 60593 **Score:** 475 **Queries matched:** 21
Tax_Id=10090 Gene_Symbol=Camk2d Isoform 4 of Calcium/calmodulin-dependent protein kinase type II subunit delta
IPI00475044 **Mass:** 55899 **Score:** 475 **Queries matched:** 21
Tax_Id=10090 Gene_Symbol=Camk2d Isoform 2 of Calcium/calmodulin-dependent protein kinase type II subunit delta
IPI00828919 **Mass:** 58492 **Score:** 475 **Queries matched:** 21
Tax_Id=10090 Gene_Symbol=Camk2d Isoform 3 of Calcium/calmodulin-dependent protein kinase type II subunit delta
IPI00857865 **Mass:** 54664 **Score:** 475 **Queries matched:** 21
Tax_Id=10090 Gene_Symbol=Camk2d Putative uncharacterized protein
IPI00858128 **Mass:** 58283 **Score:** 475 **Queries matched:** 21
Tax_Id=10090 Gene_Symbol=Camk2d calcium/calmodulin-dependent protein kinase type II subunit delta isoform 1
IPI00858144 **Mass:** 55828 **Score:** 475 **Queries matched:** 21
Tax_Id=10090 Gene_Symbol=Camk2d 55 kDa protein

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5. IPI00608020 **Mass:** 20817 **Score:** 452 **Queries matched:** 12 **emPAI:** 1.11
Tax_Id=10090 Gene_Symbol=Ftl1 ferritin light chain 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
☑	633	652.8418	1303.6690	1303.6633	4.42	1	29	0.097	1	R.LLEFQNDRGGR.A
☑	705	740.8561	1479.6976	1479.6954	1.55	0	(90)	6.4e-008	1	R.QNYSTEVEAAVNR.L
☑	706	740.8602	1479.7058	1479.6954	7.09	0	95	1.8e-008	1	R.QNYSTEVEAAVNR.L
☑	829	569.3081	1704.9025	1704.9271	-14.43	0	84	2e-007	1	K.NLNQALLDLHALGSAR.A
☑	830	569.3106	1704.9100	1704.9271	-10.03	0	(83)	2.1e-007	1	K.NLNQALLDLHALGSAR.A
☑	831	853.4784	1704.9422	1704.9271	8.90	0	(32)	0.018	1	K.NLNQALLDLHALGSAR.A
☑	832	853.4784	1704.9422	1704.9271	8.90	0	(31)	0.027	1	K.NLNQALLDLHALGSAR.A
☑	919	843.7637	2528.2693	2528.2772	-3.13	1	84	1.4e-007	1	R.RVAGPQPAQTGAPQGSLGEYLFER.L
☑	953	820.6315	3278.4969	3278.5587	-18.86	1	(72)	1.3e-006	1	R.ALFQDVQKPSQDEWGKTQEAMEAALAMEK.N
☑	954	820.6387	3278.5257	3278.5587	-10.07	1	(20)	0.28	1	R.ALFQDVQKPSQDEWGKTQEAMEAALAMEK.N
☑	955	820.6396	3278.5293	3278.5587	-8.97	1	(79)	3.8e-007	1	R.ALFQDVQKPSQDEWGKTQEAMEAALAMEK.N
☑	957	820.6479	3278.5625	3278.5587	1.15	1	84	1.1e-007	1	R.ALFQDVQKPSQDEWGKTQEAMEAALAMEK.N

Proteins matching the same set of peptides:
IPI00762203 **Mass:** 20847 **Score:** 452 **Queries matched:** 12
Tax_Id=10090 Gene_Symbol=Ftl1 Ferritin light chain 1

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6. IPI00109061 **Mass:** 50377 **Score:** 449 **Queries matched:** 16 **emPAI:** 0.88

Tax_Id=10090 Gene_Symbol=Tubb2b Tubulin beta-2B 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
	557	580.3218	1158.6290	1158.6219	6.13	0	48	0.0012	1	K.LAVNMVPFPR.L + Oxidation (M)
	783	808.4200	1614.8254	1614.8287	-2.02	0	(49)	0.00091	1	R.AILVDLEPGTMDSVR.S
	788	540.9453	1619.8141	1619.8283	-8.76	0	(53)	0.00031	1	R.LHFFMPGFAPLTSR.G
	789	810.9224	1619.8302	1619.8283	1.23	0	57	0.00013	1	R.LHFFMPGFAPLTSR.G
	790	810.9226	1619.8306	1619.8283	1.47	0	(45)	0.0019	1	R.LHFFMPGFAPLTSR.G
	797	816.4169	1630.8192	1630.8236	-2.68	0	59	0.0001	1	R.AILVDLEPGTMDSVR.S + Oxidation (M)
	819	848.9158	1695.8170	1695.8257	-5.07	0	64	2.6e-005	1	K.NSSYFVEWIPNNVK.T
	820	848.9227	1695.8308	1695.8257	3.06	0	(47)	0.0013	1	K.NSSYFVEWIPNNVK.T
	833	**854.4404**	**1706.8662**	**1706.8549**	**6.64**	**0**	**28**	**0.092**	**2**	**R.ALTVPELTQQMFDSK.N**
	877	653.6544	1957.9414	1957.9745	-16.94	0	(41)	0.0039	1	K.GHYTEGAELVDSVLDVVR.K
	878	980.0190	1958.0234	1957.9745	25.0	0	101	4.2e-009	1	K.GHYTEGAELVDSVLDVVR.K
	936	933.4480	2797.3222	2797.3361	-4.99	0	(89)	4.3e-008	1	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
	937	933.4524	2797.3354	2797.3361	-0.27	0	99	5.2e-009	1	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
	938	1399.6794	2797.3442	2797.3361	2.91	0	(71)	2.9e-006	1	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
	939	933.4583	2797.3531	2797.3361	6.06	0	(34)	0.016	1	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
☑	**951**	**776.3458**	**3101.3541**	**3101.4003**	**-14.89**	**0**	**9**	**2.8**	**1**	**K.FWEVISDEHGIDPTGSYHGDSDLQLER.I**

Proteins matching the same set of peptides:
IPI00338039 **Mass:** 50274 **Score:** 449 **Queries matched:** 16
Tax_Id=10090 Gene_Symbol=Tubb2a Tubulin beta-2A chain

7. IPI00169463 **Mass:** 50255 **Score:** 446 **Queries matched:** 17 **emPAI:** 1.01
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
	557	580.3218	1158.6290	1158.6219	6.13	0	48	0.0012	1	K.LAVNMVPFPR.L + Oxidation (M)
	643	660.3592	1318.7038	1318.6955	6.32	0	63	3.3e-005	1	R.IMNTFSVVPSPK.V
	653	668.3525	1334.6904	1334.6904	0.01	0	(8)	12	1	R.IMNTFSVVPSPK.V + Oxidation (M)
	654	668.3532	1334.6918	1334.6904	1.06	0	(4)	28	4	R.IMNTFSVVPSPK.V + Oxidation (M)
	788	540.9453	1619.8141	1619.8283	-8.76	0	(53)	0.00031	1	R.LHFFMPGFAPLTSR.G
	789	810.9224	1619.8302	1619.8283	1.23	0	57	0.00013	1	R.LHFFMPGFAPLTSR.G
	790	810.9226	1619.8306	1619.8283	1.47	0	(45)	0.0019	1	R.LHFFMPGFAPLTSR.G
☑	**816**	**846.4307**	**1690.8468**	**1690.8600**	**-7.78**	**0**	**43**	**0.0034**	**1**	**R.ALTVPELTQQMFDAK.N**
	819	848.9158	1695.8170	1695.8257	-5.07	0	64	2.6e-005	1	K.NSSYFVEWIPNNVK.T
	820	848.9227	1695.8308	1695.8257	3.06	0	(47)	0.0013	1	K.NSSYFVEWIPNNVK.T
☑	833	854.4404	1706.8662	1706.8549	6.64	0	(38)	0.0095	1	R.ALTVPELTQQMFDAK.N + Oxidation (M)
	877	653.6544	1957.9414	1957.9745	-16.94	0	(41)	0.0039	1	K.GHYTEGAELVDSVLDVVR.K
	878	980.0190	1958.0234	1957.9745	25.0	0	101	4.2e-009	1	K.GHYTEGAELVDSVLDVVR.K
	936	933.4480	2797.3222	2797.3361	-4.99	0	(89)	4.3e-008	1	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
	937	933.4524	2797.3354	2797.3361	-0.27	0	99	5.2e-009	1	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
	938	1399.6794	2797.3442	2797.3361	2.91	0	(71)	2.9e-006	1	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
	939	933.4583	2797.3531	2797.3361	6.06	0	(34)	0.016	1	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G

8. IPI00124695 **Mass:** 60254 **Score:** 412 **Queries matched:** 18 **emPAI:** 0.79
Tax_Id=10090 Gene_Symbol=Camk2g Isoform 1 of Calcium/calmodulin-dependent protein kinase type II 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
	155	445.2853	444.2780	444.2696	18.9	0	5	23	1	K.GAAVK.L
	424	446.2583	890.5020	890.5086	-7.40	1	8	12	2	K.GAFSVVRR.C
	489	510.2411	1018.4676	1018.4688	-1.14	0	37	0.011	1	R.STVASMMHR.Q
	495	518.2553	1034.4960	1034.4637	31.2	0	(28)	0.13	1	R.STVASMMHR.Q + Oxidation (M)
☑	**549**	**563.7897**	**1125.5648**	**1125.5666**	**-1.53**	**1**	**50**	**0.00076**	**1**	**K.KTSTQEYAAK.I**
	558	**580.8033**	**1159.5920**	**1159.5913**	**0.61**	**0**	**2**	**56**	**6**	**K.FYFENLLSK.N**
	656	670.8677	1339.7208	1339.7711	-37.49	0	(77)	1.1e-006	1	R.DLKPENLLLASK.C
	657	670.8842	1339.7538	1339.7711	-12.86	0	78	7.5e-007	1	R.DLKPENLLLASK.C
	658	447.5925	1339.7557	1339.7711	-11.49	0	(59)	6e-005	1	R.DLKPENLLLASK.C
	688	468.5813	1402.7221	1402.7317	-6.87	0	(26)	0.16	1	R.LTQYIDGQGRPR.T
	689	468.5816	1402.7230	1402.7317	-6.23	0	(40)	0.0067	1	R.LTQYIDGQGRPR.T
	690	702.3738	1402.7330	1402.7317	0.96	0	(37)	0.015	1	R.LTQYIDGQGRPR.T
	691	702.3776	1402.7406	1402.7317	6.38	0	51	0.00048	1	R.LTQYIDGQGRPR.T
	707	743.4136	1484.8126	1484.8021	7.13	0	75	1.7e-006	1	K.NLINQMLTINPAK.R + Oxidation (M)
☑	**782**	**802.8676**	**1603.7206**	**1603.7406**	**-12.44**	**0**	**90**	**3.8e-008**	**1**	**R.FTDDYQLFEELGK.G**
	794	542.6372	1624.8898	1624.9082	-11.37	1	89	5.7e-008	1	K.NLINQMLTINPAKR.I
	795	813.4636	1624.9126	1624.9082	2.71	1	(55)	9.8e-005	1	K.NLINQMLTINPAKR.I
	883	1040.9640	2079.9134	2079.9426	-13.99	0	78	5.2e-007	1	K.AGAYDFPSPEWDTVTPEAK.N

Proteins matching the same set of peptides:
IPI00228044 **Mass:** 59013 **Score:** 412 **Queries matched:** 18
Tax_Id=10090 Gene_Symbol=Camk2g Isoform 2 of Calcium/calmodulin-dependent protein kinase type II subunit gamma
IPI00228045 **Mass:** 56610 **Score:** 412 **Queries matched:** 18
Tax_Id=10090 Gene_Symbol=Camk2g Isoform 3 of Calcium/calmodulin-dependent protein kinase type II subunit gamma

9. IPI00117348 **Mass:** 50804 **Score:** 341 **Queries matched:** 12 **emPAI:** 0.46
Tax_Id=10090 Gene_Symbol=Tuba1b Tubulin alpha-1B 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
☑	**708**	**744.4436**	**1486.8726**	**1486.8719**	**0.52**	**0**	**90**	**2.2e-008**	**1**	**R.LISQIVSSITASLR.F**
☑	**822**	**851.4536**	**1700.8926**	**1700.8985**	**-3.45**	**0**	**64**	**2.3e-005**	**1**	**R.AVFVDLEPTVIDEVR.T**
☑	**823**	**851.4573**	**1700.9000**	**1700.8985**	**0.90**	**0**	**(60)**	**5.7e-005**	**1**	**R.AVFVDLEPTVIDEVR.T**

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	841	878.9860	1755.9574	1755.9559	0.86	0	67	8.3e-006	1	R.IHFPLATYAPVISAEK.A
☑	842	878.9954	1755.9762	1755.9559	11.6	0	(66)	9.9e-006	1	R.IHFPLATYAPVISAEK.A
☑	857	912.9819	1823.9492	1823.9782	-15.85	0	(26)	0.13	1	K.VGINYQPPTVVPGGDLAK.V
☑	858	913.0020	1823.9894	1823.9782	6.19	0	29	0.054	1	K.VGINYQPPTVVPGGDLAK.V
☑	914	1205.1045	2408.1944	2408.2012	-2.82	0	128	7.5e-012	1	R.FDGALNVDLTEFQTNLVPYPR.I
☑	915	604.5469	2414.1585	2414.1978	-16.29	1	(39)	0.0058	1	R.QLFHPEQLITGKEDAANNYAR.G
☑	916	604.5476	2414.1613	2414.1978	-15.13	1	54	0.0002	1	R.QLFHPEQLITGKEDAANNYAR.G
☑	917	604.5506	2414.1733	2414.1978	-10.16	1	(24)	0.19	1	R.QLFHPEQLITGKEDAANNYAR.G
☑	918	604.5528	2414.1821	2414.1978	-6.52	1	(18)	0.68	1	R.QLFHPEQLITGKEDAANNYAR.G

Proteins matching the same set of peptides:
IPI00129028 **Mass:** 50689 **Score:** 341 **Queries matched:** 12
Tax_Id=10090 Gene_Symbol=Gm5620 Uncharacterized protein
IPI00403810 **Mass:** 50562 **Score:** 341 **Queries matched:** 12
Tax_Id=10090 Gene_Symbol=Tuba1c Tubulin alpha-1C chain

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10. IPI00230145 **Mass:** 21224 **Score:** 297 **Queries matched:** 10 **emPAI:** 1.09
Tax_Id=10090 Gene_Symbol=Fth1 Ferritin 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
☑	605	423.2317	1266.6733	1266.6932	-15.71	0	58	9.9e-005	1	K.SVNQSLLELHK.L
☑	606	634.3522	1266.6898	1266.6932	-2.63	0	(57)	0.0001	1	K.SVNQSLLELHK.L
☑	607	634.3550	1266.6954	1266.6932	1.79	0	(57)	9.5e-005	1	K.SVNQSLLELHK.L
☑	718	765.3590	1528.7034	1528.7018	1.06	0	(64)	1.9e-005	1	R.QNYHQDAEAAINR.Q
☑	719	765.3598	1528.7050	1528.7018	2.11	0	72	3e-006	1	R.QNYHQDAEAAINR.Q
☑	920	641.5282	2562.0837	2562.1155	-12.42	1	(41)	0.0013	1	K.MGAPEAGMAEYLFDKHTLGHGDES.-
☑	921	855.0369	2562.0889	2562.1155	-10.40	1	(26)	0.045	1	K.MGAPEAGMAEYLFDKHTLGHGDES.-
☑	922	641.5305	2562.0929	2562.1155	-8.83	1	(13)	0.83	1	K.MGAPEAGMAEYLFDKHTLGHGDES.-
☑	923	855.0422	2562.1048	2562.1155	-4.19	1	111	1.6e-010	1	K.MGAPEAGMAEYLFDKHTLGHGDES.-
☑	924	855.0442	2562.1108	2562.1155	-1.85	1	(46)	0.00051	1	K.MGAPEAGMAEYLFDKHTLGHGDES.-

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11. IPI00112251 **Mass:** 50842 **Score:** 277 **Queries matched:** 14 **emPAI:** 0.76
Tax_Id=10090 Gene_Symbol=Tubb3 Tubulin beta-3 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
557	580.3218	1158.6290	1158.6219	6.13	0	48	0.0012	1	K.LAVNMVPFPR.L + Oxidation (M)
643	660.3592	1318.7038	1318.6955	6.32	0	63	3.3e-005	1	R.IMNTFSVVPSPK.V
653	668.3525	1334.6904	1334.6904	0.01	0	(8)	12	1	R.IMNTFSVVPSPK.V + Oxidation (M)
654	668.3532	1334.6918	1334.6904	1.06	0	(4)	28	4	R.IMNTFSVVPSPK.V + Oxidation (M)
783	808.4200	1614.8254	1614.8287	-2.02	0	(49)	0.00091	1	R.AILVDLEPGTMDSVR.S
789	810.9224	1619.8302	1619.8283	1.23	0	18	0.99	2	R.LHFFMPGFAPLTAR.G + Oxidation (M)
790	810.9226	1619.8306	1619.8283	1.47	0	(17)	1.3	2	R.LHFFMPGFAPLTAR.G + Oxidation (M)
797	816.4169	1630.8192	1630.8236	-2.68	0	59	0.0001	1	R.AILVDLEPGTMDSVR.S + Oxidation (M)
816	846.4307	1690.8468	1690.8600	-7.78	0	43	0.0034	1	R.ALTVPELTQQMFDAK.N
819	848.9158	1695.8170	1695.8257	-5.07	0	64	2.6e-005	1	K.NSSYFVEWIPNNVK.V
820	848.9227	1695.8308	1695.8257	3.06	0	(47)	0.0013	1	K.NSSYFVEWIPNNVK.V
833	854.4404	1706.8662	1706.8549	6.64	0	(38)	0.0095	1	R.ALTVPELTQQMFDAK.N + Oxidation (M)
877	653.6544	1957.9414	1957.9745	-16.94	0	(41)	0.0039	1	K.GHYTEGAELVDSVLDVVR.K
878	980.0190	1958.0234	1957.9745	25.0	0	101	4.2e-009	1	K.GHYTEGAELVDSVLDVVR.K

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12. IPI00115546 **Mass:** 40524 **Score:** 212 **Queries matched:** 4 **emPAI:** 0.27
Tax_Id=10090 Gene_Symbol=Gnao1 Isoform Alpha-2 of Guanine nucleotide-binding protein G(o) 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
☑	509	529.3168	1056.6190	1056.6179	1.10	0	45	0.0021	1	K.LLLLGAGESGK.S
☑	811	838.4183	1674.8220	1674.8213	0.44	0	98	1.1e-008	1	R.IGAGDYQPTEQDILR.T
☑	812	838.4184	1674.8222	1674.8213	0.56	0	(59)	8.4e-005	1	R.IGAGDYQPTEQDILR.T
☑	876	979.4533	1956.8920	1956.8631	14.8	0	106	9.8e-010	1	R.MEDTEPFSAELLSAMMR.L

Proteins matching the same set of peptides:
IPI00230192 **Mass:** 40629 **Score:** 212 **Queries matched:** 4
Tax_Id=10090 Gene_Symbol=Gnao1 Isoform Alpha-1 of Guanine nucleotide-binding protein G(o) subunit alpha

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13. IPI00138892 **Mass:** 15004 **Score:** 171 **Queries matched:** 3 **emPAI:** 0.51
Tax_Id=10090 Gene_Symbol=Uba52 Ubiquitin-60S ribosomal protein L40
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	712	762.3933	1522.7720	1522.7740	-1.25	1	(66)	1.8e-005	1	K.IQDKEGIPPDQQR.L
☑	713	762.4007	1522.7868	1522.7740	8.47	1	83	3.2e-007	1	K.IQDKEGIPPDQQR.L
☑	881	663.0222	1986.0448	1986.0521	-3.68	1	86	1.3e-007	1	K.TITLEVEPSDTIENVKAK.I

Proteins matching the same set of peptides:
IPI00470152 **Mass:** 18282 **Score:** 171 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=Rps27a Ubiquitin-40S ribosomal protein S27a
IPI00895319 **Mass:** 22277 **Score:** 171 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=2810422J05Rik 22 kDa protein
IPI00895479 **Mass:** 27181 **Score:** 171 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=2810422J05Rik 27 kDa protein

IPI00918763 **Mass:** 11021 **Score:** 171 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=Uba52 Ubiqutin subunit 1
IPI00750889 **Mass:** 22822 **Score:** 171 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=Ubc Ubc protein
IPI00923013 **Mass:** 26603 **Score:** 171 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=Ubb Ubiquitin B
IPI00923037 **Mass:** 22578 **Score:** 171 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=Ubc Putative uncharacterized protein
IPI00139518 **Mass:** 34348 **Score:** 171 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=Ubb Polyubiquitin-B
IPI00969323 **Mass:** 82603 **Score:** 171 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=Ubc Polyubiquitin-C
IPI00755916 **Mass:** 82614 **Score:** 171 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=Ubc ubiquitin

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14. IPI00122048 **Mass:** 113045 **Score:** 130 **Queries matched:** 4 **emPAI:** 0.09
Tax_Id=10090 Gene_Symbol=Atp1a3 Sodium/potassium-transporting ATPase subunit alpha-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
☑	592	618.8615	1235.7084	1235.6986	7.96	0	40	0.0032	1	R.LNIPVSQVNPR.D
☑	859	915.4680	1828.9214	1828.9167	2.62	0	109	7.1e-010	1	K.GVGIISEGNETVEDIAAR.L
☑	944	956.1194	2865.3364	2865.3490	-4.42	1	42	0.0022	1	K.EQPLDEEMKEAFQNAYLELGGLGER.V
☑	945	956.1257	2865.3553	2865.3490	2.18	1	(31)	0.03	1	K.EQPLDEEMKEAFQNAYLELGGLGER.V

Proteins matching the same set of peptides:
IPI00752412 **Mass:** 117548 **Score:** 130 **Queries matched:** 4
Tax_Id=10090 Gene_Symbol=Atp1a3 ATPase, Na+/K+ transporting, alpha 3 polypeptide, isoform CRA_c

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15. IPI00121038 **Mass:** 368613 **Score:** 123 **Queries matched:** 2 **emPAI:** 0.02
Tax_Id=10090 Gene_Symbol=Vcan Isoform V0 of Versican core 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
☑	639	657.8640	1313.7134	1313.7092	3.26	0	81	5e-007	1	R.LATVGELQAAWR.N
☑	694	709.3778	1416.7410	1416.7283	9.03	1	73	4.4e-006	1	K.METSPPVKGSLSGK.V

Proteins matching the same set of peptides:
IPI00230441 **Mass:** 264594 **Score:** 123 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=Vcan Isoform V1 of Versican core protein
IPI00469172 **Mass:** 76209 **Score:** 123 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=Vcan versican core protein isoform 4
IPI00469565 **Mass:** 180325 **Score:** 123 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=Vcan versican core protein isoform 3
IPI00473932 **Mass:** 41850 **Score:** 123 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=Vcan versican core protein isoform 5
IPI00656277 **Mass:** 41758 **Score:** 123 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=Vcan Versican
IPI00875672 **Mass:** 368720 **Score:** 123 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=Vcan versican core protein isoform 1

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16. IPI00621468 **Mass:** 23411 **Score:** 114 **Queries matched:** 3 **emPAI:** 0.14
Tax_Id=10090 Gene_Symbol=Gm7866 similar to ubiquitin A-52 residue ribosomal protein fusion product 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
	712	762.3933	1522.7720	1522.7740	-1.25	1	(66)	1.8e-005	1	K.IQDKEGIPPDQQR.L
	713	762.4007	1522.7868	1522.7740	8.47	1	83	3.2e-007	1	K.IQDKEGIPPDQQR.L
☑	836	582.9590	1745.8552	1745.8402	8.59	0	7	13	1	K.QFTAALIMMTALMEK.I + 3 Oxidation (M)

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17. IPI00110850 **Mass:** 42052 **Score:** 107 **Queries matched:** 6 **emPAI:** 0.16
Tax_Id=10090 Gene_Symbol=Actb Actin, cytoplasmic 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
☑	576	599.8588	1197.7030	1197.6982	4.03	0	24	0.13	1	R.AVFPSIVGRPR.H
	791	812.4296	1622.8446	1622.8338	6.70	1	3	30	3	R.LDLAGRDLTDYLMK.I
☑	849	895.9518	1789.8890	1789.8846	2.47	0	21	0.43	1	K.SYELPDGQVITIGNER.F
	874	652.0251	1953.0535	1953.0571	-1.86	0	5	12	2	R.VAPEEHPVLLTEAPLNPK.A
☑	897	1108.0496	2214.0846	2214.0627	9.92	0	71	3.8e-006	1	K.DLYANTVLSGGTTMYPGIADR.M
☑	952	796.6569	3182.5985	3182.6071	-2.69	0	67	5.2e-006	1	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L

Proteins matching the same set of peptides:
IPI00473320 **Mass:** 42115 **Score:** 107 **Queries matched:** 6
Tax_Id=10090 Gene_Symbol=Actb Putative uncharacterized protein
IPI00652436 **Mass:** 42053 **Score:** 107 **Queries matched:** 6
Tax_Id=10090 Gene_Symbol=Actg1 Putative uncharacterized protein
IPI00874482 **Mass:** 42108 **Score:** 107 **Queries matched:** 6
Tax_Id=10090 Gene_Symbol=Actg1 Actin, cytoplasmic 2

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18. IPI00136929 **Mass:** 44029 **Score:** 107 **Queries matched:** 5 **emPAI:** 0.16
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
791	812.4296	1622.8446	1622.8338	6.70	1	3	30	3	R.LDLAGRDLTDYLMK.I
849	895.9518	1789.8890	1789.8846	2.47	0	21	0.43	1	K.SYELPDGQVITIGNER.F
874	652.0251	1953.0535	1953.0571	-1.86	0	5	12	2	R.VAPEEHPVLLTEAPLNPK.R
897	1108.0496	2214.0846	2214.0627	9.92	0	71	3.8e-006	1	K.DLYANTVLSGGTTMYPGLADR.M
952	796.6569	3182.5985	3182.6071	-2.69	0	67	5.2e-006	1	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L

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19. IPI00123176 **Mass:** 36804 **Score:** 99 **Queries matched:** 3 **emPAI:** 0.19
Tax_Id=10090 Gene_Symbol=Gm6316 Glyceraldehyde-3-phosphate dehydrogenase

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

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	678	**685.3767**	**1368.7388**	**1368.7361**	**2.01**	**0**	**51**	**0.00049**	**1**	**R.GAAQNIIPASTGAAK.A**
☑	679	**685.3803**	**1368.7460**	**1368.7361**	**7.27**	**0**	**(27)**	**0.1**	**1**	**R.GAAQNIIPASTGAAK.A**
☑	846	**890.4040**	**1778.7934**	**1778.7900**	**1.95**	**0**	**85**	**1.4e-007**	**1**	**K.LISWYDNEYGYSNR.M**

Proteins matching the same set of peptides:

IPI00135284 **Mass:** 36092 **Score:** 99 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=Gm16374 Glyceraldehyde-3-phosphate dehydrogenase

IPI00271869 **Mass:** 36293 **Score:** 99 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=- 36 kDa protein

IPI00273646 **Mass:** 36072 **Score:** 99 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=Gapdh;LOC100042025 Glyceraldehyde-3-phosphate dehydrogenase

IPI00622795 **Mass:** 36074 **Score:** 99 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=- 36 kDa protein

IPI00752289 **Mass:** 36308 **Score:** 99 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=Gm10290 Glyceraldehyde-3-phosphate dehydrogenase

IPI00848801 **Mass:** 36100 **Score:** 99 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=- 36 kDa protein

IPI00849045 **Mass:** 36072 **Score:** 99 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=- 36 kDa protein

IPI00850337 **Mass:** 44633 **Score:** 99 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=LOC100048117 similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) isoform 1

IPI00850377 **Mass:** 35975 **Score:** 99 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=- 36 kDa protein

IPI00850779 **Mass:** 36076 **Score:** 99 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=- 36 kDa protein

IPI00874682 **Mass:** 36038 **Score:** 99 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=- 36 kDa protein

IPI00874964 **Mass:** 36512 **Score:** 99 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=- 36 kDa protein

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20. IPI00114642 **Mass:** 13928 **Score:** 97 **Queries matched:** 1 **emPAI:** 0.25
Tax_Id=10090 Gene_Symbol=Hist1h2bn;Hist1h2bl;Hist1h2bj;Hist1h2bf Histone H2B type 1-F/J/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
☑	835	**872.4168**	**1742.8190**	**1742.8120**	**4.05**	**0**	**97**	**1.2e-008**	**1**	**K.AMGIMNSFVNDIFER.I**

Proteins matching the same set of peptides:

IPI00124518 **Mass:** 13359 **Score:** 97 **Queries matched:** 1
Tax_Id=10090 Gene_Symbol=Hist2h2bb Hist2h2bb protein

IPI00134534 **Mass:** 14879 **Score:** 97 **Queries matched:** 1
Tax_Id=10090 Gene_Symbol=Gm11277;Gm13646 Histone H2B

IPI00187543 **Mass:** 13985 **Score:** 97 **Queries matched:** 1
Tax_Id=10090 Gene_Symbol=Hist2h2be Histone H2B type 2-E

IPI00227930 **Mass:** 13912 **Score:** 97 **Queries matched:** 1
Tax_Id=10090 Gene_Symbol=Hist1h2bh Histone H2B type 1-H

IPI00229539 **Mass:** 17248 **Score:** 97 **Queries matched:** 1
Tax_Id=10090 Gene_Symbol=Hist3h2bb-ps histone H2B type 3-B

IPI00265768 **Mass:** 13912 **Score:** 97 **Queries matched:** 1
Tax_Id=10090 Gene_Symbol=Hist1h2bk Histone H2B type 1-K

IPI00282266 **Mass:** 13898 **Score:** 97 **Queries matched:** 1
Tax_Id=10090 Gene_Symbol=Hist1h2bg;Hist1h2be;Gm9998;Hist1h2bc Histone H2B type 1-C/E/G

IPI00282269 **Mass:** 13928 **Score:** 97 **Queries matched:** 1
Tax_Id=10090 Gene_Symbol=Hist1h2bm Histone H2B type 1-M

IPI00348270 **Mass:** 13912 **Score:** 97 **Queries matched:** 1
Tax_Id=10090 Gene_Symbol=Hist2h2bb Histone H2B type 2-B

IPI00453744 **Mass:** 15968 **Score:** 97 **Queries matched:** 1
Tax_Id=10090 Gene_Symbol=Hist1h2bp 16 kDa protein

IPI00461514 **Mass:** 14987 **Score:** 97 **Queries matched:** 1
Tax_Id=10090 Gene_Symbol=Gm13646 Histone H2B

IPI00553774 **Mass:** 13986 **Score:** 97 **Queries matched:** 1
Tax_Id=10090 Gene_Symbol=Hist3h2ba Histone H2B type 3-A

IPI00554853 **Mass:** 13944 **Score:** 97 **Queries matched:** 1
Tax_Id=10090 Gene_Symbol=Hist1h2bb Histone H2B type 1-B

IPI00648991 **Mass:** 13984 **Score:** 97 **Queries matched:** 1
Tax_Id=10090 Gene_Symbol=Hist1h2bp Isoform 1 of Histone H2B type 1-P

IPI00761713 **Mass:** 15555 **Score:** 97 **Queries matched:** 1
Tax_Id=10090 Gene_Symbol=Hist1h2bp Isoform 2 of Histone H2B type 1-P

IPI00874492 **Mass:** 14746 **Score:** 97 **Queries matched:** 1
Tax_Id=10090 Gene_Symbol=Hist1h2bm 15 kDa protein

IPI00874654 **Mass:** 14787 **Score:** 97 **Queries matched:** 1
Tax_Id=10090 Gene_Symbol=Hist1h2bg;Hist1h2be;Gm9998;Hist1h2bc Histone H2B

```
      IPI00874970    Mass: 14951    Score: 97     Queries matched: 1
      Tax_Id=10090 Gene_Symbol=Hist1h2bn;Hist1h2bl;Hist1h2bj;Hist1h2bf Histone H2B
      IPI00875277    Mass: 14242    Score: 97     Queries matched: 1
      Tax_Id=10090 Gene_Symbol=Hist1h2bk 14 kDa protein
      IPI00875523    Mass: 14900    Score: 97     Queries matched: 1
      Tax_Id=10090 Gene_Symbol=Hist1h2bh Histone H2B
      IPI00875901    Mass: 14806    Score: 97     Queries matched: 1
      Tax_Id=10090 Gene_Symbol=Hist1h2bk Histone H2B
      IPI00876167    Mass: 14126    Score: 97     Queries matched: 1
      Tax_Id=10090 Gene_Symbol=Hist1h2bn;Hist1h2bl;Hist1h2bj;Hist1h2bf 14 kDa protein
      IPI00876432    Mass: 14148    Score: 97     Queries matched: 1
      Tax_Id=10090 Gene_Symbol=Hist1h2bn;Hist1h2bl;Hist1h2bj;Hist1h2bf Histone H2B
      IPI00876549    Mass: 14902    Score: 97     Queries matched: 1
      Tax_Id=10090 Gene_Symbol=Hist1h2bn;Hist1h2bl;Hist1h2bj;Hist1h2bf Histone H2B
      IPI00876550    Mass: 14812    Score: 97     Queries matched: 1
      Tax_Id=10090 Gene_Symbol=- 15 kDa protein
```

```
21.   IPI00380227    Mass: 7720     Score: 76     Queries matched: 1    emPAI: 0.45
      Tax_Id=10090 Gene_Symbol=Nrgn Neurogranin
    ☐ Check to include this hit in error tolerant search or archive report

     Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score   Expect Rank  Peptide
  ☑    573  596.8132  1191.6118  1191.6109   0.81    1    76  2.1e-006    1   R.KGPGPGGPGGAGGAR.G
```

```
22.   IPI00135106    Mass: 19584    Score: 71     Queries matched: 4    emPAI: 0.61
      Tax_Id=10090 Gene_Symbol=Mobp Isoform 1 of Myelin-associated oligodendrocyte basic 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  449.7448   897.4750   897.4781  -3.35    1     3       33    7  R.GGSPTRAPR.F
  ☑    477  498.7868   995.5590   995.5586   0.46    0    46   0.0011    1  K.SPLMPAKPR.S
  ☑    546  557.8030  1113.5914  1113.5891   2.14    1    38    0.012    1  R.SSPLRGPGTSR.G
  ☑    559  580.8307  1159.6468  1159.6462   0.56    0    48  0.00095    1  K.HQPAASPVVVR.A
```

```
23.   IPI00221528    Mass: 42319    Score: 67     Queries matched: 4    emPAI: 0.08
      Tax_Id=10090 Gene_Symbol=Actbl2 Beta-actin-like 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
       791  812.4296  1622.8446  1622.8338   6.70    1     3        30    3   R.LDLAGRDLTDYLMK.I
       849  895.9518  1789.8890  1789.8846   2.47    0    21      0.43    1   R.SYELPDGQVITIGNER.F
  ☑    874  652.0251  1953.0535  1953.0571  -1.86    0     6        10    1   R.VAPDEHPILLTEAPLNPK.I
       952  796.6569  3182.5985  3182.6071  -2.69    0    67  5.2e-006    1   R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L
```

```
24.   IPI00136703    Mass: 42971    Score: 58     Queries matched: 1    emPAI: 0.08
      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
  ☑    807  828.9211  1655.8276  1655.8188   5.31    0    58  9.4e-005    1   R.LEQGQAIDDLMPAQK.-
```

```
25.   IPI00404590    Mass: 19412    Score: 53     Queries matched: 2    emPAI: 0.38
      Tax_Id=10090 Gene_Symbol=H1f0 Putative uncharacterized 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
  ☑    514  530.7678  1059.5210  1059.5196   1.33    0    42 0.0063    1  K.VGENADSQIK.L
  ☑    624  651.3369  1300.6592  1300.6623  -2.32    0    48 0.0013    1  M.TENSTSAPAAKPK.R


      Proteins matching the same set of peptides:
      IPI00467914    Mass: 20848    Score: 53     Queries matched: 2
      Tax_Id=10090 Gene_Symbol=H1f0 Histone H1.0
```

```
26.   IPI00131366    Mass: 60627    Score: 50     Queries matched: 1    emPAI: 0.05
      Tax_Id=10090 Gene_Symbol=Krt6b Keratin, type II cytoskeletal 6B
    ☐ Check to include this hit in error tolerant search or archive report

     Query  Observed   Mr(expt)   Mr(calc)     ppm  Miss Score  Expect Rank  Peptide
  ☑    627  651.8530  1301.6914  1301.7078  -12.58    0    50 0.00072    1   R.SLDLDSIIAEVK.A


      Proteins matching the same set of peptides:
      IPI00131368    Mass: 59641    Score: 50     Queries matched: 1
      Tax_Id=10090 Gene_Symbol=Krt6a Keratin, type II cytoskeletal 6A
      IPI00139301    Mass: 61957    Score: 50     Queries matched: 1
      Tax_Id=10090 Gene_Symbol=Krt5 Keratin, type II cytoskeletal 5
      IPI00221797    Mass: 59932    Score: 50     Queries matched: 1
      Tax_Id=10090 Gene_Symbol=Krt75 Keratin, type II cytoskeletal 75
      IPI00330480    Mass: 35315    Score: 50     Queries matched: 1
      Tax_Id=10090 Gene_Symbol=- 35 kDa protein
      IPI00470126    Mass: 60553    Score: 50     Queries matched: 1
      Tax_Id=10090 Gene_Symbol=Krt5 Uncharacterized protein
      IPI00762364    Mass: 50641    Score: 50     Queries matched: 1
```

Tax_Id=10090 Gene_Symbol=Krt6a Uncharacterized protein
IPI00785403 **Mass:** 59832 **Score:** 50 **Queries matched:** 1
Tax_Id=10090 Gene_Symbol=Krt6b keratin, type II cytoskeletal 6B

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27. IPI00348094 **Mass:** 51093 **Score:** 48 **Queries matched:** 2 **emPAI:** 0.06
Tax_Id=10090 Gene_Symbol=Tubb1 Tubulin, 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
557	580.3218	1158.6290	1158.6219	6.13	0	48	0.0012	1	K.LAVNMVPFPR.L + Oxidation (M)
643	660.3592	1318.7038	1318.6955	6.33	0	11	6	2	R.ILNSFSVMPSPK.V

---

28. IPI00229525 **Score:** 45 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=Gnal Guanine nucleotide-binding protein G(olf) 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
509	529.3168	1056.6190	1056.6179	1.10	0	45	0.0021	1	R.LLLLGAGESGK.S
571	**595.8328**	**1189.6510**	**1189.6165**	**29.0**	**1**	**0**	**76**	**6**	**R.MHLKQYELL.- + Oxidation (M)**

Proteins matching the same set of peptides:
IPI00272681 **Score:** 45 **Queries matched:** 2

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29. IPI00118569 **Mass:** 44369 **Score:** 45 **Queries matched:** 1 **emPAI:** 0.07
Tax_Id=10090 Gene_Symbol=Gna13 Guanine nucleotide-binding protein subunit alpha-13
☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
509	529.3168	1056.6190	1056.6179	1.10	0	45	0.0021	1	K.ILLLGAGESGK.S

Proteins matching the same set of peptides:
IPI00230191 **Mass:** 44238 **Score:** 45 **Queries matched:** 1
Tax_Id=10090 Gene_Symbol=Gna12 Guanine nucleotide-binding protein subunit alpha-12
IPI00649388 **Mass:** 20095 **Score:** 45 **Queries matched:** 1
Tax_Id=10090 Gene_Symbol=Gna13 Putative uncharacterized protein

---

30. IPI00119067 **Mass:** 23731 **Score:** 44 **Queries matched:** 1 **emPAI:** 0.14
Tax_Id=10090 Gene_Symbol=Tppp Tubulin polymerization-promoting 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
☑	871	**948.9888**	**1895.9630**	**1895.9516**	**6.02**	**0**	**44**	**0.0026**	**1**	**R.TITFEQFQEALEELAK.K**

Peptide matches not assigned to protein hits: (no details means no match)

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	684	**696.3746**	**1390.7346**	**1390.7245**	**7.29**	**0**	**28**	**0.094**	**1**	**LEGVVFPYQPSR**
☑	792	**812.4532**	**1622.8918**	**1622.8992**	**-4.50**	**0**	**28**	**0.068**	**1**	**LAGTQPLEVLEAVQR**
☑	685	**697.3685**	**1392.7224**	**1392.7038**	**13.4**	**0**	**25**	**0.22**	**1**	**ELGGEVFYVGPAR**
☑	960	**1259.2880**	**3774.8422**	**3774.8417**	**0.12**	**0**	**23**	**0.092**	**1**	**ADTPIEEFTPTPAFPALQYLESVDEGGVAWQAGLR**
☑	595	**622.7920**	**1243.5694**	**1243.5581**	**9.10**	**1**	**22**	**0.34**	**1**	**ESQAYYDGRR**
☑	663	**673.8612**	**1345.7078**	**1345.6925**	**11.4**	**1**	**22**	**0.54**	**1**	**AGGQGFKMALNPR**
☑	404	**421.7574**	**841.5002**	**841.4810**	**22.9**	**0**	**21**	**0.48**	**1**	**AVLTWPR**
☑	515	**530.7717**	**1059.5288**	**1059.5713**	**-40.04**	**0**	**17**	**2**	**1**	**AGSLAFPELR**
☑	304	**346.2065**	**690.3984**	**690.3912**	**10.5**	**1**	**17**	**1.4**	**1**	**KDVTTK**
☑	565	**587.8109**	**1173.6072**	**1173.6353**	**-23.93**	**0**	**17**	**2**	**1**	**NATITQALTNK**
☑	488	**508.7708**	**1015.5270**	**1015.5298**	**-2.76**	**0**	**16**	**2.6**	**1**	**QHTVTTTTK**
☑	551	**566.2957**	**1130.5768**	**1130.5720**	**4.27**	**0**	**16**	**2.2**	**1**	**TTHYGSLPQK**
☑	496	**346.2080**	**1035.6022**	**1035.5964**	**5.55**	**0**	**16**	**0.9**	**1**	**KPIPLEDPK**
☑	508	**529.2868**	**1056.5590**	**1056.5716**	**-11.89**	**1**	**15**	**2.4**	**1**	**KPDWDLKR**
☑	394	**411.2468**	**820.4790**	**820.4668**	**15.0**	**1**	**15**	**1.5**	**1**	**RQPAPPR**
☑	709	**746.3885**	**1490.7624**	**1490.7841**	**-14.54**	**0**	**14**	**2.9**	**1**	**VIEDGPEPRPNLR**
☑	604	**633.3046**	**1264.5946**	**1264.6425**	**-37.83**	**1**	**14**	**2.7**	**1**	**FQQEAPHPRR**
☑	424	446.2583	890.5020	890.5226	-23.04	1	14	3.3	1	GVQFVIKT
☑	475	**329.1741**	**984.5005**	**984.4923**	**8.26**	**1**	**14**	**2.8**	**1**	**CVHKQTGR**
☑	436	**449.7468**	**897.4790**	**897.4920**	**-14.39**	**0**	**14**	**3**	**1**	**KPEGKPDK**
☑	470	**487.3048**	**972.5950**	**972.5869**	**8.38**	**0**	**13**	**1.5**	**1**	**VPGHLPVVR**
☑	418	**441.2692**	**880.5238**	**880.5355**	**-13.24**	**0**	**13**	**1.1**	**1**	**RPTVRPR**
☑	539	**551.8070**	**1101.5994**	**1101.5455**	**49.0**	**1**	**13**	**4**	**1**	**KDSGYYTLR**
☑	507	**529.2727**	**1056.5308**	**1056.5676**	**-34.77**	**1**	**13**	**3.6**	**1**	**QLGDLERAR**
☑	634	**653.3388**	**1304.6630**	**1304.6143**	**37.4**	**1**	**13**	**4.3**	**1**	**LGADMEDLRNR + Oxidation (M)**
☑	641	**659.8417**	**1317.6688**	**1317.7115**	**-32.35**	**0**	**12**	**4.4**	**1**	**LLYMAIDGVAPR**
☑	723	**776.3270**	**1550.6394**	**1550.6759**	**-23.48**	**1**	**12**	**0.97**	**1**	**GYDLAFRFCSCR**
☑	358	**780.3290**	**779.3217**	**779.3054**	**20.9**	**0**	**12**	**2**	**1**	**ANECMR**
☑	615	**643.8413**	**1285.6680**	**1285.7064**	**-29.81**	**1**	**12**	**5**	**1**	**TIMKDEIAIPR**
☑	478	**499.2877**	**996.5608**	**996.5141**	**46.9**	**0**	**12**	**3**	**1**	**VPWGSAQPR**
☑	324	**743.4591**	**742.4518**	**742.4198**	**43.1**	**1**	**12**	**5.5**	**1**	**RGAAVGGR**
☑	582	**606.7893**	**1211.5640**	**1211.6007**	**-30.23**	**1**	**11**	**4.1**	**1**	**DSLAEATRGHR**
☑	455	**470.7701**	**939.5256**	**939.5548**	**-31.07**	**1**	**11**	**3.5**	**1**	**MRKPRPR**
☑	519	**531.2891**	**1060.5636**	**1060.5665**	**-2.70**	**0**	**11**	**6.6**	**1**	**YLLASNAPGR**
☑	491	**517.2959**	**1032.5772**	**1032.6001**	**-22.17**	**1**	**11**	**5.1**	**1**	**KVIAAMTVGK + Oxidation (M)**
☑	569	**595.8130**	**1189.6114**	**1189.6489**	**-31.45**	**1**	**11**	**8**	**1**	**KTNIIDSMLR**

☑	683	458.9068	1373.6986	1373.7085	-7.24	1	10	7.5	1	VTAAAMAGNKSTPR
☑	710	756.8234	1511.6322	1511.6939	-40.80	1	10	2.3	1	YYGTSMHERVNR
☑	687	699.8989	1397.7832	1397.7263	40.8	1	10	4.7	1	ELKTDNLPNQAR
☑	614	643.3510	1284.6874	1284.7150	-21.41	1	10	6.8	1	QKNSINIQAAAK
☑	480	500.2594	998.5042	998.5509	-46.69	0	10	6.7	1	VQIQQAANK
☑	435	449.7448	897.4750	897.4556	21.7	0	10	7.2	1	DAETPLPR
☑	809	834.9677	1667.9208	1667.8970	14.3	1	10	4.4	1	QPFFPTHMGPIKLR
☑	301	685.3705	684.3632	684.3667	-5.08	0	10	4.9	1	GAERPR
☑	840	878.4757	1754.9368	1754.9567	-11.28	1	10	4.7	1	ELLDLVASHFNLKEK
☑	594	622.7913	1243.5680	1243.5681	-0.00	1	10	5.4	1	KQGGSPDEPDSK
☑	443	455.2521	908.4896	908.4790	11.8	0	10	6.8	1	ELVMFVR + Oxidation (M)
☑	506	528.7111	1055.4076	1055.4310	-22.17	1	10	1	1	MGNGMCSRK + Oxidation (M)
☑	517	530.8016	1059.5886	1059.5672	20.2	1	10	8.9	1	SERDTLLAR
☑	400	417.2493	832.4840	832.4443	47.7	0	9	5.6	1	SLPVDFR
☑	518	530.8044	1059.5942	1059.5672	25.5	1	9	8.5	1	SERDTLLAR
☑	635	653.8335	1305.6524	1305.6751	-17.32	1	9	8.3	1	YEALKEPMVAR
☑	479	499.7479	997.4812	997.4507	30.6	1	9	6.6	1	MAMAMRQK + 2 Oxidation (M)
☑	273	320.1377	638.2608	638.2880	-42.53	0	9	2.7	1	SMVMR + Oxidation (M)
☑	501	523.2865	1044.5584	1044.5101	46.3	1	9	12	1	KGAAGWEGGGR
☑	584	607.3194	1212.6242	1212.6211	2.61	1	9	9.2	1	LSASPSPADRGR
☑	668	678.3817	1354.7488	1354.7820	-24.48	0	9	6.7	1	IVQLLAGVADQTK
☑	680	458.5831	1372.7275	1372.7184	6.58	1	9	9.5	1	QAQHGRRPGNPR
☑	522	532.2796	1062.5446	1062.4917	49.9	0	9	13	1	AGEMAQWVR + Oxidation (M)
☑	516	530.8014	1059.5882	1059.5672	19.8	1	8	11	1	SERDTLLAR
☑	180	487.3051	486.2978	486.2914	13.2	0	8	19	1	AGAIR
☑	498	520.2791	1038.5436	1038.5458	-2.05	0	8	9.6	1	AQASAPAQAPK
☑	810	838.3979	1674.7812	1674.8246	-25.91	1	8	8.7	1	ALDGLQREAMEELGK + Oxidation (M)
☑	201	518.2473	517.2400	517.2609	-40.29	0	8	9.8	1	AGGTGR
☑	654	668.3532	1334.6918	1334.7050	-9.86	1	8	12	1	DKPLISRTMMK + Oxidation (M)
☑	854	903.4784	1804.9422	1805.0121	-38.69	0	8	9.1	1	MAGLVFLGLALSSGATVAK
☑	538	548.2862	1094.5578	1094.5253	29.8	0	8	11	1	LWVMDMIR + 2 Oxidation (M)
☑	608	639.2949	1276.5752	1276.6380	-49.15	1	8	8	1	GIRTCLICER
☑	426	446.2641	890.5136	890.5226	-10.02	1	8	10	1	GVQFVIKT
☑	454	467.7639	933.5132	933.4702	46.1	0	7	13	1	LSNNMLAR + Oxidation (M)
☑	406	423.2285	844.4424	844.4767	-40.51	0	7	22	1	IGTSLAQR
☑	256	607.3195	606.3122	606.3047	12.4	0	7	15	1	MDVVK + Oxidation (M)
☑	504	525.7818	1049.5490	1049.5943	-43.14	0	7	15	1	VLFAVLNMK + Oxidation (M)
☑	682	687.8503	1373.6860	1373.6939	-5.73	0	7	15	1	EVYAHAGTTLQGK
☑	537	545.2896	1088.5646	1088.5978	-30.49	1	7	17	1	KDFTVNLPR
☑	442	452.7382	903.4618	903.4522	10.7	1	7	20	1	GAATADSRR
☑	306	350.1603	698.3060	698.3096	-5.09	0	7	4.1	1	SAHGDGR
☑	560	581.3129	1160.6112	1160.5859	21.8	0	7	19	1	QMPSTIAIER + Oxidation (M)
☑	460	475.7495	949.4844	949.4406	46.2	0	7	18	1	GQEQWFR
☑	567	595.3054	1188.5962	1188.6033	-5.95	1	7	18	1	QMQASRLSPR + Oxidation (M)
☑	503	525.2869	1048.5592	1048.5084	48.5	1	7	17	1	MAGLARGDSR + Oxidation (M)
☑	303	343.7281	685.4416	685.4235	26.5	1	7	12	1	GAKALAR
☑	597	623.3267	1244.6388	1244.5819	45.7	0	7	19	1	QDMPKPSEAAR + Oxidation (M)
☑	873	956.4583	1910.9020	1910.9964	-49.39	1	6	11	1	LFEDMGLFEAFKIPVR
☑	572	596.3065	1190.5984	1190.5649	28.2	1	6	19	1	RCSMTGQPVR
☑	664	675.3417	1348.6688	1348.6735	-3.47	0	6	20	1	GADAASPPPVAGSPR
☑	461	476.2360	950.4574	950.4682	-11.33	0	6	18	1	QAPGAHGASR
☑	743	785.8390	1569.6634	1569.6664	-1.90	1	6	5.9	1	WTEGTCKGSTQCR
☑	593	622.7913	1243.5680	1243.5581	7.97	1	6	13	1	ESQAYYDGRR
☑	293	675.3319	674.3246	674.3347	-14.99	0	6	25	1	SSAASPR
☑	927	881.7323	2642.1751	2642.2348	-22.59	1	6	7.6	1	ENSHPHHHHQQPPPQPGPSGERR
☑	453	463.2427	924.4708	924.4310	43.1	0	6	17	1	FLCACVR
☑	667	677.8867	1353.7588	1353.7001	43.4	1	6	11	1	TESGGALRDLAHK
☑	213	531.2889	530.2816	530.2635	34.2	0	6	44	1	MAGPR
☑	640	659.3407	1316.6668	1316.6725	-4.26	1	6	24	1	LVKEAFQDDPR
☑	666	676.3508	1350.6870	1350.6271	44.4	1	5	22	1	EAMSKALDPAMR + 2 Oxidation (M)
☑	600	630.3074	1258.6002	1258.6153	-11.97	1	5	19	1	KEVVEEAENGR
☑	329	379.7334	757.4522	757.4698	-23.12	1	5	32	1	KELLQK
☑	558	580.8033	1159.5920	1159.6131	-18.19	1	5	27	1	MQLAELQRR + Oxidation (M)
☑	619	645.8328	1289.6510	1289.7013	-38.97	1	5	24	1	AEGTVVMKLAQK + Oxidation (M)
☑	652	667.3491	1332.6836	1332.6972	-10.20	0	5	24	1	LGGLPGPGPMANPR
☑	302	343.2315	684.4484	684.4646	-23.64	1	5	14	1	KAVVIR
☑	677	684.3544	1366.6942	1366.6551	28.6	0	5	22	1	EGMVTFSNTLPR + Oxidation (M)
☑	555	577.2852	1152.5558	1152.5564	-0.45	0	5	22	1	EAFGFEQAVR
☑	850	897.9155	1793.8164	1793.8941	-43.31	1	5	17	1	TERSNTLNTAIVNMSK + Oxidation (M)
☑	441	452.2508	902.4870	902.4709	17.9	1	5	36	1	KSDPELSK
☑	476	496.2224	990.4302	990.4744	-44.54	0	5	12	1	LGGNHSNHR
☑	571	595.8328	1189.6510	1189.6819	-25.93	1	5	27	1	KLFVQDLATR
☑	669	678.8935	1355.7724	1355.7846	-8.98	1	5	16	1	QDPKLLLMLAAK + Oxidation (M)
☑	626	651.8315	1301.6484	1301.6463	1.66	0	4	28	1	KPTAQEDSADLK
☑	934	916.4277	2746.2613	2746.2996	-13.94	1	4	12	1	QAPPQYTFIGELNSMGIWYRMGR + 2 Oxidation (M)
☑	556	577.2904	1152.5662	1152.6147	-42.08	1	4	26	1	LTGRLMFMGK
☑	636	655.3013	1308.5880	1308.5252	48.0	0	4	17	1	DINDQMDESSR
☑	520	531.8290	1061.6434	1061.6386	4.60	1	4	7.9	1	SFLILWKR
☑	898	1110.6010	2219.1874	2219.1950	-3.39	1	4	15	1	QLFLEPSQKLEGPPALPEAR
☑	487	505.7451	1009.4756	1009.4829	-7.15	0	4	24	1	EATPGEPGPR
☑	570	595.8189	1189.6232	1189.6012	18.5	1	4	40	1	KQDIEAVMEK

☑	642	660.3415	1318.6684	1318.6526	12.0	0	4	32	1	LTGAIMHFGNMK
☑	578	604.7988	1207.5830	1207.5615	17.8	1	4	33	1	KGETSAANMQR + Oxidation (M)
☑	817	847.9592	1693.9038	1693.8423	36.3	0	4	23	1	LRPIYDYLDNGNNK
☑	711	756.8477	1511.6808	1511.6939	-8.65	1	4	21	1	YYGTSMHERVNR
☑	425	446.2607	890.5068	890.4875	21.7	1	3	33	1	FQRWVR
☑	791	812.4296	1622.8446	1622.9144	-42.98	0	3	27	1	FSAELIQHIPLSLR
☑	568	595.8109	1189.6072	1189.6489	-34.98	1	3	46	1	KTNIIDSMLR
☑	305	697.3679	696.3606	696.3919	-44.86	0	3	22	1	LPSPQR
☑	784	809.3986	1616.7826	1616.8279	-27.99	1	3	32	1	KMGNKPHMIQVYR + Oxidation (M)
☑	382	810.4398	809.4325	809.3953	46.0	0	3	24	1	MSLTNTK + Oxidation (M)
☑	271	631.3865	630.3792	630.3813	-3.27	1	3	61	1	KQISR
☑	274	320.1440	638.2734	638.3024	-45.33	0	3	15	1	HLDPAS
☑	947	961.7438	2882.2096	2882.3141	-36.26	0	3	5.7	1	DPGSPQLNQEAMADGVEGTPWSAEKPR + Oxidation (M)
☑	879	980.4991	1958.9836	1958.9810	1.36	0	3	32	1	SNNGTDVNAGQIPQLLYR
☑	486	504.2251	1006.4356	1006.4693	-33.42	0	3	18	1	QSHSQQHR
☑	270	631.3174	630.3101	630.3198	-15.29	1	3	43	1	QDGRR
☑	536	545.2885	1088.5624	1088.6012	-35.59	1	3	51	1	KALTGSMPIR + Oxidation (M)
☑	620	647.3015	1292.5884	1292.6183	-23.12	0	3	30	1	WTVVTPMSSNR + Oxidation (M)
☑	292	672.3444	671.3371	671.3602	-34.42	0	2	24	1	LGETPR
☑	773	785.8511	1569.6876	1569.7068	-12.20	1	2	20	1	KFPEWMSMQSQR + Oxidation (M)
☑	777	795.4383	1588.8620	1588.9044	-26.68	1	2	31	1	LLKAGVISALACMVK + Oxidation (M)
☑	577	600.2880	1198.5614	1198.5441	14.5	0	2	35	1	MGFPEAASSFR
☑	943	1414.1135	2826.2124	2826.2840	-25.32	0	2	12	1	EYTESMCLLENELEAQLGEFHLR + Oxidation (M)
☑	381	809.4304	808.4231	808.4443	-26.18	1	1	46	1	AVGKYSGK
☑	629	652.2864	1302.5582	1302.6099	-39.65	1	1	20	1	RCADVPGASGTGR
☑	245	600.3077	599.3004	599.3027	-3.83	0	1	21	1	DNPVR
☑	250	601.3277	600.3204	600.3231	-4.49	0	1	36	1	ETVPR
☑	545	556.8411	1111.6676	1111.6462	19.3	1	1	21	1	KPQLDTRVR
☑	942	1400.1620	2798.3094	2798.3075	0.68	1	1	27	1	LGTNMYSASRPVETHMSATSKNAASR + 2 Oxidation (M)
☑	903	762.0558	2283.1456	2283.0334	49.1	1	1	36	1	KCSCVICSPTYVPEDLEAR
☑	421	445.2847	888.5548	888.5280	30.2	1	1	16	1	KDSSLIVK
☑	887	1048.9823	2095.9500	2095.9469	1.52	0	1	33	1	SNPFHYPSNSVFFPFYF
☑	715	510.2402	1527.6988	1527.6922	4.29	1	1	42	1	CNDPVMNEKLHR + Oxidation (M)
☑	896	738.0253	2211.0541	2211.0477	2.86	0	0	45	1	GPELMAIEGLENGEGPTTAGPR + Oxidation (M)
☑	941	933.7730	2798.2972	2798.3075	-3.71	1	0	32	1	LGTNMYSASRPVETHMSATSKNAASR + 2 Oxidation (M)
☑	1	300.0226	299.0153							
☑	2	301.1499	300.1426							
☑	3	301.1562	300.1489							
☑	4	301.1611	300.1538							
☑	5	301.1714	300.1641							
☑	6	305.9528	304.9455							
☑	7	307.9514	306.9441							
☑	8	308.0271	307.0198							
☑	9	309.0632	308.0559							
☑	10	309.0973	308.0900							
☑	11	311.1737	310.1664							
☑	12	312.9832	311.9759							
☑	13	313.0961	312.0888							
☑	14	315.0642	314.0569							
☑	15	315.0667	314.0594							
☑	16	315.0670	314.0597							
☑	17	315.0680	314.0607							
☑	18	315.0689	314.0616							
☑	19	315.2316	314.2243							
☑	20	315.2350	314.2277							
☑	21	317.0646	316.0573							
☑	22	322.0896	321.0823							
☑	23	322.9079	321.9006							
☑	24	322.9219	321.9146							
☑	25	324.0315	323.0242							
☑	26	325.0964	324.0891							
☑	27	332.9781	331.9708							
☑	28	333.0402	332.0329							
☑	29	333.6491	332.6418							
☑	30	338.8961	337.8888							
☑	31	340.0163	339.0090							
☑	32	340.8851	339.8778							
☑	33	341.0215	340.0142							
☑	34	341.0225	340.0152							
☑	35	341.0247	340.0174							
☑	36	341.0261	340.0188							
☑	37	341.0267	340.0194							
☑	38	341.0269	340.0196							
☑	39	341.0484	340.0411							
☑	40	341.0866	340.0793							
☑	41	342.0295	341.0222							
☑	42	342.0844	341.0771							
☑	43	342.0868	341.0795							
☑	44	342.0894	341.0821							
☑	45	342.0905	341.0832							
☑	46	342.0916	341.0843							

☑	47	342.9606	341.9533
☑	48	343.0220	342.0147
☑	49	343.7295	342.7222
☑	50	344.2295	343.2222
☑	51	344.9496	343.9423
☑	52	345.0750	344.0677
☑	53	345.2236	344.2163
☑	54	346.9440	345.9367
☑	55	354.9622	353.9549
☑	56	354.9651	353.9578
☑	57	355.0676	354.0603
☑	58	355.0696	354.0623
☑	59	355.0723	354.0650
☑	60	355.0738	354.0665
☑	61	355.0746	354.0673
☑	62	355.0752	354.0679
☑	63	355.0760	354.0687
☑	64	355.0764	354.0691
☑	65	355.0774	354.0701
☑	66	355.0786	354.0713
☑	67	355.0806	354.0733
☑	68	355.0832	354.0759
☑	69	356.0023	354.9950
☑	70	356.0729	355.0656
☑	71	356.0748	355.0675
☑	72	356.0748	355.0675
☑	73	356.0791	355.0718
☑	74	356.9736	355.9663
☑	75	357.0002	355.9929
☑	76	357.0729	356.0656
☑	77	359.0438	358.0365
☑	78	365.9749	364.9676
☑	79	366.1819	365.1746
☑	80	371.2194	370.2121
☑	81	374.2417	373.2344
☑	82	375.0931	374.0858
☑	83	375.0943	374.0870
☑	84	375.0979	374.0906
☑	85	375.0984	374.0911
☑	86	375.0995	374.0922
☑	87	376.9003	375.8930
☑	88	377.0886	376.0813
☑	89	377.0909	376.0836
☑	90	377.1556	376.1483
☑	91	378.2327	377.2254
☑	92	378.9160	377.9087
☑	93	385.8234	384.8161
☑	94	402.1234	401.1161
☑	95	404.2323	403.2250
☑	96	414.8633	413.8560
☑	97	414.8758	413.8685
☑	98	414.9092	413.9019
☑	99	415.0326	414.0253
☑	100	415.0343	414.0270
☑	101	415.0360	414.0287
☑	102	415.0377	414.0304
☑	103	415.0380	414.0307
☑	104	415.0395	414.0322
☑	105	415.0411	414.0338
☑	106	415.0453	414.0380
☑	107	415.0509	414.0436
☑	108	415.0523	414.0450
☑	109	415.0569	414.0496
☑	110	415.0619	414.0546
☑	111	415.8512	414.8439
☑	112	415.8564	414.8491
☑	113	415.8646	414.8573
☑	114	415.8731	414.8658
☑	115	416.0414	415.0341
☑	116	416.0461	415.0388
☑	117	417.0393	416.0320
☑	118	417.2494	416.2421
☑	119	417.8458	416.8385
☑	120	417.8559	416.8486
☑	121	417.8654	416.8581
☑	122	418.1017	417.0944
☑	123	418.9891	417.9818
☑	124	425.9435	424.9362
☑	125	426.0362	425.0289
☑	126	429.0944	428.0871
☑	127	429.0957	428.0884

☑	128	*429.0975*	*428.0902*
☑	129	*430.0917*	*429.0844*
☑	130	*430.0920*	*429.0847*
☑	131	*430.0957*	*429.0884*
☑	132	*430.0992*	*429.0919*
☑	133	*431.0923*	*430.0850*
☑	134	*431.0932*	*430.0859*
☑	135	*431.0937*	*430.0864*
☑	136	*431.0951*	*430.0878*
☑	137	*431.0982*	*430.0909*
☑	138	*432.0933*	*431.0860*
☑	139	*432.0939*	*431.0866*
☑	140	*432.0958*	*431.0885*
☑	141	*432.0974*	*431.0901*
☑	142	*433.0854*	*432.0781*
☑	143	*433.0930*	*432.0857*
☑	144	*445.1251*	*444.1178*
☑	145	*445.1266*	*444.1193*
☑	146	*445.1275*	*444.1202*
☑	147	*445.1280*	*444.1207*
☑	148	*445.1287*	*444.1214*
☑	149	*445.1289*	*444.1216*
☑	150	*445.1302*	*444.1229*
☑	151	*445.1305*	*444.1232*
☑	152	*445.1331*	*444.1258*
☑	153	*445.1368*	*444.1295*
☑	154	*445.2821*	*444.2748*
☑	156	*445.8061*	*444.7988*
☑	157	*446.1269*	*445.1196*
☑	158	*446.1286*	*445.1213*
☑	159	*446.1309*	*445.1236*
☑	160	*446.1360*	*445.1287*
☑	161	*446.1412*	*445.1339*
☑	162	*446.2843*	*445.2770*
☑	163	*446.2873*	*445.2800*
☑	164	*446.2876*	*445.2803*
☑	165	*446.2899*	*445.2826*
☑	166	*446.2906*	*445.2833*
☑	167	*447.0993*	*446.0920*
☑	168	*447.1175*	*446.1102*
☑	169	*447.1263*	*446.1190*
☑	170	*447.1268*	*446.1195*
☑	171	*447.1297*	*446.1224*
☑	172	*447.1343*	*446.1270*
☑	173	*447.1383*	*446.1310*
☑	174	*448.1143*	*447.1070*
☑	175	*449.7466*	*448.7393*
☑	176	*450.2478*	*449.2405*
☑	177	*461.2213*	*460.2140*
☑	178	*461.7260*	*460.7187*
☑	179	*472.2944*	*471.2871*
☑	181	*500.5695*	*499.5622*
☑	182	*500.5753*	*499.5680*
☑	183	*500.5760*	*499.5687*
☑	184	*500.9095*	*499.9022*
☑	185	*500.9131*	*499.9058*
☑	186	*500.9177*	*499.9104*
☑	187	*501.2471*	*500.2398*
☑	188	*501.2475*	*500.2402*
☑	189	*503.1157*	*502.1084*
☑	190	*503.1174*	*502.1101*
☑	191	*503.1176*	*502.1103*
☑	192	*503.1184*	*502.1111*
☑	193	*503.1201*	*502.1128*
☑	194	*503.1308*	*502.1235*
☑	195	*504.1160*	*503.1087*
☑	196	*504.1167*	*503.1094*
☑	197	*505.1104*	*504.1031*
☑	198	*505.1158*	*504.1085*
☑	199	*505.1231*	*504.1158*
☑	200	*506.1123*	*505.1050*
☑	202	*519.1440*	*518.1367*
☑	203	*519.1457*	*518.1384*
☑	204	*519.1489*	*518.1416*
☑	205	*519.1493*	*518.1420*
☑	206	*519.3159*	*518.3086*
☑	207	*519.3237*	*518.3164*
☑	208	*521.1315*	*520.1242*
☑	209	*521.1358*	*520.1285*
☑	210	*525.7811*	*524.7738*
☑	211	*528.3071*	*527.2998*

☑	212	529.7824	528.7751
☑	214	536.1706	535.1633
☑	215	536.1713	535.1640
☑	216	536.1730	535.1657
☑	217	536.1737	535.1664
☑	218	536.1744	535.1671
☑	219	536.1745	535.1672
☑	220	536.1812	535.1739
☑	221	536.8585	535.8512
☑	222	536.8828	535.8755
☑	223	537.1801	536.1728
☑	224	538.1652	537.1579
☑	225	538.1685	537.1612
☑	226	538.7639	537.7566
☑	227	539.1697	538.1624
☑	228	540.8604	539.8531
☑	229	540.8785	539.8712
☑	230	553.0611	552.0538
☑	231	556.0690	555.0617
☑	232	580.8301	579.8228
☑	233	581.3103	580.3030
☑	234	581.7997	580.7924
☑	235	582.2520	581.2447
☑	236	582.9348	581.9275
☑	237	588.3419	587.3346
☑	238	597.8699	596.8626
☑	239	598.2394	597.2321
☑	240	598.2418	597.2345
☑	241	598.2443	597.2370
☑	242	300.0219	598.0292
☑	243	599.2518	598.2445
☑	244	600.3033	599.2960
☑	246	600.7967	599.7894
☑	247	600.8087	599.8014
☑	248	301.0960	600.1774
☑	249	301.1556	600.2966
☑	251	301.1781	600.3416
☑	252	301.1829	600.3512
☑	253	605.0685	604.0612
☑	254	304.0132	606.0118
☑	255	607.0647	606.0574
☑	257	607.8162	606.8089
☑	258	610.1964	609.1891
☑	259	610.2040	609.1967
☑	260	305.9519	609.8892
☑	261	307.9505	613.8864
☑	262	308.0223	614.0300
☑	263	311.6292	621.2438
☑	264	312.9918	623.9690
☑	265	313.1710	624.3274
☑	266	315.0595	628.1044
☑	267	315.0653	628.1160
☑	268	315.0656	628.1166
☑	269	315.0695	628.1244
☑	272	631.8058	630.7985
☑	275	321.0964	640.1782
☑	276	322.0926	642.1706
☑	277	645.7817	644.7744
☑	278	647.1479	646.1406
☑	279	647.2982	646.2909
☑	280	648.3733	647.3660
☑	281	325.1739	648.3332
☑	282	651.8560	650.8487
☑	283	653.6557	652.6484
☑	284	653.9991	652.9918
☑	285	654.3298	653.3225
☑	286	655.8140	654.8067
☑	287	329.1692	656.3238
☑	288	333.0366	664.0586
☑	289	333.0381	664.0616
☑	290	671.8058	670.7985
☑	291	672.2556	671.2483
☑	294	676.8664	675.8591
☑	295	341.0230	680.0314
☑	296	341.0260	680.0374
☑	297	341.6445	681.2744
☑	298	342.0403	682.0660
☑	299	342.0908	682.1670
☑	300	343.0520	684.0894
☑	307	355.0086	708.0026
☑	308	355.0699	708.1252

☑	309	*355.0714*	*708.1282*
☑	310	*355.0716*	*708.1286*
☑	311	*355.0768*	*708.1390*
☑	312	*357.0765*	*712.1384*
☑	313	*357.0783*	*712.1420*
☑	314	*357.0813*	*712.1480*
☑	315	*715.0626*	*714.0553*
☑	316	*717.2094*	*716.2021*
☑	317	*719.2115*	*718.2042*
☑	318	*363.9105*	*725.8064*
☑	319	*365.9737*	*729.9328*
☑	320	*367.9813*	*733.9480*
☑	321	*735.2515*	*734.2442*
☑	322	*735.6586*	*734.6513*
☑	323	*371.2217*	*740.4288*
☑	325	*743.7808*	*742.7735*
☑	326	*377.0889*	*752.1632*
☑	327	*377.1041*	*752.1936*
☑	328	*378.7470*	*755.4794*
☑	330	*380.1723*	*758.3300*
☑	331	*764.6671*	*763.6598*
☑	332	*766.6816*	*765.6743*
☑	333	*768.4365*	*767.4292*
☑	334	*768.6876*	*767.6803*
☑	335	*768.9266*	*767.9193*
☑	336	*769.0150*	*768.0077*
☑	337	*776.5955*	*775.5882*
☑	338	*776.6066*	*775.5993*
☑	339	*776.7003*	*775.6930*
☑	340	*776.8279*	*775.8206*
☑	341	*776.8330*	*775.8257*
☑	342	*776.8347*	*775.8274*
☑	343	*776.8354*	*775.8281*
☑	344	*776.8408*	*775.8335*
☑	345	*776.8497*	*775.8424*
☑	346	*776.8613*	*775.8540*
☑	347	*777.0920*	*776.0847*
☑	348	*777.0993*	*776.0920*
☑	349	*777.3115*	*776.3042*
☑	350	*777.3357*	*776.3284*
☑	351	*777.3363*	*776.3290*
☑	352	*777.3436*	*776.3363*
☑	353	*777.3442*	*776.3369*
☑	354	*778.4701*	*777.4628*
☑	355	*778.7656*	*777.7583*
☑	356	*779.8745*	*778.8672*
☑	357	*779.8841*	*778.8768*
☑	359	*391.8338*	*781.6530*
☑	360	*783.7374*	*782.7301*
☑	361	*784.0562*	*783.0489*
☑	362	*784.3928*	*783.3855*
☑	363	*785.8331*	*784.8258*
☑	364	*785.8378*	*784.8305*
☑	365	*785.8421*	*784.8348*
☑	366	*785.8471*	*784.8398*
☑	367	*786.3374*	*785.3301*
☑	368	*786.3397*	*785.3324*
☑	369	*786.3427*	*785.3354*
☑	370	*786.3428*	*785.3355*
☑	371	*786.3466*	*785.3393*
☑	372	*786.8060*	*785.7987*
☑	373	*786.8641*	*785.8568*
☑	374	*787.3468*	*786.3395*
☑	375	*787.3529*	*786.3456*
☑	376	*788.7139*	*787.7066*
☑	377	*798.4542*	*797.4469*
☑	378	*798.4572*	*797.4499*
☑	379	*798.8981*	*797.8908*
☑	380	*801.2337*	*800.2264*
☑	383	*812.9364*	*811.9291*
☑	384	*813.4753*	*812.4680*
☑	385	*815.6945*	*814.6872*
☑	386	*816.2376*	*815.2303*
☑	387	*816.8932*	*815.8859*
☑	388	*817.4152*	*816.4079*
☑	389	*817.4265*	*816.4192*
☑	390	*818.4018*	*817.3945*
☑	391	*819.3159*	*818.3086*
☑	392	*820.6399*	*819.6326*
☑	393	*821.1201*	*820.1128*
☑	395	*823.3724*	*822.3651*

☑	396	823.7456	822.7383
☑	397	414.8913	827.7680
☑	398	415.0452	828.0758
☑	399	830.2775	829.2702
☑	401	837.4243	836.4170
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☑	403	841.7367	840.7294
☑	405	845.1757	844.1684
☑	407	849.6374	848.6301
☑	408	849.7866	848.7793
☑	409	851.4526	850.4453
☑	410	857.9733	856.9660
☑	411	860.7335	859.7262
☑	412	431.0923	860.1700
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☑	420	445.1362	888.2578
☑	422	446.1226	890.2306
☑	423	446.1356	890.2566
☑	427	446.2776	890.5406
☑	428	446.2813	890.5480
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☑	431	447.1323	892.2500
☑	432	896.6285	895.6212
☑	433	897.0573	896.0500
☑	434	898.1887	897.1814
☑	437	899.5178	898.5105
☑	438	899.6995	898.6922
☑	439	900.0301	899.0228
☑	440	902.5184	901.5111
☑	444	913.8610	912.8537
☑	445	915.2546	914.2473
☑	446	915.5565	914.5492
☑	447	915.7029	914.6956
☑	448	915.7895	914.7822
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☑	452	924.2578	923.2505
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☑	521	355.0849	1062.2329
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☑	721	768.7252	1535.4358
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☑	803	816.9065	1631.7984
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☑	806	820.8856	1639.7566
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☑	814	842.7434	1683.4722
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☑	868	1883.1820	1882.1747
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☑	875	978.5511	1955.0876
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☑	882	1039.9951	2077.9756
☑	884	1048.4742	2094.9338
☑	885	1048.9790	2095.9434
☑	886	1048.9817	2095.9488
☑	888	699.7144	2096.1214
☑	889	1056.4691	2110.9236
☑	892	1064.9711	2127.9276
☑	893	1072.9751	2143.9356
☑	894	1072.9877	2143.9608
☑	895	737.0175	2208.0307
☑	899	1111.1013	2220.1880
☑	900	1131.2676	2260.5206
☑	901	761.3976	2281.1710
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☑	932	893.7734	2678.2984
☑	933	894.0991	2679.2755
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☑	940	933.7698	2798.2876
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☑	948	961.7506	2882.2300
☑	949	972.4224	2914.2454
☑	950	978.5491	2932.6255
☑	956	820.6473	3278.5601
☑	958	1130.5444	3388.6114
☑	959	1130.5486	3388.6240
☑	961	1493.0217	4476.0433

Search Parameters

```
Type of search         : MS/MS Ion Search
Enzyme                 : Trypsin
Fixed modifications    : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values            : Monoisotopic
Protein Mass           : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages   : 1
Instrument type        : ESI-QUAD-TOF
Number of queries      : 961
```

Mascot: http://www.matrixscience.com/

Mascot Search Results

```
User                   : Dominic
Email                  : dominic.kurian@bbsrc.ac.uk
Search title           : IPI Mouse_15-02-2010
MS data file           : C:\Program Files\Matrix Science\Mascot Daemon\mgf\31 MSadmin\mascot_daemon_merge.mgf
Database               : IPI_mouse MOUSE_v3_79 (54943 sequences; 24917557 residues)
Timestamp              : 15 Feb 2011 at 11:16:52 GMT
Enzyme                 : Trypsin
Fixed modifications    : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values            : Monoisotopic
Protein Mass           : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages   : 1
Instrument type        : ESI-QUAD-TOF
Number of queries      : 1043
Protein hits           : IPI00420725 Tax_Id=10090 Gene_Symbol=Camk2a Uncharacterized protein
                         IPI00474502 Tax_Id=10090 Gene_Symbol=Camk2b Calcium/calmodulin-dependent protein kinase type II subunit beta
                         IPI00473320 Tax_Id=10090 Gene_Symbol=Actb Putative uncharacterized protein
                         IPI00136929 Tax_Id=10090 Gene_Symbol=Actg1 Gamma actin-like protein
                         IPI00112584 Tax_Id=10090 Gene_Symbol=Camk2d Isoform 1 of Calcium/calmodulin-dependent protein kinase type II
                         IPI00124695 Tax_Id=10090 Gene_Symbol=Camk2g Isoform 1 of Calcium/calmodulin-dependent protein kinase type II
                         IPI00221528 Tax_Id=10090 Gene_Symbol=Actbl2 Beta-actin-like protein 2
                         IPI00169463 Tax_Id=10090 Gene_Symbol=Tubb2c Tubulin beta-2C chain
                         IPI00109073 Tax_Id=10090 Gene_Symbol=Tubb4 Tubulin beta-4 chain
                         IPI00109061 Tax_Id=10090 Gene_Symbol=Tubb2b Tubulin beta-2B chain
                         IPI00136703 Tax_Id=10090 Gene_Symbol=Ckb Creatine kinase B-type
                         IPI00420569 Tax_Id=10090 Gene_Symbol=Atp1a2 Sodium/potassium-transporting ATPase subunit alpha-2
                         IPI00122048 Tax_Id=10090 Gene_Symbol=Atp1a3 Sodium/potassium-transporting ATPase subunit alpha-3
                         IPI00117352 Tax_Id=10090 Gene_Symbol=Tubb5 Tubulin beta-5 chain
                         IPI00115546 Tax_Id=10090 Gene_Symbol=Gnao1 Isoform Alpha-2 of Guanine nucleotide-binding protein G(o) subunit
                         IPI00110753 Tax_Id=10090 Gene_Symbol=Tuba1a Tubulin alpha-1A chain
                         IPI00120793 Tax_Id=10090 Gene_Symbol=Prnp Major prion protein
                         IPI00112251 Tax_Id=10090 Gene_Symbol=Tubb3 Tubulin beta-3 chain
                         IPI00122928 Tax_Id=10090 Gene_Symbol=Tubb6 Tubulin beta-6 chain
                         IPI00135284 Tax_Id=10090 Gene_Symbol=Gm16374 Glyceraldehyde-3-phosphate dehydrogenase
                         IPI00135106 Tax_Id=10090 Gene_Symbol=Mobp Isoform 1 of Myelin-associated oligodendrocyte basic protein
                         IPI00114375 Tax_Id=10090 Gene_Symbol=Dpysl2 Dihydropyrimidinase-related protein 2
                         IPI00132042 Tax_Id=10090 Gene_Symbol=Pdhb Pyruvate dehydrogenase E1 component subunit beta, mitochondrial
                         IPI00138892 Tax_Id=10090 Gene_Symbol=Uba52 Ubiquitin-60S ribosomal protein L40
                         IPI00121038 Tax_Id=10090 Gene_Symbol=Vcan Isoform V0 of Versican core protein
                         IPI00323571 Tax_Id=10090 Gene_Symbol=Apoe Apolipoprotein E
                         IPI00229525 Tax_Id=10090 Gene_Symbol=Gnal Guanine nucleotide-binding protein G(olf) subunit alpha
                         IPI00118569 Tax_Id=10090 Gene_Symbol=Gna13 Guanine nucleotide-binding protein subunit alpha-13
                         IPI00129240 Tax_Id=10090 Gene_Symbol=Vtn Vitronectin
                         IPI00323357 Tax_Id=10090 Gene_Symbol=Hspa8 Heat shock cognate 71 kDa protein
                         IPI00131366 Tax_Id=10090 Gene_Symbol=Krt6b Keratin, type II cytoskeletal 6B
                         IPI00134344 Tax_Id=10090 Gene_Symbol=Spnb3 Putative uncharacterized protein
                         IPI00123313 Tax_Id=10090 Gene_Symbol=Uba1 Ubiquitin-like modifier-activating enzyme 1
                         IPI00113112 Tax_Id=10090 Gene_Symbol=Rab3b Ras-related protein Rab-3B
                         IPI00116697 Tax_Id=10090 Gene_Symbol=Rab6 Isoform 1 of Ras-related protein Rab-6A
                         IPI00136271 Tax_Id=10090 Gene_Symbol=Rab33b Putative uncharacterized protein
                         IPI00170032 Tax_Id=10090 Gene_Symbol=Rab15 Ras-related protein Rab-15
                         IPI00656325 Tax_Id=10090 Gene_Symbol=Nsf Vesicle-fusing ATPase
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	IPI_mouse	Decoy	False discovery rate
Peptide matches above identity threshold	123	0	0.00 %
Peptide matches above homology or identity threshold	143	2	1.40 %

Select Summary Report

Format As | Select Summary (protein hits) | Help

Significance threshold p< 0.01 | Max. number of hits AUTO

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

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

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1.     IPI00420725     Mass: 55882     Score: 883     Queries matched: 42     emPAI: 1.23
       Tax_Id=10090 Gene_Symbol=Camk2a Uncharacterized protein
      Query   Observed   Mr(expt)   Mr(calc)    ppm  Miss Score    Expect Rank  Peptide
        245   432.7284   863.4422   863.4501  -9.12    0    17       2.1    1   R.SGAPSVLPH.-
        261   446.2625   890.5104   890.5086   2.03    1     4        22    2   K.GAFSVVRR.C
        283   463.2463   924.4780   924.4777   0.37    1    25       0.2    1   R.DHQKLER.E 282 284
        373   525.2643  1048.5140  1048.5553 -39.33    0    53   0.00048    1   K.VLAGQEYAAK.I 374
        384   530.3027  1058.5908  1058.5906   0.21    1  (43)    0.0034    1   K.MLTINPSKR.I 383 385
        398   538.2980  1074.5814  1074.5855  -3.81    1    52   0.00054    1   K.MLTINPSKR.I 399 400 401
        424   545.3502  1088.6858  1088.6818   3.70    1    37     0.003    1   R.LLKHPNIVR.L
        480   574.3285  1146.6424  1146.6431  -0.54    0    64  2.5e-005    1   K.GAILTTMLATR.N
        497   582.3258  1162.6370  1162.6380  -0.81    0  (59)  8.6e-005    1   K.GAILTTMLATR.N 498
        586   631.3029  1260.5912  1260.5927  -1.19    0    58    0.0001    1   R.FYFENLWSR.N 585 587
        628   652.3355  1302.6564  1302.6932 -28.21    0    73  4.2e-006    1   R.ITQYLDAGGIPR.T 629 630 632
        669   670.8956  1339.7766  1339.7711   4.16    0    74  1.2e-006    1   R.DLKPENLLLASK.L 664 665 666 667 668
        836   816.8978  1631.7810  1631.7719   5.62    0    68  1.1e-005    1   R.FTEEYQLFEELGK.G 832 835
        937  1040.9652  2079.9158  2079.9426 -12.84    0    77  6.5e-007    1   K.AGAYDFPSPEWDTVTPEAK.D 936
        983   783.7271  2348.1595  2348.1689  -4.00    1    78  7.4e-007    1   R.FTEEYQLFEELGKGAFSVVR.R 982 984
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      1005    888.7645  2663.2717  2663.2755   -1.44   1   101  3.3e-009   1   K.AGAYDFPSPEWDTVTPEAKDLINK.M 1004 1006

     Proteins matching the same set of peptides:
     IPI00621806     Mass: 54651    Score: 883    Queries matched: 42
     Tax_Id=10090 Gene_Symbol=Camk2a Isoform Alpha CaMKII of Calcium/calmodulin-dependent protein kinase type II subunit alpha

2.   IPI00474502     Mass: 61164    Score: 771    Queries matched: 36   emPAI: 1.57
     Tax_Id=10090 Gene_Symbol=Camk2b Calcium/calmodulin-dependent protein kinase type II subunit beta
    Query   Observed   Mr(expt)   Mr(calc)    ppm  Miss Score   Expect Rank  Peptide
      261   446.2625   890.5104   890.5086   2.03    1     4       22    2   K.GAFSVVRR.C
      283   463.2463   924.4780   924.4777   0.37    1    25      0.2    1   R.DHQKLER.E 282 284
      376   526.2389  1050.4632  1050.4586   4.38    0    21      0.3    1   R.STVASMMHR.Q
      477   572.8038  1143.5930  1143.5964  -2.95    0    15      2.9    1   R.FYFENLLAK.N 478
      480   574.3285  1146.6424  1146.6431  -0.54    0    64  2.5e-005   1   K.GAILTTMLATR.N
      497   582.3258  1162.6370  1162.6380  -0.81    0  (59) 8.6e-005   1   K.GAILTTMLATR.N 498
      573   623.3220  1244.6294  1244.6361  -5.33    0    43   0.0047    1   K.ADGVKPQTNSTK.N
      669   670.8956  1339.7766  1339.7711   4.16    0    74  1.2e-006   1   R.DLKPENLLLASK.C 664 665 666 667 668
      692   458.5797  1372.7173  1372.7310 -10.02    1    24     0.27    1   K.KADGVKPQTNSTK.N
      712   702.3754  1402.7362  1402.7317   3.24    0    60  6.5e-005   1   R.LTQYIDGQGRPR.T 711 713
      821   810.8781  1619.7416  1619.7355   3.79    0    80  5.2e-007   1   R.FTDEYQLYEDIGK.G
      827   542.6376  1624.8910  1624.9082 -10.63    1    72  2.8e-006   1   K.NLINQMLTINPAKR.I 826
      937  1040.9652  2079.9158  2079.9426 -12.84    0    77  6.5e-007   1   K.AGAYDFPSPEWDTVTPEAK.N 936
      945  1057.0130  2112.0114  2112.0011   4.90    0    90     5e-008   1   K.TTEQLIEAVNNGDFEAYAK.I 942 944
      981   779.7127  2336.1163  2336.1325  -6.94    1    98  6.8e-009   1   R.FTDEYQLYEDIGKGAFSVVR.R 979 980
      988  1177.0770  2352.1394  2352.1301   3.97    0    92  2.6e-008   1   R.QTTAPATMSTAASGTTMGLVEQAK.S 986
      989   785.4238  2353.2496  2353.2642  -6.20    0    61  2.7e-005   1   K.GSLPPAALEPQTTVIHNPVDGIK.E
      991  1185.0753  2368.1360  2368.1250   4.65    0  (66) 1.1e-005   1   R.QTTAPATMSTAASGTTMGLVEQAK.S

     Proteins matching the same set of peptides:
     IPI00649778     Mass: 73827    Score: 771    Queries matched: 36
     Tax_Id=10090 Gene_Symbol=Camk2b Calcium/calmodulin-dependent protein kinase II, beta, isoform CRA_b
     IPI00875723     Mass: 68686    Score: 771    Queries matched: 36
     Tax_Id=10090 Gene_Symbol=Camk2b 68 kDa protein

3.   IPI00473320     Mass: 42115    Score: 665    Queries matched: 20   emPAI: 1.13
     Tax_Id=10090 Gene_Symbol=Actb Putative uncharacterized protein
    Query   Observed   Mr(expt)   Mr(calc)    ppm  Miss Score  Expect Rank  Peptide
       94   630.2972   629.2899   629.2769   20.7   0    21     0.16    1   R.GDDAPR.A
      494   581.3107  1160.6068  1160.6111  -3.65   0    23     0.45    1   K.EITALAPSTMK.I
      530   599.8568  1197.6990  1197.6982   0.69   0    51  0.00032    1   R.AVFPSIVGRPR.H 531
      676   677.8154  1353.6162  1353.6161   0.14   1    80  5.7e-007   1   K.DSYVGDEAQSKR.G
      757   774.9159  1547.8172  1547.8051   7.85   1    93  3.4e-008   1   R.MQKEITALAPSTMK.I 755 756
      824   812.4301  1622.8456  1622.8338   7.32   1    16      1.3    1   R.LDLAGRDLTDYLMK.I
      885   895.9537  1789.8928  1789.8846   4.59   0   103  3.1e-009   1   K.SYELPDGQVITIGNER.F 886
      918   652.0211  1953.0415  1953.0571  -8.00   0    73    2e-006   1   R.VAPEEHPVLLTEAPLNPK.A 917 919
      966  1108.0448  2214.0750  2214.0627   5.58   0    71  3.7e-006   1   K.DLYANTVLSGGTTMYPGIADR.M
     1038  1061.8691  3182.5855  3182.6071  -6.78   0   109  3.5e-010   1   R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L 1035 1036 1037
     1039   800.6558  3198.5941  3198.6020  -2.46   0  (84) 1.2e-007   1   R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L

4.   IPI00136929     Mass: 44029    Score: 627    Queries matched: 17   emPAI: 0.92
     Tax_Id=10090 Gene_Symbol=Actg1 Gamma actin-like protein
    Query   Observed   Mr(expt)   Mr(calc)    ppm  Miss Score  Expect Rank  Peptide
      494   581.3107  1160.6068  1160.6111  -3.65   0    23     0.45    1   K.EITALAPSTMK.I
      676   677.8154  1353.6162  1353.6161   0.14   1    80  5.7e-007   1   K.DSYVGDEAQSKR.G
      757   774.9159  1547.8172  1547.8051   7.85   1    93  3.4e-008   1   R.MQKEITALAPSTMK.I 755 756
      824   812.4301  1622.8456  1622.8338   7.32   1    16      1.3    1   R.LDLAGRDLTDYLMK.I
      885   895.9537  1789.8928  1789.8846   4.59   0   103  3.1e-009   1   K.SYELPDGQVITIGNER.F 886
      918   652.0211  1953.0415  1953.0571  -8.00   0    73    2e-006   1   R.VAPEEHPVLLTEAPLNPK.R 917 919
      966  1108.0448  2214.0750  2214.0627   5.58   0    71  3.7e-006   1   K.DLYANTVLSGGTTMYPGLADR.M
     1038  1061.8691  3182.5855  3182.6071  -6.78   0   109  3.5e-010   1   R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L 1035 1036 1037
     1039   800.6558  3198.5941  3198.6020  -2.46   0  (84) 1.2e-007   1   R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L

5.   IPI00112584     Mass: 56961    Score: 456    Queries matched: 24   emPAI: 0.66
     Tax_Id=10090 Gene_Symbol=Camk2d Isoform 1 of Calcium/calmodulin-dependent protein kinase type II subunit delta
    Query   Observed   Mr(expt)   Mr(calc)    ppm  Miss Score   Expect Rank  Peptide
      261   446.2625   890.5104   890.5086   2.03    1     4       22    2   K.GAFSVVRR.C
      283   463.2463   924.4780   924.4777   0.37    1    25      0.2    1   R.DHQKLER.E 282 284
      376   526.2389  1050.4632  1050.4586   4.38    0    21      0.3    1   R.STVASMMHR.Q
      383   530.2958  1058.5770  1058.5906 -12.82    1    20     0.97    2   K.MLTINPAKR.I
      424   545.3502  1088.6858  1088.6818   3.70    1    37    0.003    1   R.LLKHPNIVR.L
      460   559.7792  1117.5438  1117.5444  -0.48    0    13      4.2    1   R.FYFENALSK.S
      480   574.3285  1146.6424  1146.6431  -0.54    0    64  2.5e-005   1   K.GAILTTMLATR.N
      497   582.3258  1162.6370  1162.6380  -0.81    0  (59) 8.6e-005   1   K.GAILTTMLATR.N 498
      669   670.8956  1339.7766  1339.7711   4.16    0    74  1.2e-006   1   R.DLKPENLLLASK.S 664 665 666 667 668
      679   680.3028  1358.5910  1358.5846   4.72    0    20      0.3    1   R.LTQYMDGSGMPK.T
      819   809.8877  1617.7608  1617.7562   2.85    0    59  6.8e-005   1   R.FTDEYQLFEELGK.G
      937  1040.9652  2079.9158  2079.9426 -12.84    0    77  6.5e-007   1   K.AGAYDFPSPEWDTVTPEAK.D 936
     1005   888.7645  2663.2717  2663.2755  -1.44    1   101  3.3e-009   1   K.AGAYDFPSPEWDTVTPEAKDLINK.M 1004 1006

     Proteins matching the same set of peptides:
     IPI00406790     Mass: 60593    Score: 456    Queries matched: 24
     Tax_Id=10090 Gene_Symbol=Camk2d Isoform 4 of Calcium/calmodulin-dependent protein kinase type II subunit delta
     IPI00475044     Mass: 55899    Score: 456    Queries matched: 24
     Tax_Id=10090 Gene_Symbol=Camk2d Isoform 2 of Calcium/calmodulin-dependent protein kinase type II subunit delta
     IPI00828919     Mass: 58492    Score: 456    Queries matched: 24
     Tax_Id=10090 Gene_Symbol=Camk2d Isoform 3 of Calcium/calmodulin-dependent protein kinase type II subunit delta
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        IPI00857865     Mass: 54664     Score: 456     Queries matched: 24
        Tax_Id=10090 Gene_Symbol=Camk2d Putative uncharacterized protein
        IPI00858128     Mass: 58283     Score: 456     Queries matched: 24
        Tax_Id=10090 Gene_Symbol=Camk2d calcium/calmodulin-dependent protein kinase type II subunit delta isoform 1
        IPI00858144     Mass: 55828     Score: 456     Queries matched: 24
        Tax_Id=10090 Gene_Symbol=Camk2d 55 kDa protein

6.      IPI00124695     Mass: 60254     Score: 420     Queries matched: 21   emPAI: 0.79
        Tax_Id=10090 Gene_Symbol=Camk2g Isoform 1 of Calcium/calmodulin-dependent protein kinase type II subunit gamma
       Query    Observed    Mr(expt)    Mr(calc)     ppm  Miss Score    Expect Rank  Peptide
         261    446.2625    890.5104    890.5086    2.03    1     4        22    2  K.GAFSVVRR.C
         283    463.2463    924.4780    924.4777    0.37    1    25       0.2    1  R.DHQKLER.E 282 284
         376    526.2389   1050.4632   1050.4586    4.38    0    21       0.3    1  R.STVASMMHR.Q
         424    545.3502   1088.6858   1088.6818    3.70    1    37     0.003    1  R.LLKHPNIVR.L
         669    670.8956   1339.7766   1339.7711    4.16    0    74  1.2e-006    1  R.DLKPENLLLASK.C 664 665 666 667 668
         712    702.3754   1402.7362   1402.7317    3.24    0    60  6.5e-005    1  R.LTQYIDGQGRPR.T 711 713
         811    802.8796   1603.7446   1603.7406    2.52    0    77    1e-006    1  R.FTDDYQLFEELGK.G
         827    542.6376   1624.8910   1624.9082  -10.63    1    72  2.8e-006    1  K.NLINQMLTINPAKR.I 826
         937   1040.9652   2079.9158   2079.9426  -12.84    0    77  6.5e-007    1  K.AGAYDFPSPEWDTVTPEAK.N 936
         978    774.3764   2320.1074   2320.1376  -13.02    1    53   0.00023    1  R.FTDDYQLFEELGKGAFSVVR.R


        Proteins matching the same set of peptides:
        IPI00228044     Mass: 59013     Score: 420     Queries matched: 21
        Tax_Id=10090 Gene_Symbol=Camk2g Isoform 2 of Calcium/calmodulin-dependent protein kinase type II subunit gamma
        IPI00228045     Mass: 56610     Score: 420     Queries matched: 21
        Tax_Id=10090 Gene_Symbol=Camk2g Isoform 3 of Calcium/calmodulin-dependent protein kinase type II subunit gamma

7.      IPI00221528     Mass: 42319     Score: 401     Queries matched: 11   emPAI: 0.46
        Tax_Id=10090 Gene_Symbol=Actbl2 Beta-actin-like protein 2
       Query    Observed    Mr(expt)    Mr(calc)     ppm  Miss Score    Expect Rank  Peptide
         824    812.4301   1622.8456   1622.8338    7.32    1    16       1.3    1  R.LDLAGRDLTDYLMK.I
         885    895.9537   1789.8928   1789.8846    4.59    0   103  3.1e-009    1  R.SYELPDGQVITIGNER.F 886
         918    652.0211   1953.0415   1953.0571   -8.00    0    47   0.00096    2  R.VAPDEHPILLTEAPLNPK.I 917 919
        1038   1061.8691   3182.5855   3182.6071   -6.78    0   109  3.5e-010    1  R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L 1035 1036 1037
        1039    800.6558   3198.5941   3198.6020   -2.46    0  (84)  1.2e-007    1  R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L


8.      IPI00169463     Mass: 50255     Score: 392     Queries matched: 19   emPAI: 1.01
        Tax_Id=10090 Gene_Symbol=Tubb2c Tubulin beta-2C chain
       Query  Observed    Mr(expt)    Mr(calc)     ppm  Miss Score    Expect Rank  Peptide
         404  539.2755   1076.5364   1076.5250    10.6    1    21      0.68    1  K.IREEYPDR.I 405
         554  615.3074   1228.6002   1228.5910    7.50    0    66  1.6e-005    1  R.ISEQFTAMFR.R
         651  660.3555   1318.6964   1318.6955    0.71    0    70    7e-006    1  R.IMNTFSVVPSPK.V
         806  801.4128   1600.8110   1600.8131   -1.26    0    62  4.4e-005    1  R.AVLVDLEPGTMDSVR.S
         817  809.4195   1616.8244   1616.8080    10.2    0  (37)     0.014    1  R.AVLVDLEPGTMDSVR.S 818
         823  540.9528   1619.8366   1619.8283    5.13    0    53   0.00035    1  R.LHFFMPGFAPLTSR.G 822
         838  818.9071   1635.7996   1635.8232  -14.39    0  (15)       2.2    1  R.LHFFMPGFAPLTSR.G
         849  846.4417   1690.8688   1690.8600    5.23    0    71    5e-006    1  R.ALTVPELTQQMFDAK.N
         850  848.9232   1695.8318   1695.8257    3.65    0    53    0.0003    1  K.NSSYFVEWIPNNVK.T 851
         905  929.4750   1856.9354   1856.9342    0.66    0    35     0.017    2  K.MSATFIGNSTAIQELFK.R
         924  979.9998   1957.9850   1957.9745    5.37    0    44    0.0021    1  K.GHYTEGAELVDSVLDVVR.K
         931  672.0128   2013.0166   2013.0353   -9.32    1    98  9.4e-009    1  K.MSATFIGNSTAIQELFKR.I
        1012  933.4506   2797.3300   2797.3361   -2.20    0    88  5.4e-008    1  R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G 1011 1013


9.      IPI00109073     Mass: 50010     Score: 375     Queries matched: 17   emPAI: 0.89
        Tax_Id=10090 Gene_Symbol=Tubb4 Tubulin beta-4 chain
       Query  Observed    Mr(expt)    Mr(calc)     ppm  Miss Score    Expect Rank  Peptide
         389  531.2863   1060.5580   1060.5301    26.3    1    10       8.7    5  K.IREEFPDR.I
         554  615.3074   1228.6002   1228.5910    7.50    0    66  1.6e-005    1  R.ISEQFTAMFR.R
         651  660.3555   1318.6964   1318.6955    0.71    0    70    7e-006    1  R.IMNTFSVVPSPK.V
         806  801.4128   1600.8110   1600.8131   -1.26    0    62  4.4e-005    1  R.AVLVDLEPGTMDSVR.S
         817  809.4195   1616.8244   1616.8080    10.2    0  (37)     0.014    1  R.AVLVDLEPGTMDSVR.S 818
         823  540.9528   1619.8366   1619.8283    5.13    0    53   0.00035    1  R.LHFFMPGFAPLTSR.G 822
         838  818.9071   1635.7996   1635.8232  -14.39    0  (15)       2.2    1  R.LHFFMPGFAPLTSR.G
         849  846.4417   1690.8688   1690.8600    5.23    0    71    5e-006    1  R.ALTVPELTQQMFDAK.N
         850  848.9232   1695.8318   1695.8257    3.65    0    53    0.0003    1  K.NSSYFVEWIPNNVK.T 851
         905  929.4750   1856.9354   1856.9342    0.66    0    37     0.012    1  K.MAATFIGNSTAIQELFK.R
         931  672.0128   2013.0166   2013.0353   -9.32    1    98  9.8e-009    2  K.MAATFIGNSTAIQELFKR.I
        1012  933.4506   2797.3300   2797.3361   -2.20    0    88  5.4e-008    1  R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G 1011 1013


10.     IPI00109061     Mass: 50377     Score: 358     Queries matched: 20   emPAI: 0.88
        Tax_Id=10090 Gene_Symbol=Tubb2b Tubulin beta-2B chain
       Query  Observed    Mr(expt)    Mr(calc)     ppm  Miss Score    Expect Rank  Peptide
         404  539.2755   1076.5364   1076.5250    10.6    1    21      0.68    1  K.IREEYPDR.I 405
         554  615.3074   1228.6002   1228.5910    7.50    0    66  1.6e-005    1  R.ISEQFTAMFR.R
         675  676.3422   1350.6698   1350.6676    1.69    0    73  3.5e-006    1  R.IMNTFSVMPSPK.V
         814  808.4207   1614.8268   1614.8287   -1.15    0    47    0.0015    1  R.AILVDLEPGTMDSVR.S
         823  540.9528   1619.8366   1619.8283    5.13    0    53   0.00035    1  R.LHFFMPGFAPLTSR.G 822
         829  816.4133   1630.8120   1630.8236   -7.10    0  (41)    0.0058    1  R.AILVDLEPGTMDSVR.S 830 831
         838  818.9071   1635.7996   1635.8232  -14.39    0  (15)       2.2    1  R.LHFFMPGFAPLTSR.G
         850  848.9232   1695.8318   1695.8257    3.65    0    53    0.0003    1  K.NSSYFVEWIPNNVK.T 851
         905  929.4750   1856.9354   1856.9342    0.66    0    35     0.017    2  K.MSATFIGNSTAIQELFK.R
         924  979.9998   1957.9850   1957.9745    5.37    0    44    0.0021    1  K.GHYTEGAELVDSVLDVVR.K
         931  672.0128   2013.0166   2013.0353   -9.32    1    98  9.4e-009    1  K.MSATFIGNSTAIQELFKR.I
        1012  933.4506   2797.3300   2797.3361   -2.20    0    88  5.4e-008    1  R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G 1011 1013
        1034  776.3489   3101.3665   3101.4003  -10.89    0     7       4.2    1  K.FWEVISDEHGIDPTGSYHGDSDLQLER.I
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      Proteins matching the same set of peptides:
      IPI00338039     Mass: 50274     Score: 358     Queries matched: 20
      Tax_Id=10090 Gene_Symbol=Tubb2a Tubulin beta-2A chain

11.   IPI00136703     Mass: 42971     Score: 341     Queries matched: 8    emPAI: 0.45
      Tax_Id=10090 Gene_Symbol=Ckb Creatine kinase B-type
     Query  Observed    Mr(expt)   Mr(calc)     ppm  Miss Score    Expect  Rank   Peptide
       632  652.3672  1302.7198  1302.7183     1.17    0     84  2.2e-007    1    K.VLTPELYAELR.A 631
       809  801.9227  1601.8308  1601.8260     3.00    0     96  1.7e-008    1    K.LAVEALSSLDGDLSGR.Y
       841  828.9185  1655.8224  1655.8188     2.17    0     72  4.3e-006    1    R.LEQGQAIDDLMPAQK.-
       903  924.9891  1847.9636  1847.9703    -3.60    0     31     0.044    1    R.LGFSEVELVQMVVDGVK.L
      1040  897.6892  3586.7277  3586.7800   -14.57    0     87  4.9e-008    1    K.SMTEAEQQQLIDDHFLFDKPVSPLLLASGMAR.D 1041 1042

12.   IPI00420569     Mass: 113457    Score: 312     Queries matched: 7    emPAI: 0.12
      Tax_Id=10090 Gene_Symbol=Atp1a2 Sodium/potassium-transporting ATPase subunit alpha-2
     Query  Observed    Mr(expt)   Mr(calc)    ppm  Miss Score    Expect  Rank  Peptide
       558  618.8573  1235.7000  1235.6986    1.17    0     52   0.00022    1   R.LNIPVSQVNPR.E 559
       590  634.8586  1267.7026  1267.7071   -3.48    0     22       0.3    1   K.NMVPQQALVIR.E
       898  906.4799  1810.9452  1810.9425    1.51    0    103  2.8e-009    1   R.QGAIVAVTGDGVNDSPALK.K 897
       902  915.4670  1828.9194  1828.9167    1.53    0    124  2.5e-011    1   K.GVGIISEGNETVEDIAAR.L
      1020  952.1171  2853.3295  2853.3313   -0.64    1     53   0.00017    1   K.EIPLDKEMQDAFQNAYMELGGLGER.V

      Proteins matching the same set of peptides:
      IPI00762871     Mass: 104717    Score: 312     Queries matched: 7
      Tax_Id=10090 Gene_Symbol=Atp1a2 Uncharacterized protein

13.   IPI00122048     Mass: 113045    Score: 309     Queries matched: 7    emPAI: 0.12
      Tax_Id=10090 Gene_Symbol=Atp1a3 Sodium/potassium-transporting ATPase subunit alpha-3
     Query  Observed    Mr(expt)   Mr(calc)    ppm  Miss Score    Expect  Rank  Peptide
       558  618.8573  1235.7000  1235.6986    1.17    0     52   0.00022    1   R.LNIPVSQVNPR.D 559
       590  634.8586  1267.7026  1267.7071   -3.48    0     22       0.3    1   K.NMVPQQALVIR.E
       898  906.4799  1810.9452  1810.9425    1.51    0    103  2.8e-009    1   R.QGAIVAVTGDGVNDSPALK.K 897
       902  915.4670  1828.9194  1828.9167    1.53    0    124  2.5e-011    1   K.GVGIISEGNETVEDIAAR.L
      1022  956.1228  2865.3466  2865.3490   -0.86    1     48   0.00055    1   K.EQPLDEEMKEAFQNAYLELGGLGER.V

      Proteins matching the same set of peptides:
      IPI00752412     Mass: 117548    Score: 309     Queries matched: 7
      Tax_Id=10090 Gene_Symbol=Atp1a3 ATPase, Na+/K+ transporting, alpha 3 polypeptide, isoform CRA_c

14.   IPI00117352     Mass: 50095     Score: 290     Queries matched: 17    emPAI: 0.78
      Tax_Id=10090 Gene_Symbol=Tubb5 Tubulin beta-5 chain
     Query  Observed    Mr(expt)   Mr(calc)     ppm  Miss Score    Expect  Rank   Peptide
       404  539.2755  1076.5364  1076.5250     10.6    1     21      0.68    1    K.IREEYPDR.I 405
       554  615.3074  1228.6002  1228.5910     7.50    0     66  1.6e-005    1    R.ISEQFTAMFR.R
       651  660.3555  1318.6964  1318.6955     0.71    0     70    7e-006    1    R.IMNTFSVVPSPK.V
       814  808.4207  1614.8268  1614.8287    -1.15    0     47    0.0015    1    R.AILVDLEPGTMDSVR.S
       823  540.9528  1619.8366  1619.8283     5.13    0     53   0.00035    1    R.LHFFMPGFAPLTSR.G 822
       829  816.4133  1630.8120  1630.8236    -7.10    0    (41)    0.0058    1    R.AILVDLEPGTMDSVR.S 830 831
       838  818.9071  1635.7996  1635.8232   -14.39    0    (15)       2.2    1    R.LHFFMPGFAPLTSR.G
       850  848.9232  1695.8318  1695.8257     3.65    0     53    0.0003    1    K.NSSYFVEWIPNNVK.T 851
       924  979.9998  1957.9850  1957.9745     5.37    0     44    0.0021    1    K.GHYTEGAELVDSVLDVVR.K
      1012  933.4506  2797.3300  2797.3361    -2.20    0     88  5.4e-008    1    R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G 1011 1013

15.   IPI00115546     Mass: 40524     Score: 278     Queries matched: 6    emPAI: 0.37
      Tax_Id=10090 Gene_Symbol=Gnao1 Isoform Alpha-2 of Guanine nucleotide-binding protein G(o) subunit alpha
     Query  Observed    Mr(expt)   Mr(calc)    ppm  Miss Score    Expect  Rank  Peptide
       380  529.3142  1056.6138  1056.6179   -3.82    0     77  1.3e-006    1   K.LLLLGAGESGK.S 381
       799  792.3738  1582.7330  1582.7297    2.11    1     53   0.00024    1   R.AMDTLGVEYGDKER.K
       845  838.4210  1674.8274  1674.8213    3.67    0    101  5.3e-009    1   R.IGAGDYQPTEQDILR.T 844
       922  979.4433  1956.8720  1956.8631    4.58    0     69  4.7e-006    1   R.MEDTEPFSAELLSAMMR.L

      Proteins matching the same set of peptides:
      IPI00230192     Mass: 40629     Score: 278     Queries matched: 6
      Tax_Id=10090 Gene_Symbol=Gnao1 Isoform Alpha-1 of Guanine nucleotide-binding protein G(o) subunit alpha

16.   IPI00110753     Mass: 50788     Score: 246     Queries matched: 7    emPAI: 0.29
      Tax_Id=10090 Gene_Symbol=Tuba1a Tubulin alpha-1A chain
     Query   Observed    Mr(expt)   Mr(calc)    ppm  Miss Score    Expect  Rank   Peptide
       351   508.2901  1014.5656  1014.5709   -5.21    0      8        15    5    K.DVNAAIATIK.T
       739   729.4378  1456.8610  1456.8613   -0.18    0     20       0.2    1    R.LIGQIVSSITASLR.F
       855   851.4660  1700.9174  1700.8985    11.1    0     91  3.7e-008    1    R.AVFVDLEPTVIDEVR.T 854
       868   586.3238  1755.9496  1755.9559   -3.62    0     49   0.00055    1    R.IHFPLATYAPVISAEK.A
       900   913.0059  1823.9972  1823.9782    10.5    0     32     0.021    1    K.VGINYQPPTVVPGGDLAK.V
       994  1205.1074  2408.2002  2408.2012   -0.41    0    112  2.7e-010    1    R.FDGALNVDLTEFQTNLVPYPR.I

17.   IPI00120793     Mass: 28131     Score: 236     Queries matched: 13    emPAI: 0.75
      Tax_Id=10090 Gene_Symbol=Prnp Major prion protein
     Query  Observed    Mr(expt)   Mr(calc)    ppm  Miss Score    Expect  Rank  Peptide
       354  508.7722  1015.5298  1015.5298    0.00    0     32     0.074    1   K.QHTVTTTTK.G
       421  544.7347  1087.4548  1087.4570   -2.01    0     41    0.0017    1   K.ESQAYYDGR.R
       474  570.2632  1138.5118  1138.5142   -2.10    0     36     0.012    1   K.GENFTETDVK.M 475
       566  622.7841  1243.5536  1243.5581   -3.61    1     37    0.0081    1   K.ESQAYYDGRR.S 567 568 569 570 571
       951  713.0164  2136.0274  2136.0335   -2.88    1    110  4.9e-010    1   K.QHTVTTTTKGENFTETDVK.M 950 952

18.   IPI00112251     Mass: 50842     Score: 228     Queries matched: 11    emPAI: 0.55
```

```
        Tax_Id=10090 Gene_Symbol=Tubb3 Tubulin beta-3 chain
       Query  Observed    Mr(expt)   Mr(calc)    ppm  Miss Score    Expect Rank  Peptide
         554  615.3074  1228.6002  1228.5910   7.50   0     66  1.6e-005    1   R.ISEQFTAMFR.R
         651  660.3555  1318.6964  1318.6955   0.71   0     70    7e-006    1   R.IMNTFSVVPSPK.V
         814  808.4207  1614.8268  1614.8287  -1.15   0     47    0.0015    1   R.AILVDLEPGTMDSVR.S
         822  810.9188  1619.8230  1619.8283  -3.22   0     13       3.2    2   R.LHFFMPGFAPLTAR.G
         829  816.4133  1630.8120  1630.8236  -7.10   0    (41)   0.0058    1   R.AILVDLEPGTMDSVR.S 830 831
         849  846.4417  1690.8688  1690.8600   5.23   0     71    5e-006    1   R.ALTVPELTQQMFDAK.N
         850  848.9232  1695.8318  1695.8257   3.65   0     53    0.0003    1   K.NSSYFVEWIPNNVK.V 851
         924  979.9998  1957.9850  1957.9745   5.37   0     44    0.0021    1   K.GHYTEGAELVDSVLDVVR.K

19.     IPI00122928     Mass: 50514     Score: 208     Queries matched: 10    emPAI: 0.37
        Tax_Id=10090 Gene_Symbol=Tubb6 Tubulin beta-6 chain
       Query  Observed    Mr(expt)   Mr(calc)    ppm  Miss Score    Expect Rank  Peptide
         404  539.2755  1076.5364  1076.5250   10.6   1     21      0.68    1   K.IREEYPDR.I 405
         675  676.3422  1350.6698  1350.6676   1.69   0     73  3.5e-006    1   R.IMNTFSVMPSPK.V
         822  810.9188  1619.8230  1619.8283  -3.22   0     13       3.2    2   R.LHFFMPGFAPLTAR.G
         849  846.4417  1690.8688  1690.8600   5.23   0     71    5e-006    1   R.ALTVPELTQQMFDAK.N
         850  848.9232  1695.8318  1695.8257   3.65   0     53    0.0003    1   K.NSSYFVEWIPNNVK.V 851
         905  929.4750  1856.9354  1856.9342   0.66   0     31     0.046    3   K.MASTFIGNSTAIQELFK.R
         924  979.9998  1957.9850  1957.9745   5.37   0     44    0.0021    1   K.GHYTEGAELVDSVLDVVR.K
         931  672.0128  2013.0166  2013.0353  -9.32   1     82  3.9e-007    3   K.MASTFIGNSTAIQELFKR.I

20.     IPI00135284     Mass: 36092     Score: 186     Queries matched: 4    emPAI: 0.30
        Tax_Id=10090 Gene_Symbol=Gm16374 Glyceraldehyde-3-phosphate dehydrogenase
       Query  Observed    Mr(expt)   Mr(calc)    ppm  Miss Score    Expect Rank  Peptide
         688  685.3770  1368.7394  1368.7361   2.45   0     61  4.6e-005    1   R.GAAQNIIPASTGAAK.A
         691  686.8327  1371.6508  1371.6414   6.89   1     52   0.00038    1   R.VVDLMAYMASKE.-
         875  890.4037  1778.7928  1778.7900   1.61   0     85  1.5e-007    1   K.LISWYDNEYGYSNR.V 876


        Proteins matching the same set of peptides:
        IPI00271869     Mass: 36293     Score: 186     Queries matched: 4
        Tax_Id=10090 Gene_Symbol=- 36 kDa protein
        IPI00273646     Mass: 36072     Score: 186     Queries matched: 4
        Tax_Id=10090 Gene_Symbol=Gapdh;LOC100042025 Glyceraldehyde-3-phosphate dehydrogenase
        IPI00622795     Mass: 36074     Score: 186     Queries matched: 4
        Tax_Id=10090 Gene_Symbol=- 36 kDa protein
        IPI00752289     Mass: 36308     Score: 186     Queries matched: 4
        Tax_Id=10090 Gene_Symbol=Gm10290 Glyceraldehyde-3-phosphate dehydrogenase
        IPI00848801     Mass: 36100     Score: 186     Queries matched: 4
        Tax_Id=10090 Gene_Symbol=- 36 kDa protein
        IPI00849045     Mass: 36072     Score: 186     Queries matched: 4
        Tax_Id=10090 Gene_Symbol=- 36 kDa protein
        IPI00850337     Mass: 44633     Score: 186     Queries matched: 4
        Tax_Id=10090 Gene_Symbol=LOC100048117 similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) isoform 1
        IPI00850377     Mass: 35975     Score: 186     Queries matched: 4
        Tax_Id=10090 Gene_Symbol=- 36 kDa protein
        IPI00850779     Mass: 36076     Score: 186     Queries matched: 4
        Tax_Id=10090 Gene_Symbol=- 36 kDa protein
        IPI00874682     Mass: 36038     Score: 186     Queries matched: 4
        Tax_Id=10090 Gene_Symbol=- 36 kDa protein
        IPI00874964     Mass: 36512     Score: 186     Queries matched: 4
        Tax_Id=10090 Gene_Symbol=- 36 kDa protein

21.     IPI00135106     Mass: 19584     Score: 113     Queries matched: 12    emPAI: 0.89
        Tax_Id=10090 Gene_Symbol=Mobp Isoform 1 of Myelin-associated oligodendrocyte basic protein
       Query  Observed    Mr(expt)   Mr(calc)    ppm  Miss Score    Expect Rank  Peptide
         271  449.7446   897.4746   897.4781  -3.80   1     10         7    1   R.GGSPTRAPR.F 270
         332  498.7873   995.5600   995.5586   1.46   0     59  5.6e-005    1   K.SPLMPAKPR.S 333
         343  503.3052  1004.5958  1004.5879   7.89   0     22       0.2    1   R.SPPRPAKPR.S 342
         349  506.7819  1011.5492  1011.5535  -4.22   0    (49)  0.00066    1   K.SPLMPAKPR.S
         453  557.8041  1113.5936  1113.5891   4.11   1     36     0.019    1   R.SSPLRGPGTSR.G 452 454
         491  580.8288  1159.6430  1159.6462  -2.71   0     53   0.00038    1   K.HQPAASPVVVR.A 492

22.     IPI00114375     Mass: 62638     Score: 110     Queries matched: 1    emPAI: 0.05
        Tax_Id=10090 Gene_Symbol=Dpysl2 Dihydropyrimidinase-related protein 2
       Query  Observed    Mr(expt)   Mr(calc)    ppm  Miss Score    Expect Rank  Peptide
         911  956.0205  1910.0264  1910.0149   6.03   0    110  4.8e-010    1   R.FQLTDSQIYEVLSVIR.D

23.     IPI00132042     Mass: 39254     Score: 105     Queries matched: 1    emPAI: 0.08
        Tax_Id=10090 Gene_Symbol=Pdhb Pyruvate dehydrogenase E1 component subunit beta, mitochondrial
       Query  Observed    Mr(expt)   Mr(calc)    ppm  Miss Score    Expect Rank  Peptide
         867  874.4476  1746.8806  1746.8763   2.48   0    105  1.9e-009    1   R.IMEGPAFNFLDAPAVR.V

24.     IPI00138892     Mass: 15004     Score: 101     Queries matched: 2    emPAI: 0.23
        Tax_Id=10090 Gene_Symbol=Uba52 Ubiquitin-60S ribosomal protein L40
       Query  Observed    Mr(expt)   Mr(calc)    ppm  Miss Score    Expect Rank  Peptide
         883  894.4674  1786.9202  1786.9200   0.13   0    101  5.2e-009    1   K.TITLEVEPSDTIENVK.A 884


        Proteins matching the same set of peptides:
        IPI00470152     Mass: 18282     Score: 101     Queries matched: 2
        Tax_Id=10090 Gene_Symbol=Rps27a Ubiquitin-40S ribosomal protein S27a
        IPI00895319     Mass: 22277     Score: 101     Queries matched: 2
        Tax_Id=10090 Gene_Symbol=2810422J05Rik 22 kDa protein
```

```
      IPI00895479    Mass: 27181    Score: 101    Queries matched: 2
      Tax_Id=10090 Gene_Symbol=2810422J05Rik 27 kDa protein
      IPI00918763    Mass: 11021    Score: 101    Queries matched: 2
      Tax_Id=10090 Gene_Symbol=Uba52 Ubiqutin subunit 1
      IPI00750889    Mass: 22822    Score: 101    Queries matched: 2
      Tax_Id=10090 Gene_Symbol=Ubc Ubc protein
      IPI00923013    Mass: 26603    Score: 101    Queries matched: 2
      Tax_Id=10090 Gene_Symbol=Ubb Ubiquitin B
      IPI00923037    Mass: 22578    Score: 101    Queries matched: 2
      Tax_Id=10090 Gene_Symbol=Ubc Putative uncharacterized protein
      IPI00139518    Mass: 34348    Score: 101    Queries matched: 2
      Tax_Id=10090 Gene_Symbol=Ubb Polyubiquitin-B
      IPI00755916    Mass: 82614    Score: 101    Queries matched: 2
      Tax_Id=10090 Gene_Symbol=Ubc ubiquitin
      IPI00969323    Mass: 82603    Score: 101    Queries matched: 2
      Tax_Id=10090 Gene_Symbol=Ubc Polyubiquitin-C
```

```
25.   IPI00121038    Mass: 368613   Score: 100    Queries matched: 3   emPAI: 0.02
      Tax_Id=10090 Gene_Symbol=Vcan Isoform V0 of Versican core protein
     Query  Observed   Mr(expt)   Mr(calc)   ppm  Miss Score   Expect Rank  Peptide
       641  657.8627  1313.7108  1313.7092   1.28   0    15      2.3    1   R.LATVGELQAAWR.N
       716  709.3745  1416.7344  1416.7283   4.37   1    45   0.0023    1   K.METSPPVKGSLSGK.V
       926  656.6585  1966.9537  1966.9670  -6.79   0    87  1.2e-007   1   R.VSVPTHPDDVGDASLTMVK.L


      Proteins matching the same set of peptides:
      IPI00230441    Mass: 264594   Score: 100    Queries matched: 3
      Tax_Id=10090 Gene_Symbol=Vcan Isoform V1 of Versican core protein
      IPI00469172    Mass: 76209    Score: 100    Queries matched: 3
      Tax_Id=10090 Gene_Symbol=Vcan versican core protein isoform 4
      IPI00469565    Mass: 180325   Score: 100    Queries matched: 3
      Tax_Id=10090 Gene_Symbol=Vcan versican core protein isoform 3
      IPI00473932    Mass: 41850    Score: 100    Queries matched: 3
      Tax_Id=10090 Gene_Symbol=Vcan versican core protein isoform 5
      IPI00656277    Mass: 41758    Score: 100    Queries matched: 3
      Tax_Id=10090 Gene_Symbol=Vcan Versican
      IPI00875672    Mass: 368720   Score: 100    Queries matched: 3
      Tax_Id=10090 Gene_Symbol=Vcan versican core protein isoform 1
```

```
26.   IPI00323571    Mass: 35901    Score: 92     Queries matched: 7   emPAI: 0.30
      Tax_Id=10090 Gene_Symbol=Apoe Apolipoprotein E
     Query  Observed   Mr(expt)   Mr(calc)   ppm  Miss Score   Expect Rank  Peptide
       315  484.7793   967.5440   967.5451  -1.06   0    23     0.19    1   R.LGPLVEQGR.Q
       506  585.8336  1169.6526  1169.6516   0.86   1    68  9.6e-006   1   R.LGKEVQAAQAR.L 507
       550  614.8275  1227.6404  1227.6320   6.90   1    40   0.0081    1   R.GRLEEVGNQAR.D
       749  755.9121  1509.8096  1509.8012   5.62   1    10      4.9    1   R.TANLGAGAAQPLRDR.A
       805  800.4014  1598.7882  1598.7787   5.94   0    47   0.0014    1   K.ELEEQLGPVAEETR.A
       927  997.5323  1993.0500  1993.0480   1.03   0    18     0.84    1   K.IQASVATNPIITPVAQENQ.-
```

```
27.   IPI00229525    Score: 88     Queries matched: 3
      Tax_Id=10090 Gene_Symbol=Gnal Guanine nucleotide-binding protein G(olf) subunit alpha
     Query  Observed   Mr(expt)   Mr(calc)   ppm  Miss Score   Expect Rank  Peptide
       380  529.3142  1056.6138  1056.6179  -3.82   0    77  1.3e-006   1   R.LLLLGAGESGK.S 381
       527  595.8279  1189.6412  1189.6165   20.8   1     0       84    9   R.MHLKQYELL.-


      Proteins matching the same set of peptides:
      IPI00272681    Score: 88     Queries matched: 3
```

```
28.   IPI00118569    Mass: 44369    Score: 88     Queries matched: 2   emPAI: 0.07
      Tax_Id=10090 Gene_Symbol=Gna13 Guanine nucleotide-binding protein subunit alpha-13
     Query  Observed   Mr(expt)   Mr(calc)   ppm  Miss Score   Expect Rank  Peptide
       380  529.3142  1056.6138  1056.6179  -3.82   0    77  1.3e-006   1   K.ILLLGAGESGK.S 381


      Proteins matching the same set of peptides:
      IPI00230191    Mass: 44238    Score: 88     Queries matched: 2
      Tax_Id=10090 Gene_Symbol=Gna12 Guanine nucleotide-binding protein subunit alpha-12
      IPI00649388    Mass: 20095    Score: 88     Queries matched: 2
      Tax_Id=10090 Gene_Symbol=Gna13 Putative uncharacterized protein
```

```
29.   IPI00129240    Mass: 55613    Score: 54     Queries matched: 1   emPAI: 0.06
      Tax_Id=10090 Gene_Symbol=Vtn Vitronectin
     Query   Observed   Mr(expt)   Mr(calc)   ppm  Miss Score  Expect Rank  Peptide
       929  1001.0344  2000.0542  2000.0367   8.76   0    54  0.00022   1   K.LIQDVWGIEGPIDAAFTR.I
```

```
30.   IPI00323357    Mass: 71055    Score: 52     Queries matched: 2   emPAI: 0.05
      Tax_Id=10090 Gene_Symbol=Hspa8 Heat shock cognate 71 kDa protein
     Query  Observed   Mr(expt)   Mr(calc)   ppm  Miss Score  Expect Rank  Peptide
       551  614.8422  1227.6698  1227.6207   40.0   0     1      52    4   K.VEIIANDQGNR.T
       816  808.9132  1615.8118  1615.7804   19.5   0    52  0.00038   1   K.SFYPEEVSSMVLTK.M


      Proteins matching the same set of peptides:
      IPI00886297    Mass: 68964    Score: 52     Queries matched: 2
      Tax_Id=10090 Gene_Symbol=Hspa8 Hspa8 protein
```

```
31.   IPI00131366    Mass: 60627    Score: 50     Queries matched: 1   emPAI: 0.05
      Tax_Id=10090 Gene_Symbol=Krt6b Keratin, type II cytoskeletal 6B
```

```
      Query  Observed   Mr(expt)   Mr(calc)   ppm  Miss Score  Expect Rank  Peptide
        627  651.8628  1301.7110  1301.7078  2.48   0    50  0.00059   1   R.SLDLDSIIAEVK.A


       Proteins matching the same set of peptides:
       IPI00131368     Mass: 59641     Score: 50     Queries matched: 1
       Tax_Id=10090 Gene_Symbol=Krt6a Keratin, type II cytoskeletal 6A
       IPI00139301     Mass: 61957     Score: 50     Queries matched: 1
       Tax_Id=10090 Gene_Symbol=Krt5 Keratin, type II cytoskeletal 5
       IPI00221797     Mass: 59932     Score: 50     Queries matched: 1
       Tax_Id=10090 Gene_Symbol=Krt75 Keratin, type II cytoskeletal 75
       IPI00330480     Mass: 35315     Score: 50     Queries matched: 1
       Tax_Id=10090 Gene_Symbol=- 35 kDa protein
       IPI00470126     Mass: 60553     Score: 50     Queries matched: 1
       Tax_Id=10090 Gene_Symbol=Krt5 Uncharacterized protein
       IPI00762364     Mass: 50641     Score: 50     Queries matched: 1
       Tax_Id=10090 Gene_Symbol=Krt6a Uncharacterized protein
       IPI00785403     Mass: 59832     Score: 50     Queries matched: 1
       Tax_Id=10090 Gene_Symbol=Krt6b keratin, type II cytoskeletal 6B
```

```
32.    IPI00134344     Mass: 272022    Score: 48     Queries matched: 1   emPAI: 0.01
       Tax_Id=10090 Gene_Symbol=Spnb3 Putative uncharacterized protein
      Query   Observed    Mr(expt)   Mr(calc)    ppm  Miss Score  Expect Rank  Peptide
        930  1001.5367  2001.0588  2001.0531   2.88   0    48  0.00063   1   R.LVSQDNFGLELAAVEAAVR.K
```

```
33.    IPI00123313     Mass: 118931    Score: 47     Queries matched: 1   emPAI: 0.03
       Tax_Id=10090 Gene_Symbol=Uba1 Ubiquitin-like modifier-activating enzyme 1
      Query  Observed   Mr(expt)   Mr(calc)   ppm  Miss Score  Expect Rank  Peptide
        825  812.4624  1622.9102  1622.8992  6.84   0    47  0.00062   1   R.LAGTQPLEVLEAVQR.S
```

```
34.    IPI00113112     Score: 38     Queries matched: 1
       Tax_Id=10090 Gene_Symbol=Rab3b Ras-related protein Rab-3B
      Query  Observed   Mr(expt)   Mr(calc)   ppm  Miss Score Expect Rank  Peptide
        642  658.8356  1315.6566  1315.6521  3.49   0    38   0.011   1   K.LQIWDTAGQER.Y


       Proteins matching the same set of peptides:
       IPI00113127     Score: 38     Queries matched: 1
       IPI00114560     Score: 38     Queries matched: 1
       IPI00116688     Score: 38     Queries matched: 1
       IPI00122965     Score: 38     Queries matched: 1
       IPI00123180     Score: 38     Queries matched: 1
       IPI00126042     Score: 38     Queries matched: 1
       IPI00130118     Score: 38     Queries matched: 1
       IPI00130489     Score: 38     Queries matched: 1
       IPI00133706     Score: 38     Queries matched: 1
       IPI00169699     Score: 38     Queries matched: 1
       IPI00223332     Score: 38     Queries matched: 1
       IPI00224319     Score: 38     Queries matched: 1
       IPI00271059     Score: 38     Queries matched: 1
       IPI00272230     Score: 38     Queries matched: 1
       IPI00316495     Score: 38     Queries matched: 1
       IPI00331128     Score: 38     Queries matched: 1
       IPI00331205     Score: 38     Queries matched: 1
       IPI00404357     Score: 38     Queries matched: 1
       IPI00411115     Score: 38     Queries matched: 1
       IPI00468209     Score: 38     Queries matched: 1
       IPI00648888     Score: 38     Queries matched: 1
       IPI00651876     Score: 38     Queries matched: 1
       IPI00654255     Score: 38     Queries matched: 1
       IPI00671283     Score: 38     Queries matched: 1
       IPI00751303     Score: 38     Queries matched: 1
       IPI00757464     Score: 38     Queries matched: 1
       IPI00830932     Score: 38     Queries matched: 1
       IPI00894915     Score: 38     Queries matched: 1
       IPI00895100     Score: 38     Queries matched: 1
       IPI00944081     Score: 38     Queries matched: 1
```

```
35.    IPI00116697     Score: 38     Queries matched: 1
       Tax_Id=10090 Gene_Symbol=Rab6 Isoform 1 of Ras-related protein Rab-6A
      Query  Observed   Mr(expt)   Mr(calc)   ppm  Miss Score Expect Rank  Peptide
        642  658.8356  1315.6566  1315.6521  3.49   0    38   0.011   1   R.LQLWDTAGQER.F


       Proteins matching the same set of peptides:
       IPI00221836     Score: 38     Queries matched: 1
       IPI00230011     Score: 38     Queries matched: 1
       IPI00378145     Score: 38     Queries matched: 1
       IPI00757748     Score: 38     Queries matched: 1
```

```
36.    IPI00136271     Score: 38     Queries matched: 1
       Tax_Id=10090 Gene_Symbol=Rab33b Putative uncharacterized protein
      Query  Observed   Mr(expt)   Mr(calc)   ppm  Miss Score Expect Rank  Peptide
        642  658.8356  1315.6566  1315.6521  3.49   0    38   0.011   1   K.IQLWDTAGQER.F


       Proteins matching the same set of peptides:
       IPI00890284     Score: 38     Queries matched: 1
```

```
37.    IPI00170032     Mass: 24588     Score: 38     Queries matched: 1   emPAI: 0.14
       Tax_Id=10090 Gene_Symbol=Rab15 Ras-related protein Rab-15
```

```
      Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score Expect Rank  Peptide
        642  658.8356  1315.6566  1315.6521   3.49   0     38   0.011    1   R.IQIWDTAGQER.Y


       Proteins matching the same set of peptides:
       IPI00622236     Mass: 19558     Score: 38      Queries matched: 1
       Tax_Id=10090 Gene_Symbol=Rab15 Rab15 protein
       IPI00880661     Mass: 21411     Score: 38      Queries matched: 1
       Tax_Id=10090 Gene_Symbol=Rab15 Uncharacterized protein
       IPI00880893     Mass: 19333     Score: 38      Queries matched: 1
       Tax_Id=10090 Gene_Symbol=Rab15 Uncharacterized protein
       IPI00881140     Mass: 13439     Score: 38      Queries matched: 1
       Tax_Id=10090 Gene_Symbol=Rab15 Uncharacterized protein
       IPI00881258     Mass: 16230     Score: 38      Queries matched: 1
       Tax_Id=10090 Gene_Symbol=Rab15 Uncharacterized protein
       IPI00884469     Mass: 24602     Score: 38      Queries matched: 1
       Tax_Id=10090 Gene_Symbol=Rab15 ras-related protein Rab-15
```

```
38.    IPI00656325     Mass: 83131     Score: 37      Queries matched: 2    emPAI: 0.04
       Tax_Id=10090 Gene_Symbol=Nsf Vesicle-fusing ATPase
      Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score Expect Rank  Peptide
        615  646.3392  1290.6638  1290.6568   5.46   0     37   0.015    1   K.NFSGAELEGLVR.A
        738  729.3986  1456.7826  1456.7773   3.65   0     17     1.1    1   R.VLDDGELLVQQTK.N


       Proteins matching the same set of peptides:
       IPI00876255     Mass: 83174     Score: 37      Queries matched: 2
       Tax_Id=10090 Gene_Symbol=Nsf 83 kDa protein
```

Mascot: http://www.matrixscience.com/

Mascot Search Results

```
User                 : Dominic
Email                : dominic.kurian@bbsrc.ac.uk
Search title         : IPI Mouse_15-02-2010
MS data file         : C:\Program Files\Matrix Science\Mascot Daemon\mgf\32 10755\mascot_daemon_merge.mgf
Database             : IPI_mouse MOUSE_v3_79 (54943 sequences; 24917557 residues)
Timestamp            : 15 Feb 2011 at 11:28:31 GMT
Enzyme               : Trypsin
Fixed modifications  : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values          : Monoisotopic
Protein Mass         : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type      : ESI-QUAD-TOF
Number of queries    : 1078
Protein hits         : IPI00110850 Tax_Id=10090 Gene_Symbol=Actb Actin, cytoplasmic 1
                       IPI00136929 Tax_Id=10090 Gene_Symbol=Actg1 Gamma actin-like protein
                       IPI00169463 Tax_Id=10090 Gene_Symbol=Tubb2c Tubulin beta-2C chain
                       IPI00109073 Tax_Id=10090 Gene_Symbol=Tubb4 Tubulin beta-4 chain
                       IPI00338039 Tax_Id=10090 Gene_Symbol=Tubb2a Tubulin beta-2A chain
                       IPI00117352 Tax_Id=10090 Gene_Symbol=Tubb5 Tubulin beta-5 chain
                       IPI00221528 Tax_Id=10090 Gene_Symbol=Actbl2 Beta-actin-like protein 2
                       IPI00117348 Tax_Id=10090 Gene_Symbol=Tuba1b Tubulin alpha-1B chain
                       IPI00110753 Tax_Id=10090 Gene_Symbol=Tuba1a Tubulin alpha-1A chain
                       IPI00112251 Tax_Id=10090 Gene_Symbol=Tubb3 Tubulin beta-3 chain
                       IPI00122048 Tax_Id=10090 Gene_Symbol=Atp1a3 Sodium/potassium-transporting ATPase subunit alpha-3
                       IPI00420725 Tax_Id=10090 Gene_Symbol=Camk2a Uncharacterized protein
                       IPI00122928 Tax_Id=10090 Gene_Symbol=Tubb6 Tubulin beta-6 chain
                       IPI00115546 Tax_Id=10090 Gene_Symbol=Gnao1 Isoform Alpha-2 of Guanine nucleotide-binding protein G(o) subunit
                       IPI00117350 Tax_Id=10090 Gene_Symbol=Tuba4a Tubulin alpha-4A chain
                       IPI00120793 Tax_Id=10090 Gene_Symbol=Prnp Major prion protein
                       IPI00135284 Tax_Id=10090 Gene_Symbol=Gm16374 Glyceraldehyde-3-phosphate dehydrogenase
                       IPI00123176 Tax_Id=10090 Gene_Symbol=Gm6316 Glyceraldehyde-3-phosphate dehydrogenase
                       IPI00474502 Tax_Id=10090 Gene_Symbol=Camk2b Calcium/calmodulin-dependent protein kinase type II subunit beta
                       IPI00119063 Tax_Id=10090 Gene_Symbol=Lrp1 Prolow-density lipoprotein receptor-related protein 1
                       IPI00136703 Tax_Id=10090 Gene_Symbol=Ckb Creatine kinase B-type
                       IPI00319602 Tax_Id=10090 Gene_Symbol=Cnp Isoform CNPII of 2',3'-cyclic-nucleotide 3'-phosphodiesterase
                       IPI00138892 Tax_Id=10090 Gene_Symbol=Uba52 Ubiquitin-60S ribosomal protein L40
                       IPI00323357 Tax_Id=10090 Gene_Symbol=Hspa8 Heat shock cognate 71 kDa protein
                       IPI00348094 Tax_Id=10090 Gene_Symbol=Tubb1 Tubulin, beta 1
                       IPI00608020 Tax_Id=10090 Gene_Symbol=Ftl1 ferritin light chain 1
                       IPI00136372 Tax_Id=10090 Gene_Symbol=Syn1 Isoform Ib of Synapsin-1
                       IPI00555023 Tax_Id=10090 Gene_Symbol=Gstp1 Glutathione S-transferase P 1
                       IPI00114375 Tax_Id=10090 Gene_Symbol=Dpysl2 Dihydropyrimidinase-related protein 2
                       IPI00652902 Tax_Id=10090 Gene_Symbol=Gnai2 Putative uncharacterized protein
                       IPI00114642 Tax_Id=10090 Gene_Symbol=Hist1h2bn;Hist1h2bl;Hist1h2bj;Hist1h2bf Histone H2B type 1-F/J/L
                       IPI00118569 Tax_Id=10090 Gene_Symbol=Gna13 Guanine nucleotide-binding protein subunit alpha-13
                       IPI00310091 Tax_Id=10090 Gene_Symbol=Ppp2r1a Serine/threonine-protein phosphatase 2A 65 kDa regulatory subuni
                       IPI00130280 Tax_Id=10090 Gene_Symbol=Atp5a1 ATP synthase subunit alpha, mitochondrial
                       IPI00625729 Tax_Id=10090 Gene_Symbol=Krt1 Keratin, type II cytoskeletal 1
                       IPI00462140 Tax_Id=10090 Gene_Symbol=Krt77 Keratin, type II cytoskeletal 1b
                       IPI00408378 Tax_Id=10090 Gene_Symbol=Ywhaq Isoform 1 of 14-3-3 protein theta
                       IPI00119067 Tax_Id=10090 Gene_Symbol=Tppp Tubulin polymerization-promoting protein
                       IPI00323571 Tax_Id=10090 Gene_Symbol=Apoe Apolipoprotein E
                       IPI00272878 Tax_Id=10090 Gene_Symbol=Dnm1 Isoform 1 of Dynamin-1
                       IPI00230145 Tax_Id=10090 Gene_Symbol=Fth1 Ferritin heavy chain
                       IPI00123313 Tax_Id=10090 Gene_Symbol=Uba1 Ubiquitin-like modifier-activating enzyme 1
                       IPI00131366 Tax_Id=10090 Gene_Symbol=Krt6b Keratin, type II cytoskeletal 6B
                       IPI00462072 Tax_Id=10090 Gene_Symbol=Eno1;Gm5506 Alpha-enolase
                       IPI00266188 Tax_Id=10090 Gene_Symbol=Cfl2 Cofilin-2
                       IPI00230680 Tax_Id=10090 Gene_Symbol=Atp4a Potassium-transporting ATPase alpha chain 1
                       IPI00268145 Tax_Id=10090 Gene_Symbol=Atp12a Potassium-transporting ATPase alpha chain 2
                       IPI00222632 Tax_Id=10090 Gene_Symbol=Rab31 ras-related protein Rab-31
                       IPI00755181 Tax_Id=10090 Gene_Symbol=Krt10 keratin, type I cytoskeletal 10
                       IPI00134492 Tax_Id=10090 Gene_Symbol=Syn2 Isoform IIb of Synapsin-2
                       IPI00415402 Tax_Id=10090 Gene_Symbol=Stxbp1 Isoform 1 of Syntaxin-binding protein 1
                       IPI00656325 Tax_Id=10090 Gene_Symbol=Nsf Vesicle-fusing ATPase
                       IPI00135106 Tax_Id=10090 Gene_Symbol=Mobp Isoform 1 of Myelin-associated oligodendrocyte basic protein
```

	IPI_mouse	**Decoy**	**False discovery rate**
Peptide matches above identity threshold	145	0	0.00 %
Peptide matches above homology or identity threshold	161	0	0.00 %

Select Summary Report

Format As | Select Summary (protein hits) | Help

Significance threshold p< 0.01 | Max. number of hits AUTO

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

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

```
1.     IPI00110850     Mass: 42052     Score: 818     Queries matched: 24    emPAI: 1.88
       Tax_Id=10090 Gene_Symbol=Actb Actin, cytoplasmic 1
      Query   Observed    Mr(expt)   Mr(calc)     ppm  Miss Score    Expect Rank  Peptide
```

279	488.7281	975.4416	975.4410	0.65	0	22	0.31	1	K.AGFAGDDAPR.A
403	566.7664	1131.5182	1131.5197	-1.24	0	39	0.0064	1	R.GYSFTTTAER.E
437	581.3213	1160.6280	1160.6111	14.6	0	44	0.0035	1	K.EITALAPSTMK.I 436
450	586.2927	1170.5708	1170.5638	6.02	0	41	0.0053	1	R.HQGVMVGMGQK.D 451
456	589.3190	1176.6234	1176.6060	14.8	0	(5)	21	5	K.EITALAPSTMK.I
482	599.8567	1197.6988	1197.6982	0.52	0	60	3.5e-005	1	R.AVFPSIVGRPR.H 483
488	602.2874	1202.5602	1202.5536	5.50	0	(34)	0.027	1	R.HQGVMVGMGQK.D
665	677.8166	1353.6186	1353.6161	1.91	1	74	2.2e-006	1	K.DSYVGDEAQSKR.G 664
763	774.9140	1547.8134	1547.8051	5.39	1	91	5.1e-008	1	R.MQKEITALAPSTMK.I
854	812.4282	1622.8418	1622.8338	4.98	1	52	0.00033	1	R.LDLAGRDLTDYLMK.I
923	895.9495	1789.8844	1789.8846	-0.10	0	95	1.9e-008	1	K.SYELPDGQVITIGNER.F 922 924 925
972	652.0197	1953.0373	1953.0571	-10.15	0	68	7.4e-006	1	R.VAPEEHPVLLTEAPLNPK.A 973
1011	1108.0479	2214.0812	2214.0627	8.39	0	66	1.3e-005	1	K.DLYANTVLSGGTTMYPGIADR.M
1068	1061.8734	3182.5984	3182.6071	-2.73	0	159	3.8e-015	1	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L 1066 1067

Proteins matching the same set of peptides:
IPI00874482 **Mass:** 42108 **Score:** 818 **Queries matched:** 24
Tax_Id=10090 Gene_Symbol=Actg1 Actin, cytoplasmic 2

---

2. IPI00136929 **Mass:** 44029 **Score:** 726 **Queries matched:** 18 **emPAI:** 1.21
Tax_Id=10090 Gene_Symbol=Actg1 Gamma actin-like protein

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
403	566.7664	1131.5182	1131.5197	-1.24	0	39	0.0064	1	R.GYSFTTTAER.E
437	581.3213	1160.6280	1160.6111	14.6	0	44	0.0035	1	K.EITALAPSTMK.I 436
456	589.3190	1176.6234	1176.6060	14.8	0	(5)	21	5	K.EITALAPSTMK.I
665	677.8166	1353.6186	1353.6161	1.91	1	74	2.2e-006	1	K.DSYVGDEAQSKR.G 664
763	774.9140	1547.8134	1547.8051	5.39	1	91	5.1e-008	1	R.MQKEITALAPSTMK.I
854	812.4282	1622.8418	1622.8338	4.98	1	52	0.00033	1	R.LDLAGRDLTDYLMK.I
923	895.9495	1789.8844	1789.8846	-0.10	0	95	1.9e-008	1	K.SYELPDGQVITIGNER.F 922 924 925
972	652.0197	1953.0373	1953.0571	-10.15	0	68	7.4e-006	1	R.VAPEEHPVLLTEAPLNPK.R 973
1011	1108.0479	2214.0812	2214.0627	8.39	0	66	1.3e-005	1	K.DLYANTVLSGGTTMYPGLADR.M
1068	1061.8734	3182.5984	3182.6071	-2.73	0	159	3.8e-015	1	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L 1066 1067

---

3. IPI00169463 **Mass:** 50255 **Score:** 656 **Queries matched:** 29 **emPAI:** 1.94
Tax_Id=10090 Gene_Symbol=Tubb2c Tubulin beta-2C chain

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
339	539.2715	1076.5284	1076.5250	3.17	1	35	0.026	1	K.IREEYPDR.I 338 340
409	572.3189	1142.6232	1142.6270	-3.31	0	(64)	3.3e-005	1	K.LAVNMVPFPR.L 410
431	580.3211	1158.6276	1158.6219	4.92	0	83	4.5e-007	1	K.LAVNMVPFPR.L
521	615.3052	1228.5958	1228.5910	3.92	0	68	1.2e-005	1	R.ISEQFTAMFR.R
541	623.2966	1244.5786	1244.5860	-5.87	0	(6)	14	1	R.ISEQFTAMFR.R
632	660.3535	1318.6924	1318.6955	-2.32	0	72	5e-006	1	R.IMNTFSVVPSPK.V 633
643	664.8295	1327.6444	1327.6408	2.74	0	70	6.3e-006	1	R.INVYYNEATGGK.Y
648	668.3517	1334.6888	1334.6904	-1.19	0	(50)	0.00078	1	R.IMNTFSVVPSPK.V
708	723.8540	1445.6934	1445.6820	7.90	0	59	8.6e-005	1	K.EVDEQMLNVQNK.N
837	801.4127	1600.8108	1600.8131	-1.38	0	(28)	0.098	1	R.AVLVDLEPGTMDSVR.S
844	809.4111	1616.8076	1616.8080	-0.21	0	39	0.0077	1	R.AVLVDLEPGTMDSVR.S
849	540.9459	1619.8159	1619.8283	-7.65	0	47	0.0014	1	R.LHFFMPGFAPLTSR.G 850
875	846.4407	1690.8668	1690.8600	4.05	0	72	4.3e-006	1	R.ALTVPELTQQMFDAK.N 874
878	848.9237	1695.8328	1695.8257	4.24	0	50	0.00065	1	K.NSSYFVEWIPNNVK.T 877
887	854.4349	1706.8552	1706.8549	0.19	0	(53)	0.00036	2	R.ALTVPELTQQMFDAK.N 889 890
949	929.4739	1856.9332	1856.9342	-0.52	0	46	0.0016	1	K.MSATFIGNSTAIQELFK.R
992	672.0167	2013.0283	2013.0353	-3.50	1	134	1.9e-012	1	K.MSATFIGNSTAIQELFKR.I
1048	933.4539	2797.3399	2797.3361	1.34	0	104	1.4e-009	1	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G 1047 1049

---

4. IPI00109073 **Mass:** 50010 **Score:** 638 **Queries matched:** 25 **emPAI:** 1.60
Tax_Id=10090 Gene_Symbol=Tubb4 Tubulin beta-4 chain

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
409	572.3189	1142.6232	1142.6270	-3.31	0	(64)	3.3e-005	1	K.LAVNMVPFPR.L 410
431	580.3211	1158.6276	1158.6219	4.92	0	83	4.5e-007	1	K.LAVNMVPFPR.L
521	615.3052	1228.5958	1228.5910	3.92	0	68	1.2e-005	1	R.ISEQFTAMFR.R
541	623.2966	1244.5786	1244.5860	-5.87	0	(6)	14	1	R.ISEQFTAMFR.R
632	660.3535	1318.6924	1318.6955	-2.32	0	72	5e-006	1	R.IMNTFSVVPSPK.V 633
648	668.3517	1334.6888	1334.6904	-1.19	0	(50)	0.00078	1	R.IMNTFSVVPSPK.V
837	801.4127	1600.8108	1600.8131	-1.38	0	(28)	0.098	1	R.AVLVDLEPGTMDSVR.S
844	809.4111	1616.8076	1616.8080	-0.21	0	39	0.0077	1	R.AVLVDLEPGTMDSVR.S
849	540.9459	1619.8159	1619.8283	-7.65	0	47	0.0014	1	R.LHFFMPGFAPLTSR.G 850
875	846.4407	1690.8668	1690.8600	4.05	0	72	4.3e-006	1	R.ALTVPELTQQMFDAK.N 874
878	848.9237	1695.8328	1695.8257	4.24	0	50	0.00065	1	K.NSSYFVEWIPNNVK.T 877
887	854.4349	1706.8552	1706.8549	0.19	0	(53)	0.00036	2	R.ALTVPELTQQMFDAK.N 889 890
937	915.4451	1828.8756	1828.8744	0.69	0	114	2.2e-010	1	R.INVYYNEATGGNYVPR.A
949	929.4739	1856.9332	1856.9342	-0.52	0	43	0.0029	2	K.MAATFIGNSTAIQELFK.R
992	672.0167	2013.0283	2013.0353	-3.50	1	116	1.3e-010	3	K.MAATFIGNSTAIQELFKR.I
1048	933.4539	2797.3399	2797.3361	1.34	0	104	1.4e-009	1	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G 1047 1049

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5. IPI00338039 **Mass:** 50274 **Score:** 600 **Queries matched:** 30 **emPAI:** 1.76
Tax_Id=10090 Gene_Symbol=Tubb2a Tubulin beta-2A chain

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
339	539.2715	1076.5284	1076.5250	3.17	1	35	0.026	1	K.IREEYPDR.I 338 340
409	572.3189	1142.6232	1142.6270	-3.31	0	(64)	3.3e-005	1	K.LAVNMVPFPR.L 410
431	580.3211	1158.6276	1158.6219	4.92	0	83	4.5e-007	1	K.LAVNMVPFPR.L
521	615.3052	1228.5958	1228.5910	3.92	0	68	1.2e-005	1	R.ISEQFTAMFR.R
541	623.2966	1244.5786	1244.5860	-5.87	0	(6)	14	1	R.ISEQFTAMFR.R
660	676.3409	1350.6672	1350.6676	-0.24	0	63	3.8e-005	1	R.IMNTFSVMPSPK.V 659
708	723.8540	1445.6934	1445.6820	7.90	0	59	8.6e-005	1	K.EVDEQMLNVQNK.N
841	808.4230	1614.8314	1614.8287	1.70	0	77	1.5e-006	1	R.AILVDLEPGTMDSVR.S 842
849	540.9459	1619.8159	1619.8283	-7.65	0	47	0.0014	1	R.LHFFMPGFAPLTSR.G 850

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     858   816.4194  1630.8242  1630.8236    0.38   0   (58)  0.00011    1   R.AILVDLEPGTMDSVR.S 859
     878   848.9237  1695.8328  1695.8257    4.24   0    50   0.00065    1   K.NSSYFVEWIPNNVK.T 877
     887   854.4349  1706.8552  1706.8549    0.19   0    66  1.6e-005    1   R.ALTVPELTQQMFDSK.N 889 890
     896   862.4366  1722.8586  1722.8498    5.11   0   (11)      4.4    1   R.ALTVPELTQQMFDSK.N
     949   929.4739  1856.9332  1856.9342   -0.52   0    46    0.0016    1   K.MSATFIGNSTAIQELFK.R
     958   624.3088  1869.9046  1869.9373  -17.50   1    33     0.028    1   R.INVYYNEAAGNKYVPR.A
     992   672.0167  2013.0283  2013.0353   -3.50   1   134  1.9e-012    1   K.MSATFIGNSTAIQELFKR.I
    1048   933.4539  2797.3399  2797.3361    1.34   0   104  1.4e-009    1   R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G 1047 1049
    1065   776.3421  3101.3393  3101.4003  -19.66   0    29     0.022    1   K.FWEVISDEHGIDPTGSYHGDSDLQLER.I
```

```
6.   IPI00117352     Mass: 50095     Score: 553     Queries matched: 25    emPAI: 1.60
     Tax_Id=10090 Gene_Symbol=Tubb5 Tubulin beta-5 chain
    Query  Observed   Mr(expt)   Mr(calc)     ppm  Miss Score    Expect Rank  Peptide
     339   539.2715  1076.5284  1076.5250    3.17   1    35     0.026    1   K.IREEYPDR.I 338 340
     409   572.3189  1142.6232  1142.6270   -3.31   0   (64) 3.3e-005    1   K.LAVNMVPFPR.L 410
     431   580.3211  1158.6276  1158.6219    4.92   0    83  4.5e-007    1   K.LAVNMVPFPR.L
     521   615.3052  1228.5958  1228.5910    3.92   0    68  1.2e-005    1   R.ISEQFTAMFR.R
     541   623.2966  1244.5786  1244.5860   -5.87   0    (6)       14    1   R.ISEQFTAMFR.R
     608   651.3157  1300.6168  1300.6299  -10.05   0    52   0.00041    1   R.ISVYYNEATGGK.Y
     632   660.3535  1318.6924  1318.6955   -2.32   0    72     5e-006    1   R.IMNTFSVVPSPK.V 633
     648   668.3517  1334.6888  1334.6904   -1.19   0   (50)  0.00078    1   R.IMNTFSVVPSPK.V
     708   723.8540  1445.6934  1445.6820    7.90   0    59  8.6e-005    1   K.EVDEQMLNVQNK.N
     841   808.4230  1614.8314  1614.8287    1.70   0    77  1.5e-006    1   R.AILVDLEPGTMDSVR.S 842
     849   540.9459  1619.8159  1619.8283   -7.65   0    47    0.0014    1   R.LHFFMPGFAPLTSR.G 850
     858   816.4194  1630.8242  1630.8236    0.38   0   (58)  0.00011    1   R.AILVDLEPGTMDSVR.S 859
     864   830.4438  1658.8730  1658.8879   -8.98   0    72  3.8e-006    1   R.ALTVPELTQQVFDAK.N
     878   848.9237  1695.8328  1695.8257    4.24   0    50   0.00065    1   K.NSSYFVEWIPNNVK.T 877
    1048   933.4539  2797.3399  2797.3361    1.34   0   104  1.4e-009    1   R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G 1047 1049
```

```
7.   IPI00221528     Mass: 42319     Score: 498     Queries matched: 13    emPAI: 0.83
     Tax_Id=10090 Gene_Symbol=Actbl2 Beta-actin-like protein 2
    Query   Observed   Mr(expt)   Mr(calc)     ppm  Miss Score    Expect  Rank  Peptide
     450    586.2927  1170.5708  1170.5638    6.02    0    41    0.0053    1   R.HQGVMVGMGQK.D 451
     488    602.2874  1202.5602  1202.5536    5.50    0   (34)    0.027    1   R.HQGVMVGMGQK.D
     854    812.4282  1622.8418  1622.8338    4.98    1    52   0.00033    1   R.LDLAGRDLTDYLMK.I
     923    895.9495  1789.8844  1789.8846   -0.10    0    95  1.9e-008    1   R.SYELPDGQVITIGNER.F 922 924 925
     972    652.0197  1953.0373  1953.0571  -10.15    0    50   0.00051    2   R.VAPDEHPILLTEAPLNPK.I 973
    1068   1061.8734  3182.5984  3182.6071   -2.73    0   159  3.8e-015    1   R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L 1066 1067
```

```
8.   IPI00117348     Mass: 50804     Score: 427     Queries matched: 16    emPAI: 0.55
     Tax_Id=10090 Gene_Symbol=Tuba1b Tubulin alpha-1B chain
    Query   Observed   Mr(expt)   Mr(calc)    ppm  Miss Score    Expect Rank  Peptide
     243    455.2580   908.5014   908.4967   5.21    1     2        33    2   R.LSVDYGKK.S
     294    508.2930  1014.5714  1014.5709   0.50    0    26      0.19    1   K.DVNAAIATIK.T
     736    744.4408  1486.8670  1486.8719  -3.24    0    18      0.45    1   R.LISQIVSSITASLR.F
     883    851.4699  1700.9252  1700.8985   15.7    0    80  4.4e-007    1   R.AVFVDLEPTVIDEVR.T 882
     893    859.9458  1717.8770  1717.8747   1.36    0    67  1.3e-005    1   R.NLDIERPTYTNLNR.L 894
     934    912.9977  1823.9808  1823.9782   1.47    0    29     0.052    1   K.VGINYQPPTVVPGGDLAK.V 935
     990   1004.4575  2006.9004  2006.8858   7.30    0    89  5.8e-008    1   K.TIGGGDDSFNTFFSETGAGK.H
    1028   1205.1035  2408.1924  2408.2012  -3.65    0   125  1.4e-011    1   R.FDGALNVDLTEFQTNLVPYPR.I
    1033    805.7347  2414.1823  2414.1978  -6.44    1    78    8e-007    1   R.QLFHPEQLITGKEDAANNYAR.G 1030 1031 1032 1034


     Proteins matching the same set of peptides:
     IPI00403810     Mass: 50562     Score: 427     Queries matched: 16
     Tax_Id=10090 Gene_Symbol=Tuba1c Tubulin alpha-1C chain
```

```
9.   IPI00110753     Mass: 50788     Score: 427     Queries matched: 16    emPAI: 0.55
     Tax_Id=10090 Gene_Symbol=Tuba1a Tubulin alpha-1A chain
    Query   Observed   Mr(expt)   Mr(calc)    ppm  Miss Score    Expect Rank  Peptide
     243    455.2580   908.5014   908.4967   5.21    1     2        33    2   R.LSVDYGKK.S
     294    508.2930  1014.5714  1014.5709   0.50    0    26      0.19    1   K.DVNAAIATIK.T
     713    729.4382  1456.8618  1456.8613   0.37    0     8       2.8    1   R.LIGQIVSSITASLR.F
     883    851.4699  1700.9252  1700.8985   15.7    0    80  4.4e-007    1   R.AVFVDLEPTVIDEVR.T 882
     893    859.9458  1717.8770  1717.8747   1.36    0    67  1.3e-005    1   R.NLDIERPTYTNLNR.L 894
     934    912.9977  1823.9808  1823.9782   1.47    0    29     0.052    1   K.VGINYQPPTVVPGGDLAK.V 935
     990   1004.4575  2006.9004  2006.8858   7.30    0    89  5.8e-008    1   K.TIGGGDDSFNTFFSETGAGK.H
    1028   1205.1035  2408.1924  2408.2012  -3.65    0   125  1.4e-011    1   R.FDGALNVDLTEFQTNLVPYPR.I
    1033    805.7347  2414.1823  2414.1978  -6.44    1    78    8e-007    1   R.QLFHPEQLITGKEDAANNYAR.G 1030 1031 1032 1034
```

```
10.  IPI00112251     Mass: 50842     Score: 426     Queries matched: 21    emPAI: 0.87
     Tax_Id=10090 Gene_Symbol=Tubb3 Tubulin beta-3 chain
    Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score    Expect Rank  Peptide
     332   532.2687  1062.5228  1062.5094   12.7   1    25      0.26    1   K.VREEYPDR.I
     409   572.3189  1142.6232  1142.6270  -3.31   0   (64) 3.3e-005    1   K.LAVNMVPFPR.L 410
     431   580.3211  1158.6276  1158.6219   4.92   0    83  4.5e-007    1   K.LAVNMVPFPR.L
     521   615.3052  1228.5958  1228.5910   3.92   0    68  1.2e-005    1   R.ISEQFTAMFR.R
     541   623.2966  1244.5786  1244.5860  -5.87   0    (6)       14    1   R.ISEQFTAMFR.R
     632   660.3535  1318.6924  1318.6955  -2.32   0    72     5e-006    1   R.IMNTFSVVPSPK.V 633
     648   668.3517  1334.6888  1334.6904  -1.19   0   (50)  0.00078    1   R.IMNTFSVVPSPK.V
     841   808.4230  1614.8314  1614.8287   1.70   0    77  1.5e-006    1   R.AILVDLEPGTMDSVR.S 842
     850   810.9166  1619.8186  1619.8283  -5.94   0    19      0.83    2   R.LHFFMPGFAPLTAR.G
     858   816.4194  1630.8242  1630.8236   0.38   0   (58)  0.00011    1   R.AILVDLEPGTMDSVR.S 859
     875   846.4407  1690.8668  1690.8600   4.05   0    72  4.3e-006    1   R.ALTVPELTQQMFDAK.N 874
     878   848.9237  1695.8328  1695.8257   4.24   0    50   0.00065    1   K.NSSYFVEWIPNNVK.V 877
     887   854.4349  1706.8552  1706.8549   0.19   0   (53)  0.00036    2   R.ALTVPELTQQMFDAK.N 889 890
```

```
11.   IPI00122048     Mass: 113045    Score: 397    Queries matched: 12   emPAI: 0.22
      Tax_Id=10090 Gene_Symbol=Atp1a3 Sodium/potassium-transporting ATPase subunit alpha-3
     Query  Observed   Mr(expt)   Mr(calc)   ppm  Miss Score   Expect Rank  Peptide
       327  528.2854  1054.5562  1054.5520  4.07   1    18       1.1    1   K.GGDRVPADLR.I
       529  618.8585  1235.7024  1235.6986  3.11   0    54   0.00015    1   R.LNIPVSQVNPR.D 530
       573  634.8594  1267.7042  1267.7071 -2.22   0    40    0.0054    1   K.NMVPQQALVIR.E 574
       685  691.3808  1380.7470  1380.7435  2.55   0    57   0.00012    1   K.VIMVTGDHPITAK.A
       931  906.4794  1810.9442  1810.9425  0.96   0    91  4.8e-008    1   R.QGAIVAVTGDGVNDSPALK.K
       938  915.4692  1828.9238  1828.9167  3.93   0   116  1.6e-010    1   K.GVGIISEGNETVEDIAAR.L
       970  647.3470  1939.0192  1939.0375 -9.43   1    33     0.025    1   R.QGAIVAVTGDGVNDSPALKK.A
      1039 1232.6124  2463.2102  2463.1951  6.13   0   133  2.6e-012    1   K.QAADMILLDDNFASIVTGVEEGR.L
      1057  956.1147  2865.3223  2865.3490 -9.34   1    64  1.1e-005    1   K.EQPLDEEMKEAFQNAYLELGGLGER.V 1058


      Proteins matching the same set of peptides:
      IPI00752412     Mass: 117548    Score: 397    Queries matched: 12
      Tax_Id=10090 Gene_Symbol=Atp1a3 ATPase, Na+/K+ transporting, alpha 3 polypeptide, isoform CRA_c
```

```
12.   IPI00420725     Mass: 55882    Score: 371    Queries matched: 16   emPAI: 0.67
      Tax_Id=10090 Gene_Symbol=Camk2a Uncharacterized protein
     Query  Observed   Mr(expt)   Mr(calc)   ppm  Miss Score   Expect Rank  Peptide
       323  525.2839  1048.5532  1048.5553 -1.94   0    22      0.58    1   K.VLAGQEYAAK.I
       330  530.3022  1058.5898  1058.5906 -0.73   1    51   0.00061    1   K.MLTINPSKR.I 331
       417  574.3328  1146.6510  1146.6431  6.96   0    62  3.2e-005    1   K.GAILTTMLATR.N
       568  631.3073  1260.6000  1260.5927  5.79   0    62  4.9e-005    1   R.FYFENLWSR.N 566
       614  652.3557  1302.6968  1302.6932  2.81   0    71     5e-006    1   R.ITQYLDAGGIPR.T 613
       653  670.8925  1339.7704  1339.7711 -0.47   0    63     2e-005    1   R.DLKPENLLLASK.L 654
       860  816.8933  1631.7720  1631.7719  0.10   0    69  7.9e-006    1   R.FTEEYQLFEELGK.G
       996 1040.9818  2079.9490  2079.9426  3.12   0    76     1e-006    1   K.AGAYDFPSPEWDTVTPEAK.D 997
      1024  783.7260  2348.1562  2348.1689 -5.40   1    52   0.00029    1   R.FTEEYQLFEELGKGAFSVVR.R
      1046  888.7650  2663.2732  2663.2755 -0.87   1    47   0.00083    1   K.AGAYDFPSPEWDTVTPEAKDLINK.M 1045


      Proteins matching the same set of peptides:
      IPI00621806     Mass: 54651    Score: 371    Queries matched: 16
      Tax_Id=10090 Gene_Symbol=Camk2a Isoform Alpha CaMKII of Calcium/calmodulin-dependent protein kinase type II subunit alpha
```

```
13.   IPI00122928     Mass: 50514    Score: 368    Queries matched: 18   emPAI: 0.66
      Tax_Id=10090 Gene_Symbol=Tubb6 Tubulin beta-6 chain
     Query Observed   Mr(expt)   Mr(calc)    ppm  Miss Score   Expect Rank  Peptide
       339 539.2715  1076.5284  1076.5250   3.17   1    35     0.026    1   K.IREEYPDR.I 338 340
       409 572.3189  1142.6232  1142.6270  -3.31   0   (64) 3.3e-005    1   K.LAVNMVPFPR.L 410
       431 580.3211  1158.6276  1158.6219   4.92   0    83  4.5e-007    1   K.LAVNMVPFPR.L
       660 676.3409  1350.6672  1350.6676  -0.24   0    63  3.8e-005    1   R.IMNTFSVMPSPK.V 659
       850 810.9166  1619.8186  1619.8283  -5.94   0    19      0.83    2   R.LHFFMPGFAPLTAR.G
       875 846.4407  1690.8668  1690.8600   4.05   0    72  4.3e-006    1   R.ALTVPELTQQMFDAK.N 874
       878 848.9237  1695.8328  1695.8257   4.24   0    50   0.00065    1   K.NSSYFVEWIPNNVK.V 877
       887 854.4349  1706.8552  1706.8549   0.19   0   (53)  0.00036    2   R.ALTVPELTQQMFDAK.N 889 890
       949 929.4739  1856.9332  1856.9342  -0.52   0    36     0.016    3   K.MASTFIGNSTAIQELFK.R
       992 672.0167  2013.0283  2013.0353  -3.50   1   116  1.3e-010    2   K.MASTFIGNSTAIQELFKR.I
```

```
14.   IPI00115546     Mass: 40524    Score: 367    Queries matched: 10   emPAI: 0.48
      Tax_Id=10090 Gene_Symbol=Gnao1 Isoform Alpha-2 of Guanine nucleotide-binding protein G(o) subunit alpha
     Query Observed   Mr(expt)   Mr(calc)    ppm  Miss Score   Expect Rank  Peptide
       233 446.2509   890.4872   890.4610   29.4   0    14       3.5    1   R.LFDVGGQR.S
       329 529.3133  1056.6120  1056.6179  -5.53   0    72  4.1e-006    1   K.LLLLGAGESGK.S
       416 573.3207  1144.6268  1144.6088   15.8   1     4        34    8   K.NLKEDGISAAK.D
       707 723.3447  1444.6748  1444.6834  -5.94   0     8       9.9    2   K.IIHEDGFSGEDVK.Q
       834 792.3745  1582.7344  1582.7297   3.00   1    62  3.2e-005    1   R.AMDTLGVEYGDKER.K
       871 838.4184  1674.8222  1674.8213   0.56   0   115  2.1e-010    1   R.IGAGDYQPTEQDILR.T 872
       976 979.4461  1956.8776  1956.8631   7.44   0   101  2.8e-009    1   R.MEDTEPFSAELLSAMMR.L 975
       986 987.4356  1972.8566  1972.8580  -0.69   0   (47)  0.00058    1   R.MEDTEPFSAELLSAMMR.L


      Proteins matching the same set of peptides:
      IPI00230192     Mass: 40629    Score: 367    Queries matched: 10
      Tax_Id=10090 Gene_Symbol=Gnao1 Isoform Alpha-1 of Guanine nucleotide-binding protein G(o) subunit alpha
```

```
15.   IPI00117350     Mass: 50634    Score: 316    Queries matched: 13   emPAI: 0.46
      Tax_Id=10090 Gene_Symbol=Tuba4a Tubulin alpha-4A chain
     Query  Observed   Mr(expt)   Mr(calc)   ppm  Miss Score   Expect Rank  Peptide
       243  455.2580   908.5014   908.4967  5.21   1     2        33    2   R.LSVDYGKK.S
       736  744.4408  1486.8670  1486.8719 -3.24   0    18      0.45    1   R.LISQIVSSITASLR.F
       893  859.9458  1717.8770  1717.8747  1.36   0    67  1.3e-005    1   R.NLDIERPTYTNLNR.L 894
       934  912.9977  1823.9808  1823.9782  1.47   0    29     0.052    1   K.VGINYQPPTVVPGGDLAK.V 935
      1021  768.4006  2302.1800  2302.1957 -6.85   1    45    0.0013    1   R.AVFVDLEPTVIDEIRNGPYR.Q
      1028 1205.1035  2408.1924  2408.2012 -3.65   0   125  1.4e-011    1   R.FDGALNVDLTEFQTNLVPYPR.I
      1033  805.7347  2414.1823  2414.1978 -6.44   1    78     8e-007    1   R.QLFHPEQLITGKEDAANNYAR.G 1030 1031 1032 1034
```

```
16.   IPI00120793     Mass: 28131    Score: 282    Queries matched: 11   emPAI: 0.40
      Tax_Id=10090 Gene_Symbol=Prnp Major prion protein
     Query Observed   Mr(expt)   Mr(calc)    ppm  Miss Score   Expect Rank  Peptide
       295 508.7724  1015.5302  1015.5298   0.40   0    23      0.55    1   K.QHTVTTTTK.G
       349 544.7376  1087.4606  1087.4570   3.33   0    41    0.0019    1   K.ESQAYYDGR.R
       406 570.2620  1138.5094  1138.5142  -4.21   0    23       0.2    1   K.GENFTETDVK.M
       539 622.7877  1243.5608  1243.5581   2.18   1    39     0.005    1   K.ESQAYYDGRR.S 536 537 538
      1002 713.0141  2136.0205  2136.0335  -6.11   1   106  1.2e-009    1   K.QHTVTTTTKGENFTETDVK.M 1003 1004 1005
```

```
17.   IPI00135284     Mass: 36092     Score: 250     Queries matched: 12    emPAI: 0.42
      Tax_Id=10090 Gene_Symbol=Gm16374 Glyceraldehyde-3-phosphate dehydrogenase
     Query  Observed   Mr(expt)   Mr(calc)     ppm  Miss Score    Expect Rank  Peptide
        61  596.3636   595.3563   595.3442    20.4    0     8       4.6    2   K.AGAHLK.G
       243  455.2580   908.5014   908.5192  -19.52    1     0        52    8   K.AGAHLKGGAK.R
       667  678.8332  1355.6518  1355.6465    3.96    1    51   0.00049    1   R.VVDLMAYMASKE.- 666
       675  685.3760  1368.7374  1368.7361    0.99    0    59  6.8e-005    1   R.GAAQNIIPASTGAAK.A 674
       676  686.8303  1371.6460  1371.6414    3.39    1  (13)       3.2    1   R.VVDLMAYMASKE.-
       690  694.8303  1387.6460  1387.6363    7.01    1  (21)      0.49    1   R.VVDLMAYMASKE.-
       879  849.4503  1696.8860  1696.8856    0.25    1    76  1.5e-006    1   R.DGRGAAQNIIPASTGAAK.A 880
       914  890.4036  1778.7926  1778.7900    1.50    0    85  1.5e-007    1   K.LISWYDNEYGYSNR.V 913


      Proteins matching the same set of peptides:
      IPI00273646     Mass: 36072     Score: 250     Queries matched: 12
      Tax_Id=10090 Gene_Symbol=Gapdh;LOC100042025 Glyceraldehyde-3-phosphate dehydrogenase
      IPI00622795     Mass: 36074     Score: 250     Queries matched: 12
      Tax_Id=10090 Gene_Symbol=- 36 kDa protein
      IPI00848801     Mass: 36100     Score: 250     Queries matched: 12
      Tax_Id=10090 Gene_Symbol=- 36 kDa protein
      IPI00849045     Mass: 36072     Score: 250     Queries matched: 12
      Tax_Id=10090 Gene_Symbol=- 36 kDa protein
      IPI00850337     Mass: 44633     Score: 250     Queries matched: 12
      Tax_Id=10090 Gene_Symbol=LOC100048117 similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) isoform 1
      IPI00850377     Mass: 35975     Score: 250     Queries matched: 12
      Tax_Id=10090 Gene_Symbol=- 36 kDa protein
      IPI00874682     Mass: 36038     Score: 250     Queries matched: 12
      Tax_Id=10090 Gene_Symbol=- 36 kDa protein
      IPI00874964     Mass: 36512     Score: 250     Queries matched: 12
      Tax_Id=10090 Gene_Symbol=- 36 kDa protein
```

```
18.   IPI00123176     Mass: 36804     Score: 236     Queries matched: 9    emPAI: 0.29
      Tax_Id=10090 Gene_Symbol=Gm6316 Glyceraldehyde-3-phosphate dehydrogenase
     Query  Observed   Mr(expt)   Mr(calc)     ppm  Miss Score    Expect Rank  Peptide
        61  596.3636   595.3563   595.3442    20.4    0     8       4.6    2   K.AGAHLK.G
       243  455.2580   908.5014   908.5192  -19.52    1     0        52    8   K.AGAHLKGGAK.R
       675  685.3760  1368.7374  1368.7361    0.99    0    59  6.8e-005    1   R.GAAQNIIPASTGAAK.A 674
       841  808.4230  1614.8314  1614.8512  -12.23    1     0        70    6   R.VPTRNVSVVDLTCR.L
       879  849.4503  1696.8860  1696.8856    0.25    1    76  1.5e-006    1   R.DGRGAAQNIIPASTGAAK.A 880
       914  890.4036  1778.7926  1778.7900    1.50    0    85  1.5e-007    1   K.LISWYDNEYGYSNR.M 913
```

```
19.   IPI00474502     Mass: 61164     Score: 171     Queries matched: 10    emPAI: 0.23
      Tax_Id=10090 Gene_Symbol=Camk2b Calcium/calmodulin-dependent protein kinase type II subunit beta
     Query   Observed   Mr(expt)   Mr(calc)    ppm  Miss Score    Expect Rank  Peptide
       414   572.8060  1143.5974  1143.5964   0.90    0    18       1.6    1   R.FYFENLLAK.N
       417   574.3328  1146.6510  1146.6431   6.96    0    62  3.2e-005    1   K.GAILTTMLATR.N
       653   670.8925  1339.7704  1339.7711  -0.47    0    63    2e-005    1   R.DLKPENLLLASK.C 654
       678   687.3762  1372.7378  1372.7310   4.96    1    23      0.38    1   K.KADGVKPQTNSTK.N 677
       696   702.3779  1402.7412  1402.7317   6.80    0    46    0.0019    1   R.LTQYIDGQGRPR.T
       848   810.8851  1619.7556  1619.7355   12.4    0     9       7.7    1   R.FTDEYQLYEDIGK.G
       996  1040.9818  2079.9490  2079.9426   3.12    0    76    1e-006    1   K.AGAYDFPSPEWDTVTPEAK.N 997


      Proteins matching the same set of peptides:
      IPI00475302     Mass: 60053     Score: 171     Queries matched: 10
      Tax_Id=10090 Gene_Symbol=Camk2b calcium/calmodulin-dependent protein kinase type II subunit beta isoform 3
      IPI00515669     Mass: 57159     Score: 171     Queries matched: 10
      Tax_Id=10090 Gene_Symbol=Camk2b Calcium/calmodulin-dependent protein kinase II, beta
      IPI00648630     Mass: 58788     Score: 171     Queries matched: 10
      Tax_Id=10090 Gene_Symbol=Camk2b Calcium/calmodulin-dependent protein kinase II, beta
      IPI00649778     Mass: 73827     Score: 171     Queries matched: 10
      Tax_Id=10090 Gene_Symbol=Camk2b Calcium/calmodulin-dependent protein kinase II, beta, isoform CRA_b
      IPI00875723     Mass: 68686     Score: 171     Queries matched: 10
      Tax_Id=10090 Gene_Symbol=Camk2b 68 kDa protein
      IPI00470962     Mass: 61436     Score: 171     Queries matched: 10
      Tax_Id=10090 Gene_Symbol=Camk2b calcium/calmodulin-dependent protein kinase type II subunit beta isoform 1
      IPI00649296     Mass: 65906     Score: 171     Queries matched: 10
      Tax_Id=10090 Gene_Symbol=Camk2b Calcium/calmodulin-dependent protein kinase II, beta
```

```
20.   IPI00119063     Mass: 523342     Score: 170     Queries matched: 4    emPAI: 0.02
      Tax_Id=10090 Gene_Symbol=Lrp1 Prolow-density lipoprotein receptor-related protein 1
     Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score    Expect Rank  Peptide
       679  687.8944  1373.7742  1373.7667   5.50    0    73  2.2e-006    1   R.YVVISQGLDKPR.A 680
       851  811.4091  1620.8036  1620.8148  -6.85    0    75  2.2e-006    1   K.AVTDEEPFLIFANR.Y
       891  854.9852  1707.9558  1707.9308   14.7    0    51   0.00023    1   K.TVLWPNGLSLDIPAGR.L
```

```
21.   IPI00136703     Mass: 42971     Score: 170     Queries matched: 5    emPAI: 0.35
      Tax_Id=10090 Gene_Symbol=Ckb Creatine kinase B-type
     Query  Observed   Mr(expt)   Mr(calc)     ppm  Miss Score    Expect Rank  Peptide
       305  516.2994  1030.5842  1030.5481    35.1    0    15       2.4    1   K.LLIEMEQR.L
       838  801.9229  1601.8312  1601.8260    3.25    0    96  1.6e-008    1   K.LAVEALSSLDGDLSGR.Y
       863  828.9160  1655.8174  1655.8188   -0.85    0    59  8.3e-005    1   R.LEQGQAIDDLMPAQK.-
       944  924.9993  1847.9840  1847.9703    7.44    0    56   0.00012    1   R.LGFSEVELVQMVVDGVK.L
      1075  897.6848  3586.7101  3586.7800  -19.48    0    54  9.8e-005    1   K.SMTEAEQQQLIDDHFLFDKPVSPLLLASGMAR.D
```

```
22.   IPI00319602     Mass: 47493     Score: 159     Queries matched: 3    emPAI: 0.14
      Tax_Id=10090 Gene_Symbol=Cnp Isoform CNPII of 2',3'-cyclic-nucleotide 3'-phosphodiesterase
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      Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score   Expect Rank  Peptide
        291  500.7604   999.5062   999.4808   25.5   1      1        57    3   -.MNTSFTRK.S
        560  628.8163  1255.6180  1255.6157   1.89   0     70  6.3e-006    1   K.GGSQGEAVGELPR.G
        861  824.9201  1647.8256  1647.8216   2.45   1    124  2.8e-011    1   K.AAGAEEYAQQEVVKR.S

23.    IPI00138892     Mass: 15004     Score: 158     Queries matched: 4    emPAI: 0.85
       Tax_Id=10090 Gene_Symbol=Uba52 Ubiquitin-60S ribosomal protein L40
      Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score   Expect Rank  Peptide
         82  648.4186   647.4113   647.4006   16.5   0     35    0.0084    1   R.LIFAGK.Q
        752  762.3943  1522.7740  1522.7740   0.06   1     82    4e-007    1   K.IQDKEGIPPDQQR.L 753
        921  894.4671  1786.9196  1786.9200  -0.20   0     82  3.7e-007    1   K.TITLEVEPSDTIENVK.A


       Proteins matching the same set of peptides:
       IPI00470152     Mass: 18282     Score: 158     Queries matched: 4
       Tax_Id=10090 Gene_Symbol=Rps27a Ubiquitin-40S ribosomal protein S27a
       IPI00895319     Mass: 22277     Score: 158     Queries matched: 4
       Tax_Id=10090 Gene_Symbol=2810422J05Rik 22 kDa protein
       IPI00895479     Mass: 27181     Score: 158     Queries matched: 4
       Tax_Id=10090 Gene_Symbol=2810422J05Rik 27 kDa protein
       IPI00918763     Mass: 11021     Score: 158     Queries matched: 4
       Tax_Id=10090 Gene_Symbol=Uba52 Ubiquitin subunit 1
       IPI00750889     Mass: 22822     Score: 158     Queries matched: 4
       Tax_Id=10090 Gene_Symbol=Ubc Ubc protein
       IPI00923013     Mass: 26603     Score: 158     Queries matched: 4
       Tax_Id=10090 Gene_Symbol=Ubb Ubiquitin B
       IPI00923037     Mass: 22578     Score: 158     Queries matched: 4
       Tax_Id=10090 Gene_Symbol=Ubc Putative uncharacterized protein
       IPI00139518     Mass: 34348     Score: 158     Queries matched: 4
       Tax_Id=10090 Gene_Symbol=Ubb Polyubiquitin-B
       IPI00969323     Mass: 82603     Score: 158     Queries matched: 4
       Tax_Id=10090 Gene_Symbol=Ubc Polyubiquitin-C
       IPI00755916     Mass: 82614     Score: 158     Queries matched: 4
       Tax_Id=10090 Gene_Symbol=Ubc ubiquitin

24.    IPI00323357     Mass: 71055     Score: 136     Queries matched: 7    emPAI: 0.09
       Tax_Id=10090 Gene_Symbol=Hspa8 Heat shock cognate 71 kDa protein
      Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score   Expect Rank  Peptide
        464  590.8160  1179.6174  1179.6135   3.31   1     25      0.25    1   K.VQVEYKGETK.S
        520  614.8207  1227.6268  1227.6207   4.97   0     14         3    2   K.VEIIANDQGNR.T
        612  652.3111  1302.6076  1302.5914   12.5   0      5        16    2   K.NSLESYAFNMK.A
        733  744.3572  1486.6998  1486.6940   3.93   0     69  7.6e-006    1   R.TTPSYVAFTDTER.L 734
        843  808.9025  1615.7904  1615.7804   6.25   0      3        35    2   K.SFYPEEVSSMVLTK.M
        987  991.5050  1980.9954  1980.9905   2.49   0     59  6.2e-005    1   K.TVTNAVVTVPAYFNDSQR.Q

25.    IPI00348094     Mass: 51093     Score: 133     Queries matched: 8    emPAI: 0.21
       Tax_Id=10090 Gene_Symbol=Tubb1 Tubulin, beta 1
      Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score   Expect Rank  Peptide
        339  539.2715  1076.5284  1076.5250   3.17   1     35     0.026    1   K.IREEYPDR.I 338 340
        409  572.3189  1142.6232  1142.6270  -3.31   0   (64)  3.3e-005    1   K.LAVNMVPFPR.L 410
        431  580.3211  1158.6276  1158.6219   4.92   0     83  4.5e-007    1   K.LAVNMVPFPR.L
        632  660.3535  1318.6924  1318.6955  -2.31   0     11       6.1    2   R.ILNSFSVMPSPK.V 633

26.    IPI00608020     Mass: 20817     Score: 116     Queries matched: 2    emPAI: 0.35
       Tax_Id=10090 Gene_Symbol=Ftl1 ferritin light chain 1
      Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score   Expect Rank  Peptide
        730  740.8624  1479.7102  1479.6954   10.1   0     87  1.2e-007    1   R.QNYSTEVEAAVNR.L
       1071  820.6419  3278.5385  3278.5587  -6.17   1     62  1.9e-005    1   R.ALFQDVQKPSQDEWGKTQEAMEAALAMEK.N


       Proteins matching the same set of peptides:
       IPI00762203     Mass: 20847     Score: 116     Queries matched: 2
       Tax_Id=10090 Gene_Symbol=Ftl1 Ferritin light chain 1

27.    IPI00136372     Mass: 70163     Score: 94      Queries matched: 5    emPAI: 0.10
       Tax_Id=10090 Gene_Symbol=Syn1 Isoform Ib of Synapsin-1
      Query  Observed   Mr(expt)   Mr(calc)     ppm  Miss Score  Expect Rank  Peptide
        238  450.2198   898.4250   898.4621  -41.20   0      6       11    2   R.QAGAPQATR.Q
        470  594.3597  1186.7048  1186.7074   -2.14   0     24     0.15    1   R.SLKPDFVLIR.Q
        639  663.8334  1325.6522  1325.6503    1.46   0     57  0.00014    1   K.TYATAEPFIDAK.Y 640
        897  862.9027  1723.7908  1723.7869    2.29   0     47  0.00094    1   K.TNTGSAMLEQIAMSDR.Y


       Proteins matching the same set of peptides:
       IPI00649467     Mass: 71610     Score: 94      Queries matched: 5
       Tax_Id=10090 Gene_Symbol=Syn1 Isoform 3 of Synapsin-1
       IPI00649886     Mass: 74223     Score: 94      Queries matched: 5
       Tax_Id=10090 Gene_Symbol=Syn1 Isoform Ia of Synapsin-1

28.    IPI00555023     Mass: 23765     Score: 91      Queries matched: 2    emPAI: 0.14
       Tax_Id=10090 Gene_Symbol=Gstp1 Glutathione S-transferase P 1
      Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score   Expect Rank  Peptide
        662  676.3783  1350.7420  1350.7336   6.25   0     70  5.6e-006    1   M.PPYTIVYFPVR.G 661

29.    IPI00114375     Mass: 62638     Score: 88      Queries matched: 1    emPAI: 0.05
       Tax_Id=10090 Gene_Symbol=Dpysl2 Dihydropyrimidinase-related protein 2
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      Query  Observed   Mr(expt)   Mr(calc)   ppm  Miss Score   Expect Rank  Peptide
        967  956.0165  1910.0184  1910.0149  1.85    0     88  7.4e-008    1   R.FQLTDSQIYEVLSVIR.D

30.   IPI00652902    Mass: 41033    Score: 88     Queries matched: 2   emPAI: 0.17
      Tax_Id=10090 Gene_Symbol=Gnai2 Putative uncharacterized protein
      Query  Observed   Mr(expt)   Mr(calc)   ppm  Miss Score   Expect Rank  Peptide
        329  529.3133  1056.6120  1056.6179 -5.53    0     72  4.1e-006    1   K.LLLLGAGESGK.S
        902  868.9853  1735.9560  1735.9542  1.05    0     50   0.00034    1   R.AVVYSNTIQSIMAIVK.A

31.   IPI00114642    Mass: 13928    Score: 77     Queries matched: 2   emPAI: 0.25
      Tax_Id=10090 Gene_Symbol=Hist1h2bn;Hist1h2bl;Hist1h2bj;Hist1h2bf Histone H2B type 1-F/J/L
      Query  Observed   Mr(expt)   Mr(calc)   ppm  Miss Score   Expect Rank  Peptide
        903  872.4119  1742.8092  1742.8120 -1.58    0     75  1.9e-006    1   K.AMGIMNSFVNDIFER.I 904


      Proteins matching the same set of peptides:
      IPI00124518    Mass: 13359    Score: 77     Queries matched: 2
      Tax_Id=10090 Gene_Symbol=Hist2h2bb Hist2h2bb protein
      IPI00134534    Mass: 14879    Score: 77     Queries matched: 2
      Tax_Id=10090 Gene_Symbol=Gm11277;Gm13646 Histone H2B
      IPI00187543    Mass: 13985    Score: 77     Queries matched: 2
      Tax_Id=10090 Gene_Symbol=Hist2h2be Histone H2B type 2-E
      IPI00227930    Mass: 13912    Score: 77     Queries matched: 2
      Tax_Id=10090 Gene_Symbol=Hist1h2bh Histone H2B type 1-H
      IPI00229539    Mass: 17248    Score: 77     Queries matched: 2
      Tax_Id=10090 Gene_Symbol=Hist3h2bb-ps histone H2B type 3-B
      IPI00265768    Mass: 13912    Score: 77     Queries matched: 2
      Tax_Id=10090 Gene_Symbol=Hist1h2bk Histone H2B type 1-K
      IPI00282266    Mass: 13898    Score: 77     Queries matched: 2
      Tax_Id=10090 Gene_Symbol=Hist1h2bg;Hist1h2be;Gm9998;Hist1h2bc Histone H2B type 1-C/E/G
      IPI00282269    Mass: 13928    Score: 77     Queries matched: 2
      Tax_Id=10090 Gene_Symbol=Hist1h2bm Histone H2B type 1-M
      IPI00348270    Mass: 13912    Score: 77     Queries matched: 2
      Tax_Id=10090 Gene_Symbol=Hist2h2bb Histone H2B type 2-B
      IPI00453744    Mass: 15968    Score: 77     Queries matched: 2
      Tax_Id=10090 Gene_Symbol=Hist1h2bp 16 kDa protein
      IPI00461514    Mass: 14987    Score: 77     Queries matched: 2
      Tax_Id=10090 Gene_Symbol=Gm13646 Histone H2B
      IPI00553774    Mass: 13986    Score: 77     Queries matched: 2
      Tax_Id=10090 Gene_Symbol=Hist3h2ba Histone H2B type 3-A
      IPI00554853    Mass: 13944    Score: 77     Queries matched: 2
      Tax_Id=10090 Gene_Symbol=Hist1h2bb Histone H2B type 1-B
      IPI00648991    Mass: 13984    Score: 77     Queries matched: 2
      Tax_Id=10090 Gene_Symbol=Hist1h2bp Isoform 1 of Histone H2B type 1-P
      IPI00761713    Mass: 15555    Score: 77     Queries matched: 2
      Tax_Id=10090 Gene_Symbol=Hist1h2bp Isoform 2 of Histone H2B type 1-P
      IPI00874492    Mass: 14746    Score: 77     Queries matched: 2
      Tax_Id=10090 Gene_Symbol=Hist1h2bm 15 kDa protein
      IPI00874654    Mass: 14787    Score: 77     Queries matched: 2
      Tax_Id=10090 Gene_Symbol=Hist1h2bg;Hist1h2be;Gm9998;Hist1h2bc Histone H2B
      IPI00874970    Mass: 14951    Score: 77     Queries matched: 2
      Tax_Id=10090 Gene_Symbol=Hist1h2bn;Hist1h2bl;Hist1h2bj;Hist1h2bf Histone H2B
      IPI00875277    Mass: 14242    Score: 77     Queries matched: 2
      Tax_Id=10090 Gene_Symbol=Hist1h2bk 14 kDa protein
      IPI00875523    Mass: 14900    Score: 77     Queries matched: 2
      Tax_Id=10090 Gene_Symbol=Hist1h2bh Histone H2B
      IPI00875901    Mass: 14806    Score: 77     Queries matched: 2
      Tax_Id=10090 Gene_Symbol=Hist1h2bk Histone H2B
      IPI00876167    Mass: 14126    Score: 77     Queries matched: 2
      Tax_Id=10090 Gene_Symbol=Hist1h2bn;Hist1h2bl;Hist1h2bj;Hist1h2bf 14 kDa protein
      IPI00876432    Mass: 14148    Score: 77     Queries matched: 2
      Tax_Id=10090 Gene_Symbol=Hist1h2bn;Hist1h2bl;Hist1h2bj;Hist1h2bf Histone H2B
      IPI00876549    Mass: 14902    Score: 77     Queries matched: 2
      Tax_Id=10090 Gene_Symbol=Hist1h2bn;Hist1h2bl;Hist1h2bj;Hist1h2bf Histone H2B
      IPI00876550    Mass: 14812    Score: 77     Queries matched: 2
      Tax_Id=10090 Gene_Symbol=- 15 kDa protein

32.   IPI00118569    Mass: 44369    Score: 72     Queries matched: 1   emPAI: 0.07
      Tax_Id=10090 Gene_Symbol=Gna13 Guanine nucleotide-binding protein subunit alpha-13
      Query  Observed   Mr(expt)   Mr(calc)   ppm  Miss Score   Expect Rank  Peptide
        329  529.3133  1056.6120  1056.6179 -5.53    0     72  4.1e-006    1   K.ILLLGAGESGK.S


      Proteins matching the same set of peptides:
      IPI00230191    Mass: 44238    Score: 72     Queries matched: 1
      Tax_Id=10090 Gene_Symbol=Gna12 Guanine nucleotide-binding protein subunit alpha-12
      IPI00649388    Mass: 20095    Score: 72     Queries matched: 1
      Tax_Id=10090 Gene_Symbol=Gna13 Putative uncharacterized protein

33.   IPI00310091    Mass: 66079    Score: 72     Queries matched: 1   emPAI: 0.05
      Tax_Id=10090 Gene_Symbol=Ppp2r1a Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform
      Query  Observed   Mr(expt)   Mr(calc)   ppm  Miss Score   Expect Rank  Peptide
       1008  732.0782  2193.2128  2193.2256 -5.86    0     72  1.5e-006    1   K.IGPILDNSTLQSEVKPILEK.L

34.   IPI00130280    Mass: 59830    Score: 72     Queries matched: 1   emPAI: 0.05
      Tax_Id=10090 Gene_Symbol=Atp5a1 ATP synthase subunit alpha, mitochondrial
      Query   Observed   Mr(expt)   Mr(calc)   ppm  Miss Score   Expect Rank  Peptide
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      1023  1169.5824  2337.1502  2337.1601  -4.21   0    72  2.9e-006   1    R.EVAAFAQFGSDLDAATQQLLSR.G


     Proteins matching the same set of peptides:
     IPI00857439     Mass: 54675     Score: 72      Queries matched: 1
     Tax_Id=10090 Gene_Symbol=Atp5a1 ATP synthase subunit alpha

35.  IPI00625729     Mass: 66079     Score: 70      Queries matched: 3   emPAI: 0.05
     Tax_Id=10090 Gene_Symbol=Krt1 Keratin, type II cytoskeletal 1
    Query  Observed    Mr(expt)    Mr(calc)     ppm  Miss Score    Expect Rank  Peptide
      694  697.3569  1392.6992  1392.7249  -18.40    1     0        75    8   R.TNAENEFVTIKK.D
      728  738.4001  1474.7856  1474.7780    5.20    0    70  6.4e-006    1   R.FLEQQNQVLQTK.W
      880  849.4527  1696.8908  1696.8342    33.4    1     3        28    4   K.DVDSAYMTKVELQAK.A

36.  IPI00462140     Mass: 61379     Score: 70      Queries matched: 2   emPAI: 0.05
     Tax_Id=10090 Gene_Symbol=Krt77 Keratin, type II cytoskeletal 1b
    Query  Observed    Mr(expt)    Mr(calc)     ppm  Miss Score    Expect Rank  Peptide
      681  689.3424  1376.6702  1376.7300  -43.38    1     1        65    9   R.TNAENDFVVLKK.D
      728  738.4001  1474.7856  1474.7780    5.20    0    70  6.4e-006    1   R.FLEQQNQVLQTK.W

37.  IPI00408378     Mass: 28046     Score: 69      Queries matched: 1   emPAI: 0.12
     Tax_Id=10090 Gene_Symbol=Ywhaq Isoform 1 of 14-3-3 protein theta
    Query  Observed    Mr(expt)    Mr(calc)    ppm  Miss Score    Expect Rank  Peptide
      755  766.8602  1531.7058  1531.7114  -3.62    0    69  7.3e-006    1   K.AVTEQGAELSNEER.N


     Proteins matching the same set of peptides:
     IPI00656269     Mass: 28025     Score: 69      Queries matched: 1
     Tax_Id=10090 Gene_Symbol=Ywhaq Isoform 2 of 14-3-3 protein theta
     IPI00754545     Mass: 35930     Score: 69      Queries matched: 1
     Tax_Id=10090 Gene_Symbol=Gm2423 similar to Ywhaq protein
     IPI00853924     Mass: 34613     Score: 69      Queries matched: 1
     Tax_Id=10090 Gene_Symbol=Ywhaq 34 kDa protein

38.  IPI00119067     Mass: 23731     Score: 68      Queries matched: 1   emPAI: 0.14
     Tax_Id=10090 Gene_Symbol=Tppp Tubulin polymerization-promoting protein
    Query  Observed    Mr(expt)    Mr(calc)    ppm  Miss Score    Expect Rank  Peptide
      964  948.9969  1895.9792  1895.9516   14.6    0    68  1.1e-005    1   R.TITFEQFQEALEELAK.K

39.  IPI00323571     Mass: 35901     Score: 67      Queries matched: 5   emPAI: 0.30
     Tax_Id=10090 Gene_Symbol=Apoe Apolipoprotein E
    Query  Observed    Mr(expt)    Mr(calc)    ppm  Miss Score Expect Rank  Peptide
      448  585.8325  1169.6504  1169.6516  -1.02    1    43  0.0027    1   R.LGKEVQAAQAR.L 447
      520  614.8207  1227.6268  1227.6320  -4.17    1    45  0.0025    1   R.GRLEEVGNQAR.D
      681  689.3424  1376.6702  1376.6718  -1.12    1    36   0.021    1   R.SKMEEQTQQIR.L
      749  755.9105  1509.8064  1509.8012   3.50    1     6      14    1   R.TANLGAGAAQPLRDR.A

40.  IPI00272878     Mass: 98140     Score: 66      Queries matched: 2   emPAI: 0.03
     Tax_Id=10090 Gene_Symbol=Dnm1 Isoform 1 of Dynamin-1
    Query  Observed    Mr(expt)    Mr(calc)    ppm  Miss Score    Expect Rank  Peptide
      328  529.2714  1056.5282  1056.5200   7.82    0     6        15    1   R.SPTSSPTPQR.R
      657  672.8652  1343.7158  1343.7045   8.46    0    66  1.4e-005    1   K.TSGNQDEILVIR.K


     Proteins matching the same set of peptides:
     IPI00331293     Mass: 97762     Score: 66      Queries matched: 2
     Tax_Id=10090 Gene_Symbol=Dnm1 Isoform 4 of Dynamin-1
     IPI00465648     Mass: 96209     Score: 66      Queries matched: 2
     Tax_Id=10090 Gene_Symbol=Dnm1 Isoform 3 of Dynamin-1
     IPI00753037     Mass: 96395     Score: 66      Queries matched: 2
     Tax_Id=10090 Gene_Symbol=Dnm1 Isoform 5 of Dynamin-1
     IPI00890133     Mass: 97954     Score: 66      Queries matched: 2
     Tax_Id=10090 Gene_Symbol=Dnm1 Uncharacterized protein

41.  IPI00230145     Mass: 21224     Score: 62      Queries matched: 3   emPAI: 0.16
     Tax_Id=10090 Gene_Symbol=Fth1 Ferritin heavy chain
    Query  Observed    Mr(expt)    Mr(calc)    ppm  Miss Score    Expect Rank  Peptide
      422  577.3004  1152.5862  1152.5887  -2.15    0    11         6    1   K.ELGDHVTNLR.K
      571  634.3499  1266.6852  1266.6932  -6.26    0    59  7.2e-005    1   K.SVNQSLLELHK.L 572

42.  IPI00123313     Mass: 118931    Score: 62      Queries matched: 1   emPAI: 0.03
     Tax_Id=10090 Gene_Symbol=Uba1 Ubiquitin-like modifier-activating enzyme 1
    Query  Observed    Mr(expt)    Mr(calc)    ppm  Miss Score    Expect Rank  Peptide
      962  943.0261  1884.0376  1884.0357   1.06    0    62  2.1e-005    1   R.AAVASLLQSVQVPEFTPK.S

43.  IPI00131366     Mass: 60627     Score: 61      Queries matched: 4   emPAI: 0.05
     Tax_Id=10090 Gene_Symbol=Krt6b Keratin, type II cytoskeletal 6B
    Query  Observed    Mr(expt)    Mr(calc)     ppm  Miss Score    Expect Rank  Peptide
      610  651.8621  1301.7096  1301.7078    1.40    0    61  4.7e-005    1   R.SLDLDSIIAEVK.A
      705  717.8544  1433.6942  1433.7375  -30.17    1     0        57    3   R.GYSASSARVPGLNR.S
      880  849.4527  1696.8908  1696.8342    33.4    1     3        28    4   K.DVDAAYMTKVELQAK.A 879


     Proteins matching the same set of peptides:
     IPI00785403     Mass: 59832     Score: 61      Queries matched: 4
     Tax_Id=10090 Gene_Symbol=Krt6b keratin, type II cytoskeletal 6B
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44.   IPI00462072     Mass: 47453     Score: 60     Queries matched: 2    emPAI: 0.07
      Tax_Id=10090 Gene_Symbol=Eno1;Gm5506 Alpha-enolase
     Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score   Expect Rank  Peptide
       706  720.3782  1438.7418  1438.7344   5.19   0    60  7.3e-005   1   R.YITPDQLADLYK.S
      1062  990.7887  2969.3443  2969.3508  -2.21   0    14      0.96   1   K.SFVQNYPVVSIEDPFDQDDWGAWQK.F


      Proteins matching the same set of peptides:
      IPI00648821     Mass: 40099     Score: 60     Queries matched: 2
      Tax_Id=10090 Gene_Symbol=Eno1 Enolase

45.   IPI00266188     Mass: 18812     Score: 58     Queries matched: 2    emPAI: 0.18
      Tax_Id=10090 Gene_Symbol=Cfl2 Cofilin-2
     Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score  Expect Rank  Peptide
       651  669.3212  1336.6278  1336.6187   6.87   0    54  0.00022   1   R.YALYDATYETK.E 650


      Proteins matching the same set of peptides:
      IPI00407543     Mass: 25293     Score: 58     Queries matched: 2
      Tax_Id=10090 Gene_Symbol=Cfl1 Putative uncharacterized protein
      IPI00848816     Mass: 18731     Score: 58     Queries matched: 2
      Tax_Id=10090 Gene_Symbol=LOC100048522 similar to Cofilin-1
      IPI00890117     Mass: 18776     Score: 58     Queries matched: 2
      Tax_Id=10090 Gene_Symbol=Cfl1 Cofilin-1

46.   IPI00230680     Mass: 115702    Score: 57     Queries matched: 2    emPAI: 0.03
      Tax_Id=10090 Gene_Symbol=Atp4a Potassium-transporting ATPase alpha chain 1
     Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score  Expect Rank  Peptide
       327  528.2854  1054.5562  1054.5520   4.07   1    18      1.1   1   K.GGDRVPADIR.I
       685  691.3808  1380.7470  1380.7435   2.55   0    57  0.00012   1   R.VIMVTGDHPITAK.A


47.   IPI00268145     Mass: 115394    Score: 57     Queries matched: 3    emPAI: 0.03
      Tax_Id=10090 Gene_Symbol=Atp12a Potassium-transporting ATPase alpha chain 2
     Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score  Expect Rank  Peptide
       447  585.8287  1169.6428  1169.6516  -7.52   1    11      4.9   2   R.NIAVEQVNKR.E 448
       685  691.3808  1380.7470  1380.7435   2.55   0    57  0.00012   1   K.VIMVTGDHPITAK.A


      Proteins matching the same set of peptides:
      IPI00877215     Mass: 115395    Score: 57     Queries matched: 3
      Tax_Id=10090 Gene_Symbol=Atp12a potassium-transporting ATPase alpha chain 2

48.   IPI00222632     Mass: 21791     Score: 52     Queries matched: 1    emPAI: 0.15
      Tax_Id=10090 Gene_Symbol=Rab31 ras-related protein Rab-31
     Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score  Expect Rank  Peptide
       839  802.4271  1602.8396  1602.8365   1.94   0    52  0.00043   1   K.NAINIEELFQGISR.Q


49.   IPI00755181     Mass: 57178     Score: 49     Queries matched: 1    emPAI: 0.06
      Tax_Id=10090 Gene_Symbol=Krt10 keratin, type I cytoskeletal 10
     Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score  Expect Rank  Peptide
       683  691.3288  1380.6430  1380.6408   1.60   0    49  0.00076   1   R.ALEESNYELEGK.I


      Proteins matching the same set of peptides:
      IPI00798492     Mass: 57906     Score: 49     Queries matched: 1
      Tax_Id=10090 Gene_Symbol=Krt10 Isoform 1 of Keratin, type I cytoskeletal 10
      IPI00828744     Mass: 57197     Score: 49     Queries matched: 1
      Tax_Id=10090 Gene_Symbol=Krt10 Isoform 2 of Keratin, type I cytoskeletal 10

50.   IPI00134492     Mass: 52818     Score: 47     Queries matched: 2    emPAI: 0.13
      Tax_Id=10090 Gene_Symbol=Syn2 Isoform IIb of Synapsin-2
     Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score  Expect Rank  Peptide
       726  737.4225  1472.8304  1472.8313  -0.57   0    29    0.051   1   R.EMLTLPTFPVVVK.I
       897  862.9027  1723.7908  1723.7869   2.29   0    47  0.00094   1   K.TNTGSAMLEQIAMSDR.Y


      Proteins matching the same set of peptides:
      IPI00469548     Mass: 63618     Score: 47     Queries matched: 2
      Tax_Id=10090 Gene_Symbol=Syn2 Isoform IIa of Synapsin-2

51.   IPI00415402     Mass: 67925     Score: 47     Queries matched: 1    emPAI: 0.05
      Tax_Id=10090 Gene_Symbol=Stxbp1 Isoform 1 of Syntaxin-binding protein 1
     Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score Expect Rank  Peptide
       516  612.8163  1223.6180  1223.6146   2.82   0    47  0.0014   1   R.ISEQTYQLSR.W


      Proteins matching the same set of peptides:
      IPI00415403     Mass: 69091     Score: 47     Queries matched: 1
      Tax_Id=10090 Gene_Symbol=Stxbp1 Isoform 2 of Syntaxin-binding protein 1
      IPI00756061     Mass: 49457     Score: 47     Queries matched: 1
      Tax_Id=10090 Gene_Symbol=Stxbp1 49 kDa protein

52.   IPI00656325     Mass: 83131     Score: 45     Queries matched: 2    emPAI: 0.04
      Tax_Id=10090 Gene_Symbol=Nsf Vesicle-fusing ATPase
     Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score Expect Rank  Peptide
       712  729.3977  1456.7808  1456.7773   2.42   0    45  0.0018   1   R.VLDDGELLVQQTK.N 711


      Proteins matching the same set of peptides:
```

```
     IPI00876255    Mass: 83174    Score: 45     Queries matched: 2
     Tax_Id=10090 Gene_Symbol=Nsf 83 kDa protein
```

```
53.  IPI00135106    Mass: 19584    Score: 41     Queries matched: 4    emPAI: 0.37
     Tax_Id=10090 Gene_Symbol=Mobp Isoform 1 of Myelin-associated oligodendrocyte basic protein
    Query  Observed   Mr(expt)   Mr(calc)   ppm  Miss Score Expect Rank  Peptide
      377  557.8031  1113.5916  1113.5891   2.32   1    33   0.041    1   R.SSPLRGPGTSR.G 378
      433  580.8276  1159.6406  1159.6462  -4.78   0    38   0.011    1   K.HQPAASPVVVR.A 434
```

Mascot: http://www.matrixscience.com/

Mascot Search Results

```
User          : Dominic
Email         : dominic.kurian@bbsrc.ac.uk
Search title  : IPI Mouse_15-02-2010
MS data file  : D:\Peaklist\Dominic Kurian\QTofDK20010803 GATC P 0010881.pkl
Database      : IPI_mouse MOUSE_v3_79 (54943 sequences; 24917557 residues)
Timestamp     : 15 Feb 2011 at 15:10:35 GMT
Protein hits  : IPI00420725 Tax_Id=10090 Gene_Symbol=Camk2a Uncharacterized protein
                IPI00474502 Tax_Id=10090 Gene_Symbol=Camk2b Calcium/calmodulin-dependent protein kinase type II subunit beta
                IPI00112584 Tax_Id=10090 Gene_Symbol=Camk2d Isoform 1 of Calcium/calmodulin-dependent protein kinase type II subunit
                IPI00124695 Tax_Id=10090 Gene_Symbol=Camk2g Isoform 1 of Calcium/calmodulin-dependent protein kinase type II subunit
                IPI00109073 Tax_Id=10090 Gene_Symbol=Tubb4 Tubulin beta-4 chain
                IPI00115546 Tax_Id=10090 Gene_Symbol=Gnao1 Isoform Alpha-2 of Guanine nucleotide-binding protein G(o) subunit alpha
                IPI00323571 Tax_Id=10090 Gene_Symbol=Apoe Apolipoprotein E
                IPI00112251 Tax_Id=10090 Gene_Symbol=Tubb3 Tubulin beta-3 chain
                IPI00110850 Tax_Id=10090 Gene_Symbol=Actb Actin, cytoplasmic 1
                IPI00109061 Tax_Id=10090 Gene_Symbol=Tubb2b Tubulin beta-2B chain
                IPI00122048 Tax_Id=10090 Gene_Symbol=Atp1a3 Sodium/potassium-transporting ATPase subunit alpha-3
                IPI00138892 Tax_Id=10090 Gene_Symbol=Uba52 Ubiquitin-60S ribosomal protein L40
                IPI00120793 Tax_Id=10090 Gene_Symbol=Prnp Major prion protein
                IPI00122928 Tax_Id=10090 Gene_Symbol=Tubb6 Tubulin beta-6 chain
                IPI00225062 Tax_Id=10090 Gene_Symbol=Srrm2 Isoform 3 of Serine/arginine repetitive matrix protein 2
                IPI00221528 Tax_Id=10090 Gene_Symbol=Actbl2 Beta-actin-like protein 2
                IPI00404590 Tax_Id=10090 Gene_Symbol=H1f0 Putative uncharacterized protein
                IPI00323357 Tax_Id=10090 Gene_Symbol=Hspa8 Heat shock cognate 71 kDa protein
                IPI00469012 Tax_Id=10090 Gene_Symbol=Tbc1d10b TBC1 domain family member 10B
                IPI00223714 Tax_Id=10090 Gene_Symbol=Hist1h1e Histone H1.4
                IPI00656325 Tax_Id=10090 Gene_Symbol=Nsf Vesicle-fusing ATPase
                IPI00377681 Tax_Id=10090 Gene_Symbol=N28178 Isoform 2 of Protein KIAA1045
                IPI00122069 Tax_Id=10090 Gene_Symbol=Prkcc Protein kinase C gamma type
                IPI00136703 Tax_Id=10090 Gene_Symbol=Ckb Creatine kinase B-type
                IPI00347110 Tax_Id=10090 Gene_Symbol=Krt73 Keratin, type II cytoskeletal 73
                IPI00403219 Tax_Id=10090 Gene_Symbol=Gm14496 Novel vomeronasal 2, receptor family protein
                IPI00119853 Tax_Id=10090 Gene_Symbol=Gnas Isoform Gnas-1 of Guanine nucleotide-binding protein G(s) subunit alpha is
                IPI00347770 Tax_Id=10090 Gene_Symbol=Gnat3 Guanine nucleotide-binding protein G(t) subunit alpha-3
                IPI00118569 Tax_Id=10090 Gene_Symbol=Gna13 Guanine nucleotide-binding protein subunit alpha-13
                IPI00123176 Tax_Id=10090 Gene_Symbol=Gm6316 Glyceraldehyde-3-phosphate dehydrogenase
                IPI00348094 Tax_Id=10090 Gene_Symbol=Tubb1 Tubulin, beta 1
                IPI00116074 Tax_Id=10090 Gene_Symbol=Aco2 Aconitate hydratase, mitochondrial
                IPI00119063 Tax_Id=10090 Gene_Symbol=Lrp1 Prolow-density lipoprotein receptor-related protein 1
```

	IPI_mouse	Decoy	False discovery rate
Peptide matches above identity threshold	161	0	0.00 %
Peptide matches above homology or identity threshold	181	0	0.00 %

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 > 37 indicate identity or extensive homology (p<0.01).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.

Score Distribution

Peptide Summary Report

Format As | Peptide Summary | Help

Significance threshold p< 0.01 | Max. number of hits AUTO

Standard scoring ○ MudPIT scoring ● | Ions score or expect cut-off 0 | 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.     IPI00420725     Mass: 55882     Score: 1434    Queries matched: 119    emPAI: 0.99
       Tax_Id=10090 Gene_Symbol=Camk2a Uncharacterized 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
☑	33	602.3627	601.3554	601.3435	19.8	0	20	1.6	1	K.DLINK.M
☑	81	432.7283	863.4420	863.4501	-9.35	0	(7)	20	1	R.SGAPSVLPH.-
☑	82	432.7314	863.4482	863.4501	-2.17	0	(12)	6.1	1	R.SGAPSVLPH.-
☑	83	432.7319	863.4492	863.4501	-1.01	0	20	0.94	1	R.SGAPSVLPH.-
☑	118	452.2494	902.4842	902.4895	-5.84	0	(13)	5.2	1	K.MLTINPSK.R

☑	119	452.2506	902.4866	902.4895	-3.18	0	15	3.5	1	K.MLTINPSK.R
☑	125	461.2198	920.4250	920.4199	5.57	0	43	0.0033	1	R.TAQSEETR.V
☑	126	463.2444	924.4742	924.4777	-3.74	1	11	5.1	1	R.DHQKLER.E
☑	197	525.2842	1048.5538	1048.5553	-1.37	0	(33)	0.046	1	K.VLAGQEYAAK.I
☑	198	525.2860	1048.5574	1048.5553	2.06	0	(53)	0.0004	1	K.VLAGQEYAAK.I
☑	199	525.2860	1048.5574	1048.5553	2.06	0	55	0.00028	1	K.VLAGQEYAAK.I
☑	200	525.2863	1048.5580	1048.5553	2.64	0	(41)	0.0067	1	K.VLAGQEYAAK.I
☑	201	525.2864	1048.5582	1048.5553	2.83	0	(48)	0.0013	1	K.VLAGQEYAAK.I
☑	202	525.2868	1048.5590	1048.5553	3.59	0	(51)	0.00065	1	K.VLAGQEYAAK.I
	205	530.2988	1058.5830	1058.5906	-7.15	1	(10)	9.3	2	K.MLTINPSKR.I
☑	206	530.2996	1058.5846	1058.5906	-5.64	1	(11)	6.5	1	K.MLTINPSKR.I
☑	207	530.3001	1058.5856	1058.5906	-4.70	1	41	0.0064	1	K.MLTINPSKR.I
☑	208	530.3005	1058.5864	1058.5906	-3.94	1	(40)	0.0086	1	K.MLTINPSKR.I
☑	209	530.3017	1058.5888	1058.5906	-1.68	1	(31)	0.054	1	K.MLTINPSKR.I
☑	210	530.3018	1058.5890	1058.5906	-1.49	1	(14)	3.1	1	K.MLTINPSKR.I
☑	211	530.3021	1058.5896	1058.5906	-0.92	1	(34)	0.028	1	K.MLTINPSKR.I
☑	212	530.3030	1058.5914	1058.5906	0.78	1	(36)	0.017	1	K.MLTINPSKR.I
☑	213	530.3034	1058.5922	1058.5906	1.54	1	(29)	0.09	1	K.MLTINPSKR.I
☑	214	530.3041	1058.5936	1058.5906	2.86	1	(34)	0.031	1	K.MLTINPSKR.I
☑	215	530.3043	1058.5940	1058.5906	3.24	1	(36)	0.017	1	K.MLTINPSKR.I
☑	216	530.3059	1058.5972	1058.5906	6.26	1	(6)	19	1	K.MLTINPSKR.I
	217	530.3068	1058.5990	1058.5906	7.96	1	(5)	23	2	K.MLTINPSKR.I
	220	530.3162	1058.6178	1058.5906	25.7	1	(7)	9.3	2	K.MLTINPSKR.I
☑	280	574.3269	1146.6392	1146.6431	-3.33	0	(48)	0.00085	1	K.GAILTTMLATR.N
☑	281	574.3270	1146.6394	1146.6431	-3.16	0	54	0.00024	1	K.GAILTTMLATR.N
☑	282	574.3282	1146.6418	1146.6431	-1.06	0	(46)	0.0015	1	K.GAILTTMLATR.N
☑	334	631.3043	1260.5940	1260.5927	1.04	0	(33)	0.032	1	R.FYFENLWSR.N
☑	335	631.3046	1260.5946	1260.5927	1.51	0	(54)	0.00029	1	R.FYFENLWSR.N
☑	336	631.3046	1260.5946	1260.5927	1.51	0	(54)	0.00029	1	R.FYFENLWSR.N
☑	337	631.3046	1260.5946	1260.5927	1.51	0	(38)	0.0095	1	R.FYFENLWSR.N
☑	338	631.3051	1260.5956	1260.5927	2.30	0	58	0.00011	1	R.FYFENLWSR.N
☑	339	631.3056	1260.5966	1260.5927	3.10	0	(54)	0.00026	1	R.FYFENLWSR.N
☑	340	631.3057	1260.5968	1260.5927	3.26	0	(54)	0.00029	1	R.FYFENLWSR.N
☑	341	631.3057	1260.5968	1260.5927	3.26	0	(38)	0.012	1	R.FYFENLWSR.N
☑	342	631.3059	1260.5972	1260.5927	3.57	0	(34)	0.025	1	R.FYFENLWSR.N
☑	343	631.3104	1260.6062	1260.5927	10.7	0	(53)	0.00038	1	R.FYFENLWSR.N
☑	344	631.3109	1260.6072	1260.5927	11.5	0	(54)	0.00033	1	R.FYFENLWSR.N
☑	357	652.3538	1302.6930	1302.6932	-0.11	0	(72)	4.3e-006	1	R.ITQYLDAGGIPR.T
☑	358	652.3549	1302.6952	1302.6932	1.58	0	81	5.8e-007	1	R.ITQYLDAGGIPR.T
☑	359	652.3557	1302.6968	1302.6932	2.81	0	(79)	9.7e-007	1	R.ITQYLDAGGIPR.T
☑	360	652.3559	1302.6972	1302.6932	3.11	0	(59)	9.2e-005	1	R.ITQYLDAGGIPR.T
☑	361	652.3559	1302.6972	1302.6932	3.11	0	(55)	0.00023	1	R.ITQYLDAGGIPR.T
☑	362	652.3560	1302.6974	1302.6932	3.27	0	(66)	1.6e-005	1	R.ITQYLDAGGIPR.T
☑	370	670.8879	1339.7612	1339.7711	-7.33	0	(37)	0.0084	1	R.DLKPENLLLASK.L
☑	371	670.8884	1339.7622	1339.7711	-6.59	0	(26)	0.11	1	R.DLKPENLLLASK.L
☑	372	670.8900	1339.7654	1339.7711	-4.20	0	(26)	0.1	1	R.DLKPENLLLASK.L
☑	373	670.8904	1339.7662	1339.7711	-3.60	0	(41)	0.0029	1	R.DLKPENLLLASK.L
☑	374	670.8911	1339.7676	1339.7711	-2.56	0	67	7.6e-006	1	R.DLKPENLLLASK.L
☑	375	670.8915	1339.7684	1339.7711	-1.96	0	(39)	0.0044	1	R.DLKPENLLLASK.L
☑	376	670.8923	1339.7700	1339.7711	-0.76	0	(27)	0.069	1	R.DLKPENLLLASK.L
☑	377	670.8923	1339.7700	1339.7711	-0.76	0	(34)	0.015	1	R.DLKPENLLLASK.L
☑	378	670.8926	1339.7706	1339.7711	-0.32	0	(45)	0.0012	1	R.DLKPENLLLASK.L
☑	379	670.8926	1339.7706	1339.7711	-0.32	0	(39)	0.0046	1	R.DLKPENLLLASK.L
☑	380	670.8930	1339.7714	1339.7711	0.28	0	(36)	0.01	1	R.DLKPENLLLASK.L
☑	381	670.8934	1339.7722	1339.7711	0.88	0	(35)	0.011	1	R.DLKPENLLLASK.L
☑	382	670.8936	1339.7726	1339.7711	1.18	0	(32)	0.026	1	R.DLKPENLLLASK.L
☑	383	670.8938	1339.7730	1339.7711	1.47	0	(28)	0.054	1	R.DLKPENLLLASK.L
☑	384	670.8939	1339.7732	1339.7711	1.62	0	(47)	0.00072	1	R.DLKPENLLLASK.L
	385	670.8940	1339.7734	1339.7711	1.77	0	(1)	30	9	R.DLKPENLLLASK.L
☑	386	670.8944	1339.7742	1339.7711	2.37	0	(32)	0.02	1	R.DLKPENLLLASK.L
☑	387	670.8953	1339.7760	1339.7711	3.71	0	(47)	0.00064	1	R.DLKPENLLLASK.L
☑	388	670.8953	1339.7760	1339.7711	3.71	0	(47)	0.00077	1	R.DLKPENLLLASK.L
☑	389	670.8954	1339.7762	1339.7711	3.86	0	(21)	0.31	1	R.DLKPENLLLASK.L
☑	390	670.8956	1339.7766	1339.7711	4.16	0	(38)	0.006	1	R.DLKPENLLLASK.L
☑	500	816.8917	1631.7688	1631.7719	-1.86	0	(17)	1.2	1	R.FTEEYQLFEELGK.G
☑	501	816.8925	1631.7704	1631.7719	-0.88	0	(49)	0.00075	1	R.FTEEYQLFEELGK.G
☑	503	816.8930	1631.7714	1631.7719	-0.27	0	(52)	0.00039	1	R.FTEEYQLFEELGK.G
☑	504	816.8939	1631.7732	1631.7719	0.84	0	(63)	2.9e-005	1	R.FTEEYQLFEELGK.G
☑	505	816.8942	1631.7738	1631.7719	1.21	0	(36)	0.015	1	R.FTEEYQLFEELGK.G
☑	506	816.8947	1631.7748	1631.7719	1.82	0	(18)	1	1	R.FTEEYQLFEELGK.G
☑	507	816.8947	1631.7748	1631.7719	1.82	0	(60)	6.1e-005	1	R.FTEEYQLFEELGK.G
☑	508	816.8950	1631.7754	1631.7719	2.19	0	(42)	0.0042	1	R.FTEEYQLFEELGK.G
☑	509	816.8950	1631.7754	1631.7719	2.19	0	(59)	8.7e-005	1	R.FTEEYQLFEELGK.G
☑	510	816.8951	1631.7756	1631.7719	2.31	0	(61)	4.6e-005	1	R.FTEEYQLFEELGK.G
☑	511	816.8951	1631.7756	1631.7719	2.31	0	(30)	0.065	1	R.FTEEYQLFEELGK.G
☑	512	816.8953	1631.7760	1631.7719	2.55	0	67	1.2e-005	1	R.FTEEYQLFEELGK.G
☑	513	816.8953	1631.7760	1631.7719	2.55	0	(53)	0.0003	1	R.FTEEYQLFEELGK.G
☑	515	816.8961	1631.7776	1631.7719	3.53	0	(44)	0.0026	1	R.FTEEYQLFEELGK.G
☑	516	816.8964	1631.7782	1631.7719	3.90	0	(30)	0.062	1	R.FTEEYQLFEELGK.G
☑	517	816.8969	1631.7792	1631.7719	4.51	0	(42)	0.0043	1	R.FTEEYQLFEELGK.G
☑	518	816.8969	1631.7792	1631.7719	4.51	0	(48)	0.0011	1	R.FTEEYQLFEELGK.G

☑	520	816.8972	1631.7798	1631.7719	4.88	0	(56)	0.00017	1	R.FTEEYQLFEELGK.G
	521	816.8972	1631.7798	1631.7719	4.88	0	(0)	58	9	R.FTEEYQLFEELGK.G
☑	523	816.8978	1631.7810	1631.7719	5.62	0	(52)	0.00042	1	R.FTEEYQLFEELGK.G
☑	524	816.8982	1631.7818	1631.7719	6.11	0	(52)	0.00039	1	R.FTEEYQLFEELGK.G
☑	526	816.9008	1631.7870	1631.7719	9.29	0	(29)	0.082	1	R.FTEEYQLFEELGK.G
☑	528	816.9053	1631.7960	1631.7719	14.8	0	(35)	0.022	1	R.FTEEYQLFEELGK.G
☑	578	694.3150	2079.9232	2079.9426	-9.32	0	75	1e-006	1	K.AGAYDFPSPEWDTVTPEAK.D
☑	579	694.3163	2079.9271	2079.9426	-7.44	0	(64)	1.4e-005	1	K.AGAYDFPSPEWDTVTPEAK.D
☑	580	1040.9812	2079.9478	2079.9426	2.55	0	(28)	0.064	1	K.AGAYDFPSPEWDTVTPEAK.D
☑	581	1040.9817	2079.9488	2079.9426	3.03	0	(51)	0.00036	1	K.AGAYDFPSPEWDTVTPEAK.D
☑	582	1040.9819	2079.9492	2079.9426	3.22	0	(60)	4.1e-005	1	K.AGAYDFPSPEWDTVTPEAK.D
☑	583	1040.9828	2079.9510	2079.9426	4.09	0	(58)	6.4e-005	1	K.AGAYDFPSPEWDTVTPEAK.D
☑	584	1040.9840	2079.9534	2079.9426	5.24	0	(36)	0.01	1	K.AGAYDFPSPEWDTVTPEAK.D
☑	590	715.3455	2143.0147	2143.0321	-8.12	0	60	5.1e-005	1	K.VTEQLIEAISNGDFESYTK.M
☑	657	888.7528	2663.2366	2663.2755	-14.62	1	(19)	0.51	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
	658	888.7558	2663.2456	2663.2755	-11.24	1	(7)	7.8	2	K.AGAYDFPSPEWDTVTPEAKDLINK.M
☑	659	888.7559	2663.2459	2663.2755	-11.12	1	(26)	0.11	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
☑	660	888.7564	2663.2474	2663.2755	-10.56	1	(47)	0.00075	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
☑	661	888.7583	2663.2531	2663.2755	-8.42	1	(17)	0.87	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
☑	662	888.7584	2663.2534	2663.2755	-8.31	1	(63)	1.9e-005	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
☑	663	888.7586	2663.2540	2663.2755	-8.08	1	(54)	0.00018	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
☑	664	888.7588	2663.2546	2663.2755	-7.86	1	(63)	2e-005	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
☑	665	888.7589	2663.2549	2663.2755	-7.74	1	(64)	1.8e-005	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
☑	666	888.7592	2663.2558	2663.2755	-7.41	1	(26)	0.12	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
☑	667	888.7593	2663.2561	2663.2755	-7.29	1	(17)	0.85	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
☑	668	888.7594	2663.2564	2663.2755	-7.18	1	(45)	0.0012	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
☑	669	888.7597	2663.2573	2663.2755	-6.84	1	80	4e-007	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
☑	670	888.7598	2663.2576	2663.2755	-6.73	1	(75)	1.2e-006	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
☑	671	888.7599	2663.2579	2663.2755	-6.62	1	(21)	0.33	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
☑	672	888.7599	2663.2579	2663.2755	-6.62	1	(4)	15	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
☑	674	888.7605	2663.2597	2663.2755	-5.94	1	(28)	0.072	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
☑	675	888.7608	2663.2606	2663.2755	-5.60	1	(67)	8e-006	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
☑	676	888.7608	2663.2606	2663.2755	-5.60	1	(27)	0.086	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M

Proteins matching the same set of peptides:
IPI00621806 **Mass:** 54651 **Score:** 1434 **Queries matched:** 119
Tax_Id=10090 Gene_Symbol=Camk2a Isoform Alpha CaMKII of Calcium/calmodulin-dependent protein kinase type II subunit alpha

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2. IPI00474502 **Mass:** 61164 **Score:** 978 **Queries matched:** 66 **emPAI:** 0.78
Tax_Id=10090 Gene_Symbol=Camk2b Calcium/calmodulin-dependent protein kinase type II subunit 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
☑	120	452.7383	903.4620	903.4661	-4.53	0	(11)	7.7	1	K.NSSAITSPK.G
	121	452.7405	903.4664	903.4661	0.34	0	(4)	43	3	K.NSSAITSPK.G
☑	122	452.7416	903.4686	903.4661	2.77	0	31	0.089	1	K.NSSAITSPK.G
☑	123	452.7432	903.4718	903.4661	6.32	0	(28)	0.16	1	K.NSSAITSPK.G
	126	463.2444	924.4742	924.4777	-3.74	1	11	5.1	1	R.DHQKLER.E
☑	132	469.2222	936.4298	936.4148	16.0	0	26	0.16	1	R.TSQSEETR.V
☑	274	572.8061	1143.5976	1143.5964	1.07	0	(22)	0.51	1	R.FYFENLLAK.N
☑	275	572.8066	1143.5986	1143.5964	1.95	0	(12)	5.4	1	R.FYFENLLAK.N
☑	276	572.8070	1143.5994	1143.5964	2.65	0	23	0.44	1	R.FYFENLLAK.N
☑	277	572.8071	1143.5996	1143.5964	2.82	0	(11)	7.5	1	R.FYFENLLAK.N
☑	278	572.8080	1143.6014	1143.5964	4.40	0	(16)	2.1	1	R.FYFENLLAK.N
	280	574.3269	1146.6392	1146.6431	-3.33	0	(48)	0.00085	1	K.GAILTTMLATR.N
	281	574.3270	1146.6394	1146.6431	-3.16	0	54	0.00024	1	K.GAILTTMLATR.N
	282	574.3282	1146.6418	1146.6431	-1.06	0	(46)	0.0015	1	K.GAILTTMLATR.N
	370	670.8879	1339.7612	1339.7711	-7.33	0	(37)	0.0084	1	R.DLKPENLLLASK.C
	371	670.8884	1339.7622	1339.7711	-6.59	0	(26)	0.11	1	R.DLKPENLLLASK.C
	372	670.8900	1339.7654	1339.7711	-4.20	0	(26)	0.1	1	R.DLKPENLLLASK.C
	373	670.8904	1339.7662	1339.7711	-3.60	0	(41)	0.0029	1	R.DLKPENLLLASK.C
	374	670.8911	1339.7676	1339.7711	-2.56	0	67	7.6e-006	1	R.DLKPENLLLASK.C
	375	670.8915	1339.7684	1339.7711	-1.96	0	(39)	0.0044	1	R.DLKPENLLLASK.C
	376	670.8923	1339.7700	1339.7711	-0.76	0	(27)	0.069	1	R.DLKPENLLLASK.C
	377	670.8923	1339.7700	1339.7711	-0.76	0	(34)	0.015	1	R.DLKPENLLLASK.C
	378	670.8926	1339.7706	1339.7711	-0.32	0	(45)	0.0012	1	R.DLKPENLLLASK.C
	379	670.8926	1339.7706	1339.7711	-0.32	0	(39)	0.0046	1	R.DLKPENLLLASK.C
	380	670.8930	1339.7714	1339.7711	0.28	0	(36)	0.01	1	R.DLKPENLLLASK.C
	381	670.8934	1339.7722	1339.7711	0.88	0	(35)	0.011	1	R.DLKPENLLLASK.C
	382	670.8936	1339.7726	1339.7711	1.18	0	(32)	0.026	1	R.DLKPENLLLASK.C
	383	670.8938	1339.7730	1339.7711	1.47	0	(28)	0.054	1	R.DLKPENLLLASK.C
	384	670.8939	1339.7732	1339.7711	1.62	0	(47)	0.00072	1	R.DLKPENLLLASK.C
	385	670.8940	1339.7734	1339.7711	1.77	0	(1)	30	9	R.DLKPENLLLASK.C
	386	670.8944	1339.7742	1339.7711	2.37	0	(32)	0.02	1	R.DLKPENLLLASK.C
	387	670.8953	1339.7760	1339.7711	3.71	0	(47)	0.00064	1	R.DLKPENLLLASK.C
	388	670.8953	1339.7760	1339.7711	3.71	0	(47)	0.00077	1	R.DLKPENLLLASK.C
	389	670.8954	1339.7762	1339.7711	3.86	0	(21)	0.31	1	R.DLKPENLLLASK.C
	390	670.8956	1339.7766	1339.7711	4.16	0	(38)	0.006	1	R.DLKPENLLLASK.C
☑	414	702.3716	1402.7286	1402.7317	-2.18	0	(2)	41	1	R.LTQYIDGQGRPR.T
	415	702.3759	1402.7372	1402.7317	3.95	0	5	23	2	R.LTQYIDGQGRPR.T
☑	429	735.4117	1468.8088	1468.8071	1.16	0	(58)	6.9e-005	1	K.NLINQMLTINPAK.R
☑	430	735.4119	1468.8092	1468.8071	1.43	0	(63)	2.2e-005	1	K.NLINQMLTINPAK.R
☑	431	735.4133	1468.8120	1468.8071	3.34	0	(74)	2e-006	1	K.NLINQMLTINPAK.R
☑	432	735.4143	1468.8140	1468.8071	4.70	0	76	1.2e-006	1	K.NLINQMLTINPAK.R

☑	539	871.3708	1740.7270	1740.7173	5.57	0	(7)	3.6	1	K.ESSDSTNTTIEDEDAK.A
☑	540	871.3715	1740.7284	1740.7173	6.38	0	17	0.37	1	K.ESSDSTNTTIEDEDAK.A
☑	572	656.9528	1967.8366	1967.8556	-9.65	1	94	8.3e-009	1	K.ESSDSTNTTIEDEDAKAR.K
	578	694.3150	2079.9232	2079.9426	-9.32	0	75	1e-006	1	K.AGAYDFPSPEWDTVTPEAK.N
	579	694.3163	2079.9271	2079.9426	-7.44	0	(64)	1.4e-005	1	K.AGAYDFPSPEWDTVTPEAK.N
	580	1040.9812	2079.9478	2079.9426	2.55	0	(28)	0.064	1	K.AGAYDFPSPEWDTVTPEAK.N
	581	1040.9817	2079.9488	2079.9426	3.03	0	(51)	0.00036	1	K.AGAYDFPSPEWDTVTPEAK.N
	582	1040.9819	2079.9492	2079.9426	3.22	0	(60)	4.1e-005	1	K.AGAYDFPSPEWDTVTPEAK.N
	583	1040.9828	2079.9510	2079.9426	4.09	0	(58)	6.4e-005	1	K.AGAYDFPSPEWDTVTPEAK.N
	584	1040.9840	2079.9534	2079.9426	5.24	0	(36)	0.01	1	K.AGAYDFPSPEWDTVTPEAK.N
☑	588	705.0029	2111.9869	2112.0011	-6.74	0	71	3.9e-006	1	K.TTEQLIEAVNNGDFEAYAK.I
☑	634	779.7132	2336.1178	2336.1325	-6.29	1	17	0.81	1	R.FTDEYQLYEDIGKGAFSVVR.R
☑	635	779.7135	2336.1187	2336.1325	-5.91	1	(9)	6	1	R.FTDEYQLYEDIGKGAFSVVR.R
☑	637	779.7166	2336.1280	2336.1325	-1.93	1	(15)	1.4	1	R.FTDEYQLYEDIGKGAFSVVR.R
☑	643	785.0448	2352.1126	2352.1301	-7.46	0	(89)	4.8e-008	1	R.QTTAPATMSTAASGTTMGLVEQAK.S
☑	644	785.0455	2352.1147	2352.1301	-6.56	0	(88)	6.7e-008	1	R.QTTAPATMSTAASGTTMGLVEQAK.S
☑	645	1177.0762	2352.1378	2352.1301	3.29	0	(96)	1e-008	1	R.QTTAPATMSTAASGTTMGLVEQAK.S
☑	646	1177.0767	2352.1388	2352.1301	3.71	0	98	7.3e-009	1	R.QTTAPATMSTAASGTTMGLVEQAK.S
☑	647	785.4142	2353.2208	2353.2642	-18.44	0	(35)	0.013	1	K.GSLPPAALEPQTTVIHNPVDGIK.E
☑	648	785.4187	2353.2343	2353.2642	-12.70	0	64	1.6e-005	1	K.GSLPPAALEPQTTVIHNPVDGIK.E
☑	649	785.4208	2353.2406	2353.2642	-10.02	0	(62)	2.2e-005	1	K.GSLPPAALEPQTTVIHNPVDGIK.E
☑	650	785.4230	2353.2472	2353.2642	-7.22	0	(44)	0.0014	1	K.GSLPPAALEPQTTVIHNPVDGIK.E
☑	651	785.4244	2353.2514	2353.2642	-5.43	0	(40)	0.0036	1	K.GSLPPAALEPQTTVIHNPVDGIK.E
☑	652	790.3753	2368.1041	2368.1250	-8.85	0	(85)	1.2e-007	1	R.QTTAPATMSTAASGTTMGLVEQAK.S + Oxidation (M)
☑	653	790.3780	2368.1122	2368.1250	-5.43	0	(79)	4.5e-007	1	R.QTTAPATMSTAASGTTMGLVEQAK.S + Oxidation (M)

Proteins matching the same set of peptides:
IPI00875723 **Mass:** 68686 **Score:** 978 **Queries matched:** 66
Tax_Id=10090 Gene_Symbol=Camk2b 68 kDa protein

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3. IPI00112584 **Mass:** 56961 **Score:** 636 **Queries matched:** 57 **emPAI:** 0.48
Tax_Id=10090 Gene_Symbol=Camk2d Isoform 1 of Calcium/calmodulin-dependent protein kinase type II subunit 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
	33	602.3627	601.3554	601.3435	19.8	0	20	1.6	1	K.DLINK.M
	126	463.2444	924.4742	924.4777	-3.74	1	11	5.1	1	R.DHQKLER.E
☑	241	539.2839	1076.5532	1076.5502	2.83	0	10	8.9	1	K.IPTGQEYAAK.I
	280	574.3269	1146.6392	1146.6431	-3.33	0	(48)	0.00085	1	K.GAILTTMLATR.N
	281	574.3270	1146.6394	1146.6431	-3.16	0	54	0.00024	1	K.GAILTTMLATR.N
	282	574.3282	1146.6418	1146.6431	-1.06	0	(46)	0.0015	1	K.GAILTTMLATR.N
☑	366	664.3086	1326.6026	1326.5948	5.91	0	59	6.2e-005	1	R.LTQYMDGSGMPK.T
☑	367	664.3100	1326.6054	1326.5948	8.02	0	(46)	0.0015	1	R.LTQYMDGSGMPK.T
	370	670.8879	1339.7612	1339.7711	-7.33	0	(37)	0.0084	1	R.DLKPENLLLASK.S
	371	670.8884	1339.7622	1339.7711	-6.59	0	(26)	0.11	1	R.DLKPENLLLASK.S
	372	670.8900	1339.7654	1339.7711	-4.20	0	(26)	0.1	1	R.DLKPENLLLASK.S
	373	670.8904	1339.7662	1339.7711	-3.60	0	(41)	0.0029	1	R.DLKPENLLLASK.S
	374	670.8911	1339.7676	1339.7711	-2.56	0	67	7.6e-006	1	R.DLKPENLLLASK.S
	375	670.8915	1339.7684	1339.7711	-1.96	0	(39)	0.0044	1	R.DLKPENLLLASK.S
	376	670.8923	1339.7700	1339.7711	-0.76	0	(27)	0.069	1	R.DLKPENLLLASK.S
	377	670.8923	1339.7700	1339.7711	-0.76	0	(34)	0.015	1	R.DLKPENLLLASK.S
	378	670.8926	1339.7706	1339.7711	-0.32	0	(45)	0.0012	1	R.DLKPENLLLASK.S
	379	670.8926	1339.7706	1339.7711	-0.32	0	(39)	0.0046	1	R.DLKPENLLLASK.S
	380	670.8930	1339.7714	1339.7711	0.28	0	(36)	0.01	1	R.DLKPENLLLASK.S
	381	670.8934	1339.7722	1339.7711	0.88	0	(35)	0.011	1	R.DLKPENLLLASK.S
	382	670.8936	1339.7726	1339.7711	1.18	0	(32)	0.026	1	R.DLKPENLLLASK.S
	383	670.8938	1339.7730	1339.7711	1.47	0	(28)	0.054	1	R.DLKPENLLLASK.S
	384	670.8939	1339.7732	1339.7711	1.62	0	(47)	0.00072	1	R.DLKPENLLLASK.S
	385	670.8940	1339.7734	1339.7711	1.77	0	(1)	30	9	R.DLKPENLLLASK.S
	386	670.8944	1339.7742	1339.7711	2.37	0	(32)	0.02	1	R.DLKPENLLLASK.S
	387	670.8953	1339.7760	1339.7711	3.71	0	(47)	0.00064	1	R.DLKPENLLLASK.S
	388	670.8953	1339.7760	1339.7711	3.71	0	(47)	0.00077	1	R.DLKPENLLLASK.S
	389	670.8954	1339.7762	1339.7711	3.86	0	(21)	0.31	1	R.DLKPENLLLASK.S
	390	670.8956	1339.7766	1339.7711	4.16	0	(38)	0.006	1	R.DLKPENLLLASK.S
☑	492	809.8878	1617.7610	1617.7562	2.97	0	64	2e-005	1	R.FTDEYQLFEELGK.G
☑	493	809.8892	1617.7638	1617.7562	4.70	0	(49)	0.00078	1	R.FTDEYQLFEELGK.G
	578	694.3150	2079.9232	2079.9426	-9.32	0	75	1e-006	1	K.AGAYDFPSPEWDTVTPEAK.D
	579	694.3163	2079.9271	2079.9426	-7.44	0	(64)	1.4e-005	1	K.AGAYDFPSPEWDTVTPEAK.D
	580	1040.9812	2079.9478	2079.9426	2.55	0	(28)	0.064	1	K.AGAYDFPSPEWDTVTPEAK.D
	581	1040.9817	2079.9488	2079.9426	3.03	0	(51)	0.00036	1	K.AGAYDFPSPEWDTVTPEAK.D
	582	1040.9819	2079.9492	2079.9426	3.22	0	(60)	4.1e-005	1	K.AGAYDFPSPEWDTVTPEAK.D
	583	1040.9828	2079.9510	2079.9426	4.09	0	(58)	6.4e-005	1	K.AGAYDFPSPEWDTVTPEAK.D
	584	1040.9840	2079.9534	2079.9426	5.24	0	(36)	0.01	1	K.AGAYDFPSPEWDTVTPEAK.D
	657	888.7528	2663.2366	2663.2755	-14.62	1	(19)	0.51	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
	658	888.7558	2663.2456	2663.2755	-11.24	1	(7)	7.8	2	K.AGAYDFPSPEWDTVTPEAKDLINK.M
	659	888.7559	2663.2459	2663.2755	-11.12	1	(26)	0.11	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
	660	888.7564	2663.2474	2663.2755	-10.56	1	(47)	0.00075	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
	661	888.7583	2663.2531	2663.2755	-8.42	1	(17)	0.87	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
	662	888.7584	2663.2534	2663.2755	-8.31	1	(63)	1.9e-005	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
	663	888.7586	2663.2540	2663.2755	-8.08	1	(54)	0.00018	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
	664	888.7588	2663.2546	2663.2755	-7.86	1	(63)	2e-005	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
	665	888.7589	2663.2549	2663.2755	-7.74	1	(64)	1.8e-005	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
	666	888.7592	2663.2558	2663.2755	-7.41	1	(26)	0.12	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
	667	888.7593	2663.2561	2663.2755	-7.29	1	(17)	0.85	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
	668	888.7594	2663.2564	2663.2755	-7.18	1	(45)	0.0012	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
	669	888.7597	2663.2573	2663.2755	-6.84	1	80	4e-007	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
	670	888.7598	2663.2576	2663.2755	-6.73	1	(75)	1.2e-006	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M

	671	888.7599	2663.2579	2663.2755	-6.62	1	(21)	0.33	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
	672	888.7599	2663.2579	2663.2755	-6.62	1	(4)	15	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
	674	888.7605	2663.2597	2663.2755	-5.94	1	(28)	0.072	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
	675	888.7608	2663.2606	2663.2755	-5.60	1	(67)	8e-006	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
	676	888.7608	2663.2606	2663.2755	-5.60	1	(27)	0.086	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M

Proteins matching the same set of peptides:
IPI00406790 **Mass:** 60593 **Score:** 636 **Queries matched:** 57
Tax_Id=10090 Gene_Symbol=Camk2d Isoform 4 of Calcium/calmodulin-dependent protein kinase type II subunit delta
IPI00475044 **Mass:** 55899 **Score:** 636 **Queries matched:** 57
Tax_Id=10090 Gene_Symbol=Camk2d Isoform 2 of Calcium/calmodulin-dependent protein kinase type II subunit delta
IPI00828919 **Mass:** 58492 **Score:** 636 **Queries matched:** 57
Tax_Id=10090 Gene_Symbol=Camk2d Isoform 3 of Calcium/calmodulin-dependent protein kinase type II subunit delta
IPI00857865 **Mass:** 54664 **Score:** 636 **Queries matched:** 57
Tax_Id=10090 Gene_Symbol=Camk2d Putative uncharacterized protein
IPI00858128 **Mass:** 58283 **Score:** 636 **Queries matched:** 57
Tax_Id=10090 Gene_Symbol=Camk2d calcium/calmodulin-dependent protein kinase type II subunit delta isoform 1
IPI00858144 **Mass:** 55828 **Score:** 636 **Queries matched:** 57
Tax_Id=10090 Gene_Symbol=Camk2d 55 kDa protein

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4. IPI00124695 **Mass:** 60254 **Score:** 516 **Queries matched:** 39 **emPAI:** 0.30
Tax_Id=10090 Gene_Symbol=Camk2g Isoform 1 of Calcium/calmodulin-dependent protein kinase type II 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
	126	463.2444	924.4742	924.4777	-3.74	1	11	5.1	1	R.DHQKLER.E
	132	469.2222	936.4298	936.4148	16.0	0	26	0.16	1	R.TSQSEETR.V
☑	165	**499.7433**	**997.4720**	**997.4716**	**0.43**	**0**	**23**	**0.27**	**1**	**K.TSTQEYAAK.I**
	370	670.8879	1339.7612	1339.7711	-7.33	0	(37)	0.0084	1	R.DLKPENLLLASK.C
	371	670.8884	1339.7622	1339.7711	-6.59	0	(26)	0.11	1	R.DLKPENLLLASK.C
	372	670.8900	1339.7654	1339.7711	-4.20	0	(26)	0.1	1	R.DLKPENLLLASK.C
	373	670.8904	1339.7662	1339.7711	-3.60	0	(41)	0.0029	1	R.DLKPENLLLASK.C
	374	670.8911	1339.7676	1339.7711	-2.56	0	67	7.6e-006	1	R.DLKPENLLLASK.C
	375	670.8915	1339.7684	1339.7711	-1.96	0	(39)	0.0044	1	R.DLKPENLLLASK.C
	376	670.8923	1339.7700	1339.7711	-0.76	0	(27)	0.069	1	R.DLKPENLLLASK.C
	377	670.8923	1339.7700	1339.7711	-0.76	0	(34)	0.015	1	R.DLKPENLLLASK.C
	378	670.8926	1339.7706	1339.7711	-0.32	0	(45)	0.0012	1	R.DLKPENLLLASK.C
	379	670.8926	1339.7706	1339.7711	-0.32	0	(39)	0.0046	1	R.DLKPENLLLASK.C
	380	670.8930	1339.7714	1339.7711	0.28	0	(36)	0.01	1	R.DLKPENLLLASK.C
	381	670.8934	1339.7722	1339.7711	0.88	0	(35)	0.011	1	R.DLKPENLLLASK.C
	382	670.8936	1339.7726	1339.7711	1.18	0	(32)	0.026	1	R.DLKPENLLLASK.C
	383	670.8938	1339.7730	1339.7711	1.47	0	(28)	0.054	1	R.DLKPENLLLASK.C
	384	670.8939	1339.7732	1339.7711	1.62	0	(47)	0.00072	1	R.DLKPENLLLASK.C
	385	670.8940	1339.7734	1339.7711	1.77	0	(1)	30	9	R.DLKPENLLLASK.C
	386	670.8944	1339.7742	1339.7711	2.37	0	(32)	0.02	1	R.DLKPENLLLASK.C
	387	670.8953	1339.7760	1339.7711	3.71	0	(47)	0.00064	1	R.DLKPENLLLASK.C
	388	670.8953	1339.7760	1339.7711	3.71	0	(47)	0.00077	1	R.DLKPENLLLASK.C
	389	670.8954	1339.7762	1339.7711	3.86	0	(21)	0.31	1	R.DLKPENLLLASK.C
	390	670.8956	1339.7766	1339.7711	4.16	0	(38)	0.006	1	R.DLKPENLLLASK.C
	414	702.3716	1402.7286	1402.7317	-2.18	0	(2)	41	1	R.LTQYIDGQGRPR.T
	415	702.3759	1402.7372	1402.7317	3.95	0	5	23	2	R.LTQYIDGQGRPR.T
	429	735.4117	1468.8088	1468.8071	1.16	0	(58)	6.9e-005	1	K.NLINQMLTINPAK.R
	430	735.4119	1468.8092	1468.8071	1.43	0	(63)	2.2e-005	1	K.NLINQMLTINPAK.R
	431	735.4133	1468.8120	1468.8071	3.34	0	(74)	2e-006	1	K.NLINQMLTINPAK.R
	432	735.4143	1468.8140	1468.8071	4.70	0	76	1.2e-006	1	K.NLINQMLTINPAK.R
☑	484	**802.8825**	**1603.7504**	**1603.7406**	**6.14**	**0**	**(68)**	**9.3e-006**	**1**	**R.FTDDYQLFEELGK.G**
☑	485	**802.8837**	**1603.7528**	**1603.7406**	**7.64**	**0**	**69**	**7.7e-006**	**1**	**R.FTDDYQLFEELGK.G**
	578	694.3150	2079.9232	2079.9426	-9.32	0	75	1e-006	1	K.AGAYDFPSPEWDTVTPEAK.N
	579	694.3163	2079.9271	2079.9426	-7.44	0	(64)	1.4e-005	1	K.AGAYDFPSPEWDTVTPEAK.N
	580	1040.9812	2079.9478	2079.9426	2.55	0	(28)	0.064	1	K.AGAYDFPSPEWDTVTPEAK.N
	581	1040.9817	2079.9488	2079.9426	3.03	0	(51)	0.00036	1	K.AGAYDFPSPEWDTVTPEAK.N
	582	1040.9819	2079.9492	2079.9426	3.22	0	(60)	4.1e-005	1	K.AGAYDFPSPEWDTVTPEAK.N
	583	1040.9828	2079.9510	2079.9426	4.09	0	(58)	6.4e-005	1	K.AGAYDFPSPEWDTVTPEAK.N
	584	1040.9840	2079.9534	2079.9426	5.24	0	(36)	0.01	1	K.AGAYDFPSPEWDTVTPEAK.N

Proteins matching the same set of peptides:
IPI00228044 **Mass:** 59013 **Score:** 516 **Queries matched:** 39
Tax_Id=10090 Gene_Symbol=Camk2g Isoform 2 of Calcium/calmodulin-dependent protein kinase type II subunit gamma
IPI00228045 **Mass:** 56610 **Score:** 516 **Queries matched:** 39
Tax_Id=10090 Gene_Symbol=Camk2g Isoform 3 of Calcium/calmodulin-dependent protein kinase type II subunit gamma

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5. IPI00109073 **Mass:** 50010 **Score:** 259 **Queries matched:** 11 **emPAI:** 0.29
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
☑	273	**572.3212**	**1142.6278**	**1142.6270**	**0.72**	**0**	**42**	**0.0049**	**1**	**K.LAVNMVPFPR.L**
	317	**615.2972**	**1228.5798**	**1228.5910**	**-9.10**	**0**	**1**	**43**	**2**	**R.ISEQFTAMFR.R**
☑	364	**660.3562**	**1318.6978**	**1318.6955**	**1.77**	**0**	**85**	**2.5e-007**	**1**	**R.IMNTFSVVPSPK.V**
☑	365	**660.3578**	**1318.7010**	**1318.6955**	**4.20**	**0**	**(84)**	**2.7e-007**	**1**	**R.IMNTFSVVPSPK.V**
☑	481	**801.4144**	**1600.8142**	**1600.8131**	**0.74**	**0**	**82**	**3.6e-007**	**1**	**R.AVLVDLEPGTMDSVR.S**
☑	482	**801.4154**	**1600.8162**	**1600.8131**	**1.99**	**0**	**(67)**	**1.2e-005**	**1**	**R.AVLVDLEPGTMDSVR.S**
☑	483	**801.4161**	**1600.8176**	**1600.8131**	**2.86**	**0**	**(60)**	**5.9e-005**	**1**	**R.AVLVDLEPGTMDSVR.S**
☑	532	**846.4391**	**1690.8636**	**1690.8600**	**2.16**	**0**	**(20)**	**0.66**	**1**	**R.ALTVPELTQQMFDAK.N**
☑	533	**846.4404**	**1690.8662**	**1690.8600**	**3.69**	**0**	**40**	**0.0061**	**1**	**R.ALTVPELTQQMFDAK.N**
☑	534	**848.9236**	**1695.8326**	**1695.8257**	**4.12**	**0**	**15**	**2.1**	**1**	**K.NSSYFVEWIPNNVK.T**
	537	**854.4365**	**1706.8584**	**1706.8549**	**2.07**	**0**	**(30)**	**0.064**	**2**	**R.ALTVPELTQQMFDAK.N + Oxidation (M)**

Proteins matching the same set of peptides:
IPI00169463 **Mass:** 50255 **Score:** 259 **Queries matched:** 11
Tax_Id=10090 Gene_Symbol=Tubb2c Tubulin beta-2C chain

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6. IPI00115546 **Mass:** 40524 **Score:** 227 **Queries matched:** 5 **emPAI:** 0.27
Tax_Id=10090 Gene_Symbol=Gnao1 Isoform Alpha-2 of Guanine nucleotide-binding protein G(o) 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
☑	203	529.3122	1056.6098	1056.6179	-7.61	0	(18)	0.98	1	K.LLLLGAGESGK.S
☑	204	529.3124	1056.6102	1056.6179	-7.23	0	44	0.0026	1	K.LLLLGAGESGK.S
☑	531	838.4189	1674.8232	1674.8213	1.16	0	113	3.4e-010	1	R.IGAGDYQPTEQDILR.T
☑	570	979.4428	1956.8710	1956.8631	4.07	0	87	7.1e-008	1	R.MEDTEPFSAELLSAMMR.L
☑	571	979.4498	1956.8850	1956.8631	11.2	0	(83)	1.8e-007	1	R.MEDTEPFSAELLSAMMR.L

Proteins matching the same set of peptides:
IPI00230192 **Mass:** 40629 **Score:** 227 **Queries matched:** 5
Tax_Id=10090 Gene_Symbol=Gnao1 Isoform Alpha-1 of Guanine nucleotide-binding protein G(o) subunit alpha

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7. IPI00323571 **Mass:** 35901 **Score:** 226 **Queries matched:** 18 **emPAI:** 0.86
Tax_Id=10090 Gene_Symbol=Apoe Apolipoprotein E
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	152	484.7774	967.5402	967.5451	-4.99	0	(50)	0.00041	1	R.LGPLVEQGR.Q
☑	153	484.7776	967.5406	967.5451	-4.57	0	52	0.00027	1	R.LGPLVEQGR.Q
☑	155	487.7528	973.4910	973.4828	8.42	1	46	0.0023	1	R.DAEDLQKR.L
☑	184	510.2458	1018.4770	1018.4753	1.69	0	56	0.00017	1	R.LGADMEDLR.N
☑	185	510.2510	1018.4874	1018.4753	11.9	0	(43)	0.0033	1	R.LGADMEDLR.N
☑	187	510.2557	1018.4968	1018.4906	6.16	0	15	2.6	1	R.QWANLMEK.I
☑	238	538.2985	1074.5824	1074.5822	0.26	0	(40)	0.0082	1	R.LQAEIFQAR.L
☑	239	538.2990	1074.5834	1074.5822	1.19	0	52	0.00055	1	R.LQAEIFQAR.L
☑	240	538.3007	1074.5868	1074.5822	4.35	0	(36)	0.021	1	R.LQAEIFQAR.L
☑	287	581.7828	1161.5510	1161.5448	5.38	0	(42)	0.0051	1	K.MEEQTQQIR.L
☑	288	581.7836	1161.5526	1161.5448	6.76	0	(42)	0.0053	1	K.MEEQTQQIR.L
☑	289	581.7837	1161.5528	1161.5448	6.93	0	(24)	0.3	1	K.MEEQTQQIR.L
☑	290	581.7856	1161.5566	1161.5448	10.2	0	49	0.001	1	K.MEEQTQQIR.L
☑	479	800.4014	1598.7882	1598.7787	5.94	0	63	2.9e-005	1	K.ELEEQLGPVAEETR.A
☑	480	800.4103	1598.8060	1598.7787	17.1	0	(54)	0.00027	1	K.ELEEQLGPVAEETR.A
☑	573	997.5337	1993.0528	1993.0480	2.43	0	25	0.14	1	K.IQASVATNPIITPVAQENQ.-
☑	702	1308.9537	3923.8393	3923.8656	-6.72	0	32	0.01	1	R.WVQTLSDQVQEELQSSQVTQELTALMEDTMTEVK.A
☑	705	1308.9666	3923.8780	3923.8656	3.15	0	(10)	1.8	1	R.WVQTLSDQVQEELQSSQVTQELTALMEDTMTEVK.A

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8. IPI00112251 **Mass:** 50842 **Score:** 198 **Queries matched:** 12 **emPAI:** 0.29
Tax_Id=10090 Gene_Symbol=Tubb3 Tubulin beta-3 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
	273	572.3212	1142.6278	1142.6270	0.72	0	42	0.0049	1	K.LAVNMVPFPR.L
	317	615.2972	1228.5798	1228.5910	-9.10	0	1	43	2	R.ISEQFTAMFR.R
	364	660.3562	1318.6978	1318.6955	1.77	0	85	2.5e-007	1	R.IMNTFSVVPSPK.V
	365	660.3578	1318.7010	1318.6955	4.20	0	(84)	2.7e-007	1	R.IMNTFSVVPSPK.V
☑	486	808.4135	1614.8124	1614.8287	-10.07	0	(41)	0.0062	1	R.AILVDLEPGTMDSVR.S
☑	487	808.4182	1614.8218	1614.8287	-4.25	0	(35)	0.026	1	R.AILVDLEPGTMDSVR.S
☑	488	808.4218	1614.8290	1614.8287	0.21	0	71	6.3e-006	1	R.AILVDLEPGTMDSVR.S
☑	497	816.4215	1630.8284	1630.8236	2.96	0	(31)	0.059	1	R.AILVDLEPGTMDSVR.S + Oxidation (M)
	532	846.4391	1690.8636	1690.8600	2.16	0	(20)	0.66	1	R.ALTVPELTQQMFDAK.N
	533	846.4404	1690.8662	1690.8600	3.69	0	40	0.0061	1	R.ALTVPELTQQMFDAK.N
	534	848.9236	1695.8326	1695.8257	4.12	0	15	2.1	1	K.NSSYFVEWIPNNVK.V
	537	854.4365	1706.8584	1706.8549	2.07	0	(30)	0.064	2	R.ALTVPELTQQMFDAK.N + Oxidation (M)

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9. IPI00110850 **Mass:** 42052 **Score:** 175 **Queries matched:** 9 **emPAI:** 0.35
Tax_Id=10090 Gene_Symbol=Actb Actin, cytoplasmic 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
☑	285	581.3162	1160.6178	1160.6111	5.83	0	(27)	0.17	1	K.EITALAPSTMK.I
☑	286	581.3204	1160.6262	1160.6111	13.1	0	36	0.018	1	K.EITALAPSTMK.I
☑	307	599.7695	1197.5244	1197.5150	7.93	0	41	0.0029	1	K.DSYVGDEAQSK.R
☑	550	895.9509	1789.8872	1789.8846	1.46	0	85	2e-007	1	K.SYELPDGQVITIGNER.F
☑	551	895.9536	1789.8926	1789.8846	4.48	0	(73)	3.1e-006	1	K.SYELPDGQVITIGNER.F
☑	566	652.0146	1953.0220	1953.0571	-17.99	0	(34)	0.019	1	R.VAPEEHPVLLTEAPLNPK.A
☑	567	652.0152	1953.0238	1953.0571	-17.06	0	52	0.00028	1	R.VAPEEHPVLLTEAPLNPK.A
☑	568	652.0201	1953.0385	1953.0571	-9.54	0	(32)	0.028	1	R.VAPEEHPVLLTEAPLNPK.A
☑	569	652.0240	1953.0502	1953.0571	-3.55	0	(38)	0.0068	1	R.VAPEEHPVLLTEAPLNPK.A

Proteins matching the same set of peptides:
IPI00136929 **Mass:** 44029 **Score:** 175 **Queries matched:** 9
Tax_Id=10090 Gene_Symbol=Actg1 Gamma actin-like protein
IPI00473320 **Mass:** 42115 **Score:** 175 **Queries matched:** 9

Tax_Id=10090 Gene_Symbol=Actb Putative uncharacterized protein
IPI00652436 **Mass:** 42053 **Score:** 175 **Queries matched:** 9
Tax_Id=10090 Gene_Symbol=Actg1 Putative uncharacterized protein
IPI00874482 **Mass:** 42108 **Score:** 175 **Queries matched:** 9
Tax_Id=10090 Gene_Symbol=Actg1 Actin, cytoplasmic 2

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10. IPI00109061 **Mass:** 50377 **Score:** 175 **Queries matched:** 10 **emPAI:** 0.29
Tax_Id=10090 Gene_Symbol=Tubb2b Tubulin beta-2B 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
	273	572.3212	1142.6278	1142.6270	0.72	0	42	0.0049	1	K.LAVNMVPFPR.L
	317	615.2972	1228.5798	1228.5910	-9.10	0	1	43	2	R.ISEQFTAMFR.R
☑	397	**676.3429**	**1350.6712**	**1350.6676**	**2.72**	**0**	**(67)**	**1.4e-005**	**1**	**R.IMNTFSVMPSPK.V**
☑	398	**676.3460**	**1350.6774**	**1350.6676**	**7.31**	**0**	**79**	**1e-006**	**1**	**R.IMNTFSVMPSPK.V**
	486	808.4135	1614.8124	1614.8287	-10.07	0	(41)	0.0062	1	R.AILVDLEPGTMDSVR.S
	487	808.4182	1614.8218	1614.8287	-4.25	0	(35)	0.026	1	R.AILVDLEPGTMDSVR.S
	488	808.4218	1614.8290	1614.8287	0.21	0	71	6.3e-006	1	R.AILVDLEPGTMDSVR.S
	497	816.4215	1630.8284	1630.8236	2.96	0	(31)	0.059	1	R.AILVDLEPGTMDSVR.S + Oxidation (M)
	534	848.9236	1695.8326	1695.8257	4.12	0	15	2.1	1	K.NSSYFVEWIPNNVK.T
☑	537	854.4365	1706.8584	1706.8549	2.07	0	43	0.0034	1	R.ALTVPELTQQMFDSK.N

Proteins matching the same set of peptides:
IPI00338039 **Mass:** 50274 **Score:** 175 **Queries matched:** 10
Tax_Id=10090 Gene_Symbol=Tubb2a Tubulin beta-2A chain

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11. IPI00122048 **Mass:** 113045 **Score:** 171 **Queries matched:** 5 **emPAI:** 0.09
Tax_Id=10090 Gene_Symbol=Atp1a3 Sodium/potassium-transporting ATPase subunit alpha-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
☑	318	**618.8549**	**1235.6952**	**1235.6986**	**-2.72**	**0**	**59**	**4.9e-005**	**1**	**R.LNIPVSQVNPR.D**
☑	319	**618.8561**	**1235.6976**	**1235.6986**	**-0.78**	**0**	**(36)**	**0.011**	**1**	**R.LNIPVSQVNPR.D**
☑	556	**906.4708**	**1810.9270**	**1810.9425**	**-8.54**	**0**	**(1)**	**51**	**1**	**R.QGAIVAVTGDGVNDSPALK.K**
☑	557	**906.4775**	**1810.9404**	**1810.9425**	**-1.14**	**0**	**70**	**6.2e-006**	**1**	**R.QGAIVAVTGDGVNDSPALK.K**
☑	560	**915.4684**	**1828.9222**	**1828.9167**	**3.06**	**0**	**96**	**1.3e-008**	**1**	**K.GVGIISEGNETVEDIAAR.L**

Proteins matching the same set of peptides:
IPI00420569 **Mass:** 113457 **Score:** 171 **Queries matched:** 5
Tax_Id=10090 Gene_Symbol=Atp1a2 Sodium/potassium-transporting ATPase subunit alpha-2
IPI00752412 **Mass:** 117548 **Score:** 171 **Queries matched:** 5
Tax_Id=10090 Gene_Symbol=Atp1a3 ATPase, Na+/K+ transporting, alpha 3 polypeptide, isoform CRA_c
IPI00762871 **Mass:** 104717 **Score:** 171 **Queries matched:** 5
Tax_Id=10090 Gene_Symbol=Atp1a2 Uncharacterized protein

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12. IPI00138892 **Mass:** 15004 **Score:** 170 **Queries matched:** 3 **emPAI:** 0.23
Tax_Id=10090 Gene_Symbol=Uba52 Ubiquitin-60S ribosomal protein L40
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	547	**894.4697**	**1786.9248**	**1786.9200**	**2.71**	**0**	**81**	**4.8e-007**	**1**	**K.TITLEVEPSDTIENVK.A**
☑	548	**894.4703**	**1786.9260**	**1786.9200**	**3.38**	**0**	**(78)**	**9.9e-007**	**1**	**K.TITLEVEPSDTIENVK.A**
☑	549	**894.4712**	**1786.9278**	**1786.9200**	**4.38**	**0**	**(73)**	**2.8e-006**	**1**	**K.TITLEVEPSDTIENVK.A**

Proteins matching the same set of peptides:
IPI00470152 **Mass:** 18282 **Score:** 170 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=Rps27a Ubiquitin-40S ribosomal protein S27a
IPI00895319 **Mass:** 22277 **Score:** 170 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=2810422J05Rik 22 kDa protein
IPI00895479 **Mass:** 27181 **Score:** 170 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=2810422J05Rik 27 kDa protein
IPI00918763 **Mass:** 11021 **Score:** 170 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=Uba52 Ubiqutin subunit 1
IPI00750889 **Mass:** 22822 **Score:** 170 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=Ubc Ubc protein
IPI00923013 **Mass:** 26603 **Score:** 170 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=Ubb Ubiquitin B
IPI00923037 **Mass:** 22578 **Score:** 170 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=Ubc Putative uncharacterized protein
IPI00139518 **Mass:** 34348 **Score:** 170 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=Ubb Polyubiquitin-B
IPI00755916 **Mass:** 82614 **Score:** 170 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=Ubc ubiquitin
IPI00969323 **Mass:** 82603 **Score:** 170 **Queries matched:** 3
Tax_Id=10090 Gene_Symbol=Ubc Polyubiquitin-C

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13. IPI00120793 **Mass:** 28131 **Score:** 168 **Queries matched:** 14 **emPAI:** 0.40
Tax_Id=10090 Gene_Symbol=Prnp Major prion 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
☑	242	**544.7363**	**1087.4580**	**1087.4570**	**0.94**	**0**	**43**	**0.0012**	**1**	**K.ESQAYYDGR.R**
☑	243	**544.7366**	**1087.4586**	**1087.4570**	**1.49**	**0**	**(37)**	**0.0045**	**1**	**K.ESQAYYDGR.R**
☑	244	**544.7393**	**1087.4640**	**1087.4570**	**6.45**	**0**	**(41)**	**0.0019**	**1**	**K.ESQAYYDGR.R**

☑	245	544.7401	1087.4656	1087.4570	7.92	0	(38)	0.0044	1	K.ESQAYYDGR.R
	246	545.2651	1088.5156	1088.4999	14.4	0	4	22	4	R.YPGQGSPGGNR.Y
☑	268	570.2647	1138.5148	1138.5142	0.54	0	(38)	0.008	1	K.GENFTETDVK.M
☑	269	570.2656	1138.5166	1138.5142	2.12	0	50	0.00044	1	K.GENFTETDVK.M
☑	270	570.2673	1138.5200	1138.5142	5.10	0	(46)	0.0011	1	K.GENFTETDVK.M
☑	271	570.2728	1138.5310	1138.5142	14.8	0	(44)	0.0022	1	K.GENFTETDVK.M
☑	322	622.7874	1243.5602	1243.5581	1.70	1	16	1.1	1	K.ESQAYYDGRR.S
☑	325	622.7895	1243.5644	1243.5581	5.08	1	(11)	3.5	1	K.ESQAYYDGRR.S
☑	327	622.7902	1243.5658	1243.5581	6.20	1	(4)	19	1	K.ESQAYYDGRR.S
	328	622.7919	1243.5692	1243.5581	8.94	1	(2)	34	2	K.ESQAYYDGRR.S
☑	437	756.8663	1511.7180	1511.7112	4.50	0	65	2.1e-005	1	R.VVEQMCVTQYQK.E

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14. IPI00122928 **Mass:** 50514 **Score:** 143 **Queries matched:** 7 **emPAI:** 0.21
Tax_Id=10090 Gene_Symbol=Tubb6 Tubulin beta-6 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
273	572.3212	1142.6278	1142.6270	0.72	0	42	0.0049	1	K.LAVNMVPFPR.L
397	676.3429	1350.6712	1350.6676	2.72	0	(67)	1.4e-005	1	R.IMNTFSVMPSPK.V
398	676.3460	1350.6774	1350.6676	7.31	0	79	1e-006	1	R.IMNTFSVMPSPK.V
532	846.4391	1690.8636	1690.8600	2.16	0	(20)	0.66	1	R.ALTVPELTQQMFDAK.N
533	846.4404	1690.8662	1690.8600	3.69	0	40	0.0061	1	R.ALTVPELTQQMFDAK.N
534	848.9236	1695.8326	1695.8257	4.12	0	15	2.1	1	K.NSSYFVEWIPNNVK.V
537	854.4365	1706.8584	1706.8549	2.07	0	(30)	0.064	2	R.ALTVPELTQQMFDAK.N + Oxidation (M)

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15. IPI00225062 **Mass:** 285676 **Score:** 134 **Queries matched:** 4 **emPAI:** 0.03
Tax_Id=10090 Gene_Symbol=Srrm2 Isoform 3 of Serine/arginine repetitive matrix 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
☑	404	691.3704	1380.7262	1380.7361	-7.15	0	30	0.069	1	R.TAVAPSAVNLADPR.T
☑	405	693.3643	1384.7140	1384.7133	0.57	0	64	3.2e-005	1	R.MAPALSGANLTSPR.V
☑	411	701.3675	1400.7204	1400.7259	-3.92	0	62	5.6e-005	1	R.TSAIPASVNLADSR.T
☑	443	759.4198	1516.8250	1516.8362	-7.34	0	67	1.1e-005	1	R.TPQAPTPANLVVGPR.S

Proteins matching the same set of peptides:
IPI00785240 **Mass:** 295356 **Score:** 134 **Queries matched:** 4
Tax_Id=10090 Gene_Symbol=Srrm2 Isoform 1 of Serine/arginine repetitive matrix protein 2
IPI00785384 **Mass:** 284043 **Score:** 134 **Queries matched:** 4
Tax_Id=10090 Gene_Symbol=Srrm2 Isoform 2 of Serine/arginine repetitive matrix protein 2
IPI00874854 **Mass:** 295521 **Score:** 134 **Queries matched:** 4
Tax_Id=10090 Gene_Symbol=Srrm2 Srrm2 protein

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16. IPI00221528 **Mass:** 42319 **Score:** 133 **Queries matched:** 6 **emPAI:** 0.16
Tax_Id=10090 Gene_Symbol=Actbl2 Beta-actin-like 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
550	895.9509	1789.8872	1789.8846	1.46	0	85	2e-007	1	R.SYELPDGQVITIGNER.F
551	895.9536	1789.8926	1789.8846	4.48	0	(73)	3.1e-006	1	R.SYELPDGQVITIGNER.F
566	652.0146	1953.0220	1953.0571	-17.99	0	(33)	0.023	2	R.VAPDEHPILLTEAPLNPK.I
567	652.0152	1953.0238	1953.0571	-17.06	0	39	0.0057	2	R.VAPDEHPILLTEAPLNPK.I
568	652.0201	1953.0385	1953.0571	-9.54	0	(27)	0.098	2	R.VAPDEHPILLTEAPLNPK.I
569	652.0240	1953.0502	1953.0571	-3.55	0	(36)	0.011	2	R.VAPDEHPILLTEAPLNPK.I

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17. IPI00404590 **Mass:** 19412 **Score:** 102 **Queries matched:** 10 **emPAI:** 0.38
Tax_Id=10090 Gene_Symbol=H1f0 Putative uncharacterized 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
☑	223	530.7672	1059.5198	1059.5196	0.20	0	(7)	20	1	K.VGENADSQIK.L
☑	225	530.7692	1059.5238	1059.5196	3.97	0	(48)	0.0015	1	K.VGENADSQIK.L
☑	226	530.7695	1059.5244	1059.5196	4.54	0	(33)	0.049	1	K.VGENADSQIK.L
☑	227	530.7698	1059.5250	1059.5196	5.11	0	(26)	0.27	1	K.VGENADSQIK.L
☑	228	530.7698	1059.5250	1059.5196	5.11	0	(15)	3.6	1	K.VGENADSQIK.L
☑	229	530.7701	1059.5256	1059.5196	5.67	0	62	6.9e-005	1	K.VGENADSQIK.L
☑	231	530.7714	1059.5282	1059.5196	8.13	0	(22)	0.72	1	K.VGENADSQIK.L
☑	232	530.7786	1059.5426	1059.5196	21.7	0	(19)	1.4	1	K.VGENADSQIK.L
☑	354	651.3392	1300.6638	1300.6623	1.22	0	46	0.002	1	M.TENSTSAPAAKPK.R
☑	418	719.8656	1437.7166	1437.7173	-0.48	0	30	0.079	1	K.YSDMIVAAIQAEK.N

Proteins matching the same set of peptides:
IPI00467914 **Mass:** 20848 **Score:** 102 **Queries matched:** 10
Tax_Id=10090 Gene_Symbol=H1f0 Histone H1.0

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18. IPI00323357 **Mass:** 71055 **Score:** 79 **Queries matched:** 3 **emPAI:** 0.09
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
☑	356	652.3232	1302.6318	1302.5914	31.1	0	48	0.0013	1	K.NSLESYAFNMK.A
☑	490	808.9067	1615.7988	1615.7804	11.4	0	14	2.7	1	K.SFYPEEVSSMVLTK.M

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  ☑  529  825.4030  1648.7914  1648.7879   2.15   0    64  2.6e-005   1   K.NQVAMNPTNTVFDAK.R


     Proteins matching the same set of peptides:
     IPI00886297     Mass: 68964     Score: 79     Queries matched: 3
     Tax_Id=10090 Gene_Symbol=Hspa8 Hspa8 protein
________________________________________________________________________________________________
19.  IPI00469012     Mass: 87791     Score: 76     Queries matched: 3    emPAI: 0.08
     Tax_Id=10090 Gene_Symbol=Tbc1d10b TBC1 domain family member 10B
  ☐  Check to include this hit in error tolerant search or archive report

    Query  Observed    Mr(expt)    Mr(calc)    ppm  Miss Score  Expect Rank  Peptide
  ☑  267  568.8079  1135.6012  1135.5986   2.34   0    50  0.00078    1   R.ASPVPGPGTPTR.T
  ☑  561  925.0280  1848.0414  1848.0356   3.14   0   (38)  0.0037    1   R.QQPPLGPSSSLLSLPSLK.S
  ☑  562  925.0283  1848.0420  1848.0356   3.46   0    47  0.00049    1   R.QQPPLGPSSSLLSLPSLK.S

________________________________________________________________________________________________
20.  IPI00223714     Mass: 21964     Score: 68     Queries matched: 2    emPAI: 0.15
     Tax_Id=10090 Gene_Symbol=Hist1h1e Histone H1.4
  ☐  Check to include this hit in error tolerant search or archive report

    Query  Observed    Mr(expt)    Mr(calc)    ppm  Miss Score   Expect Rank  Peptide
  ☑  314  614.8428  1227.6710  1227.6711  -0.01   0   (46)   0.0018    1   K.TSGPPVSELITK.A
  ☑  315  614.8445  1227.6744  1227.6711   2.75   0    60  6.8e-005    1   K.TSGPPVSELITK.A

________________________________________________________________________________________________
21.  IPI00656325     Mass: 83131     Score: 67     Queries matched: 2    emPAI: 0.08
     Tax_Id=10090 Gene_Symbol=Nsf Vesicle-fusing 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
  ☑  353  646.3333  1290.6520  1290.6568  -3.68   0    40   0.0086    1   K.NFSGAELEGLVR.A
  ☑  425  729.3958  1456.7770  1456.7773  -0.19   0    57  0.00012    1   R.VLDDGELLVQQTK.N


     Proteins matching the same set of peptides:
     IPI00876255     Mass: 83174     Score: 67     Queries matched: 2
     Tax_Id=10090 Gene_Symbol=Nsf 83 kDa protein
________________________________________________________________________________________________
22.  IPI00377681     Mass: 42045     Score: 62     Queries matched: 1    emPAI: 0.08
     Tax_Id=10090 Gene_Symbol=N28178 Isoform 2 of Protein KIAA1045
  ☐  Check to include this hit in error tolerant search or archive report

    Query  Observed    Mr(expt)    Mr(calc)    ppm  Miss Score   Expect Rank  Peptide
  ☑  399  680.8234  1359.6322  1359.6266   4.15   0    62  3.5e-005    1   R.ALTDEQEEQAAR.Q


     Proteins matching the same set of peptides:
     IPI00647986     Mass: 45936     Score: 62     Queries matched: 1
     Tax_Id=10090 Gene_Symbol=N28178 Isoform 1 of Protein KIAA1045
     IPI00885599     Mass: 29710     Score: 62     Queries matched: 1
     Tax_Id=10090 Gene_Symbol=N28178 Novel protein
________________________________________________________________________________________________
23.  IPI00122069     Mass: 79562     Score: 61     Queries matched: 1    emPAI: 0.04
     Tax_Id=10090 Gene_Symbol=Prkcc Protein kinase C gamma 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
  ☑  308  599.8120  1197.6094  1197.5990   8.75   0    61  5.4e-005    1   R.LGSGPDGEPTIR.A

________________________________________________________________________________________________
24.  IPI00136703     Mass: 42971     Score: 56     Queries matched: 3    emPAI: 0.08
     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
     191  516.2849  1030.5552  1030.5481   6.96   0     8       17    2   K.LLIEMEQR.L
  ☑  363  652.3676  1302.7206  1302.7183   1.78   0    56  0.00016    1   K.VLTPELYAELR.A
  ☑  530  828.9172  1655.8198  1655.8188   0.60   0    30    0.059    1   R.LEQGQAIDDLMPAQK.-

________________________________________________________________________________________________
25.  IPI00347110     Mass: 59502     Score: 50     Queries matched: 1    emPAI: 0.06
     Tax_Id=10090 Gene_Symbol=Krt73 Keratin, type II cytoskeletal 73
  ☐  Check to include this hit in error tolerant search or archive report

    Query  Observed    Mr(expt)    Mr(calc)    ppm  Miss Score  Expect Rank  Peptide
  ☑  434  738.3943  1474.7740  1474.7780  -2.67   0    50  0.00071    1   R.FLEQQNQVLQTK.W


     Proteins matching the same set of peptides:
     IPI00420970     Mass: 55340     Score: 50     Queries matched: 1
     Tax_Id=10090 Gene_Symbol=Krt74 Keratin, type II cytoskeletal 74
     IPI00462140     Mass: 61379     Score: 50     Queries matched: 1
     Tax_Id=10090 Gene_Symbol=Krt77 Keratin, type II cytoskeletal 1b
     IPI00468956     Mass: 57860     Score: 50     Queries matched: 1
     Tax_Id=10090 Gene_Symbol=Krt71 Keratin, type II cytoskeletal 71
     IPI00625729     Mass: 66079     Score: 50     Queries matched: 1
     Tax_Id=10090 Gene_Symbol=Krt1 Keratin, type II cytoskeletal 1
```

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26.   IPI00403219     Score: 46     Queries matched: 1
      Tax_Id=10090 Gene_Symbol=Gm14496 Novel vomeronasal 2, receptor family 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
        155  487.7528  973.4910  973.4617  30.1   0     46  0.0023   1   R.WEDLGAQR.I

27.   IPI00119853     Score: 44     Queries matched: 5
      Tax_Id=10090 Gene_Symbol=Gnas Isoform Gnas-1 of Guanine nucleotide-binding protein G(s) subunit alpha isoforms short
    ☐ Check to include this hit in error tolerant search or archive report

      Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score Expect Rank  Peptide
        203  529.3122  1056.6098  1056.6179  -7.61   0   (18)   0.98    1   R.LLLLGAGESGK.S
        204  529.3124  1056.6102  1056.6179  -7.23   0    44  0.0026    1   R.LLLLGAGESGK.S
        238  538.2985  1074.5824  1074.6073 -23.14   0    (9)     11    8   R.LQEALNLFK.S
        239  538.2990  1074.5834  1074.6073 -22.21   0    21    0.64    2   R.LQEALNLFK.S
        240  538.3007  1074.5868  1074.6073 -19.05   0   (11)    6.8    2   R.LQEALNLFK.S


      Proteins matching the same set of peptides:
      IPI00463891     Score: 44     Queries matched: 5
      IPI00750570     Score: 44     Queries matched: 5
      IPI00416906     Score: 44     Queries matched: 5
      IPI00469793     Score: 44     Queries matched: 5

28.   IPI00347770     Score: 44     Queries matched: 3
      Tax_Id=10090 Gene_Symbol=Gnat3 Guanine nucleotide-binding protein G(t) subunit alpha-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
        203  529.3122  1056.6098  1056.6179 -7.61   0   (18)   0.98    1   K.LLLLGAGESGK.S
        204  529.3124  1056.6102  1056.6179 -7.23   0    44  0.0026    1   K.LLLLGAGESGK.S
        221  530.3175  1058.6204  1058.5873  31.4   1    10     4.6    4   K.IIHKNGYSK.Q

29.   IPI00118569     Mass: 44369     Score: 44     Queries matched: 4   emPAI: 0.07
      Tax_Id=10090 Gene_Symbol=Gna13 Guanine nucleotide-binding protein subunit alpha-13
    ☐ Check to include this hit in error tolerant search or archive report

      Query  Observed   Mr(expt)   Mr(calc)   ppm  Miss Score Expect Rank  Peptide
        203  529.3122  1056.6098  1056.6179 -7.61   0   (18)   0.98    1   K.ILLLGAGESGK.S
        204  529.3124  1056.6102  1056.6179 -7.23   0    44  0.0026    1   K.ILLLGAGESGK.S
        335  631.3046  1260.5946  1260.5955 -0.64   0     3      34    7   R.APMAAQGMVETR.V
        340  631.3057  1260.5968  1260.5955  1.10   0    (3)     35    6   R.APMAAQGMVETR.V


      Proteins matching the same set of peptides:
      IPI00649388     Mass: 20095     Score: 44     Queries matched: 4
      Tax_Id=10090 Gene_Symbol=Gna13 Putative uncharacterized protein

30.   IPI00123176     Mass: 36804     Score: 43     Queries matched: 2   emPAI: 0.09
      Tax_Id=10090 Gene_Symbol=Gm6316 Glyceraldehyde-3-phosphate dehydrogenase
    ☐ Check to include this hit in error tolerant search or archive report

      Query  Observed   Mr(expt)   Mr(calc)   ppm  Miss Score Expect Rank  Peptide
    ☑   401  685.3772  1368.7398  1368.7361  2.74   0   (26)   0.13    1   R.GAAQNIIPASTGAAK.A
    ☑   402  685.3792  1368.7438  1368.7361  5.66   0    43  0.0027    1   R.GAAQNIIPASTGAAK.A


      Proteins matching the same set of peptides:
      IPI00135284     Mass: 36092     Score: 43     Queries matched: 2
      Tax_Id=10090 Gene_Symbol=Gm16374 Glyceraldehyde-3-phosphate dehydrogenase
      IPI00229201     Mass: 16676     Score: 43     Queries matched: 2
      Tax_Id=10090 Gene_Symbol=3000002C10Rik Putative uncharacterized protein
      IPI00271869     Mass: 36293     Score: 43     Queries matched: 2
      Tax_Id=10090 Gene_Symbol=- 36 kDa protein
      IPI00273646     Mass: 36072     Score: 43     Queries matched: 2
      Tax_Id=10090 Gene_Symbol=Gapdh;LOC100042025 Glyceraldehyde-3-phosphate dehydrogenase
      IPI00622795     Mass: 36074     Score: 43     Queries matched: 2
      Tax_Id=10090 Gene_Symbol=- 36 kDa protein
      IPI00625893     Mass: 36205     Score: 43     Queries matched: 2
      Tax_Id=10090 Gene_Symbol=Gm6981 Glyceraldehyde-3-phosphate dehydrogenase
      IPI00752289     Mass: 36308     Score: 43     Queries matched: 2
      Tax_Id=10090 Gene_Symbol=Gm10290 Glyceraldehyde-3-phosphate dehydrogenase
      IPI00848801     Mass: 36100     Score: 43     Queries matched: 2
      Tax_Id=10090 Gene_Symbol=- 36 kDa protein
      IPI00849045     Mass: 36072     Score: 43     Queries matched: 2
      Tax_Id=10090 Gene_Symbol=- 36 kDa protein
      IPI00850337     Mass: 44633     Score: 43     Queries matched: 2
      Tax_Id=10090 Gene_Symbol=LOC100048117 similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) isoform 1
      IPI00850377     Mass: 35975     Score: 43     Queries matched: 2
      Tax_Id=10090 Gene_Symbol=- 36 kDa protein
      IPI00850779     Mass: 36076     Score: 43     Queries matched: 2
      Tax_Id=10090 Gene_Symbol=- 36 kDa protein
      IPI00874682     Mass: 36038     Score: 43     Queries matched: 2
      Tax_Id=10090 Gene_Symbol=- 36 kDa protein
      IPI00874964     Mass: 36512     Score: 43     Queries matched: 2
```

Tax_Id=10090 Gene_Symbol=- 36 kDa protein

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31. IPI00348094 **Mass:** 51093 **Score:** 42 **Queries matched:** 3 **emPAI:** 0.06
Tax_Id=10090 Gene_Symbol=Tubb1 Tubulin, 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
273	572.3212	1142.6278	1142.6270	0.72	0	42	0.0049	1	K.LAVNMVPFPR.L
364	660.3562	1318.6978	1318.6955	1.78	0	10	7.7	2	R.ILNSFSVMPSPK.V
365	660.3578	1318.7010	1318.6955	4.21	0	(10)	7.9	2	R.ILNSFSVMPSPK.V

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32. IPI00116074 **Mass:** 86151 **Score:** 40 **Queries matched:** 1 **emPAI:** 0.04
Tax_Id=10090 Gene_Symbol=Aco2 Aconitate hydratase, 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
☑	428	732.3771	1462.7396	1462.7416	-1.34	0	40	0.009	1	K.SQFTITPGSEQIR.A

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33. IPI00119063 **Mass:** 523342 **Score:** 37 **Queries matched:** 3 **emPAI:** 0.01
Tax_Id=10090 Gene_Symbol=Lrp1 Prolow-density lipoprotein receptor-related 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
	152	484.7774	967.5402	967.4975	44.2	0	(5)	15	5	R.GIPLDPNDK.S
	153	484.7776	967.5406	967.4975	44.6	0	9	5.4	3	R.GIPLDPNDK.S
☑	333	626.3710	1250.7274	1250.7347	-5.78	0	37	0.0059	1	R.GVAGAPPTVTLLR.S

Peptide matches not assigned to protein hits: (no details means no match)

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	407	696.3701	1390.7256	1390.7245	0.82	0	30	0.064	1	LEGVVFPYQPSR
☑	196	523.2819	1044.5492	1044.5564	-6.80	0	29	0.12	1	INDITLNSR
☑	154	487.3037	972.5928	972.5505	43.6	1	29	0.045	1	VRDFLAPR
☑	195	520.2805	1038.5464	1038.5458	0.65	0	28	0.1	1	AQASAPAQAPK
☑	309	599.8347	1197.6548	1197.6605	-4.71	0	27	0.12	1	ASGPPVSELITK
☑	368	669.3201	1336.6256	1336.6187	5.22	0	27	0.13	1	YALYDATYETK
☑	558	912.9982	1823.9818	1823.9782	2.02	0	22	0.24	1	VGINYQPPTVVPGGDLAK
☑	25	531.3553	530.3480	530.3428	9.90	0	20	0.74	1	ILASK
☑	419	720.3734	1438.7322	1438.7344	-1.48	0	19	0.76	1	YITPDQLADLYK
☑	63	408.2385	814.4624	814.4661	-4.48	1	19	1.2	1	GTVAPSKR
☑	606	737.7026	2210.0860	2210.0307	25.0	1	19	0.66	1	GLMVLQSIASRGCDTQDSEK + Oxidation (M)
☑	78	421.7573	841.5000	841.4810	22.6	0	19	0.75	1	LGTWLPR
☑	32	590.3131	589.3058	589.3006	8.87	0	18	2.1	1	ANMVR
☑	130	464.7809	927.5472	927.5502	-3.15	1	18	0.88	1	GITTVPGKR
☑	143	470.7710	939.5274	939.5614	-36.11	1	18	0.7	1	NRLPIATR
☑	313	614.3115	1226.6084	1226.6448	-29.61	0	18	0.91	1	IYYYHVITR
☑	194	520.2767	1038.5388	1038.5458	-6.67	0	18	1.1	1	AQASAPAQAPK
☑	496	812.9454	1623.8762	1623.8832	-4.28	0	17	0.91	1	TGAIVDVPVGEELLGR
☑	190	514.7952	1027.5758	1027.5774	-1.55	1	17	1.4	1	VAGSGKSPAVR
☑	151	481.7329	961.4512	961.4586	-7.62	1	16	1.9	1	RQAMPGMR + Oxidation (M)
☑	52	385.7109	769.4072	769.4446	-48.56	1	15	1.5	1	LEPKQR
☑	27	531.3663	530.3590	530.3428	30.6	0	15	0.67	1	ILASK
☑	26	531.3587	530.3514	530.3428	16.3	0	15	2.6	1	ILASK
☑	80	428.7653	855.5160	855.5112	5.61	1	15	1.7	1	ALRMLPR
☑	28	531.3701	530.3628	530.3428	37.8	0	14	0.78	1	ILASK
☑	84	435.7735	869.5324	869.4971	40.7	0	14	1.5	1	AVVESLPR
☑	221	530.3175	1058.6204	1058.6488	-26.77	1	14	1.9	1	KFLILNPSK
☑	72	415.1994	828.3842	828.4202	-43.39	1	14	1.7	1	ARGESPGR
☑	246	545.2651	1088.5156	1088.5098	5.38	0	13	3.4	1	EESADVNLGR
☑	205	530.2988	1058.5830	1058.5906	-7.15	1	13	4.6	1	MPTLKANIR + Oxidation (M)
☑	104	450.7215	899.4284	899.4097	20.8	0	13	2.7	1	STEPSHSR
☑	253	556.8272	1111.6398	1111.5985	37.2	1	13	2.2	1	QQPKEALGNK
☑	76	415.2051	828.3956	828.3838	14.3	1	12	2.6	1	NRDPDGR
☑	612	756.0484	2265.1234	2265.0770	20.5	0	12	3.1	1	MTPAGTSLPTSWLICTSPSSR + Oxidation (M)
☑	640	779.7223	2336.1451	2336.1617	-7.10	1	12	3	1	HMAAPLIGQLTRHEIEMTEK + 2 Oxidation (M)
☑	255	556.8319	1111.6492	1111.5986	45.6	0	12	2.3	1	IQENVPVGTR
☑	73	415.2014	828.3882	828.4276	-47.50	0	12	2.6	1	IHGSMLR + Oxidation (M)
☑	348	643.3405	1284.6664	1284.6561	8.02	0	12	4.8	1	LLVVDPETDER
☑	115	450.7243	899.4340	899.4726	-42.84	1	12	3.5	1	DGFHRLR
☑	150	481.7226	961.4306	961.4730	-44.01	1	11	3.5	1	QDPGARYR
☑	189	514.7838	1027.5530	1027.5927	-38.57	1	11	5.6	1	RLWPTLSR
☑	92	450.7179	899.4212	899.4461	-27.62	0	11	3.3	1	GLTADPGNR
☑	86	435.7745	869.5344	869.5123	25.5	0	11	3.1	1	VSLWLPR
☑	173	506.2323	1010.4500	1010.4703	-20.02	0	11	3.2	1	GDTTTTMLR + Oxidation (M)
☑	90	450.7172	899.4198	899.4647	-49.87	0	11	3.5	1	SLQHMLR + Oxidation (M)
☑	177	506.2389	1010.4632	1010.4855	-22.01	0	11	4	1	NLMADYLR + Oxidation (M)
☑	141	470.7696	939.5246	939.5614	-39.09	1	11	3.9	1	NRLPIATR
☑	66	412.7505	823.4864	823.4817	5.80	0	11	2.2	1	RPWLPR
☑	594	737.3668	2209.0786	2209.1491	-31.92	1	11	4.3	1	LGEHNIKVLEGNEQFVNAAK
☑	230	530.7705	1059.5264	1059.5495	-21.74	0	11	8.8	1	QALSNMLQR
☑	61	407.2281	812.4416	812.4756	-41.75	1	10	5.1	1	AGPKALEK

☑	79	428.7645	855.5144	855.4814	38.6	0	10	4.5	1	LGAETLPR
☑	140	470.7692	939.5238	939.5137	10.8	0	10	4.6	1	NPEALAAVR
☑	101	450.7208	899.4270	899.4322	-5.68	1	10	4.3	1	NRSSGSHR
☑	100	450.7206	899.4266	899.4647	-42.31	0	10	4.5	1	SLQHMLR + Oxidation (M)
☑	385	670.8940	1339.7734	1339.7506	17.0	1	10	3.5	1	AERPILGAMARR
☑	142	470.7698	939.5250	939.5515	-28.14	1	10	4.5	1	LRPGWRR
☑	295	595.3065	1188.5984	1188.6033	-4.10	1	10	7.9	1	QMQASRLSPR + Oxidation (M)
☑	70	414.2204	826.4262	826.4661	-48.20	0	10	5.4	1	VAAPNLSR
☑	107	450.7224	899.4302	899.4647	-38.31	0	10	4.9	1	SLQHMLR + Oxidation (M)
☑	75	415.2028	828.3910	828.4276	-44.12	0	10	4	1	IHGSMLR + Oxidation (M)
☑	191	516.2849	1030.5552	1030.5923	-36.00	0	10	11	1	LLIFQNQR
☑	91	450.7173	899.4200	899.4322	-13.47	1	10	4.3	1	NRSSGSHR
☑	176	506.2365	1010.4584	1010.4314	26.8	0	10	4.7	1	ACMDYPVR
☑	171	506.2305	1010.4464	1010.4781	-31.33	0	10	4.2	1	DLLHNEDR
☑	56	810.4305	809.4232	809.4139	11.5	1	10	6.3	1	KMQMLK + 2 Oxidation (M)
☑	19	503.2858	502.2785	502.2863	-15.54	0	9	24	1	AGSIR
☑	85	435.7742	869.5338	869.5123	24.8	0	9	4.6	1	VSLWLPR
☑	102	450.7211	899.4276	899.4322	-5.02	1	9	5.8	1	NRSSGSHR
☑	89	450.7172	899.4198	899.4209	-1.22	0	9	5	1	TQQGSSHR
☑	693	961.4171	2881.2295	2881.2557	-9.10	1	9	2.2	1	AVSAFQSMSGGSMFQCSWQHRFMAK + Oxidation (M)
☑	98	450.7204	899.4262	899.4324	-6.79	0	9	5.4	1	FMFNGLR + Oxidation (M)
☑	103	450.7213	899.4280	899.4322	-4.57	1	9	6	1	NRSSGSHR
☑	283	578.8117	1155.6088	1155.6108	-1.72	1	9	9.3	1	QQQQEALRR
☑	164	499.2584	996.5022	996.5062	-3.99	0	9	9.1	1	KPMSSYLR + Oxidation (M)
☑	35	616.3713	615.3640	615.3592	7.90	0	9	25	1	ALSTPK
☑	67	412.7511	823.4876	823.4817	7.25	0	9	3.7	1	RPWLPR
☑	603	737.7007	2210.0803	2210.1843	-47.07	0	9	6.9	1	CGATSLMASTVLLLLLFSWK
☑	477	795.3494	1588.6842	1588.6787	3.47	0	9	3.9	1	NNQDNTTNTDMPPK
☑	36	628.3656	627.3583	627.3704	-19.24	1	9	7.5	1	EKVPR
☑	621	762.0510	2283.1312	2283.1706	-17.28	1	8	6.8	1	ATSPSNNVDEVQIPEISLSKR
☑	349	643.3462	1284.6778	1284.6357	32.8	1	8	10	1	GRAGVCDPALNR
☑	641	783.7235	2348.1487	2348.1471	0.68	1	8	7.1	1	SFLIWVNEEDHTRVISMEK + Oxidation (M)
☑	112	450.7238	899.4330	899.4647	-35.20	0	8	7.5	1	SLQHMLR + Oxidation (M)
☑	346	636.8115	1271.6084	1271.6357	-21.44	0	8	8.3	1	LLDAESEDRPK
☑	108	450.7229	899.4312	899.4647	-37.20	0	8	7.8	1	SLQHMLR + Oxidation (M)
☑	111	450.7234	899.4322	899.4647	-36.09	0	8	7.8	1	SLQHMLR + Oxidation (M)
☑	403	458.9094	1373.7064	1373.7159	-6.94	0	8	13	1	KPALTMEVVCAR
☑	97	450.7202	899.4258	899.4097	17.9	0	8	6.9	1	HVGDDTTR
☑	220	530.3162	1058.6178	1058.5972	19.5	0	8	8.1	1	VTASLLGSPSK
☑	88	443.2438	884.4730	884.5080	-39.48	1	8	9.3	1	SPPKTTVR
☑	148	477.2345	952.4544	952.4284	27.4	1	8	11	1	KSSEEAMR + Oxidation (M)
☑	658	888.7558	2663.2456	2663.2034	15.8	1	8	6.9	1	SGYFELPTSQDCARSNHQDPLGGK
☑	237	538.2737	1074.5328	1074.5054	25.6	1	8	16	1	NSKEPGSNSR
☑	74	415.2025	828.3904	828.4051	-17.71	0	8	6.9	1	YATIMSK + Oxidation (M)
☑	625	762.0553	2283.1441	2283.1894	-19.87	0	7	8.3	1	EEVIDFSKPFMSLGISIMIK
☑	691	933.7790	2798.3152	2798.3262	-3.94	1	7	6.5	1	NLGNPPNAVLCMSQGRDPETMVQVR + Oxidation (M)
☑	99	450.7206	899.4266	899.4647	-42.31	0	7	9	1	HITNLMR + Oxidation (M)
☑	121	452.7405	903.4664	903.4774	-12.11	0	7	19	1	LGSSQVASR
☑	259	557.7951	1113.5756	1113.5891	-12.05	1	7	16	1	SSPLRGPGTSR
☑	224	530.7690	1059.5234	1059.5210	2.33	0	7	20	1	QEGHLPHSR
☑	247	545.2892	1088.5638	1088.5760	-11.18	1	7	18	1	RANNINMLK + Oxidation (M)
☑	93	450.7189	899.4232	899.4573	-37.87	1	7	8.4	1	QSQEPRR
☑	294	595.3062	1188.5978	1188.6172	-16.31	0	7	16	1	MLISAASPDIR + Oxidation (M)
☑	60	406.2201	810.4256	810.4235	2.60	1	7	12	1	AQYSSKK
☑	392	672.3433	1342.6720	1342.6364	26.5	1	7	15	1	ADAEEEAATRIPA
☑	655	888.7497	2663.2273	2663.1670	22.6	0	7	7.6	1	NLTTIGYNWEDHNIEEQCQSGR
☑	135	470.7658	939.5170	939.5614	-47.17	1	7	11	1	LPRASGALR
☑	257	557.3074	1112.6002	1112.6342	-30.54	0	7	14	1	GLFLSNVVHK
☑	265	565.3054	1128.5962	1128.6139	-15.61	0	7	17	1	TLIEQIEQR
☑	412	701.8926	1401.7706	1401.7715	-0.61	0	7	12	1	ATQPSLTELTTLK
☑	692	961.4110	2881.2112	2881.1807	10.6	1	7	3	1	NFSPDQSPEFAREADEECYSTQMK + Oxidation (M)
☑	522	816.8976	1631.7806	1631.7912	-6.46	1	7	13	1	MVNRENKPPCYPK
☑	266	565.3197	1128.6248	1128.6503	-22.51	0	7	16	1	TKPVLSSLER
☑	620	762.0505	2283.1297	2283.1190	4.67	1	7	10	1	KGTTTNATATSTSTASTAVADAQK
☑	622	762.0521	2283.1345	2283.1756	-17.99	1	7	10	1	GLVKVLFATETFAMGVNMPAR + 2 Oxidation (M)
☑	166	500.2500	998.4854	998.5145	-29.08	1	6	14	1	KAEGAPNQGK
☑	68	412.7528	823.4910	823.4817	11.4	0	6	6.5	1	RPWLPR
☑	331	622.7954	1243.5762	1243.5721	3.37	0	6	13	1	GELYDYISER
☑	685	933.4488	2797.3246	2797.3051	6.96	0	6	8.7	1	MATQNVPPPPYQDSPQMTATAQPPSK + Oxidation (M)
☑	415	702.3759	1402.7372	1402.7061	22.2	0	6	16	1	MAGVGVGPLQGMVR + 2 Oxidation (M)
☑	179	506.2391	1010.4636	1010.4314	31.9	0	6	11	1	ACMDYPVR
☑	110	450.7234	899.4322	899.4097	25.1	0	6	12	1	STEPSHSR
☑	114	450.7242	899.4338	899.4461	-13.61	0	6	12	1	GQSSAPPTR
☑	542	885.9581	1769.9016	1769.8505	28.9	1	6	15	1	EEPKEEESLSMPLPR
☑	217	530.3068	1058.5990	1058.5608	36.2	1	6	17	1	KSTESVPPSK
☑	607	737.7040	2210.0902	2210.0967	-2.97	0	6	13	1	LGEHNINVLEGNEQFIDAAK
☑	157	491.2421	980.4696	980.4233	47.3	0	6	19	1	AVSMDNSNK + Oxidation (M)
☑	71	415.1973	828.3800	828.4202	-48.46	1	6	9.4	1	REQSPGR
☑	144	470.7715	939.5284	939.5025	27.6	0	6	12	1	NPIVPTDGK
☑	105	450.7220	899.4294	899.4726	-47.95	0	6	13	1	HRPSFTR
☑	626	762.0572	2283.1498	2283.2370	-38.22	1	6	12	1	LMVMEIRNAYAVLYDIILK + Oxidation (M)

☑	133	470.2356	938.4566	938.4471	10.2	0	6	17	1	QAYHHQR
☑	369	670.3066	1338.5986	1338.6099	-8.39	0	6	12	1	NEGQPQGLMHGR + Oxidation (M)
☑	222	530.7654	1059.5162	1059.5574	-38.81	1	6	26	1	AGSGLRWTGR
☑	302	595.3110	1188.6074	1188.5921	12.9	1	6	23	1	MADAAASPVGKR + Oxidation (M)
☑	180	506.2392	1010.4638	1010.5033	-39.01	0	6	13	1	SSPVPNPNLS
☑	260	557.8024	1113.5902	1113.5414	43.8	0	6	22	1	DTNLNDLGPR
☑	136	470.7668	939.5190	939.5614	-45.05	1	6	15	1	NRLPIATR
☑	169	501.2503	1000.4860	1000.5302	-44.08	1	6	20	1	RLLVDDDR
☑	145	470.7721	939.5296	939.5515	-23.24	1	5	13	1	LRPGWRR
☑	138	470.7690	939.5234	939.4774	49.0	1	5	15	1	QAPKEPDR
☑	182	506.2429	1010.4712	1010.5033	-31.68	0	5	15	1	SSPVPNPNLS
☑	248	545.2919	1088.5692	1088.5536	14.4	0	5	27	1	MGLEEELLR
☑	424	728.8551	1455.6956	1455.6664	20.1	0	5	17	1	AGAQGDPDVPECLK
☑	279	573.7990	1145.5834	1145.5975	-12.28	1	5	26	1	AGDRVMVLNR + Oxidation (M)
☑	321	622.7869	1243.5592	1243.5946	-28.39	0	5	13	1	SPTGASDHFLGR
☑	219	530.3109	1058.6072	1058.5720	33.3	0	5	17	1	GSTLQDAVLR
☑	442	506.2327	1515.6763	1515.7053	-19.14	0	5	12	1	LDTPATSDPLSEDR
☑	310	600.2780	1198.5414	1198.5942	-44.03	0	5	12	1	GQPDTVQDALR
☑	688	933.7679	2798.2819	2798.2851	-1.15	1	5	9.9	1	APNTMWSILSSLSSEVPSSDDRTMR + 2 Oxidation (M)
☑	316	615.2961	1228.5776	1228.6386	-49.63	1	5	17	1	AIYLSGYRMR
☑	160	496.2260	990.4374	990.4487	-11.39	1	5	14	1	ASMSRHMR + Oxidation (M)
☑	162	496.2284	990.4422	990.4487	-6.54	1	5	16	1	ASMSRHMR + Oxidation (M)
☑	147	470.7730	939.5314	939.5250	6.87	1	5	14	1	IQTKASHR
☑	576	688.3119	2061.9139	2061.9426	-13.92	1	5	11	1	SKGSQGTSPFPMSPPSPDSR + Oxidation (M)
☑	417	711.3622	1420.7098	1420.6947	10.7	0	5	22	1	AGDPGLQGPAGAPGEK
☑	168	500.2616	998.5086	998.4716	37.1	0	5	23	1	HMEARPSR + Oxidation (M)
☑	600	737.6983	2210.0731	2210.0637	4.23	1	5	16	1	LAVTSYNDIQDLMDSGNKAR
☑	131	465.2120	928.4094	928.4147	-5.61	0	5	9	1	FMTEMVR + Oxidation (M)
☑	134	470.7655	939.5164	939.5515	-37.29	1	5	19	1	LRPGWRR
☑	139	470.7692	939.5238	939.5515	-29.41	1	5	17	1	LRPGWRR
☑	345	634.3837	1266.7528	1266.7296	18.4	0	5	6.7	1	KPKPTNQVEVK
☑	161	496.2276	990.4406	990.4479	-7.28	1	5	16	1	DQESRSNR
☑	605	737.7022	2210.0848	2210.1167	-14.45	1	4	18	1	ALFASQEMWLSHRQTHLR
☑	420	728.3528	1454.6910	1454.6572	23.3	1	4	22	1	QEMPQDPRAPDR + Oxidation (M)
☑	234	532.2764	1062.5382	1062.5393	-0.95	1	4	33	1	MRSLAWAGR + Oxidation (M)
☑	53	399.7266	797.4386	797.4548	-20.24	0	4	19	1	LPWLNR
☑	326	622.7897	1243.5648	1243.5615	2.66	0	4	18	1	ETMPVHSQSGR + Oxidation (M)
☑	423	728.8538	1455.6930	1455.6664	18.3	0	4	22	1	AGAQGDPDVPECLK
☑	305	595.3142	1188.6138	1188.6033	8.85	1	4	33	1	SSGVGKNCKPR
☑	94	450.7191	899.4236	899.4647	-45.65	0	4	17	1	SLQHMLR + Oxidation (M)
☑	632	779.7067	2336.0983	2336.0559	18.1	0	4	17	1	DQSQAADMLCVVVNNMEQLR + Oxidation (M)
☑	159	492.2374	982.4602	982.4508	9.58	0	4	22	1	NTEGPYFR
☑	656	888.7521	2663.2345	2663.1412	35.0	1	4	17	1	EFAPSDEELDSYRHGEEWDPQK
☑	521	816.8972	1631.7798	1631.8017	-13.42	1	4	28	1	MLFLSESSNWFKK + Oxidation (M)
☑	163	496.2305	990.4464	990.4671	-20.90	0	4	24	1	YNPASFHR
☑	677	888.7624	2663.2654	2663.2796	-5.33	1	4	19	1	VSSEVQQMWALTEMIRASHTSTR + Oxidation (M)
☑	312	612.3268	1222.6390	1222.5942	36.7	0	4	33	1	SQLQENTFTR
☑	328	622.7919	1243.5692	1243.6091	-32.08	1	4	23	1	ELPRCAATGGGR
☑	535	852.4255	1702.8364	1702.7688	39.7	1	3	29	1	SMSMSVGERVTLSCK + 2 Oxidation (M)
☑	624	762.0549	2283.1429	2283.1190	10.4	1	3	22	1	KGTTTNATATSTSTASTAVADAQK
☑	109	450.7229	899.4312	899.4712	-44.44	0	3	25	1	DLSPIAER
☑	416	711.3582	1420.7018	1420.6947	5.06	0	3	34	1	AGDPGLQGPAGAPGEK
☑	514	816.8953	1631.7760	1631.7638	7.50	1	3	32	1	TENLDDEEKLNNAK
☑	181	506.2395	1010.4644	1010.4703	-5.77	0	3	26	1	GDTTTTMLR + Oxidation (M)
☑	395	672.8402	1343.6658	1343.6681	-1.66	1	3	34	1	AQGDEQEAQLKK
☑	116	450.7244	899.4342	899.4461	-13.18	0	3	26	1	GTPGDQGLR
☑	393	672.3479	1342.6812	1342.6551	19.5	0	3	40	1	MDVQATTPLDPR
☑	47	732.3589	731.3516	731.3562	-6.26	0	3	50	1	DVSAANR
☑	433	736.3515	1470.6884	1470.7566	-46.32	0	3	27	1	LGSTPISGASIDPEK
☑	617	761.7278	2282.1616	2282.0559	46.3	0	3	25	1	VALLEQQMQACTLDFENEK + Oxidation (M)
☑	262	561.2590	1120.5034	1120.4958	6.84	0	3	32	1	MEDEIQDII + Oxidation (M)
☑	391	672.3428	1342.6710	1342.6551	11.9	0	3	41	1	MDVQATTPLDPR
☑	575	514.0181	2052.0433	2052.0211	10.8	0	3	27	1	NEMVAHIHELLVFQGGSR + Oxidation (M)
☑	552	897.9138	1793.8130	1793.8665	-29.80	0	3	27	1	VLCEALQHPGCNIQR
☑	527	816.9020	1631.7894	1631.7905	-0.65	0	2	38	1	YECIFTLYPEGIK
☑	306	595.3143	1188.6140	1188.6285	-12.14	1	2	47	1	KPATDGMAVRK + Oxidation (M)
☑	137	470.7682	939.5218	939.4886	35.4	1	2	30	1	TKHASGSPR
☑	263	561.2593	1120.5040	1120.5295	-22.71	0	2	34	1	MSLGQQQSAR + Oxidation (M)
☑	604	737.7008	2210.0806	2210.1405	-27.12	1	2	30	1	ALSMLRNVTTEQPYFIEAK
☑	422	728.3561	1454.6976	1454.7188	-14.51	1	2	37	1	KRPDEVPDAGPMK + Oxidation (M)
☑	106	450.7221	899.4296	899.4322	-2.79	1	2	29	1	NRSSGSHR
☑	577	688.3141	2061.9205	2061.9426	-10.72	1	2	22	1	SKGSQGTSPFPMSPPSPDSR + Oxidation (M)
☑	235	536.7872	1071.5598	1071.5747	-13.84	1	2	72	1	KLVGATTVHM + Oxidation (M)
☑	615	761.7188	2282.1346	2282.1623	-12.17	0	2	30	1	FPLDYYSIPFPTPTTPLTGR
☑	394	672.8397	1343.6648	1343.6470	13.3	1	2	42	1	KTASYYSPSGQR
☑	167	500.2557	998.4968	998.4743	22.6	0	2	41	1	DSMFGISVK + Oxidation (M)
☑	546	894.4644	1786.9142	1786.8849	16.4	0	2	42	1	TVSWLNEQLELGNER
☑	559	912.9985	1823.9824	1823.9782	2.35	0	2	27	1	VGINYQPPTVVPGGDLAK
☑	519	816.8969	1631.7792	1631.7937	-8.86	1	2	42	1	TEDGEGRAMITPALR + Oxidation (M)
☑	627	762.0612	2283.1618	2283.1958	-14.88	0	2	29	1	AVEILADIIQNSTLGEAEIER
☑	317	615.2972	1228.5798	1228.6387	-47.88	1	2	40	1	AVRFSFTVMR + Oxidation (M)

☑	545	596.3310	1785.9712	1785.9335	21.1	1	1	35	1	KFMTLDPVSQDALPPK
☑	554	904.9239	1807.8332	1807.7836	27.5	0	1	44	1	FGSWMTDPLAPEGDNR + Oxidation (M)
☑	324	622.7889	1243.5632	1243.6157	-42.15	1	1	34	1	KGPGAASALDDSR
☑	218	530.3070	1058.5994	1058.5794	18.9	0	1	51	1	IMSIPDVIR + Oxidation (M)
☑	193	520.2688	1038.5230	1038.5458	-21.88	0	1	50	1	AQASAPAQAPK
☑	347	638.7794	1275.5442	1275.5666	-17.53	1	1	19	1	KMYSHPQQQN + Oxidation (M)
☑	698	972.0858	2913.2356	2913.3199	-28.95	1	1	11	1	NAFERGEDPLAGDQNDHDMDSIAGVLK
☑	614	761.7159	2282.1259	2282.0559	30.7	0	1	38	1	VALLEQQMQACTLDFENEK + Oxidation (M)
☑	252	556.8272	1111.6398	1111.6349	4.41	1	1	31	1	KSPPQTVLSR
☑	610	737.7059	2210.0959	2210.0967	-0.39	0	1	40	1	LGEHNINVLEGNEQFIDAAK
☑	304	595.3141	1188.6136	1188.6714	-48.56	1	1	66	1	NETGLLSSIKK
☑	491	809.4144	1616.8142	1616.7947	12.1	1	1	54	1	WESLHQEFSAKQK
☑	301	595.3109	1188.6072	1188.5887	15.6	0	1	67	1	QLVGTNEWSR
☑	41	325.1856	648.3566	648.3442	19.2	1	1	61	1	SAESKK
☑	146	470.7728	939.5310	939.4886	45.2	1	1	37	1	TKHASGSPR
☑	597	737.6961	2210.0665	2210.0160	22.9	1	1	42	1	ARGTGEPASAGTSTGTSTGAGSSSR
☑	599	737.6978	2210.0716	2210.1167	-20.42	1	1	43	1	ALFASQEMWLSHRQTHLR
☑	39	325.1848	648.3550	648.3629	-12.06	1	0	70	1	GLGMKK + Oxidation (M)
☑	444	760.8801	1519.7456	1519.7493	-2.42	0	0	64	1	SETFLLMQPWPR + Oxidation (M)
☑	441	758.4306	1514.8466	1514.8000	30.8	1	0	42	1	APANCRLPARPHR
☑	38	325.1841	648.3536	648.3595	-9.02	0	0	76	1	AFNAVK
☑	618	762.0477	2283.1213	2283.2158	-41.38	1	0	46	1	TSGRGHPDVATMLNILALVYR
☑	311	601.3107	1200.6068	1200.5748	26.7	1	0	75	1	GAAGWEGGGRGAR
☑	40	325.1851	648.3556	648.3629	-11.14	1	0	75	1	GLGMKK + Oxidation (M)
☑	1	366.1466	365.1393							
☑	2	396.9587	395.9514							
☑	3	429.0963	428.0890							
☑	4	429.1010	428.0937							
☑	5	433.1578	432.1505							
☑	6	445.1280	444.1207							
☑	7	445.1297	444.1224							
☑	8	445.1974	444.1901							
☑	9	445.1976	444.1903							
☑	10	446.2410	445.2337							
☑	11	451.1967	450.1894							
☑	12	451.2156	450.2083							
☑	13	460.2441	459.2368							
☑	14	469.2228	468.2155							
☑	15	471.2780	470.2707							
☑	16	480.2485	479.2412							
☑	17	487.3112	486.3039							
☑	18	493.2528	492.2455							
☑	20	506.2326	505.2253							
☑	21	506.2362	505.2289							
☑	22	506.2410	505.2337							
☑	23	515.2794	514.2721							
☑	24	531.3441	530.3368							
☑	29	574.3152	573.3079							
☑	30	575.2928	574.2855							
☑	31	585.2461	584.2388							
☑	34	609.0488	608.0415							
☑	37	631.3204	630.3131							
☑	42	653.3390	652.3317							
☑	43	698.3687	697.3614							
☑	44	698.3768	697.3695							
☑	45	360.7057	719.3968							
☑	46	360.7073	719.4000							
☑	48	732.3607	731.3534							
☑	49	367.4966	732.9786							
☑	50	373.6020	745.1894							
☑	51	756.3926	755.3853							
☑	54	399.7273	797.4400							
☑	55	800.3978	799.3905							
☑	57	405.7203	809.4260							
☑	58	810.4362	809.4289							
☑	59	810.4495	809.4422							
☑	62	408.2381	814.4616							
☑	64	408.2433	814.4720							
☑	65	816.8939	815.8866							
☑	69	825.3708	824.3635							
☑	77	834.3805	833.3732							
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☑	96	450.7201	899.4256							
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☑	117	452.2079	902.4012							
☑	124	456.2869	910.5592							
☑	127	463.2484	924.4822							
☑	128	464.7739	927.5332							
☑	129	464.7761	927.5376							
☑	149	961.4308	960.4235							

☑	156	489.2438	976.4730
☑	158	491.2500	980.4854
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☑	183	510.1425	1018.2704
☑	186	510.2555	1018.4964
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☑	192	519.1511	1036.2876
☑	233	531.3477	1060.6808
☑	236	538.1265	1074.2384
☑	249	547.1017	1092.1888
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☑	251	556.8255	1111.6364
☑	254	556.8296	1111.6446
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☑	258	557.3193	1112.6240
☑	261	558.2656	1114.5166
☑	264	561.2626	1120.5106
☑	272	572.3195	1142.6244
☑	284	579.8302	1157.6458
☑	291	588.3398	1174.6650
☑	292	592.3085	1182.6024
☑	293	595.3043	1188.5940
☑	296	595.3077	1188.6008
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☑	298	595.3089	1188.6032
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☑	300	595.3095	1188.6044
☑	303	595.3124	1188.6102
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☑	323	622.7885	1243.5624
☑	329	622.7941	1243.5736
☑	330	622.7943	1243.5740
☑	332	624.3058	1246.5970
☑	350	645.3189	1288.6232
☑	351	645.8275	1289.6404
☑	352	645.8320	1289.6494
☑	355	651.8354	1301.6562
☑	396	672.8417	1343.6688
☑	400	683.9808	1365.9470
☑	406	696.3622	1390.7098
☑	408	699.8883	1397.7620
☑	409	699.8900	1397.7654
☑	410	699.8941	1397.7736
☑	413	702.3684	1402.7222
☑	421	728.3550	1454.6954
☑	426	729.4035	1456.7924
☑	427	732.3361	1462.6576
☑	435	740.3751	1478.7356
☑	436	748.8556	1495.6966
☑	438	757.8587	1513.7028
☑	439	757.8616	1513.7086
☑	440	757.8618	1513.7090
☑	445	766.8646	1531.7146
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☑	447	775.8678	1549.7210
☑	448	775.8699	1549.7252
☑	449	785.8380	1569.6614
☑	450	785.8396	1569.6646
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☑	467	785.8494	1569.6842
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☑	470	*785.8501*	*1569.6856*
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☑	474	*785.8539*	*1569.6932*
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☑	489	*808.9011*	*1615.7876*
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☑	502	*816.8928*	*1631.7710*
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☑	541	*885.9580*	*1769.9014*
☑	543	*890.3994*	*1778.7842*
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☑	553	*897.9139*	*1793.8132*
☑	555	*906.4707*	*1810.9268*
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☑	564	*973.5184*	*1945.0222*
☑	565	*650.9495*	*1949.8267*
☑	574	*1024.5062*	*2046.9978*
☑	585	*1048.9791*	*2095.9436*
☑	586	*701.6427*	*2101.9063*
☑	587	*701.6429*	*2101.9069*
☑	589	*707.3322*	*2118.9748*
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☑	593	*732.0259*	*2193.0559*
☑	595	*737.6949*	*2210.0629*
☑	596	*737.6956*	*2210.0650*
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☑	601	*737.6991*	*2210.0755*
☑	602	*737.7005*	*2210.0797*
☑	608	*737.7048*	*2210.0926*
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☑	611	*737.7095*	*2210.1067*
☑	613	*756.0691*	*2265.1855*
☑	616	*761.7196*	*2282.1370*
☑	619	*762.0505*	*2283.1297*
☑	623	*762.0542*	*2283.1408*
☑	628	*762.0628*	*2283.1666*
☑	629	*768.7164*	*2303.1274*
☑	630	*779.0418*	*2334.1036*
☑	631	*1168.5664*	*2335.1182*
☑	633	*779.7078*	*2336.1016*
☑	636	*779.7141*	*2336.1205*
☑	638	*779.7175*	*2336.1307*
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☑	642	*784.0617*	*2349.1633*
☑	654	*888.7457*	*2663.2153*
☑	673	*888.7603*	*2663.2591*
☑	678	*916.4274*	*2746.2604*
☑	679	*916.7508*	*2747.2306*
☑	680	*917.0808*	*2748.2206*
☑	681	*917.0816*	*2748.2230*
☑	682	*933.4417*	*2797.3033*
☑	683	*933.4421*	*2797.3045*
☑	684	*933.4461*	*2797.3165*
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☑	689	*933.7738*	*2798.2996*
☑	690	*933.7778*	*2798.3116*
☑	694	*961.4198*	*2881.2376*
☑	695	*961.4268*	*2881.2586*
☑	696	*961.4318*	*2881.2736*
☑	697	*961.7681*	*2882.2825*
☑	699	*972.0930*	*2913.2572*
☑	700	*972.0975*	*2913.2707*
☑	701	*972.4227*	*2914.2463*
☑	703	*1308.9585*	*3923.8537*
☑	704	*981.9737*	*3923.8657*
☑	706	*1308.9722*	*3923.8948*
☑	707	*982.2178*	*3924.8421*
☑	708	*1314.2834*	*3939.8284*
☑	709	*1130.9587*	*4519.8057*
☑	710	*1308.8093*	*5231.2081*

Search Parameters

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Type of search         : MS/MS Ion Search
Enzyme                 : Trypsin
Fixed modifications    : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values            : Monoisotopic
Protein Mass           : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages   : 1
Instrument type        : ESI-QUAD-TOF
Number of queries      : 710
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Mascot: http://www.matrixscience.com/

Mascot Search Results

```
User          : Dominic
Email         : dominic.kurian@bbsrc.ac.uk
Search title  : IPI Mouse_15-02-2010
MS data file  : D:\Peaklist\Dominic Kurian\QTofDK20010804 GATC P 0010882.pkl
Database      : IPI_mouse MOUSE_v3_79 (54943 sequences; 24917557 residues)
Timestamp     : 15 Feb 2011 at 15:23:00 GMT
Protein hits  : IPI00420725 Tax_Id=10090 Gene_Symbol=Camk2a Uncharacterized protein
                IPI00474502 Tax_Id=10090 Gene_Symbol=Camk2b Calcium/calmodulin-dependent protein kinase type II subunit beta
                IPI00109073 Tax_Id=10090 Gene_Symbol=Tubb4 Tubulin beta-4 chain
                IPI00169463 Tax_Id=10090 Gene_Symbol=Tubb2c Tubulin beta-2C chain
                IPI00124695 Tax_Id=10090 Gene_Symbol=Camk2g Isoform 1 of Calcium/calmodulin-dependent protein kinase type II subunit
                IPI00117352 Tax_Id=10090 Gene_Symbol=Tubb5 Tubulin beta-5 chain
                IPI00109061 Tax_Id=10090 Gene_Symbol=Tubb2b Tubulin beta-2B chain
                IPI00112251 Tax_Id=10090 Gene_Symbol=Tubb3 Tubulin beta-3 chain
                IPI00755181 Tax_Id=10090 Gene_Symbol=Krt10 keratin, type I cytoskeletal 10
                IPI00110753 Tax_Id=10090 Gene_Symbol=Tuba1a Tubulin alpha-1A chain
                IPI00112584 Tax_Id=10090 Gene_Symbol=Camk2d Isoform 1 of Calcium/calmodulin-dependent protein kinase type II subunit
                IPI00608020 Tax_Id=10090 Gene_Symbol=Ftl1 ferritin light chain 1
                IPI00122928 Tax_Id=10090 Gene_Symbol=Tubb6 Tubulin beta-6 chain
                IPI00347110 Tax_Id=10090 Gene_Symbol=Krt73 Keratin, type II cytoskeletal 73
                IPI00122048 Tax_Id=10090 Gene_Symbol=Atp1a3 Sodium/potassium-transporting ATPase subunit alpha-3
                IPI00138892 Tax_Id=10090 Gene_Symbol=Uba52 Ubiquitin-60S ribosomal protein L40
                IPI00625729 Tax_Id=10090 Gene_Symbol=Krt1 Keratin, type II cytoskeletal 1
                IPI00136703 Tax_Id=10090 Gene_Symbol=Ckb Creatine kinase B-type
                IPI00110850 Tax_Id=10090 Gene_Symbol=Actb Actin, cytoplasmic 1
                IPI00221797 Tax_Id=10090 Gene_Symbol=Krt75 Keratin, type II cytoskeletal 75
                IPI00348328 Tax_Id=10090 Gene_Symbol=Krt78 keratin Kb40
                IPI00322209 Tax_Id=10090 Gene_Symbol=Krt8 Keratin, type II cytoskeletal 8
                IPI00221528 Tax_Id=10090 Gene_Symbol=Actbl2 Beta-actin-like protein 2
                IPI00124499 Tax_Id=10090 Gene_Symbol=Krt79 Keratin, type II cytoskeletal 79
                IPI00230145 Tax_Id=10090 Gene_Symbol=Fth1 Ferritin heavy chain
                IPI00406377 Tax_Id=10090 Gene_Symbol=Krt7 Keratin, type II cytoskeletal 7
                IPI00222228 Tax_Id=10090 Gene_Symbol=4732456N10Rik hypothetical protein LOC239673
                IPI00135284 Tax_Id=10090 Gene_Symbol=Gm16374 Glyceraldehyde-3-phosphate dehydrogenase
                IPI00134997 Tax_Id=10090 Gene_Symbol=Dlgap3 Disks large-associated protein 3
                IPI00348094 Tax_Id=10090 Gene_Symbol=Tubb1 Tubulin, beta 1
                IPI00115546 Tax_Id=10090 Gene_Symbol=Gnao1 Isoform Alpha-2 of Guanine nucleotide-binding protein G(o) subunit alpha
                IPI00122094 Tax_Id=10090 Gene_Symbol=Dlg4 Isoform 2 of Disks large homolog 4
                IPI00119667 Tax_Id=10090 Gene_Symbol=Eef1a2 Elongation factor 1-alpha 2
                IPI00135197 Tax_Id=10090 Gene_Symbol=Krt20 Keratin, type I cytoskeletal 20
                IPI00467833 Tax_Id=10090 Gene_Symbol=Tpi1 triosephosphate isomerase
                IPI00118569 Tax_Id=10090 Gene_Symbol=Gna13 Guanine nucleotide-binding protein subunit alpha-13
                IPI00462072 Tax_Id=10090 Gene_Symbol=Eno1;Gm5506 Alpha-enolase
                IPI00120793 Tax_Id=10090 Gene_Symbol=Prnp Major prion protein
                IPI00113410 Tax_Id=10090 Gene_Symbol=Hapln2 Hyaluronan and proteoglycan link protein 2
                IPI00622240 Tax_Id=10090 Gene_Symbol=Krt2 Keratin, type II cytoskeletal 2 epidermal
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	IPI_mouse	Decoy	False discovery rate
Peptide matches above identity threshold	164	0	0.00 %
Peptide matches above homology or identity threshold	182	0	0.00 %

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 > 37 indicate identity or extensive homology (p<0.01).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.

Score Distribution

Peptide Summary Report

Format As | Peptide Summary | Help

Significance threshold p< 0.01 | Max. number of hits AUTO

Standard scoring ○ MudPIT scoring ● | Ions score or expect cut-off 0 | 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

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1.   IPI00420725   Mass: 55882   Score: 1121   Queries matched: 76   emPAI: 0.77
     Tax_Id=10090 Gene_Symbol=Camk2a Uncharacterized protein
   ☐ Check to include this hit in error tolerant search or archive report
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	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	27	588.3868	587.3795	587.3642	26.0	0	22	0.71	1	K.IINTK.K
☑	69	432.7315	863.4484	863.4501	-1.94	0	23	0.56	1	R.SGAPSVLPH.-
☑	90	452.2513	902.4880	902.4895	-1.63	0	21	0.9	1	K.MLTINPSK.R
☑	139	525.2845	1048.5544	1048.5553	-0.80	0	(45)	0.0029	1	K.VLAGQEYAAK.I
☑	140	525.2850	1048.5554	1048.5553	0.16	0	(33)	0.044	1	K.VLAGQEYAAK.I
☑	141	525.2850	1048.5554	1048.5553	0.16	0	(39)	0.01	1	K.VLAGQEYAAK.I
☑	142	525.2855	1048.5564	1048.5553	1.11	0	54	0.00031	1	K.VLAGQEYAAK.I
☑	143	525.2856	1048.5566	1048.5553	1.30	0	(22)	0.49	1	K.VLAGQEYAAK.I
☑	144	525.2864	1048.5582	1048.5553	2.83	0	(47)	0.0015	1	K.VLAGQEYAAK.I
☑	201	574.3237	1146.6328	1146.6431	-8.91	0	(39)	0.0079	1	K.GAILTTMLATR.N
☑	202	574.3245	1146.6344	1146.6431	-7.52	0	(51)	0.00057	1	K.GAILTTMLATR.N
☑	204	574.3274	1146.6402	1146.6431	-2.46	0	(36)	0.014	1	K.GAILTTMLATR.N
☑	205	574.3279	1146.6412	1146.6431	-1.59	0	(49)	0.00074	1	K.GAILTTMLATR.N
☑	206	574.3290	1146.6434	1146.6431	0.33	0	(24)	0.21	1	K.GAILTTMLATR.N
☑	207	574.3298	1146.6450	1146.6431	1.73	0	63	2.6e-005	1	K.GAILTTMLATR.N
☑	216	582.3226	1162.6306	1162.6380	-6.31	0	(28)	0.097	1	K.GAILTTMLATR.N + Oxidation (M)
☑	256	631.3042	1260.5938	1260.5927	0.88	0	62	4.5e-005	1	R.FYFENLWSR.N
☑	257	631.3046	1260.5946	1260.5927	1.51	0	(49)	0.00083	1	R.FYFENLWSR.N
☑	258	631.3048	1260.5950	1260.5927	1.83	0	(54)	0.00028	1	R.FYFENLWSR.N
☑	259	631.3049	1260.5952	1260.5927	1.99	0	(58)	0.00011	1	R.FYFENLWSR.N
☑	260	631.3054	1260.5962	1260.5927	2.78	0	(58)	0.00011	1	R.FYFENLWSR.N
☑	261	631.3054	1260.5962	1260.5927	2.78	0	(37)	0.012	1	R.FYFENLWSR.N
☑	262	631.3058	1260.5970	1260.5927	3.42	0	(41)	0.0055	1	R.FYFENLWSR.N
☑	263	631.3059	1260.5972	1260.5927	3.57	0	(58)	0.00011	1	R.FYFENLWSR.N
☑	264	631.3059	1260.5972	1260.5927	3.57	0	(35)	0.022	1	R.FYFENLWSR.N
☑	265	631.3066	1260.5986	1260.5927	4.68	0	(29)	0.086	1	R.FYFENLWSR.N
☑	266	631.3085	1260.6024	1260.5927	7.70	0	(59)	9.9e-005	1	R.FYFENLWSR.N
	268	631.3294	1260.6442	1260.5927	40.9	0	(4)	35	3	R.FYFENLWSR.N
☑	294	652.3510	1302.6874	1302.6932	-4.41	0	(72)	5e-006	1	R.ITQYLDAGGIPR.T
☑	295	652.3511	1302.6876	1302.6932	-4.26	0	(72)	5.2e-006	1	R.ITQYLDAGGIPR.T
☑	296	652.3549	1302.6952	1302.6932	1.58	0	(60)	6.7e-005	1	R.ITQYLDAGGIPR.T
☑	297	652.3553	1302.6960	1302.6932	2.19	0	(69)	8.8e-006	1	R.ITQYLDAGGIPR.T
☑	298	652.3554	1302.6962	1302.6932	2.35	0	(77)	1.4e-006	1	R.ITQYLDAGGIPR.T
☑	299	652.3554	1302.6962	1302.6932	2.35	0	77	1.3e-006	1	R.ITQYLDAGGIPR.T
☑	300	652.3558	1302.6970	1302.6932	2.96	0	(77)	1.5e-006	1	R.ITQYLDAGGIPR.T
☑	301	652.3565	1302.6984	1302.6932	4.03	0	(69)	9.5e-006	1	R.ITQYLDAGGIPR.T
☑	491	816.8912	1631.7678	1631.7719	-2.47	0	(42)	0.0039	1	R.FTEEYQLFEELGK.G
☑	492	816.8919	1631.7692	1631.7719	-1.61	0	(33)	0.034	1	R.FTEEYQLFEELGK.G
☑	493	816.8925	1631.7704	1631.7719	-0.88	0	(18)	1	1	R.FTEEYQLFEELGK.G
☑	494	816.8930	1631.7714	1631.7719	-0.27	0	(64)	2.4e-005	1	R.FTEEYQLFEELGK.G
☑	495	816.8931	1631.7716	1631.7719	-0.14	0	(38)	0.011	1	R.FTEEYQLFEELGK.G
☑	496	816.8934	1631.7722	1631.7719	0.22	0	(5)	20	1	R.FTEEYQLFEELGK.G
☑	498	816.8940	1631.7734	1631.7719	0.96	0	(65)	1.8e-005	1	R.FTEEYQLFEELGK.G
☑	500	816.8945	1631.7744	1631.7719	1.57	0	(43)	0.003	1	R.FTEEYQLFEELGK.G
☑	501	816.8950	1631.7754	1631.7719	2.19	0	(48)	0.001	1	R.FTEEYQLFEELGK.G
☑	503	816.8951	1631.7756	1631.7719	2.31	0	70	5.7e-006	1	R.FTEEYQLFEELGK.G
☑	504	816.8952	1631.7758	1631.7719	2.43	0	(3)	29	1	R.FTEEYQLFEELGK.G
☑	505	816.8954	1631.7762	1631.7719	2.68	0	(64)	2.8e-005	1	R.FTEEYQLFEELGK.G
☑	506	816.8964	1631.7782	1631.7719	3.90	0	(23)	0.35	1	R.FTEEYQLFEELGK.G
☑	507	816.8967	1631.7788	1631.7719	4.27	0	(63)	2.9e-005	1	R.FTEEYQLFEELGK.G
☑	508	816.8970	1631.7794	1631.7719	4.64	0	(48)	0.001	1	R.FTEEYQLFEELGK.G
☑	509	816.8970	1631.7794	1631.7719	4.64	0	(37)	0.014	1	R.FTEEYQLFEELGK.G
☑	510	816.8972	1631.7798	1631.7719	4.88	0	(50)	0.00068	1	R.FTEEYQLFEELGK.G
☑	511	816.8972	1631.7798	1631.7719	4.88	0	(38)	0.0091	1	R.FTEEYQLFEELGK.G
☑	512	816.8990	1631.7834	1631.7719	7.09	0	(37)	0.012	1	R.FTEEYQLFEELGK.G
☑	513	816.8997	1631.7848	1631.7719	7.95	0	(2)	42	1	R.FTEEYQLFEELGK.G
☑	646	694.3165	2079.9277	2079.9426	-7.15	0	(51)	0.0003	1	K.AGAYDFPSPEWDTVTPEAK.D
☑	647	694.3185	2079.9337	2079.9426	-4.27	0	(60)	3.8e-005	1	K.AGAYDFPSPEWDTVTPEAK.D
☑	648	1040.9807	2079.9468	2079.9426	2.07	0	(60)	4.5e-005	1	K.AGAYDFPSPEWDTVTPEAK.D
☑	649	1040.9808	2079.9470	2079.9426	2.16	0	(43)	0.0021	1	K.AGAYDFPSPEWDTVTPEAK.D
☑	650	1040.9817	2079.9488	2079.9426	3.03	0	(53)	0.0002	1	K.AGAYDFPSPEWDTVTPEAK.D
☑	651	1040.9820	2079.9494	2079.9426	3.32	0	(56)	0.00011	1	K.AGAYDFPSPEWDTVTPEAK.D
☑	652	1040.9820	2079.9494	2079.9426	3.32	0	(50)	0.00046	1	K.AGAYDFPSPEWDTVTPEAK.D
☑	653	1040.9828	2079.9510	2079.9426	4.09	0	(45)	0.0013	1	K.AGAYDFPSPEWDTVTPEAK.D
☑	654	1040.9838	2079.9530	2079.9426	5.05	0	74	1.9e-006	1	K.AGAYDFPSPEWDTVTPEAK.D
☑	655	1040.9847	2079.9548	2079.9426	5.91	0	(34)	0.019	1	K.AGAYDFPSPEWDTVTPEAK.D
☑	662	715.3441	2143.0105	2143.0321	-10.08	0	61	4.1e-005	1	K.VTEQLIEAISNGDFESYTK.M
☑	663	1072.5222	2143.0298	2143.0321	-1.04	0	(38)	0.0075	1	K.VTEQLIEAISNGDFESYTK.M
☑	664	1072.5251	2143.0356	2143.0321	1.67	0	(54)	0.00019	1	K.VTEQLIEAISNGDFESYTK.M
☑	665	1072.5334	2143.0522	2143.0321	9.41	0	(11)	4.6	1	K.VTEQLIEAISNGDFESYTK.M
☑	696	888.7555	2663.2447	2663.2755	-11.57	1	(27)	0.084	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
☑	697	888.7577	2663.2513	2663.2755	-9.10	1	(8)	6.2	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
☑	698	888.7581	2663.2525	2663.2755	-8.65	1	(5)	14	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
☑	699	888.7607	2663.2603	2663.2755	-5.72	1	(22)	0.24	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
☑	701	888.7623	2663.2651	2663.2755	-3.91	1	(8)	7.1	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
☑	703	888.7635	2663.2687	2663.2755	-2.56	1	37	0.0079	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M

Proteins matching the same set of peptides:

IPI00621806 **Mass:** 54651 **Score:** 1121 **Queries matched:** 76
Tax_Id=10090 Gene_Symbol=Camk2a Isoform Alpha CaMKII of Calcium/calmodulin-dependent protein kinase type II subunit alpha

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2. IPI00474502 **Mass:** 61164 **Score:** 595 **Queries matched:** 38 **emPAI:** 0.52
Tax_Id=10090 Gene_Symbol=Camk2b Calcium/calmodulin-dependent protein kinase type II subunit 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
	27	588.3868	587.3795	587.3642	26.0	0	22	0.71	1	K.IINTK.K
☑	193	572.8034	1143.5922	1143.5964	-3.65	0	(13)	4.4	1	R.FYFENLLAK.N
☑	194	572.8046	1143.5946	1143.5964	-1.55	0	(19)	1	1	R.FYFENLLAK.N
☑	196	572.8075	1143.6004	1143.5964	3.52	0	22	0.51	1	R.FYFENLLAK.N
☑	197	572.8082	1143.6018	1143.5964	4.75	0	(12)	4.9	1	R.FYFENLLAK.N
	198	572.8111	1143.6076	1143.5964	9.82	0	(4)	32	2	R.FYFENLLAK.N
	201	574.3237	1146.6328	1146.6431	-8.91	0	(39)	0.0079	1	K.GAILTTMLATR.N
	202	574.3245	1146.6344	1146.6431	-7.52	0	(51)	0.00057	1	K.GAILTTMLATR.N
	204	574.3274	1146.6402	1146.6431	-2.46	0	(36)	0.014	1	K.GAILTTMLATR.N
	205	574.3279	1146.6412	1146.6431	-1.59	0	(49)	0.00074	1	K.GAILTTMLATR.N
	206	574.3290	1146.6434	1146.6431	0.33	0	(24)	0.21	1	K.GAILTTMLATR.N
	207	574.3298	1146.6450	1146.6431	1.73	0	63	2.6e-005	1	K.GAILTTMLATR.N
	216	582.3226	1162.6306	1162.6380	-6.31	0	(28)	0.097	1	K.GAILTTMLATR.N + Oxidation (M)
☑	372	735.4076	1468.8006	1468.8071	-4.42	0	(18)	0.75	1	K.NLINQMLTINPAK.R
☑	373	735.4100	1468.8054	1468.8071	-1.15	0	(63)	2.7e-005	1	K.NLINQMLTINPAK.R
☑	374	735.4109	1468.8072	1468.8071	0.07	0	75	1.7e-006	1	K.NLINQMLTINPAK.R
☑	375	735.4146	1468.8146	1468.8071	5.11	0	(62)	3.1e-005	1	K.NLINQMLTINPAK.R
☑	376	735.4150	1468.8154	1468.8071	5.65	0	(71)	3.6e-006	1	K.NLINQMLTINPAK.R
☑	480	810.8856	1619.7566	1619.7355	13.1	0	(4)	26	1	R.FTDEYQLYEDIGK.G
☑	481	810.8877	1619.7608	1619.7355	15.6	0	8	9.3	1	R.FTDEYQLYEDIGK.G
☑	632	656.9538	1967.8396	1967.8556	-8.12	1	52	0.00014	1	K.ESSDSTNTTIEDEDAKAR.K
	646	694.3165	2079.9277	2079.9426	-7.15	0	(51)	0.0003	1	K.AGAYDFPSPEWDTVTPEAK.N
	647	694.3185	2079.9337	2079.9426	-4.27	0	(60)	3.8e-005	1	K.AGAYDFPSPEWDTVTPEAK.N
	648	1040.9807	2079.9468	2079.9426	2.07	0	(60)	4.5e-005	1	K.AGAYDFPSPEWDTVTPEAK.N
	649	1040.9808	2079.9470	2079.9426	2.16	0	(43)	0.0021	1	K.AGAYDFPSPEWDTVTPEAK.N
	650	1040.9817	2079.9488	2079.9426	3.03	0	(53)	0.0002	1	K.AGAYDFPSPEWDTVTPEAK.N
	651	1040.9820	2079.9494	2079.9426	3.32	0	(56)	0.00011	1	K.AGAYDFPSPEWDTVTPEAK.N
	652	1040.9820	2079.9494	2079.9426	3.32	0	(50)	0.00046	1	K.AGAYDFPSPEWDTVTPEAK.N
	653	1040.9828	2079.9510	2079.9426	4.09	0	(45)	0.0013	1	K.AGAYDFPSPEWDTVTPEAK.N
	654	1040.9838	2079.9530	2079.9426	5.05	0	74	1.9e-006	1	K.AGAYDFPSPEWDTVTPEAK.N
	655	1040.9847	2079.9548	2079.9426	5.91	0	(34)	0.019	1	K.AGAYDFPSPEWDTVTPEAK.N
☑	676	785.0440	2352.1102	2352.1301	-8.48	0	(91)	3.4e-008	1	R.QTTAPATMSTAASGTTMGLVEQAK.S
☑	677	785.0472	2352.1198	2352.1301	-4.40	0	(90)	3.9e-008	1	R.QTTAPATMSTAASGTTMGLVEQAK.S
☑	678	1177.0771	2352.1396	2352.1301	4.05	0	(32)	0.025	1	R.QTTAPATMSTAASGTTMGLVEQAK.S
☑	679	1177.0814	2352.1482	2352.1301	7.71	0	91	3.4e-008	1	R.QTTAPATMSTAASGTTMGLVEQAK.S
☑	681	785.4148	2353.2226	2353.2642	-17.67	0	(13)	1.9	1	K.GSLPPAALEPQTTVIHNPVDGIK.E
☑	682	785.4241	2353.2505	2353.2642	-5.82	0	14	1.5	1	K.GSLPPAALEPQTTVIHNPVDGIK.E
☑	685	790.3805	2368.1197	2368.1250	-2.26	0	(42)	0.0024	1	R.QTTAPATMSTAASGTTMGLVEQAK.S + Oxidation (M)

Proteins matching the same set of peptides:
IPI00875723 **Mass:** 68686 **Score:** 595 **Queries matched:** 38
Tax_Id=10090 Gene_Symbol=Camk2b 68 kDa protein

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3. IPI00109073 **Mass:** 50010 **Score:** 415 **Queries matched:** 22 **emPAI:** 0.38
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
☑	191	572.3217	1142.6288	1142.6270	1.59	0	69	1.1e-005	1	K.LAVNMVPFPR.L
☑	192	572.3229	1142.6312	1142.6270	3.69	0	(38)	0.013	1	K.LAVNMVPFPR.L
☑	308	660.3503	1318.6860	1318.6955	-7.18	0	(63)	4.2e-005	1	R.IMNTFSVVPSPK.V
☑	309	660.3552	1318.6958	1318.6955	0.26	0	(32)	0.048	1	R.IMNTFSVVPSPK.V
☑	310	660.3563	1318.6980	1318.6955	1.92	0	(71)	6.3e-006	1	R.IMNTFSVVPSPK.V
☑	311	660.3572	1318.6998	1318.6955	3.29	0	104	2.8e-009	1	R.IMNTFSVVPSPK.V
☑	454	801.4125	1600.8104	1600.8131	-1.63	0	(65)	2.2e-005	1	R.AVLVDLEPGTMDSVR.S
☑	455	801.4150	1600.8154	1600.8131	1.49	0	79	8.4e-007	1	R.AVLVDLEPGTMDSVR.S
☑	456	801.4152	1600.8158	1600.8131	1.74	0	(59)	8.6e-005	1	R.AVLVDLEPGTMDSVR.S
☑	457	801.4156	1600.8166	1600.8131	2.24	0	(60)	6.8e-005	1	R.AVLVDLEPGTMDSVR.S
☑	458	801.4175	1600.8204	1600.8131	4.61	0	(65)	1.8e-005	1	R.AVLVDLEPGTMDSVR.S
☑	475	809.4103	1616.8060	1616.8080	-1.20	0	(36)	0.017	1	R.AVLVDLEPGTMDSVR.S + Oxidation (M)
	521	846.4363	1690.8580	1690.8600	-1.16	0	(13)	3.3	2	R.ALTVPELTQQMFDAK.N
☑	522	846.4375	1690.8604	1690.8600	0.26	0	(34)	0.027	1	R.ALTVPELTQQMFDAK.N
☑	523	846.4381	1690.8616	1690.8600	0.97	0	(28)	0.099	1	R.ALTVPELTQQMFDAK.N
☑	524	846.4382	1690.8618	1690.8600	1.09	0	53	0.00034	1	R.ALTVPELTQQMFDAK.N
☑	526	848.9185	1695.8224	1695.8257	-1.89	0	12	3.8	1	K.NSSYFVEWIPNNVK.T
	558	854.4335	1706.8524	1706.8549	-1.45	0	(28)	0.11	2	R.ALTVPELTQQMFDAK.N + Oxidation (M)
	560	854.4359	1706.8572	1706.8549	1.36	0	(16)	1.5	2	R.ALTVPELTQQMFDAK.N + Oxidation (M)
☑	601	915.4471	1828.8796	1828.8744	2.87	0	65	2e-005	1	R.INVYYNEATGGNYVPR.A
☑	602	915.4512	1828.8878	1828.8744	7.36	0	(41)	0.0042	1	R.INVYYNEATGGNYVPR.A
	603	915.4561	1828.8976	1828.8744	12.7	0	(5)	18	4	R.INVYYNEATGGNYVPR.A

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4. IPI00169463 **Mass:** 50255 **Score:** 404 **Queries matched:** 20 **emPAI:** 0.37
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

	191	572.3217	1142.6288	1142.6270	1.59	0	69	1.1e-005	1	K.LAVNMVPFPR.L
	192	572.3229	1142.6312	1142.6270	3.69	0	(38)	0.013	1	K.LAVNMVPFPR.L
	308	660.3503	1318.6860	1318.6955	-7.18	0	(63)	4.2e-005	1	R.IMNTFSVVPSPK.V
	309	660.3552	1318.6958	1318.6955	0.26	0	(32)	0.048	1	R.IMNTFSVVPSPK.V
	310	660.3563	1318.6980	1318.6955	1.92	0	(71)	6.3e-006	1	R.IMNTFSVVPSPK.V
	311	660.3572	1318.6998	1318.6955	3.29	0	104	2.8e-009	1	R.IMNTFSVVPSPK.V
☑	**363**	**723.8521**	**1445.6896**	**1445.6820**	**5.28**	**0**	**61**	**5.4e-005**	**1**	**K.EVDEQMLNVQNK.N**
	454	801.4125	1600.8104	1600.8131	-1.63	0	(65)	2.2e-005	1	R.AVLVDLEPGTMDSVR.S
	455	801.4150	1600.8154	1600.8131	1.49	0	79	8.4e-007	1	R.AVLVDLEPGTMDSVR.S
	456	801.4152	1600.8158	1600.8131	1.74	0	(59)	8.6e-005	1	R.AVLVDLEPGTMDSVR.S
	457	801.4156	1600.8166	1600.8131	2.24	0	(60)	6.8e-005	1	R.AVLVDLEPGTMDSVR.S
	458	801.4175	1600.8204	1600.8131	4.61	0	(65)	1.8e-005	1	R.AVLVDLEPGTMDSVR.S
	475	809.4103	1616.8060	1616.8080	-1.20	0	(36)	0.017	1	R.AVLVDLEPGTMDSVR.S + Oxidation (M)
	521	846.4363	1690.8580	1690.8600	-1.16	0	(13)	3.3	2	R.ALTVPELTQQMFDAK.N
	522	846.4375	1690.8604	1690.8600	0.26	0	(34)	0.027	1	R.ALTVPELTQQMFDAK.N
	523	846.4381	1690.8616	1690.8600	0.97	0	(28)	0.099	1	R.ALTVPELTQQMFDAK.N
	524	846.4382	1690.8618	1690.8600	1.09	0	53	0.00034	1	R.ALTVPELTQQMFDAK.N
	526	848.9185	1695.8224	1695.8257	-1.89	0	12	3.8	1	K.NSSYFVEWIPNNVK.T
	558	854.4335	1706.8524	1706.8549	-1.45	0	(28)	0.11	2	R.ALTVPELTQQMFDAK.N + Oxidation (M)
	560	854.4359	1706.8572	1706.8549	1.36	0	(16)	1.5	2	R.ALTVPELTQQMFDAK.N + Oxidation (M)

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5. IPI00124695 **Mass:** 60254 **Score:** 386 **Queries matched:** 19 **emPAI:** 0.24
Tax_Id=10090 Gene_Symbol=Camk2g Isoform 1 of Calcium/calmodulin-dependent protein kinase type II 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
	27	588.3868	587.3795	587.3642	26.0	0	22	0.71	1	K.IINTK.K
	372	735.4076	1468.8006	1468.8071	-4.42	0	(18)	0.75	1	K.NLINQMLTINPAK.R
	373	735.4100	1468.8054	1468.8071	-1.15	0	(63)	2.7e-005	1	K.NLINQMLTINPAK.R
	374	735.4109	1468.8072	1468.8071	0.07	0	75	1.7e-006	1	K.NLINQMLTINPAK.R
	375	735.4146	1468.8146	1468.8071	5.11	0	(62)	3.1e-005	1	K.NLINQMLTINPAK.R
	376	735.4150	1468.8154	1468.8071	5.65	0	(71)	3.6e-006	1	K.NLINQMLTINPAK.R
☑	**463**	**802.8795**	**1603.7444**	**1603.7406**	**2.40**	**0**	**51**	**0.00037**	**1**	**R.FTDDYQLFEELGK.G**
☑	**464**	**802.8842**	**1603.7538**	**1603.7406**	**8.26**	**0**	**(29)**	**0.074**	**1**	**R.FTDDYQLFEELGK.G**
☑	**465**	**802.8851**	**1603.7556**	**1603.7406**	**9.38**	**0**	**(37)**	**0.011**	**1**	**R.FTDDYQLFEELGK.G**
	646	694.3165	2079.9277	2079.9426	-7.15	0	(51)	0.0003	1	K.AGAYDFPSPEWDTVTPEAK.N
	647	694.3185	2079.9337	2079.9426	-4.27	0	(60)	3.8e-005	1	K.AGAYDFPSPEWDTVTPEAK.N
	648	1040.9807	2079.9468	2079.9426	2.07	0	(60)	4.5e-005	1	K.AGAYDFPSPEWDTVTPEAK.N
	649	1040.9808	2079.9470	2079.9426	2.16	0	(43)	0.0021	1	K.AGAYDFPSPEWDTVTPEAK.N
	650	1040.9817	2079.9488	2079.9426	3.03	0	(53)	0.0002	1	K.AGAYDFPSPEWDTVTPEAK.N
	651	1040.9820	2079.9494	2079.9426	3.32	0	(56)	0.00011	1	K.AGAYDFPSPEWDTVTPEAK.N
	652	1040.9820	2079.9494	2079.9426	3.32	0	(50)	0.00046	1	K.AGAYDFPSPEWDTVTPEAK.N
	653	1040.9828	2079.9510	2079.9426	4.09	0	(45)	0.0013	1	K.AGAYDFPSPEWDTVTPEAK.N
	654	1040.9838	2079.9530	2079.9426	5.05	0	74	1.9e-006	1	K.AGAYDFPSPEWDTVTPEAK.N
	655	1040.9847	2079.9548	2079.9426	5.91	0	(34)	0.019	1	K.AGAYDFPSPEWDTVTPEAK.N

Proteins matching the same set of peptides:
IPI00228044 **Mass:** 59013 **Score:** 386 **Queries matched:** 19
Tax_Id=10090 Gene_Symbol=Camk2g Isoform 2 of Calcium/calmodulin-dependent protein kinase type II subunit gamma
IPI00228045 **Mass:** 56610 **Score:** 386 **Queries matched:** 19
Tax_Id=10090 Gene_Symbol=Camk2g Isoform 3 of Calcium/calmodulin-dependent protein kinase type II subunit gamma

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6. IPI00117352 **Mass:** 50095 **Score:** 381 **Queries matched:** 16 **emPAI:** 0.38
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
	191	572.3217	1142.6288	1142.6270	1.59	0	69	1.1e-005	1	K.LAVNMVPFPR.L
	192	572.3229	1142.6312	1142.6270	3.69	0	(38)	0.013	1	K.LAVNMVPFPR.L
	308	660.3503	1318.6860	1318.6955	-7.18	0	(63)	4.2e-005	1	R.IMNTFSVVPSPK.V
	309	660.3552	1318.6958	1318.6955	0.26	0	(32)	0.048	1	R.IMNTFSVVPSPK.V
	310	660.3563	1318.6980	1318.6955	1.92	0	(71)	6.3e-006	1	R.IMNTFSVVPSPK.V
	311	660.3572	1318.6998	1318.6955	3.29	0	104	2.8e-009	1	R.IMNTFSVVPSPK.V
	363	723.8521	1445.6896	1445.6820	5.28	0	61	5.4e-005	1	K.EVDEQMLNVQNK.N
☑	**468**	**808.4218**	**1614.8290**	**1614.8287**	**0.21**	**0**	**(36)**	**0.02**	**1**	**R.AILVDLEPGTMDSVR.S**
☑	**469**	**808.4241**	**1614.8336**	**1614.8287**	**3.06**	**0**	**(70)**	**7.9e-006**	**1**	**R.AILVDLEPGTMDSVR.S**
☑	**470**	**808.4243**	**1614.8340**	**1614.8287**	**3.31**	**0**	**(60)**	**7.8e-005**	**1**	**R.AILVDLEPGTMDSVR.S**
☑	**471**	**808.4246**	**1614.8346**	**1614.8287**	**3.68**	**0**	**70**	**7.2e-006**	**1**	**R.AILVDLEPGTMDSVR.S**
☑	**489**	**816.4179**	**1630.8212**	**1630.8236**	**-1.46**	**0**	**(48)**	**0.0011**	**1**	**R.AILVDLEPGTMDSVR.S + Oxidation (M)**
☑	**490**	**816.4210**	**1630.8274**	**1630.8236**	**2.34**	**0**	**(54)**	**0.00032**	**1**	**R.AILVDLEPGTMDSVR.S + Oxidation (M)**
☑	**518**	**830.4456**	**1658.8766**	**1658.8879**	**-6.81**	**0**	**(13)**	**2.7**	**1**	**R.ALTVPELTQQVFDAK.N**
☑	**519**	**830.4520**	**1658.8894**	**1658.8879**	**0.91**	**0**	**28**	**0.085**	**1**	**R.ALTVPELTQQVFDAK.N**
	526	848.9185	1695.8224	1695.8257	-1.89	0	12	3.8	1	K.NSSYFVEWIPNNVK.T

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7. IPI00109061 **Mass:** 50377 **Score:** 375 **Queries matched:** 16 **emPAI:** 0.46
Tax_Id=10090 Gene_Symbol=Tubb2b Tubulin beta-2B 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
	191	572.3217	1142.6288	1142.6270	1.59	0	69	1.1e-005	1	K.LAVNMVPFPR.L
	192	572.3229	1142.6312	1142.6270	3.69	0	(38)	0.013	1	K.LAVNMVPFPR.L
☑	**330**	**676.3404**	**1350.6662**	**1350.6676**	**-0.98**	**0**	**(65)**	**2.1e-005**	**1**	**R.IMNTFSVMPSPK.V**
☑	**331**	**676.3443**	**1350.6740**	**1350.6676**	**4.79**	**0**	**82**	**5.1e-007**	**1**	**R.IMNTFSVMPSPK.V**
☑	**332**	**676.3445**	**1350.6744**	**1350.6676**	**5.09**	**0**	**(64)**	**3.2e-005**	**1**	**R.IMNTFSVMPSPK.V**
	363	723.8521	1445.6896	1445.6820	5.28	0	61	5.4e-005	1	K.EVDEQMLNVQNK.N

	468	808.4218	1614.8290	1614.8287	0.21	0	(36)	0.02	1	R.AILVDLEPGTMDSVR.S
	469	808.4241	1614.8336	1614.8287	3.06	0	(70)	7.9e-006	1	R.AILVDLEPGTMDSVR.S
	470	808.4243	1614.8340	1614.8287	3.31	0	(60)	7.8e-005	1	R.AILVDLEPGTMDSVR.S
	471	808.4246	1614.8346	1614.8287	3.68	0	70	7.2e-006	1	R.AILVDLEPGTMDSVR.S
	489	816.4179	1630.8212	1630.8236	-1.46	0	(48)	0.0011	1	R.AILVDLEPGTMDSVR.S + Oxidation (M)
	490	816.4210	1630.8274	1630.8236	2.34	0	(54)	0.00032	1	R.AILVDLEPGTMDSVR.S + Oxidation (M)
	526	848.9185	1695.8224	1695.8257	-1.89	0	12	3.8	1	K.NSSYFVEWIPNNVK.T
☑	558	854.4335	1706.8524	1706.8549	-1.45	0	40	0.0068	1	R.ALTVPELTQQMFDSK.N
☑	559	**854.4358**	**1706.8570**	**1706.8549**	**1.25**	**0**	**(4)**	**27**	**1**	**R.ALTVPELTQQMFDSK.N**
☑	560	854.4359	1706.8572	1706.8549	1.36	0	(24)	0.24	1	R.ALTVPELTQQMFDSK.N

Proteins matching the same set of peptides:
IPI00338039 **Mass:** 50274 **Score:** 375 **Queries matched:** 16
Tax_Id=10090 Gene_Symbol=Tubb2a Tubulin beta-2A chain

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8. IPI00112251 **Mass:** 50842 **Score:** 372 **Queries matched:** 19 **emPAI:** 0.37
Tax_Id=10090 Gene_Symbol=Tubb3 Tubulin beta-3 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
191	572.3217	1142.6288	1142.6270	1.59	0	69	1.1e-005	1	K.LAVNMVPFPR.L
192	572.3229	1142.6312	1142.6270	3.69	0	(38)	0.013	1	K.LAVNMVPFPR.L
308	660.3503	1318.6860	1318.6955	-7.18	0	(63)	4.2e-005	1	R.IMNTFSVVPSPK.V
309	660.3552	1318.6958	1318.6955	0.26	0	(32)	0.048	1	R.IMNTFSVVPSPK.V
310	660.3563	1318.6980	1318.6955	1.92	0	(71)	6.3e-006	1	R.IMNTFSVVPSPK.V
311	660.3572	1318.6998	1318.6955	3.29	0	104	2.8e-009	1	R.IMNTFSVVPSPK.V
468	808.4218	1614.8290	1614.8287	0.21	0	(36)	0.02	1	R.AILVDLEPGTMDSVR.S
469	808.4241	1614.8336	1614.8287	3.06	0	(70)	7.9e-006	1	R.AILVDLEPGTMDSVR.S
470	808.4243	1614.8340	1614.8287	3.31	0	(60)	7.8e-005	1	R.AILVDLEPGTMDSVR.S
471	808.4246	1614.8346	1614.8287	3.68	0	70	7.2e-006	1	R.AILVDLEPGTMDSVR.S
489	816.4179	1630.8212	1630.8236	-1.46	0	(48)	0.0011	1	R.AILVDLEPGTMDSVR.S + Oxidation (M)
490	816.4210	1630.8274	1630.8236	2.34	0	(54)	0.00032	1	R.AILVDLEPGTMDSVR.S + Oxidation (M)
521	846.4363	1690.8580	1690.8600	-1.16	0	(13)	3.3	2	R.ALTVPELTQQMFDAK.N
522	846.4375	1690.8604	1690.8600	0.26	0	(34)	0.027	1	R.ALTVPELTQQMFDAK.N
523	846.4381	1690.8616	1690.8600	0.97	0	(28)	0.099	1	R.ALTVPELTQQMFDAK.N
524	846.4382	1690.8618	1690.8600	1.09	0	53	0.00034	1	R.ALTVPELTQQMFDAK.N
526	848.9185	1695.8224	1695.8257	-1.89	0	12	3.8	1	K.NSSYFVEWIPNNVK.V
558	854.4335	1706.8524	1706.8549	-1.45	0	(28)	0.11	2	R.ALTVPELTQQMFDAK.N + Oxidation (M)
560	854.4359	1706.8572	1706.8549	1.36	0	(16)	1.5	2	R.ALTVPELTQQMFDAK.N + Oxidation (M)

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9. IPI00755181 **Mass:** 57178 **Score:** 296 **Queries matched:** 11 **emPAI:** 0.32
Tax_Id=10090 Gene_Symbol=Krt10 keratin, type I cytoskeletal 10
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	170	545.7681	1089.5216	1089.5237	-1.87	0	(65)	2.8e-005	1	K.VTMQNLNDR.L
☑	171	545.7692	1089.5238	1089.5237	0.15	0	83	4.1e-007	1	K.VTMQNLNDR.L
☑	175	553.7703	1105.5260	1105.5186	6.74	0	(35)	0.029	1	K.VTMQNLNDR.L + Oxidation (M)
☑	176	553.7716	1105.5286	1105.5186	9.09	0	(50)	0.00085	1	K.VTMQNLNDR.L + Oxidation (M)
☑	217	583.2936	1164.5726	1164.5775	-4.14	0	(36)	0.019	1	R.LENEIQTYR.S
☑	218	583.2956	1164.5766	1164.5775	-0.70	0	41	0.0064	1	R.LENEIQTYR.S
☑	340	691.3282	1380.6418	1380.6408	0.73	0	(52)	0.00037	1	R.ALEESNYELEGK.I
☑	341	691.3283	1380.6420	1380.6408	0.88	0	(74)	2.5e-006	1	R.ALEESNYELEGK.I
☑	342	691.3298	1380.6450	1380.6408	3.05	0	87	1.1e-007	1	R.ALEESNYELEGK.I
☑	343	691.3315	1380.6484	1380.6408	5.51	0	(55)	0.00017	1	R.ALEESNYELEGK.I
☑	353	695.8544	1389.6942	1389.6736	14.9	0	55	0.00024	1	K.QSLEASLAETEGR.Y

Proteins matching the same set of peptides:
IPI00798492 **Mass:** 57906 **Score:** 296 **Queries matched:** 11
Tax_Id=10090 Gene_Symbol=Krt10 Isoform 1 of Keratin, type I cytoskeletal 10
IPI00828744 **Mass:** 57197 **Score:** 296 **Queries matched:** 11
Tax_Id=10090 Gene_Symbol=Krt10 Isoform 2 of Keratin, type I cytoskeletal 10

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10. IPI00110753 **Mass:** 50788 **Score:** 288 **Queries matched:** 21 **emPAI:** 0.06
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
☑	529	851.4498	1700.8850	1700.8985	-7.92	0	(1)	45	1	R.AVFVDLEPTVIDEVR.T
☑	530	851.4507	1700.8868	1700.8985	-6.86	0	(58)	8.7e-005	1	R.AVFVDLEPTVIDEVR.T
☑	532	851.4516	1700.8886	1700.8985	-5.80	0	(60)	6.1e-005	1	R.AVFVDLEPTVIDEVR.T
☑	533	851.4528	1700.8910	1700.8985	-4.39	0	(70)	5.8e-006	1	R.AVFVDLEPTVIDEVR.T
☑	534	851.4536	1700.8926	1700.8985	-3.45	0	(57)	0.00013	1	R.AVFVDLEPTVIDEVR.T
	535	851.4545	1700.8944	1700.8985	-2.39	0	(1)	47	2	R.AVFVDLEPTVIDEVR.T
☑	536	851.4548	1700.8950	1700.8985	-2.04	0	(40)	0.0052	1	R.AVFVDLEPTVIDEVR.T
☑	537	851.4554	1700.8962	1700.8985	-1.33	0	(20)	0.6	1	R.AVFVDLEPTVIDEVR.T
☑	539	851.4562	1700.8978	1700.8985	-0.39	0	(38)	0.0081	1	R.AVFVDLEPTVIDEVR.T
☑	540	851.4565	1700.8984	1700.8985	-0.04	0	(21)	0.49	1	R.AVFVDLEPTVIDEVR.T
☑	541	851.4575	1700.9004	1700.8985	1.14	0	(44)	0.0021	1	R.AVFVDLEPTVIDEVR.T
☑	542	851.4576	1700.9006	1700.8985	1.25	0	(23)	0.3	1	R.AVFVDLEPTVIDEVR.T
☑	543	851.4583	1700.9020	1700.8985	2.08	0	(49)	0.00072	1	R.AVFVDLEPTVIDEVR.T
☑	544	851.4584	1700.9022	1700.8985	2.20	0	(5)	17	1	R.AVFVDLEPTVIDEVR.T
☑	545	851.4591	1700.9036	1700.8985	3.02	0	77	1.1e-006	1	R.AVFVDLEPTVIDEVR.T
☑	546	851.4612	1700.9078	1700.8985	5.49	0	(22)	0.33	1	R.AVFVDLEPTVIDEVR.T

☑	547	851.4636	1700.9126	1700.8985	8.31	0	(56)	0.00013	1	R.AVFVDLEPTVIDEVR.T
☑	548	851.4642	1700.9138	1700.8985	9.02	0	(46)	0.0012	1	R.AVFVDLEPTVIDEVR.T
☑	597	912.9963	1823.9780	1823.9782	-0.06	0	(12)	2.8	1	K.VGINYQPPTVVPGGDLAK.V
☑	598	912.9998	1823.9850	1823.9782	3.77	0	22	0.25	1	K.VGINYQPPTVVPGGDLAK.V
☑	635	1004.4624	2006.9102	2006.8858	12.2	0	22	0.25	1	K.TIGGGDDSFNTFFSETGAGK.H

Proteins matching the same set of peptides:
IPI00117348 **Mass:** 50804 **Score:** 288 **Queries matched:** 21
Tax_Id=10090 Gene_Symbol=Tuba1b Tubulin alpha-1B chain
IPI00403810 **Mass:** 50562 **Score:** 288 **Queries matched:** 21
Tax_Id=10090 Gene_Symbol=Tuba1c Tubulin alpha-1C chain

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11. IPI00112584 **Mass:** 56961 **Score:** 284 **Queries matched:** 34 **emPAI:** 0.48
Tax_Id=10090 Gene_Symbol=Camk2d Isoform 1 of Calcium/calmodulin-dependent protein kinase type II subunit 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
	27	588.3868	587.3795	587.3642	26.0	0	22	0.71	1	K.IINTK.K
	162	539.2801	1076.5456	1076.5502	-4.23	0	(1)	72	5	K.IPTGQEYAAK.I
☑	163	539.2836	1076.5526	1076.5502	2.27	0	24	0.38	1	K.IPTGQEYAAK.I
	164	539.2836	1076.5526	1076.5502	2.27	0	(6)	21	2	K.IPTGQEYAAK.I
☑	183	559.7768	1117.5390	1117.5444	-4.78	0	35	0.025	1	R.FYFENALSK.S
☑	184	559.7831	1117.5516	1117.5444	6.50	0	(11)	6.4	1	R.FYFENALSK.S
	201	574.3237	1146.6328	1146.6431	-8.91	0	(39)	0.0079	1	K.GAILTTMLATR.N
	202	574.3245	1146.6344	1146.6431	-7.52	0	(51)	0.00057	1	K.GAILTTMLATR.N
	204	574.3274	1146.6402	1146.6431	-2.46	0	(36)	0.014	1	K.GAILTTMLATR.N
	205	574.3279	1146.6412	1146.6431	-1.59	0	(49)	0.00074	1	K.GAILTTMLATR.N
	206	574.3290	1146.6434	1146.6431	0.33	0	(24)	0.21	1	K.GAILTTMLATR.N
	207	574.3298	1146.6450	1146.6431	1.73	0	63	2.6e-005	1	K.GAILTTMLATR.N
	216	582.3226	1162.6306	1162.6380	-6.31	0	(28)	0.097	1	K.GAILTTMLATR.N + Oxidation (M)
☑	312	664.3106	1326.6066	1326.5948	8.93	0	38	0.0084	1	R.LTQYMDGSGMPK.T
☑	313	664.3110	1326.6074	1326.5948	9.53	0	(29)	0.071	1	R.LTQYMDGSGMPK.T
☑	476	809.8831	1617.7516	1617.7562	-2.84	0	(7)	11	1	R.FTDEYQLFEELGK.G
☑	477	809.8839	1617.7532	1617.7562	-1.85	0	(36)	0.012	1	R.FTDEYQLFEELGK.G
☑	478	809.8858	1617.7570	1617.7562	0.50	0	48	0.0009	1	R.FTDEYQLFEELGK.G
	646	694.3165	2079.9277	2079.9426	-7.15	0	(51)	0.0003	1	K.AGAYDFPSPEWDTVTPEAK.D
	647	694.3185	2079.9337	2079.9426	-4.27	0	(60)	3.8e-005	1	K.AGAYDFPSPEWDTVTPEAK.D
	648	1040.9807	2079.9468	2079.9426	2.07	0	(60)	4.5e-005	1	K.AGAYDFPSPEWDTVTPEAK.D
	649	1040.9808	2079.9470	2079.9426	2.16	0	(43)	0.0021	1	K.AGAYDFPSPEWDTVTPEAK.D
	650	1040.9817	2079.9488	2079.9426	3.03	0	(53)	0.0002	1	K.AGAYDFPSPEWDTVTPEAK.D
	651	1040.9820	2079.9494	2079.9426	3.32	0	(56)	0.00011	1	K.AGAYDFPSPEWDTVTPEAK.D
	652	1040.9820	2079.9494	2079.9426	3.32	0	(50)	0.00046	1	K.AGAYDFPSPEWDTVTPEAK.D
	653	1040.9828	2079.9510	2079.9426	4.09	0	(45)	0.0013	1	K.AGAYDFPSPEWDTVTPEAK.D
	654	1040.9838	2079.9530	2079.9426	5.05	0	74	1.9e-006	1	K.AGAYDFPSPEWDTVTPEAK.D
	655	1040.9847	2079.9548	2079.9426	5.91	0	(34)	0.019	1	K.AGAYDFPSPEWDTVTPEAK.D
	696	888.7555	2663.2447	2663.2755	-11.57	1	(27)	0.084	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
	697	888.7577	2663.2513	2663.2755	-9.10	1	(8)	6.2	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
	698	888.7581	2663.2525	2663.2755	-8.65	1	(5)	14	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
	699	888.7607	2663.2603	2663.2755	-5.72	1	(22)	0.24	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
	701	888.7623	2663.2651	2663.2755	-3.91	1	(8)	7.1	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
	703	888.7635	2663.2687	2663.2755	-2.56	1	37	0.0079	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M

Proteins matching the same set of peptides:
IPI00406790 **Mass:** 60593 **Score:** 284 **Queries matched:** 34
Tax_Id=10090 Gene_Symbol=Camk2d Isoform 4 of Calcium/calmodulin-dependent protein kinase type II subunit delta
IPI00475044 **Mass:** 55899 **Score:** 284 **Queries matched:** 34
Tax_Id=10090 Gene_Symbol=Camk2d Isoform 2 of Calcium/calmodulin-dependent protein kinase type II subunit delta
IPI00828919 **Mass:** 58492 **Score:** 284 **Queries matched:** 34
Tax_Id=10090 Gene_Symbol=Camk2d Isoform 3 of Calcium/calmodulin-dependent protein kinase type II subunit delta
IPI00857865 **Mass:** 54664 **Score:** 284 **Queries matched:** 34
Tax_Id=10090 Gene_Symbol=Camk2d Putative uncharacterized protein
IPI00858128 **Mass:** 58283 **Score:** 284 **Queries matched:** 34
Tax_Id=10090 Gene_Symbol=Camk2d calcium/calmodulin-dependent protein kinase type II subunit delta isoform 1
IPI00858144 **Mass:** 55828 **Score:** 284 **Queries matched:** 34
Tax_Id=10090 Gene_Symbol=Camk2d 55 kDa protein

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12. IPI00608020 **Mass:** 20817 **Score:** 247 **Queries matched:** 6 **emPAI:** 0.35
Tax_Id=10090 Gene_Symbol=Ftl1 ferritin light chain 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
☑	125	517.7652	1033.5158	1033.5192	-3.28	0	(39)	0.012	1	R.LLEFQNDR.G
☑	126	517.7660	1033.5174	1033.5192	-1.73	0	(35)	0.033	1	R.LLEFQNDR.G
☑	128	517.7683	1033.5220	1033.5192	2.72	0	46	0.0026	1	R.LLEFQNDR.G
☑	686	791.7253	2372.1541	2372.1761	-9.27	0	(73)	2.1e-006	1	R.VAGPQPAQTGAPQGSLGEYLFER.L
☑	687	791.7254	2372.1544	2372.1761	-9.15	0	110	4.8e-010	1	R.VAGPQPAQTGAPQGSLGEYLFER.L
☑	688	791.7254	2372.1544	2372.1761	-9.15	0	(92)	2.8e-008	1	R.VAGPQPAQTGAPQGSLGEYLFER.L

Proteins matching the same set of peptides:
IPI00625129 **Mass:** 20783 **Score:** 247 **Queries matched:** 6
Tax_Id=10090 Gene_Symbol=Ftl2 ferritin light chain 2
IPI00762203 **Mass:** 20847 **Score:** 247 **Queries matched:** 6
Tax_Id=10090 Gene_Symbol=Ftl1 Ferritin light chain 1

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13. IPI00122928 **Mass:** 50514 **Score:** 219 **Queries matched:** 12 **emPAI:** 0.21

Tax_Id=10090 Gene_Symbol=Tubb6 Tubulin beta-6 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
     191  572.3217  1142.6288  1142.6270   1.59   0    69  1.1e-005    1   K.LAVNMVPFPR.L
     192  572.3229  1142.6312  1142.6270   3.69   0   (38)     0.013    1   K.LAVNMVPFPR.L
     330  676.3404  1350.6662  1350.6676  -0.98   0   (65) 2.1e-005    1   R.IMNTFSVMPSPK.V
     331  676.3443  1350.6740  1350.6676   4.79   0    82  5.1e-007    1   R.IMNTFSVMPSPK.V
     332  676.3445  1350.6744  1350.6676   5.09   0   (64) 3.2e-005    1   R.IMNTFSVMPSPK.V
     521  846.4363  1690.8580  1690.8600  -1.16   0   (13)       3.3    2   R.ALTVPELTQQMFDAK.N
     522  846.4375  1690.8604  1690.8600   0.26   0   (34)     0.027    1   R.ALTVPELTQQMFDAK.N
     523  846.4381  1690.8616  1690.8600   0.97   0   (28)     0.099    1   R.ALTVPELTQQMFDAK.N
     524  846.4382  1690.8618  1690.8600   1.09   0    53   0.00034    1   R.ALTVPELTQQMFDAK.N
     526  848.9185  1695.8224  1695.8257  -1.89   0    12       3.8    1   K.NSSYFVEWIPNNVK.V
     558  854.4335  1706.8524  1706.8549  -1.45   0   (28)      0.11    2   R.ALTVPELTQQMFDAK.N + Oxidation (M)
     560  854.4359  1706.8572  1706.8549   1.36   0   (16)       1.5    2   R.ALTVPELTQQMFDAK.N + Oxidation (M)
```

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14. IPI00347110 **Mass:** 59502 **Score:** 208 **Queries matched:** 9 **emPAI:** 0.11
Tax_Id=10090 Gene_Symbol=Krt73 Keratin, type II cytoskeletal 73
☐ Check to include this hit in error tolerant search or archive report

```
   Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score    Expect  Rank  Peptide
☑    279  639.3514  1276.6882  1276.7027 -11.29   0    (9)       9.3    1   K.LALDIEIATYR.K
☑    280  639.3543  1276.6940  1276.7027  -6.75   0   (46)    0.0019    1   K.LALDIEIATYR.K
☑    281  639.3561  1276.6976  1276.7027  -3.93   0   (47)    0.0012    1   K.LALDIEIATYR.K
☑    282  639.3570  1276.6994  1276.7027  -2.52   0    54   0.00024    1   K.LALDIEIATYR.K
☑    283  639.3654  1276.7162  1276.7027   10.6   0   (28)     0.071    1   K.LALDIEIATYR.K
☑    395  738.3946  1474.7746  1474.7780  -2.26   0   (68) 9.4e-006    1   R.FLEQQNQVLQTK.W
☑    396  738.3973  1474.7800  1474.7780   1.40   0    83  2.9e-007    1   R.FLEQQNQVLQTK.W
☑    397  738.3979  1474.7812  1474.7780   2.21   0   (66) 1.6e-005    1   R.FLEQQNQVLQTK.W
☑    398  738.3981  1474.7816  1474.7780   2.48   0   (43)    0.0036    1   R.FLEQQNQVLQTK.W
```

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15. IPI00122048 **Mass:** 113045 **Score:** 198 **Queries matched:** 8 **emPAI:** 0.12
Tax_Id=10090 Gene_Symbol=Atp1a3 Sodium/potassium-transporting ATPase subunit alpha-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
☑    246  618.8546  1235.6946  1235.6986  -3.20   0   (54)   0.00019    1   R.LNIPVSQVNPR.D
☑    247  618.8594  1235.7042  1235.6986   4.56   0    66  9.5e-006    1   R.LNIPVSQVNPR.D
☑    277  634.8717  1267.7288  1267.7071   17.2   0    33     0.021    1   K.NMVPQQALVIR.E
☑    595  906.4749  1810.9352  1810.9425  -4.01   0    60  6.4e-005    1   R.QGAIVAVTGDGVNDSPALK.K
☑    596  906.4772  1810.9398  1810.9425  -1.47   0   (56)   0.00013    1   R.QGAIVAVTGDGVNDSPALK.K
     600  915.4284  1828.8422  1828.9167 -40.68   0    (6)        12    7   K.GVGIISEGNETVEDIAAR.L
☑    603  915.4561  1828.8976  1828.9167 -10.39   0   (52)   0.00038    1   K.GVGIISEGNETVEDIAAR.L
☑    604  915.4638  1828.9130  1828.9167  -1.97   0    70  6.2e-006    1   K.GVGIISEGNETVEDIAAR.L
```

Proteins matching the same set of peptides:
IPI00420569 **Mass:** 113457 **Score:** 198 **Queries matched:** 8
Tax_Id=10090 Gene_Symbol=Atp1a2 Sodium/potassium-transporting ATPase subunit alpha-2
IPI00752412 **Mass:** 117548 **Score:** 198 **Queries matched:** 8
Tax_Id=10090 Gene_Symbol=Atp1a3 ATPase, Na+/K+ transporting, alpha 3 polypeptide, isoform CRA_c
IPI00762871 **Mass:** 104717 **Score:** 198 **Queries matched:** 8
Tax_Id=10090 Gene_Symbol=Atp1a2 Uncharacterized protein

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16. IPI00138892 **Mass:** 15004 **Score:** 187 **Queries matched:** 5 **emPAI:** 0.23
Tax_Id=10090 Gene_Symbol=Uba52 Ubiquitin-60S ribosomal protein L40
☐ Check to include this hit in error tolerant search or archive report

```
   Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score    Expect  Rank  Peptide
☑    578  894.4645  1786.9144  1786.9200  -3.11   0    (9)       8.9    1   K.TITLEVEPSDTIENVK.A
☑    579  894.4648  1786.9150  1786.9200  -2.78   0   (62) 4.5e-005    1   K.TITLEVEPSDTIENVK.A
☑    580  894.4680  1786.9214  1786.9200   0.80   0   (67) 1.2e-005    1   K.TITLEVEPSDTIENVK.A
☑    581  894.4692  1786.9238  1786.9200   2.15   0   (77) 1.4e-006    1   K.TITLEVEPSDTIENVK.A
☑    582  894.4696  1786.9246  1786.9200   2.59   0    80    6e-007    1   K.TITLEVEPSDTIENVK.A
```

Proteins matching the same set of peptides:
IPI00470152 **Mass:** 18282 **Score:** 187 **Queries matched:** 5
Tax_Id=10090 Gene_Symbol=Rps27a Ubiquitin-40S ribosomal protein S27a
IPI00895319 **Mass:** 22277 **Score:** 187 **Queries matched:** 5
Tax_Id=10090 Gene_Symbol=2810422J05Rik 22 kDa protein
IPI00895479 **Mass:** 27181 **Score:** 187 **Queries matched:** 5
Tax_Id=10090 Gene_Symbol=2810422J05Rik 27 kDa protein
IPI00918763 **Mass:** 11021 **Score:** 187 **Queries matched:** 5
Tax_Id=10090 Gene_Symbol=Uba52 Ubiqutin subunit 1
IPI00750889 **Mass:** 22822 **Score:** 187 **Queries matched:** 5
Tax_Id=10090 Gene_Symbol=Ubc Ubc protein
IPI00923013 **Mass:** 26603 **Score:** 187 **Queries matched:** 5
Tax_Id=10090 Gene_Symbol=Ubb Ubiquitin B
IPI00923037 **Mass:** 22578 **Score:** 187 **Queries matched:** 5
Tax_Id=10090 Gene_Symbol=Ubc Putative uncharacterized protein
IPI00139518 **Mass:** 34348 **Score:** 187 **Queries matched:** 5
Tax_Id=10090 Gene_Symbol=Ubb Polyubiquitin-B
IPI00755916 **Mass:** 82614 **Score:** 187 **Queries matched:** 5

Tax_Id=10090 Gene_Symbol=Ubc ubiquitin
IPI00969323 **Mass:** 82603 **Score:** 187 **Queries matched:** 5
Tax_Id=10090 Gene_Symbol=Ubc Polyubiquitin-C

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17. IPI00625729 **Mass:** 66079 **Score:** 175 **Queries matched:** 5 **emPAI:** 0.10
Tax_Id=10090 Gene_Symbol=Krt1 Keratin, type II cytoskeletal 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
☑	273	633.3264	1264.6382	1264.6299	6.59	0	44	0.003	1	R.TNAENEFVTIK.K
	395	738.3946	1474.7746	1474.7780	-2.26	0	(68)	9.4e-006	1	R.FLEQQNQVLQTK.W
	396	738.3973	1474.7800	1474.7780	1.40	0	83	2.9e-007	1	R.FLEQQNQVLQTK.W
	397	738.3979	1474.7812	1474.7780	2.21	0	(66)	1.6e-005	1	R.FLEQQNQVLQTK.W
	398	738.3981	1474.7816	1474.7780	2.48	0	(43)	0.0036	1	R.FLEQQNQVLQTK.W

---

18. IPI00136703 **Mass:** 42971 **Score:** 160 **Queries matched:** 5 **emPAI:** 0.08
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
☑	302	652.3596	1302.7046	1302.7183	-10.50	0	(72)	4.6e-006	1	K.VLTPELYAELR.A
☑	303	652.3610	1302.7074	1302.7183	-8.35	0	(58)	0.00011	1	K.VLTPELYAELR.A
☑	304	652.3613	1302.7080	1302.7183	-7.89	0	90	6e-008	1	K.VLTPELYAELR.A
☑	462	801.9241	1601.8336	1601.8260	4.74	0	20	0.73	1	K.LAVEALSSLDGDLSGR.Y
☑	517	828.9160	1655.8174	1655.8188	-0.85	0	3	29	1	R.LEQGQAIDDLMPAQK.-

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19. IPI00110850 **Mass:** 42052 **Score:** 157 **Queries matched:** 11 **emPAI:** 0.35
Tax_Id=10090 Gene_Symbol=Actb Actin, cytoplasmic 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
☑	213	581.3192	1160.6238	1160.6111	11.0	0	43	0.004	1	K.EITALAPSTMK.I
☑	214	581.3192	1160.6238	1160.6111	11.0	0	(22)	0.51	1	K.EITALAPSTMK.I
☑	227	599.7656	1197.5166	1197.5150	1.41	0	46	0.00079	1	K.DSYVGDEAQSK.R
☑	583	895.9476	1789.8806	1789.8846	-2.22	0	(40)	0.0058	1	K.SYELPDGQVITIGNER.F
☑	584	895.9503	1789.8860	1789.8846	0.79	0	(55)	0.00017	1	K.SYELPDGQVITIGNER.F
☑	585	895.9514	1789.8882	1789.8846	2.02	0	93	2.7e-008	1	K.SYELPDGQVITIGNER.F
	613	652.0187	1953.0343	1953.0571	-11.69	0	(15)	1.3	2	R.VAPEEHPVLLTEAPLNPK.A
	614	652.0188	1953.0346	1953.0571	-11.53	0	31	0.034	2	R.VAPEEHPVLLTEAPLNPK.A
☑	615	652.0193	1953.0361	1953.0571	-10.77	0	(21)	0.39	1	R.VAPEEHPVLLTEAPLNPK.A
☑	616	652.0218	1953.0436	1953.0571	-6.93	0	(7)	8.3	1	R.VAPEEHPVLLTEAPLNPK.A
☑	618	652.0227	1953.0463	1953.0571	-5.54	0	(19)	0.5	1	R.VAPEEHPVLLTEAPLNPK.A

Proteins matching the same set of peptides:
IPI00136929 **Mass:** 44029 **Score:** 157 **Queries matched:** 11
Tax_Id=10090 Gene_Symbol=Actg1 Gamma actin-like protein
IPI00473320 **Mass:** 42115 **Score:** 157 **Queries matched:** 11
Tax_Id=10090 Gene_Symbol=Actb Putative uncharacterized protein
IPI00652436 **Mass:** 42053 **Score:** 157 **Queries matched:** 11
Tax_Id=10090 Gene_Symbol=Actg1 Putative uncharacterized protein
IPI00874482 **Mass:** 42108 **Score:** 157 **Queries matched:** 11
Tax_Id=10090 Gene_Symbol=Actg1 Actin, cytoplasmic 2

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20. IPI00221797 **Mass:** 59932 **Score:** 155 **Queries matched:** 7 **emPAI:** 0.05
Tax_Id=10090 Gene_Symbol=Krt75 Keratin, type II cytoskeletal 75
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	288	651.8494	1301.6842	1301.7078	-18.11	0	(7)	15	1	R.SLDLDSIIAEVK.A
☑	289	651.8604	1301.7062	1301.7078	-1.21	0	(30)	0.062	1	R.SLDLDSIIAEVK.A
☑	290	651.8617	1301.7088	1301.7078	0.79	0	(61)	4.8e-005	1	R.SLDLDSIIAEVK.A
☑	291	651.8624	1301.7102	1301.7078	1.86	0	(59)	7.4e-005	1	R.SLDLDSIIAEVK.A
☑	292	651.8624	1301.7102	1301.7078	1.86	0	(63)	3.1e-005	1	R.SLDLDSIIAEVK.A
☑	293	651.8641	1301.7136	1301.7078	4.47	0	63	2.9e-005	1	R.SLDLDSIIAEVK.A
☑	399	738.8942	1475.7738	1475.7984	-16.62	1	4	26	1	R.FLEQQNKVLETK.W

---

21. IPI00348328 **Mass:** 114018 **Score:** 142 **Queries matched:** 6 **emPAI:** 0.03
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
☑	114	504.7170	1007.4194	1007.4528	-33.13	0	5	7.8	1	K.QDMAQMLR.D + Oxidation (M)
☑	345	692.3474	1382.6802	1382.6830	-2.00	0	(60)	6.9e-005	1	R.SLNNQFASFIDK.V
☑	346	692.3569	1382.6992	1382.6830	11.7	0	(49)	0.00093	1	R.SLNNQFASFIDK.V
☑	347	692.3570	1382.6994	1382.6830	11.9	0	61	6.2e-005	1	R.SLNNQFASFIDK.V
☑	348	692.3643	1382.7140	1382.6830	22.4	0	(49)	0.00089	1	R.SLNNQFASFIDK.V
	399	738.8942	1475.7738	1475.7984	-16.62	1	4	26	1	R.FLEQQNKVLETK.W

---

22. IPI00322209 **Mass:** 54531 **Score:** 142 **Queries matched:** 4 **emPAI:** 0.06
Tax_Id=10090 Gene_Symbol=Krt8 Keratin, type II cytoskeletal 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
	345	692.3474	1382.6802	1382.7194	-28.31	1	(60)	6.9e-005	1	K.SLNNKFASFIDK.V
	346	692.3569	1382.6992	1382.7194	-14.57	1	(49)	0.00093	1	K.SLNNKFASFIDK.V
	347	692.3570	1382.6994	1382.7194	-14.42	1	61	6.2e-005	1	K.SLNNKFASFIDK.V
	348	692.3643	1382.7140	1382.7194	-3.86	1	(49)	0.00089	1	K.SLNNKFASFIDK.V

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23. IPI00221528 **Mass:** 42319 **Score:** 126 **Queries matched:** 8 **emPAI:** 0.16
Tax_Id=10090 Gene_Symbol=Actbl2 Beta-actin-like 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
	583	895.9476	1789.8806	1789.8846	-2.22	0	(40)	0.0058	1	R.SYELPDGQVITIGNER.F
	584	895.9503	1789.8860	1789.8846	0.79	0	(55)	0.00017	1	R.SYELPDGQVITIGNER.F
	585	895.9514	1789.8882	1789.8846	2.02	0	93	2.7e-008	1	R.SYELPDGQVITIGNER.F
☑	613	652.0187	1953.0343	1953.0571	-11.69	0	(16)	1.2	1	R.VAPDEHPILLTEAPLNPK.I
☑	614	652.0188	1953.0346	1953.0571	-11.53	0	32	0.03	1	R.VAPDEHPILLTEAPLNPK.I
	615	652.0193	1953.0361	1953.0571	-10.77	0	(13)	2.3	2	R.VAPDEHPILLTEAPLNPK.I
	616	652.0218	1953.0436	1953.0571	-6.93	0	(5)	15	3	R.VAPDEHPILLTEAPLNPK.I
	618	652.0227	1953.0463	1953.0571	-5.54	0	(16)	1.1	2	R.VAPDEHPILLTEAPLNPK.I

---

24. IPI00124499 **Mass:** 57802 **Score:** 105 **Queries matched:** 5 **emPAI:** 0.06
Tax_Id=10090 Gene_Symbol=Krt79 Keratin, type II cytoskeletal 79
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	314	**665.3632**	**1328.7118**	**1328.7187**	**-5.17**	**0**	**(34)**	**0.025**	**1**	**R.NLDLDSIIAEVK.A**
☑	315	**665.3666**	**1328.7186**	**1328.7187**	**-0.05**	**0**	**73**	**2.9e-006**	**1**	**R.NLDLDSIIAEVK.A**
☑	316	**665.3679**	**1328.7212**	**1328.7187**	**1.90**	**0**	**(41)**	**0.0055**	**1**	**R.NLDLDSIIAEVK.A**
☑	317	**665.3680**	**1328.7214**	**1328.7187**	**2.05**	**0**	**(42)**	**0.0038**	**1**	**R.NLDLDSIIAEVK.A**
	399	738.8942	1475.7738	1475.7984	-16.62	1	4	26	1	R.FLEQQNKVLETK.W

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25. IPI00230145 **Mass:** 21224 **Score:** 88 **Queries matched:** 3 **emPAI:** 0.16
Tax_Id=10090 Gene_Symbol=Fth1 Ferritin 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
	79	**438.7601**	**875.5056**	**875.5116**	**-6.85**	**0**	**7**	**12**	**5**	**R.IFLQDIK.K**
☑	487	**815.3727**	**1628.7308**	**1628.7214**	**5.78**	**0**	**(45)**	**0.0012**	**1**	**K.MGAPEAGMAEYLFDK.H**
☑	488	**815.3737**	**1628.7328**	**1628.7214**	**7.01**	**0**	**75**	**1.3e-006**	**1**	**K.MGAPEAGMAEYLFDK.H**

---

26. IPI00406377 **Mass:** 50678 **Score:** 82 **Queries matched:** 6 **emPAI:** 0.06
Tax_Id=10090 Gene_Symbol=Krt7 Keratin, type II cytoskeletal 7
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
	104	**487.2706**	**972.5266**	**972.5352**	**-8.81**	**1**	**10**	**9.1**	**8**	**K.SAKSSQLPR.I**
	279	639.3514	1276.6882	1276.7027	-11.29	0	(9)	9.3	1	K.LALDIEIATYR.K
	280	639.3543	1276.6940	1276.7027	-6.75	0	(46)	0.0019	1	K.LALDIEIATYR.K
	281	639.3561	1276.6976	1276.7027	-3.93	0	(47)	0.0012	1	K.LALDIEIATYR.K
	282	639.3570	1276.6994	1276.7027	-2.52	0	54	0.00024	1	K.LALDIEIATYR.K
	283	639.3654	1276.7162	1276.7027	10.6	0	(28)	0.071	1	K.LALDIEIATYR.K

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27. IPI00222228 **Mass:** 58587 **Score:** 82 **Queries matched:** 6 **emPAI:** 0.06
Tax_Id=10090 Gene_Symbol=4732456N10Rik hypothetical protein LOC239673
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
	279	639.3514	1276.6882	1276.7027	-11.29	0	(9)	9.3	1	K.LALDIEIATYR.K
	280	639.3543	1276.6940	1276.7027	-6.75	0	(46)	0.0019	1	K.LALDIEIATYR.K
	281	639.3561	1276.6976	1276.7027	-3.93	0	(47)	0.0012	1	K.LALDIEIATYR.K
	282	639.3570	1276.6994	1276.7027	-2.52	0	54	0.00024	1	K.LALDIEIATYR.K
	283	639.3654	1276.7162	1276.7027	10.6	0	(28)	0.071	1	K.LALDIEIATYR.K
	399	738.8942	1475.7738	1475.7984	-16.62	1	4	26	1	R.FLEQQNKVLETK.W

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28. IPI00135284 **Mass:** 36092 **Score:** 78 **Queries matched:** 7 **emPAI:** 0.19
Tax_Id=10090 Gene_Symbol=Gm16374 Glyceraldehyde-3-phosphate dehydrogenase
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	333	**678.8232**	**1355.6318**	**1355.6465**	**-10.80**	**1**	**(21)**	**0.41**	**1**	**R.VVDLMAYMASKE.-**
☑	334	**678.8466**	**1355.6786**	**1355.6465**	**23.7**	**1**	**43**	**0.0032**	**1**	**R.VVDLMAYMASKE.-**
☑	335	**685.3756**	**1368.7366**	**1368.7361**	**0.40**	**0**	**(50)**	**0.00057**	**1**	**R.GAAQNIIPASTGAAK.A**
☑	336	**685.3767**	**1368.7388**	**1368.7361**	**2.01**	**0**	**(39)**	**0.0079**	**1**	**R.GAAQNIIPASTGAAK.A**
☑	337	**685.3770**	**1368.7394**	**1368.7361**	**2.45**	**0**	**(20)**	**0.53**	**1**	**R.GAAQNIIPASTGAAK.A**
☑	338	**685.3795**	**1368.7444**	**1368.7361**	**6.10**	**0**	**58**	**9.3e-005**	**1**	**R.GAAQNIIPASTGAAK.A**
☑	573	**890.4178**	**1778.8210**	**1778.7900**	**17.5**	**0**	**25**	**0.17**	**1**	**K.LISWYDNEYGYSNR.V**

Proteins matching the same set of peptides:
IPI00271869 **Mass:** 36293 **Score:** 78 **Queries matched:** 7
Tax_Id=10090 Gene_Symbol=- 36 kDa protein

```
      IPI00273646    Mass: 36072    Score: 78     Queries matched: 7
      Tax_Id=10090 Gene_Symbol=Gapdh;LOC100042025 Glyceraldehyde-3-phosphate dehydrogenase
      IPI00622795    Mass: 36074    Score: 78     Queries matched: 7
      Tax_Id=10090 Gene_Symbol=- 36 kDa protein
      IPI00752289    Mass: 36308    Score: 78     Queries matched: 7
      Tax_Id=10090 Gene_Symbol=Gm10290 Glyceraldehyde-3-phosphate dehydrogenase
      IPI00848801    Mass: 36100    Score: 78     Queries matched: 7
      Tax_Id=10090 Gene_Symbol=- 36 kDa protein
      IPI00849045    Mass: 36072    Score: 78     Queries matched: 7
      Tax_Id=10090 Gene_Symbol=- 36 kDa protein
      IPI00850337    Mass: 44633    Score: 78     Queries matched: 7
      Tax_Id=10090 Gene_Symbol=LOC100048117 similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) isoform 1
      IPI00850377    Mass: 35975    Score: 78     Queries matched: 7
      Tax_Id=10090 Gene_Symbol=- 36 kDa protein
      IPI00850779    Mass: 36076    Score: 78     Queries matched: 7
      Tax_Id=10090 Gene_Symbol=- 36 kDa protein
      IPI00874682    Mass: 36038    Score: 78     Queries matched: 7
      Tax_Id=10090 Gene_Symbol=- 36 kDa protein
      IPI00874964    Mass: 36512    Score: 78     Queries matched: 7
      Tax_Id=10090 Gene_Symbol=- 36 kDa protein
```

```
29.   IPI00134997    Mass: 106777   Score: 78     Queries matched: 1   emPAI: 0.03
      Tax_Id=10090 Gene_Symbol=Dlgap3 Disks large-associated protein 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
   ☑   405  751.8646  1501.7146  1501.7274  -8.46   0    78  1e-006   1   R.GPAGPGPGPGSGAAPEAR.S


      Proteins matching the same set of peptides:
      IPI00648401    Mass: 105576   Score: 78     Queries matched: 1
      Tax_Id=10090 Gene_Symbol=Dlgap3 Discs, large (Drosophila) homolog-associated protein 3
```

```
30.   IPI00348094    Mass: 51093    Score: 75     Queries matched: 6   emPAI: 0.06
      Tax_Id=10090 Gene_Symbol=Tubb1 Tubulin, 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
       191  572.3217  1142.6288  1142.6270   1.59   0    69  1.1e-005    1   K.LAVNMVPFPR.L
       192  572.3229  1142.6312  1142.6270   3.69   0   (38)    0.013    1   K.LAVNMVPFPR.L
       308  660.3503  1318.6860  1318.6955  -7.16   0   (11)      5.8    2   R.ILNSFSVMPSPK.V
       309  660.3552  1318.6958  1318.6955   0.27   0   (13)      4.1    2   R.ILNSFSVMPSPK.V
       310  660.3563  1318.6980  1318.6955   1.94   0    21      0.63    2   R.ILNSFSVMPSPK.V
       311  660.3572  1318.6998  1318.6955   3.30   0   (16)      1.9    2   R.ILNSFSVMPSPK.V
```

```
31.   IPI00115546    Mass: 40524    Score: 70     Queries matched: 5   emPAI: 0.17
      Tax_Id=10090 Gene_Symbol=Gnao1 Isoform Alpha-2 of Guanine nucleotide-binding protein G(o) 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
   ☑   150  529.3204  1056.6262  1056.6179   7.91   0    45   0.0019    1   K.LLLLGAGESGK.S
   ☑   520  838.4207  1674.8268  1674.8213   3.31   0    55  0.00023    1   R.IGAGDYQPTEQDILR.T
   ☑   621  979.4400  1956.8654  1956.8631   1.21   0   (7)      5.7    1   R.MEDTEPFSAELLSAMMR.L
   ☑   622  979.4463  1956.8780  1956.8631   7.65   0   (5)       11    1   R.MEDTEPFSAELLSAMMR.L
   ☑   623  979.4526  1956.8906  1956.8631   14.1   0    10      4.2    1   R.MEDTEPFSAELLSAMMR.L


      Proteins matching the same set of peptides:
      IPI00230192    Mass: 40629    Score: 70     Queries matched: 5
      Tax_Id=10090 Gene_Symbol=Gnao1 Isoform Alpha-1 of Guanine nucleotide-binding protein G(o) subunit alpha
```

```
32.   IPI00122094    Mass: 85656    Score: 65     Queries matched: 3   emPAI: 0.08
      Tax_Id=10090 Gene_Symbol=Dlg4 Isoform 2 of Disks large homolog 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
   ☑   185  563.2996  1124.5846  1124.5938  -8.15   0    46  0.0019   1   K.IIPGGAAAQDGR.L
   ☑   561  857.9614  1713.9082  1713.9090  -0.44   0    42  0.0032   1   R.VIEDLSGPYIWVPAR.E
   ☑   562  857.9666  1713.9186  1713.9090   5.63   0   (26)   0.13   1   R.VIEDLSGPYIWVPAR.E


      Proteins matching the same set of peptides:
      IPI00622720    Mass: 80765    Score: 65     Queries matched: 3
      Tax_Id=10090 Gene_Symbol=Dlg4 Isoform 1 of Disks large homolog 4
      IPI00626797    Mass: 80395    Score: 65     Queries matched: 3
      Tax_Id=10090 Gene_Symbol=Dlg4 Isoform 3 of Disks large homolog 4
```

```
33.   IPI00119667    Mass: 50764    Score: 53     Queries matched: 1   emPAI: 0.06
      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
   ☑   116  513.3045  1024.5944  1024.6030  -8.30   0    53  0.00015    1   K.IGGIGTVPVGR.V


      Proteins matching the same set of peptides:
      IPI00307837    Mass: 50424    Score: 53     Queries matched: 1
```

```
      Tax_Id=10090 Gene_Symbol=Eef1a1 Elongation factor 1-alpha 1
____________________________________________________________________________________________________
34.   IPI00135197     Score: 53     Queries matched: 2
      Tax_Id=10090 Gene_Symbol=Krt20 Keratin, type I cytoskeletal 20
    ☐ Check to include this hit in error tolerant search or archive report

      Query  Observed    Mr(expt)    Mr(calc)    ppm  Miss Score Expect Rank  Peptide
        170  545.7681  1089.5216  1089.5237  -1.85   0    47  0.0016   2   K.LAMQNLNDR.L + Oxidation (M)
        171  545.7692  1089.5238  1089.5237   0.17   0   (45) 0.0024   2   K.LAMQNLNDR.L + Oxidation (M)

____________________________________________________________________________________________________
35.   IPI00467833     Mass: 32684     Score: 45     Queries matched: 1    emPAI: 0.10
      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
    ☑   249  624.2955  1246.5764  1246.5902  -11.03   0    45  0.0017    1   K.SNVNDGVAQSTR.I

____________________________________________________________________________________________________
36.   IPI00118569     Mass: 44369     Score: 45     Queries matched: 1    emPAI: 0.07
      Tax_Id=10090 Gene_Symbol=Gna13 Guanine nucleotide-binding protein subunit alpha-13
    ☐ Check to include this hit in error tolerant search or archive report

      Query  Observed    Mr(expt)    Mr(calc)    ppm  Miss Score Expect Rank  Peptide
        150  529.3204  1056.6262  1056.6179   7.91   0    45  0.0019   1   K.ILLLGAGESGK.S


      Proteins matching the same set of peptides:
      IPI00230191     Mass: 44238     Score: 45     Queries matched: 1
      Tax_Id=10090 Gene_Symbol=Gna12 Guanine nucleotide-binding protein subunit alpha-12
      IPI00649388     Mass: 20095     Score: 45     Queries matched: 1
      Tax_Id=10090 Gene_Symbol=Gna13 Putative uncharacterized protein
____________________________________________________________________________________________________
37.   IPI00462072     Mass: 47453     Score: 44     Queries matched: 1    emPAI: 0.07
      Tax_Id=10090 Gene_Symbol=Eno1;Gm5506 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
    ☑   362  720.3760  1438.7374  1438.7344   2.14   0    44  0.0025   1   R.YITPDQLADLYK.S


      Proteins matching the same set of peptides:
      IPI00648821     Mass: 40099     Score: 44     Queries matched: 1
      Tax_Id=10090 Gene_Symbol=Eno1 Enolase
____________________________________________________________________________________________________
38.   IPI00120793     Mass: 28131     Score: 41     Queries matched: 2    emPAI: 0.12
      Tax_Id=10090 Gene_Symbol=Prnp Major prion 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
    ☑   166  544.7459  1087.4772  1087.4570   18.6   0     8     5.6   1   K.ESQAYYDGR.R
    ☑   189  570.2626  1138.5106  1138.5142  -3.15   0    41  0.0039   1   K.GENFTETDVK.M

____________________________________________________________________________________________________
39.   IPI00113410     Mass: 38586     Score: 40     Queries matched: 2    emPAI: 0.09
      Tax_Id=10090 Gene_Symbol=Hapln2 Hyaluronan and proteoglycan link 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
    ☑   354  696.3665  1390.7184  1390.7245  -4.35   0    40  0.0065   1   R.LEGVVFPYQPSR.G
    ☑   355  696.3699  1390.7252  1390.7245   0.54   0   (29)  0.092   1   R.LEGVVFPYQPSR.G

____________________________________________________________________________________________________
40.   IPI00622240     Mass: 71336     Score: 39     Queries matched: 5    emPAI: 0.05
      Tax_Id=10090 Gene_Symbol=Krt2 Keratin, type II cytoskeletal 2 epidermal
    ☐ Check to include this hit in error tolerant search or archive report

      Query  Observed    Mr(expt)    Mr(calc)     ppm  Miss Score Expect Rank  Peptide
        182  556.7426  1111.4706  1111.4643    5.72   0     0      24    9   R.GGSGGGYGSGGGSR.G
    ☑   222  590.3031  1178.5916  1178.6183  -22.60   0   (23)   0.42    1   K.YEELQVTAVK.H
    ☑   223  590.3059  1178.5972  1178.6183  -17.85   0   (32)  0.054    1   K.YEELQVTAVK.H
    ☑   224  590.3073  1178.6000  1178.6183  -15.47   0    35   0.025    1   K.YEELQVTAVK.H
    ☑   251  627.8073  1253.6000  1253.6001   -0.00   0    39    0.01    1   R.GFSSGSAVVSGGSR.R


      Proteins matching the same set of peptides:
      IPI00875096     Mass: 71035     Score: 39     Queries matched: 5
      Tax_Id=10090 Gene_Symbol=Krt2 71 kDa protein
____________________________________________________________________________________________________
Peptide matches not assigned to protein hits: (no details means no match)

      Query    Observed    Mr(expt)    Mr(calc)     ppm  Miss Score Expect Rank  Peptide
    ☑   250    626.3681  1250.7216  1250.7347  -10.42   0    36  0.0076   1   GVAGAPPTVTLLR
    ☑   305    656.3151  1310.6156  1310.5999    12.0   0    35   0.018   1   QMYMSLPQGEK
    ☑   132    520.2753  1038.5360  1038.5458   -9.37   0    34   0.028   1   AQASAPAQAPK
    ☑   229    614.8425  1227.6704  1227.6711   -0.50   0    33   0.033   1   TSGPPVSELITK
    ☑   136    523.2849  1044.5552  1044.5564   -1.06   0    30   0.094   1   INDITLNSR
    ☑   208    578.8143  1155.6140  1155.6135    0.45   0    30   0.073   1   SLPNEEIVQK
```

☑	104	487.2706	972.5266	972.5240	2.74	0	29	0.12	1	EIISEVQR
☑	159	533.2659	1064.5172	1064.5138	3.23	0	28	0.11	1	AQYEDIAQK
☑	133	520.2761	1038.5376	1038.5458	-7.83	0	28	0.11	1	AQASAPAQAPK
☑	230	614.8445	1227.6744	1227.6711	2.75	0	25	0.23	1	TSGPPVSELITK
☑	252	628.8171	1255.6196	1255.6157	3.16	0	25	0.23	1	GGSQGEAVGELPR
☑	71	435.7725	869.5304	869.4971	38.4	0	25	0.14	1	AVVESLPR
☑	231	614.8458	1227.6770	1227.6711	4.87	0	25	0.24	1	TSGPPVSELITK
☑	160	533.2675	1064.5204	1064.5138	6.24	0	21	0.6	1	AQYEDIAQK
☑	134	523.2794	1044.5442	1044.5564	-11.59	0	20	0.87	1	INDITLNSR
☑	237	616.7883	1231.5620	1231.5680	-4.86	0	20	0.57	1	AVIESDEEQGR
☑	105	487.2718	972.5290	972.5240	5.20	0	19	1.1	1	EIISEVQR
☑	84	449.2162	896.4178	896.4214	-4.02	0	19	0.62	1	MWIEFR + Oxidation (M)
☑	66	428.7654	855.5162	855.5542	-44.32	0	19	0.62	1	TLAVLALR
☑	358	698.8622	1395.7098	1395.6630	33.6	0	19	0.92	1	ALGTSDPEGAEPPR
☑	165	543.3147	1084.6148	1084.5811	31.1	1	18	0.99	1	EAIRLAPCR
☑	112	496.2298	990.4450	990.4883	-43.65	0	17	0.94	1	AFSSHSSLR
☑	357	698.8580	1395.7014	1395.6630	27.5	0	17	1.2	1	ALGTSDPEGAEPPR
☑	437	785.8483	1569.6820	1569.7531	-45.25	0	17	0.57	1	SLMQCAGESISLFK
☑	479	810.3789	1618.7432	1618.7331	6.26	0	17	1	1	SSSMVLGSFGTDLMR + 2 Oxidation (M)
☑	56	412.7523	823.4900	823.4817	10.2	0	17	0.53	1	RPWLPR
☑	360	472.9068	1415.6986	1415.7521	-37.80	1	17	1.6	1	ELARWIGVTESR
☑	13	475.2986	474.2913	474.2802	23.5	0	17	2.5	1	LGGTK
☑	684	786.0964	2355.2674	2355.2012	28.1	0	17	0.76	1	QALQFAFYVIEQVGTQPFNR
☑	89	450.7500	899.4854	899.5076	-24.63	1	16	1.9	1	GAPKESALK
☑	212	581.2999	1160.5852	1160.5543	26.7	1	16	2.6	1	AAPGRMCSVGR
☑	624	656.6460	1966.9162	1966.9669	-25.81	1	16	1.3	1	ALVAMNESLKSQEQEFK + Oxidation (M)
☑	370	730.9049	1459.7952	1459.7453	34.2	1	15	1.6	1	VDILENRVMDTR
☑	210	579.3053	1156.5960	1156.6353	-33.92	0	15	2.6	1	VVSWNINGIR
☑	158	533.2621	1064.5096	1064.5138	-3.91	0	15	2.5	1	AQYEDIAQK
☑	41	327.7021	653.3896	653.3609	44.0	0	14	0.98	1	ALGTHR
☑	113	499.2547	996.4948	996.5352	-40.53	0	14	2.5	1	IGTQPPAASR
☑	172	546.7492	1091.4838	1091.5281	-40.52	0	14	1.8	1	TLLMENAER + Oxidation (M)
☑	94	460.2562	918.4978	918.4705	29.8	1	14	4.1	1	EVTGAMRR
☑	82	443.7305	885.4464	885.4304	18.1	1	14	2.4	1	KDPNAEGR
☑	25	574.3228	573.3155	573.3122	5.78	0	13	6.1	1	DIQAK
☑	521	846.4363	1690.8580	1690.8084	29.4	1	13	3	1	MTSTTPPGEDIKSSPK + Oxidation (M)
☑	369	730.9024	1459.7902	1459.7453	30.8	1	13	2.7	1	VDILENRVMDTR
☑	122	517.2615	1032.5084	1032.4724	35.0	0	13	4	1	VLDEEGSER
☑	219	585.3231	1168.6316	1168.6492	-15.03	1	13	2.9	1	KVSSFDVFLK
☑	236	616.3319	1230.6492	1230.6245	20.1	0	13	4.1	1	AWVEQEGVSVK
☑	763	1019.4843	4073.9081	4074.0473	-34.18	1	13	0.98	1	SSLSARLISMTDLLSSSAAPLSSALVHSSAQLSCRPDSR + Oxidation (M)
☑	79	438.7601	875.5056	875.4786	30.9	1	13	2.9	1	KMDELLK
☑	123	517.2618	1032.5090	1032.4724	35.5	0	13	4.4	1	VLDEEGSER
☑	55	412.7522	823.4898	823.4817	9.93	0	13	1.4	1	RPWLPR
☑	177	554.2685	1106.5224	1106.5251	-2.38	1	13	3.7	1	SGCGLTRSNR
☑	286	647.3292	1292.6438	1292.6336	7.96	0	13	4.2	1	TFNAPWMALAR + Oxidation (M)
☑	67	428.7656	855.5166	855.5178	-1.34	0	12	2.9	1	LLSTPGLR
☑	325	672.3442	1342.6738	1342.6729	0.73	0	11	5.3	1	QDVTLEPSPTTR
☑	77	437.7505	873.4864	873.4807	6.55	0	11	7.8	1	VAVEELSK
☑	74	435.7740	869.5334	869.5123	24.3	0	11	2.9	1	VSLWLPR
☑	73	435.7737	869.5328	869.5123	23.6	0	11	3	1	VSLWLPR
☑	269	631.7998	1261.5850	1261.5826	1.92	0	11	4.7	1	EALEVDWSGEK
☑	146	529.2684	1056.5222	1056.5464	-22.90	1	11	5.3	1	HELFREAR
☑	65	428.7642	855.5138	855.5112	3.04	1	11	4.3	1	ALRMLPR
☑	127	517.7664	1033.5182	1033.5338	-15.09	1	11	8.4	1	CISRTEIR
☑	97	461.2222	920.4298	920.4716	-45.31	0	10	7	1	ISAAGYPSR
☑	431	785.8430	1569.6714	1569.7254	-34.40	1	10	2.5	1	MSVFPRDWMVMR + Oxidation (M)
☑	62	421.7567	841.4988	841.4810	21.2	0	10	5.1	1	AVLTWPR
☑	380	738.3709	1474.7272	1474.6787	32.9	1	10	6.8	1	VDTEPKAEEASGDK
☑	274	634.3513	1266.6880	1266.7084	-16.09	1	10	5.1	1	YLYGIRVEVR
☑	162	539.2801	1076.5456	1076.5648	-17.79	1	10	8.8	1	MIGERNITK + Oxidation (M)
☑	392	738.3838	1474.7530	1474.8065	-36.24	1	10	7.1	1	VESLLENMGIKVK + Oxidation (M)
☑	245	618.2814	1234.5482	1234.5426	4.60	0	10	4.5	1	ETAGSSGSTPEGR
☑	169	545.2915	1088.5684	1088.5397	26.4	0	10	9.1	1	MGSADRPALR + Oxidation (M)
☑	466	804.3981	1606.7816	1606.8454	-39.66	0	10	6.9	1	VEVELLSYETQGLK
☑	640	1040.0016	2077.9886	2077.8876	48.6	0	10	5.1	1	LMCSLCHCPGATIGCDVK
☑	391	738.3832	1474.7518	1474.7813	-19.99	1	10	7.9	1	VKALEESAVNMLR + Oxidation (M)
☑	691	837.3803	2509.1191	2509.1301	-4.39	0	10	3.2	1	LTLQSHRPTCCCYLDFHSSK
☑	323	671.3476	1340.6806	1340.6282	39.1	0	10	7.4	1	AVSPENMVTYSK + Oxidation (M)
☑	173	546.7579	1091.5012	1091.5393	-34.88	1	10	6.2	1	KEMASGVNTR
☑	57	412.7530	823.4914	823.4817	11.9	0	10	3.1	1	RPWLPR
☑	270	631.8015	1261.5884	1261.5826	4.61	0	10	7	1	EALEVDWSGEK
☑	706	894.7648	2681.2726	2681.2755	-1.11	0	9	4.5	1	VVSAMVNSLDDNGVLIGNWTGDYSR
☑	49	379.7106	757.4066	757.3719	45.9	0	9	11	1	DGPLNSR
☑	102	485.7497	969.4848	969.5131	-29.16	0	9	7	1	VVEGPGTPSK
☑	368	730.9019	1459.7892	1459.7453	30.1	1	9	7.2	1	VDILENRVMDTR
☑	705	894.4244	2680.2514	2680.3420	-33.81	1	9	4.1	1	NLTAGMAMITCREPLLMSISTNLK + Oxidation (M)
☑	168	545.2596	1088.5046	1088.5462	-38.16	0	9	7.3	1	SSVLDANLDR
☑	324	671.3478	1340.6810	1340.7048	-17.73	0	9	9.2	1	NPQSTSLLPTGAR
☑	154	532.2648	1062.5150	1062.4764	36.4	0	9	11	1	DASISSCPAR
☑	80	438.7608	875.5070	875.4786	32.5	1	9	7.9	1	KLEMDLK

☑	149	529.2750	1056.5354	1056.5312	4.02	0	9	10	1	QADGQAGAALR
☑	564	863.3917	1724.7688	1724.7458	13.4	0	9	5.5	1	GVSEGSAAMAAGESMAQR + Oxidation (M)
☑	384	738.3768	1474.7390	1474.8065	-45.73	1	9	10	1	VESLLENMGIKVK + Oxidation (M)
☑	271	631.8031	1261.5916	1261.5826	7.15	0	8	9.1	1	EALEVDWSGEK
☑	58	412.7545	823.4944	823.4817	15.5	0	8	4	1	RPWLPR
☑	417	774.9011	1547.7876	1547.7865	0.76	1	8	10	1	MEEQGLADASLLKK + Oxidation (M)
☑	552	852.4298	1702.8450	1702.8825	-21.99	1	8	9.9	1	TQVGVKGCYAHVLGSK
☑	388	738.3810	1474.7474	1474.6787	46.6	1	8	12	1	VDTEPKAEEASGDK
☑	361	711.3162	1420.6178	1420.6681	-35.39	1	8	5.1	1	SLSSQEAKEAEDK
☑	268	631.3294	1260.6442	1260.6649	-16.36	0	8	13	1	LTDPFRPMLR + Oxidation (M)
☑	61	419.2105	836.4064	836.3810	30.4	1	8	12	1	QMKGDSR + Oxidation (M)
☑	390	738.3816	1474.7486	1474.6787	47.4	1	8	12	1	VDTEPKAEEASGDK
☑	631	656.6597	1966.9573	1966.9670	-4.96	0	8	9.3	1	VSVPTHPDDVGDASLTMVK
☑	63	421.7579	841.5012	841.4810	24.0	0	8	9.1	1	AVLTWPR
☑	275	634.3516	1266.6886	1266.7230	-27.14	1	8	9.1	1	MEPRIKPRPK + Oxidation (M)
☑	711	916.4344	2746.2814	2746.2593	8.03	0	8	5.8	1	LGYCYVEEPQEKPMPCWLYLR + Oxidation (M)
☑	103	485.7501	969.4856	969.4477	39.1	0	8	9.6	1	TMLEYADK
☑	152	530.7871	1059.5596	1059.5284	29.5	1	8	18	1	VWHTMSKR + Oxidation (M)
☑	731	958.4579	2872.3519	2872.3337	6.31	1	8	6.4	1	TQQETFLEVIANASGYMYETSYRR + Oxidation (M)
☑	70	435.2076	868.4006	868.4290	-32.70	1	8	7.8	1	GKFSTDSK
☑	18	531.2912	530.2839	530.2813	5.04	0	8	26	1	AVADR
☑	329	672.8435	1343.6724	1343.6906	-13.47	1	8	12	1	LASRQSTPSQNR
☑	199	573.7952	1145.5758	1145.5751	0.69	0	8	15	1	QMGLGEPSVTK
☑	385	738.3773	1474.7400	1474.6787	41.6	1	8	13	1	VDTEPKAEEASGDK
☑	130	519.2655	1036.5164	1036.4681	46.6	0	8	13	1	DPATMLMSR + Oxidation (M)
☑	131	519.2684	1036.5222	1036.5739	-49.84	0	8	13	1	IYCLLSLR
☑	241	618.2693	1234.5240	1234.5677	-35.37	0	8	5.3	1	STDSEVSQSPAK
☑	26	581.3032	580.2959	580.2890	11.9	0	8	11	1	SSMLK + Oxidation (M)
☑	382	738.3743	1474.7340	1474.8065	-49.12	1	8	13	1	VESLLENMGIKVK + Oxidation (M)
☑	36	644.3062	643.2989	643.2748	37.5	0	8	5.1	1	GCALSH
☑	209	579.2987	1156.5828	1156.5585	21.1	1	7	14	1	AGSEPAGERQR
☑	72	435.7737	869.5328	869.5698	-42.50	1	7	7.2	1	VLKILER
☑	164	539.2836	1076.5526	1076.5437	8.32	1	7	16	1	QGAVMKNWK + Oxidation (M)
☑	155	532.2737	1062.5328	1062.5128	18.9	1	7	17	1	QEIDRMQK + Oxidation (M)
☑	211	580.7757	1159.5368	1159.5581	-18.36	1	7	11	1	ELQDEGRSAR
☑	356	697.3420	1392.6694	1392.6919	-16.10	0	7	14	1	MTLTAASEVIGER + Oxidation (M)
☑	182	556.7426	1111.4706	1111.4638	6.20	1	7	5.5	1	EGMERESMK + Oxidation (M)
☑	422	785.3591	1568.7036	1568.7551	-32.82	1	7	8.8	1	FKYYSFFDLDPK
☑	242	618.2741	1234.5336	1234.5910	-46.49	0	7	8.1	1	MSTARPCAGLR + Oxidation (M)
☑	254	629.8081	1257.6016	1257.6248	-18.41	1	7	15	1	QRMSPGVAGSPR + Oxidation (M)
☑	153	530.7873	1059.5600	1059.5560	3.79	0	7	23	1	DTSSILATPR
☑	387	738.3804	1474.7462	1474.6908	37.6	0	7	16	1	HNLLCLENMTSK + Oxidation (M)
☑	751	833.1402	3328.5317	3328.5380	-1.89	0	7	5.3	1	AMNDIGDYVGSNLEISWLPNLDGLMEGYAR + Oxidation (M)
☑	120	516.3018	1030.5890	1030.5546	33.4	0	7	15	1	VDILDIDTK
☑	167	544.7650	1087.5154	1087.5370	-19.83	1	6	16	1	SADIGARADGR
☑	319	670.8413	1339.6680	1339.7037	-26.63	0	6	16	1	QQVSPPWVPFR
☑	320	670.8761	1339.7376	1339.7459	-6.19	1	6	13	1	KAELEGVAVTAPR
☑	600	915.4284	1828.8422	1828.9068	-35.29	0	6	11	1	ASGGSGGVSVPALWSEVNR
☑	383	738.3758	1474.7370	1474.6908	31.4	0	6	17	1	HNLLCLENMTSK + Oxidation (M)
☑	710	916.4273	2746.2601	2746.2625	-0.89	1	6	7.5	1	SSDMTCAPHRPELEMRSYLDVPR
☑	118	515.7795	1029.5444	1029.5753	-30.00	1	6	22	1	QACGVVLRK
☑	59	414.2218	826.4290	826.3933	43.2	0	6	13	1	NEQPPSR
☑	611	973.5194	1945.0242	1944.9364	45.2	1	6	11	1	VIEAYCTSASFQQGTRK
☑	119	516.3002	1030.5858	1030.6321	-44.87	1	6	16	1	MLLLTLRR + Oxidation (M)
☑	407	756.8483	1511.6820	1511.6939	-7.86	1	6	12	1	YYGTSMHERVNR
☑	244	618.2772	1234.5398	1234.5677	-22.55	1	6	10	1	SELEEKDTER
☑	157	533.2596	1064.5046	1064.5251	-19.18	0	6	17	1	VYGQGLSEGR
☑	19	532.2899	531.2826	531.2653	32.7	0	6	37	1	SSNPK
☑	377	736.3522	1470.6898	1470.6517	26.0	0	6	13	1	SMSLCNIAMTPSK + 2 Oxidation (M)
☑	178	554.2697	1106.5248	1106.5754	-45.66	1	6	18	1	KAVTDAIMSR + Oxidation (M)
☑	60	414.2234	826.4322	826.4661	-40.94	0	6	14	1	VAAPNLSR
☑	608	954.8972	1907.7798	1907.7561	12.5	1	6	3.6	1	KMGGDDVMACVHDDNGR + 2 Oxidation (M)
☑	393	738.3840	1474.7534	1474.6908	42.5	0	6	19	1	HNLLCLENMTSK + Oxidation (M)
☑	86	450.2203	898.4260	898.4621	-40.09	1	6	12	1	REPGEVGR
☑	135	523.2825	1044.5504	1044.5101	38.6	1	6	26	1	KGAAGWEGGGR
☑	359	466.8943	1397.6611	1397.6364	17.6	1	6	17	1	DSPKSWFFDNR
☑	180	555.2522	1108.4898	1108.5183	-25.62	1	6	12	1	ENTSKVEMR + Oxidation (M)
☑	156	533.2565	1064.4984	1064.5073	-8.31	0	6	18	1	NFNICLER
☑	124	517.2717	1032.5288	1032.5200	8.58	0	6	24	1	GEVVTAGASSR
☑	322	671.3471	1340.6796	1340.6248	40.9	0	6	19	1	YGYTEDPLEVR
☑	692	837.3954	2509.1644	2509.1667	-0.94	1	5	12	1	TIETEEASPSTESLKSTSSDPGTR
☑	111	496.2291	990.4436	990.4077	36.3	0	5	15	1	VCSDEPER
☑	672	761.7168	2282.1286	2282.0572	31.3	1	5	15	1	HCVSAGEPINPEVMEQWRK + Oxidation (M)
☑	235	615.3110	1228.6074	1228.6663	-47.92	0	5	22	1	TIVAVEVQDQK
☑	147	529.2686	1056.5226	1056.5716	-46.35	0	5	21	1	LPTALWSGGR
☑	318	670.3047	1338.5948	1338.5809	10.4	0	5	14	1	GGFGEVCACQVR
☑	328	672.8430	1343.6714	1343.6681	2.51	1	5	22	1	AQGDEQEAQLKK
☑	106	487.7730	973.5314	973.4950	37.5	1	5	32	1	ICPICRR
☑	412	766.3771	1530.7396	1530.7474	-5.04	1	5	23	1	AADTKHHHSMIQR
☑	743	1026.4631	3076.3675	3076.4223	-17.83	0	5	6.7	1	PDPISVSEFVAETLEDYMAPTASSFTTR + Oxidation (M)
☑	617	652.0220	1953.0442	1953.0758	-16.17	0	5	15	1	QGFCIPVEPGKPGLLLTK

☑	137	523.7651	1045.5156	1045.5127	2.78	1	5	34	1	FPPVDCRR
☑	30	601.3463	600.3390	600.3595	-34.10	0	5	26	1	QVINK
☑	643	1040.0198	2078.0250	2078.0895	-31.01	1	5	19	1	LEVAKLPLTEHELESENK
☑	198	572.8111	1143.6076	1143.6546	-41.07	1	5	31	1	QAMLRQLLR + Oxidation (M)
☑	633	656.9688	1967.8846	1967.8417	21.8	1	4	13	1	ASETQTSGRGSSASGSGAGDQA
☑	406	756.8435	1511.6724	1511.7144	-27.75	0	4	15	1	EVVESPQPPFPGET
☑	87	450.2206	898.4266	898.4192	8.34	1	4	17	1	GAHMDRGR
☑	28	590.3152	589.3079	589.3184	-17.71	0	4	57	1	TLNSR
☑	441	785.8559	1569.6972	1569.7569	-38.00	1	4	14	1	EMHEEEVLNIRR + Oxidation (M)
☑	626	656.6524	1966.9354	1966.9758	-20.53	0	4	20	1	AAFLGTFGTVLQVPCACR
☑	577	595.3222	1782.9448	1782.8862	32.9	0	4	19	1	MIQGDYIEKPDFALK + Oxidation (M)
☑	240	616.8068	1231.5990	1231.6197	-16.75	1	4	30	1	DLEKNYPTPR
☑	588	897.9125	1793.8104	1793.8366	-14.60	1	4	18	1	QTWTDEGSVSERMLR
☑	628	656.6563	1966.9471	1966.9670	-10.14	0	4	23	1	VSVPTHPDDVGDASLTMVK
☑	117	514.2878	1026.5610	1026.5763	-14.88	0	4	25	1	WVFLIGHR
☑	121	516.3024	1030.5902	1030.6209	-29.74	0	4	28	1	VLVIVMTTR
☑	78	438.7511	875.4876	875.5076	-22.79	1	4	35	1	SLSSKLNK
☑	371	730.9055	1459.7964	1459.7592	25.5	1	4	24	1	DVLEKMELLDQK
☑	429	785.8380	1569.6614	1569.6837	-14.19	0	4	9.6	1	VTDVMLCAGEMSGGK + Oxidation (M)
☑	435	785.8458	1569.6770	1569.7232	-29.41	0	4	13	1	LAGMEEEELAFSTK + Oxidation (M)
☑	110	496.2278	990.4410	990.4804	-39.74	0	4	21	1	LEDMQALR + Oxidation (M)
☑	34	630.3195	629.3122	629.3133	-1.70	0	3	18	1	SDGVPR
☑	109	496.2252	990.4358	990.4744	-38.89	0	3	20	1	LGGNHSNHR
☑	527	849.4228	1696.8310	1696.8818	-29.91	1	3	29	1	AFLGELKTQMTSTVR + Oxidation (M)
☑	93	458.7181	915.4216	915.3974	26.5	0	3	21	1	SSSWSYSL
☑	215	581.7887	1161.5628	1161.5448	15.5	0	3	41	1	MEEQTQQIR
☑	550	852.4276	1702.8406	1702.8825	-24.57	1	3	30	1	TQVGVKGCYAHVLGSK
☑	630	656.6592	1966.9558	1966.9418	7.11	1	3	27	1	ALQEFSELNERMSELR + Oxidation (M)
☑	669	737.6966	2210.0680	2210.0776	-4.37	1	3	24	1	TNSMSFLPVVKEEAEESSVK
☑	745	801.6301	3202.4913	3202.5964	-32.82	1	3	13	1	TVCYSPEGDMVAIGMKNGEFIILLVSSLK + 2 Oxidation (M)
☑	459	801.4326	1600.8506	1600.8243	16.5	1	3	27	1	CHLKLSLDNLSSSK
☑	327	672.8421	1343.6696	1343.7045	-25.91	1	3	33	1	KEASSGSTPQKPK
☑	181	556.2957	1110.5768	1110.6033	-23.83	0	3	32	1	TVISPDPNLR
☑	629	656.6565	1966.9477	1966.9385	4.67	0	3	28	1	ASLVSSSDGSFLADTHFAR
☑	267	631.3170	1260.6194	1260.5775	33.3	0	3	39	1	FYETVGQDFR
☑	276	634.3563	1266.6980	1266.6720	20.5	1	3	25	1	RNIIGYFEQK
☑	238	616.8051	1231.5956	1231.6561	-49.04	1	3	38	1	AKALESQFPNK
☑	673	762.0465	2283.1177	2283.0550	27.5	1	3	27	1	AVDSACPELTGSSGGPGSREPPR
☑	591	897.9169	1793.8192	1793.7699	27.5	1	3	28	1	MSYLKTTMEDEESSK + Oxidation (M)
☑	68	428.7694	855.5242	855.5178	7.55	0	2	25	1	VTIASLPR
☑	670	737.6982	2210.0728	2209.9984	33.7	1	2	28	1	RMLSDSGMITPHYEDSDLK + Oxidation (M)
☑	228	601.7988	1201.5830	1201.5952	-10.14	1	2	41	1	TPRSFSTHGGR
☑	239	616.8063	1231.5980	1231.5768	17.3	1	2	44	1	HNGYDPRVMK + Oxidation (M)
☑	574	890.4332	1778.8518	1778.8010	28.6	1	2	36	1	MVMTVFACLMGRGMK + 3 Oxidation (M)
☑	195	572.8048	1143.5950	1143.5924	2.32	0	2	51	1	NILYHLDEK
☑	693	837.3973	2509.1701	2509.2531	-33.11	0	2	24	1	MVQSLAWAGVMTLLMVQWGSAAK + 2 Oxidation (M)
☑	188	565.3242	1128.6338	1128.6502	-14.52	1	2	43	1	KLELEATVAR
☑	570	885.9603	1769.9060	1769.9635	-32.47	1	2	38	1	ENQRLQEQILSLTAK
☑	99	475.7538	949.4930	949.4869	6.48	0	2	52	1	IGDTIEFR
☑	620	652.3461	1954.0165	1954.0023	7.27	1	2	33	1	AVVVGFDPHFSYMKLTK + Oxidation (M)
☑	339	458.9060	1373.6962	1373.6688	20.0	1	2	50	1	QWRNISDVDNK
☑	528	851.4495	1700.8844	1700.8920	-4.41	1	2	38	1	DKDTLSIHYLMLPR
☑	639	1039.9996	2077.9846	2077.9132	34.4	0	2	32	1	CPNGHIYVITECGGAMQR + Oxidation (M)
☑	148	529.2691	1056.5236	1056.5426	-17.95	0	2	42	1	LMTELWHK
☑	704	894.0798	2679.2176	2679.3439	-47.13	1	2	20	1	EMLLKPHSRVQVFEGAEDNLPDR
☑	451	795.8800	1589.7454	1589.7508	-3.35	0	2	36	1	QASDSSMFLPPSPAR
☑	365	728.3507	1454.6868	1454.7365	-34.13	0	2	37	1	EQISQHIADLSSK
☑	638	688.3139	2061.9199	2061.9426	-11.01	1	2	24	1	SKGSQGTSPFPMSPPSPDSR + Oxidation (M)
☑	590	897.9169	1793.8192	1793.7699	27.5	1	2	34	1	MSYLKTTMEDEESSK + Oxidation (M)
☑	555	854.3911	1706.7676	1706.7794	-6.91	1	2	30	1	MNSFRANHSSLDNSK
☑	190	572.3210	1142.6274	1142.6448	-15.16	0	2	54	1	AALLDPFAAVR
☑	625	656.6497	1966.9273	1966.9418	-7.41	0	2	34	1	SCSVTDTVAEQAHLPPGAK
☑	667	1073.0267	2144.0388	2144.0911	-24.36	1	2	37	1	SLSAFAPICNPVLCPWGKK
☑	179	554.2782	1106.5418	1106.5581	-14.68	1	2	56	1	QSFSRQAQR
☑	439	785.8525	1569.6904	1569.6671	14.9	0	1	26	1	EDTGWYWCGIQR
☑	516	824.3876	1646.7606	1646.8055	-27.22	1	1	41	1	GLRTLCCCLPIER
☑	535	851.4545	1700.8944	1700.8920	1.46	1	1	42	1	NPKILVECLTPDFR
☑	715	917.0835	2748.2287	2748.3371	-39.44	1	1	19	1	RPTLTGCSLPGASCGPGRCPAGPVPAR
☑	732	958.4640	2872.3702	2872.2763	32.7	0	1	29	1	ASQSVDFDGDSFMNWYQQKPGQPPK + Oxidation (M)
☑	556	854.3937	1706.7728	1706.7794	-3.86	1	1	36	1	MNSFRANHSSLDNSK
☑	607	624.3091	1869.9055	1869.8349	37.7	0	1	48	1	FPCNGNSQAGLTTQTMK + Oxidation (M)
☑	627	656.6545	1966.9417	1967.0323	-46.10	1	1	41	1	LGSSSLTSIPEEVREHVK
☑	138	525.2727	1048.5308	1048.5263	4.33	0	1	76	1	GIDMIEFPK
☑	40	325.1874	648.3602	648.3595	1.16	0	1	49	1	AFNAVK
☑	423	785.8161	1569.6176	1569.6518	-21.76	0	1	7.1	1	DVTCDVHYENYR
☑	321	671.3409	1340.6672	1340.7201	-39.40	1	1	57	1	SLSRTPSPPPFR
☑	378	736.4106	1470.8066	1470.7943	8.40	0	1	43	1	QVLSQQSLYLHR
☑	100	476.7474	951.4802	951.5178	-39.46	1	1	65	1	RLPIGSYF
☑	656	1048.9799	2095.9452	2095.9844	-18.70	0	1	34	1	TPEVSQSILMSSFGNQDTR
☑	467	805.8967	1609.7788	1609.7592	12.2	1	1	53	1	TIDSWMNTMVPKR + 2 Oxidation (M)
☑	729	958.1341	2871.3805	2871.4628	-28.66	1	1	31	1	GFSQSGAPLLTLQSVRLQFQETDGHR

☑	39	325.1860	648.3574	648.3629	-8.36	1	1	67	1	GLGMKK + Oxidation (M)
☑	680	785.4049	2353.1929	2353.2715	-33.42	1	0	40	1	IVKYLALQDLMLLSQYSPSR + Oxidation (M)
☑	37	325.1857	648.3568	648.3629	-9.29	1	0	71	1	GLGMKK + Oxidation (M)
☑	85	449.2170	896.4194	896.4538	-38.32	1	0	46	1	GYTMAAKR
☑	734	963.4579	2887.3519	2887.4327	-27.99	0	0	33	1	FLTNMTITNDYQHLLVNSIANFFR + Oxidation (M)
☑	306	657.3536	1312.6926	1312.7099	-13.15	1	0	69	1	ADVKTPGGTALQR
☑	1	366.9022	365.8949							
☑	2	396.9575	395.9502							
☑	3	416.2356	415.2283							
☑	4	416.2481	415.2408							
☑	5	423.2329	422.2256							
☑	6	431.2560	430.2487							
☑	7	435.2127	434.2054							
☑	8	435.2151	434.2078							
☑	9	445.1303	444.1230							
☑	10	445.2416	444.2343							
☑	11	446.2505	445.2432							
☑	12	446.2646	445.2573							
☑	14	476.2701	475.2628							
☑	15	487.1823	486.1750							
☑	16	490.2626	489.2553							
☑	17	503.1149	502.1076							
☑	20	545.2539	544.2466							
☑	21	545.2953	544.2880							
☑	22	554.3151	553.3078							
☑	23	558.3015	557.2942							
☑	24	573.3213	572.3140							
☑	29	600.3272	599.3199							
☑	31	615.3143	614.3070							
☑	32	624.3177	623.3104							
☑	33	624.8013	623.7940							
☑	35	632.3370	631.3297							
☑	38	325.1857	648.3568							
☑	42	677.1953	676.1880							
☑	43	691.3529	690.3456							
☑	44	698.3786	697.3713							
☑	45	717.7251	716.7178							
☑	46	719.3228	718.3155							
☑	47	736.4116	735.4043							
☑	48	753.3764	752.3691							
☑	50	768.3764	767.3691							
☑	51	786.3768	785.3695							
☑	52	396.7395	791.4644							
☑	53	805.4037	804.3964							
☑	54	808.4230	807.4157							
☑	64	846.4410	845.4337							
☑	75	435.7748	869.5350							
☑	76	872.4955	871.4882							
☑	81	885.8868	884.8795							
☑	83	892.4476	891.4403							
☑	88	450.7097	899.4048							
☑	91	452.7321	903.4496							
☑	92	452.7397	903.4648							
☑	95	920.4788	919.4715							
☑	96	920.5129	919.5056							
☑	98	929.5637	928.5564							
☑	101	482.2186	962.4226							
☑	107	978.5477	977.5404							
☑	108	491.7354	981.4562							
☑	115	505.7493	1009.4840							
☑	129	519.1622	1036.3098							
☑	145	529.2667	1056.5188							
☑	151	530.2933	1058.5720							
☑	161	539.2780	1076.5414							
☑	174	552.2900	1102.5654							
☑	186	563.3021	1124.5896							
☑	187	565.2789	1128.5432							
☑	200	574.3109	1146.6072							
☑	203	574.3262	1146.6378							
☑	220	587.8072	1173.5998							
☑	221	588.3449	1174.6752							
☑	225	595.3173	1188.6200							
☑	226	1190.5615	1189.5542							
☑	232	615.3006	1228.5866							
☑	233	615.3041	1228.5936							
☑	234	615.3063	1228.5980							
☑	243	618.2758	1234.5370							
☑	248	622.8178	1243.6210							
☑	253	629.3243	1256.6340							
☑	255	631.2940	1260.5734							
☑	272	632.3372	1262.6598							

☑	278	*638.8154*	*1275.6162*
☑	284	*643.7996*	*1285.5846*
☑	285	*646.8150*	*1291.6154*
☑	287	*648.3736*	*1294.7326*
☑	307	*660.3164*	*1318.6182*
☑	326	*672.8339*	*1343.6532*
☑	344	*692.3312*	*1382.6478*
☑	349	*692.8626*	*1383.7106*
☑	350	*692.8760*	*1383.7374*
☑	351	*692.8798*	*1383.7450*
☑	352	*693.8698*	*1385.7250*
☑	364	*726.3497*	*1450.6848*
☑	366	*728.8524*	*1455.6902*
☑	367	*730.8618*	*1459.7090*
☑	379	*736.8534*	*1471.6922*
☑	381	*738.3735*	*1474.7324*
☑	386	*738.3793*	*1474.7440*
☑	389	*738.3812*	*1474.7478*
☑	394	*738.3854*	*1474.7562*
☑	400	*740.3684*	*1478.7222*
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☑	402	*745.8734*	*1489.7322*
☑	403	*746.8355*	*1491.6564*
☑	404	*748.8627*	*1495.7108*
☑	408	*756.8687*	*1511.7228*
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☑	410	*757.8616*	*1513.7086*
☑	411	*760.8881*	*1519.7616*
☑	413	*766.8620*	*1531.7094*
☑	414	*766.8657*	*1531.7168*
☑	415	*768.3747*	*1534.7348*
☑	416	*770.3876*	*1538.7606*
☑	418	*775.8670*	*1549.7194*
☑	419	*775.8695*	*1549.7244*
☑	420	*776.3786*	*1550.7426*
☑	421	*784.3751*	*1566.7356*
☑	424	*785.8351*	*1569.6556*
☑	425	*785.8369*	*1569.6592*
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☑	427	*785.8372*	*1569.6598*
☑	428	*785.8378*	*1569.6610*
☑	430	*785.8421*	*1569.6696*
☑	432	*785.8441*	*1569.6736*
☑	433	*785.8449*	*1569.6752*
☑	434	*785.8456*	*1569.6766*
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☑	438	*785.8497*	*1569.6848*
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☑	446	*793.4191*	*1584.8236*
☑	447	*794.3834*	*1586.7522*
☑	448	*794.8438*	*1587.6730*
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☑	450	*794.8522*	*1587.6898*
☑	452	*795.8813*	*1589.7480*
☑	453	*795.8821*	*1589.7496*
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☑	461	*801.9121*	*1601.8096*
☑	472	*808.9174*	*1615.8202*
☑	473	*808.9254*	*1615.8362*
☑	474	*808.9262*	*1615.8378*
☑	482	*810.8880*	*1619.7614*
☑	483	*810.8907*	*1619.7668*
☑	484	*810.8946*	*1619.7746*
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☑	486	*814.3635*	*1626.7124*
☑	497	*816.8936*	*1631.7726*
☑	499	*816.8942*	*1631.7738*
☑	502	*816.8950*	*1631.7754*
☑	514	*816.9001*	*1631.7856*
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☑	525	*846.9399*	*1691.8652*
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☑	538	*851.4555*	*1700.8964*
☑	549	*852.4240*	*1702.8334*
☑	551	*852.4293*	*1702.8440*
☑	553	*853.9323*	*1705.8500*
☑	554	*854.3732*	*1706.7318*

☑	557	854.4129	1706.8112
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☑	565	863.4109	1724.8072
☑	566	870.8540	1739.6934
☑	567	870.8572	1739.6998
☑	568	870.8726	1739.7306
☑	569	883.4468	1764.8790
☑	571	886.9477	1771.8808
☑	572	890.4144	1778.8142
☑	575	595.3120	1782.9142
☑	576	595.3168	1782.9286
☑	586	896.3635	1790.7124
☑	587	896.3699	1790.7252
☑	589	897.9144	1793.8142
☑	592	904.9169	1807.8192
☑	593	906.4688	1810.9230
☑	594	906.4699	1810.9252
☑	599	913.0020	1823.9894
☑	605	920.9665	1839.9184
☑	606	930.0057	1857.9968
☑	609	954.9168	1907.8190
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☑	612	650.9512	1949.8318
☑	619	652.0237	1953.0493
☑	634	1003.5219	2005.0292
☑	636	1004.9890	2007.9634
☑	637	1024.5085	2047.0024
☑	641	1040.0059	2077.9972
☑	642	1040.0195	2078.0244
☑	644	1040.5087	2079.0028
☑	645	1040.5095	2079.0044
☑	657	701.6409	2101.9009
☑	658	1057.0076	2112.0006
☑	659	707.3395	2118.9967
☑	660	707.6843	2120.0311
☑	661	1062.4869	2122.9592
☑	666	1073.0200	2144.0254
☑	668	1098.0914	2194.1682
☑	671	737.7042	2210.0908
☑	674	779.0428	2334.1066
☑	675	1168.5682	2335.1218
☑	683	785.4280	2353.2622
☑	689	837.3531	2509.0375
☑	690	837.3764	2509.1074
☑	694	651.8444	2603.3485
☑	695	888.4140	2662.2202
☑	700	888.7613	2663.2621
☑	702	888.7630	2663.2672
☑	707	911.4393	2731.2961
☑	708	912.4248	2734.2526
☑	709	916.4249	2746.2529
☑	712	917.0737	2748.1993
☑	713	917.0783	2748.2131
☑	714	917.0785	2748.2137
☑	716	917.0837	2748.2293
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☑	718	922.4142	2764.2208
☑	719	922.4227	2764.2463
☑	720	922.4397	2764.2973
☑	721	927.7492	2780.2258
☑	722	932.4215	2794.2427
☑	723	702.3979	2805.5625
☑	724	938.3890	2812.1452
☑	725	1415.1267	2828.2388
☑	726	958.1252	2871.3538
☑	727	958.1253	2871.3541
☑	728	958.1334	2871.3784
☑	730	958.1431	2871.4075
☑	733	958.4709	2872.3909
☑	735	963.4701	2887.3885
☑	736	963.7979	2888.3719
☑	737	968.7911	2903.3515
☑	738	969.1218	2904.3436
☑	739	969.1257	2904.3553
☑	740	973.4473	2917.3201
☑	741	753.3869	3009.5185
☑	742	767.4480	3065.7629
☑	744	1066.1575	3195.4507
☑	746	1082.2153	3243.6241
☑	747	816.6345	3262.5089
☑	748	1088.8136	3263.4190

☑	749	*1088.8392*	*3263.4958*
☑	750	*1106.5133*	*3316.5181*
☑	752	*841.9054*	*3363.5925*
☑	753	*854.3892*	*3413.5277*
☑	754	*1188.5891*	*3562.7455*
☑	755	*892.1990*	*3564.7669*
☑	756	*894.1323*	*3572.5001*
☑	757	*898.2284*	*3588.8845*
☑	758	*905.8012*	*3619.1757*
☑	759	*920.1791*	*3676.6873*
☑	760	*953.6735*	*3810.6649*
☑	761	*984.5250*	*3934.0709*
☑	762	*1004.2122*	*4012.8197*
☑	764	*1024.5935*	*4094.3449*
☑	765	*1088.9841*	*4351.9073*
☑	766	*1094.2787*	*4373.0857*
☑	767	*1111.0824*	*4440.3005*
☑	768	*1130.5969*	*4518.3585*

Search Parameters

```
Type of search         : MS/MS Ion Search
Enzyme                 : Trypsin
Fixed modifications    : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values            : Monoisotopic
Protein Mass           : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages   : 1
Instrument type        : ESI-QUAD-TOF
Number of queries      : 768
```

Mascot: http://www.matrixscience.com/

Mascot Search Results

```
User          : Dominic
Email         : dominic.kurian@bbsrc.ac.uk
Search title  : IPI Mouse_15-02-2010
MS data file  : D:\Peaklist\Dominic Kurian\QTofDK20010805 GATC P 0010883.pkl
Database      : IPI_mouse MOUSE_v3_79 (54943 sequences; 24917557 residues)
Timestamp     : 15 Feb 2011 at 15:25:08 GMT
Protein hits  : IPI00621806 Tax_Id=10090 Gene_Symbol=Camk2a Isoform Alpha CaMKII of Calcium/calmodulin-dependent protein kinase type
                IPI00474502 Tax_Id=10090 Gene_Symbol=Camk2b Calcium/calmodulin-dependent protein kinase type II subunit beta
                IPI00406790 Tax_Id=10090 Gene_Symbol=Camk2d Isoform 4 of Calcium/calmodulin-dependent protein kinase type II subunit
                IPI00124695 Tax_Id=10090 Gene_Symbol=Camk2g Isoform 1 of Calcium/calmodulin-dependent protein kinase type II subunit
                IPI00169463 Tax_Id=10090 Gene_Symbol=Tubb2c Tubulin beta-2C chain
                IPI00110850 Tax_Id=10090 Gene_Symbol=Actb Actin, cytoplasmic 1
                IPI00115546 Tax_Id=10090 Gene_Symbol=Gnao1 Isoform Alpha-2 of Guanine nucleotide-binding protein G(o) subunit alpha
                IPI00221528 Tax_Id=10090 Gene_Symbol=Actbl2 Beta-actin-like protein 2
                IPI00112251 Tax_Id=10090 Gene_Symbol=Tubb3 Tubulin beta-3 chain
                IPI00323571 Tax_Id=10090 Gene_Symbol=Apoe Apolipoprotein E
                IPI00117352 Tax_Id=10090 Gene_Symbol=Tubb5 Tubulin beta-5 chain
                IPI00138892 Tax_Id=10090 Gene_Symbol=Uba52 Ubiquitin-60S ribosomal protein L40
                IPI00755181 Tax_Id=10090 Gene_Symbol=Krt10 keratin, type I cytoskeletal 10
                IPI00122094 Tax_Id=10090 Gene_Symbol=Dlg4 Isoform 2 of Disks large homolog 4
                IPI00131366 Tax_Id=10090 Gene_Symbol=Krt6b Keratin, type II cytoskeletal 6B
                IPI00134997 Tax_Id=10090 Gene_Symbol=Dlgap3 Disks large-associated protein 3
                IPI00122928 Tax_Id=10090 Gene_Symbol=Tubb6 Tubulin beta-6 chain
                IPI00109061 Tax_Id=10090 Gene_Symbol=Tubb2b Tubulin beta-2B chain
                IPI00462140 Tax_Id=10090 Gene_Symbol=Krt77 Keratin, type II cytoskeletal 1b
                IPI00420970 Tax_Id=10090 Gene_Symbol=Krt74 Keratin, type II cytoskeletal 74
                IPI00131209 Tax_Id=10090 Gene_Symbol=Krt16 Keratin intermediate filament 16a
                IPI00348328 Tax_Id=10090 Gene_Symbol=Krt78 keratin Kb40
                IPI00322209 Tax_Id=10090 Gene_Symbol=Krt8 Keratin, type II cytoskeletal 8
                IPI00119063 Tax_Id=10090 Gene_Symbol=Lrp1 Prolow-density lipoprotein receptor-related protein 1
                IPI00121038 Tax_Id=10090 Gene_Symbol=Vcan Isoform V0 of Versican core protein
                IPI00122048 Tax_Id=10090 Gene_Symbol=Atp1a3 Sodium/potassium-transporting ATPase subunit alpha-3
                IPI00120793 Tax_Id=10090 Gene_Symbol=Prnp Major prion protein
                IPI00136402 Tax_Id=10090 Gene_Symbol=Dlgap1 Isoform 1 of Disks large-associated protein 1
                IPI00222548 Tax_Id=10090 Gene_Symbol=Rpl29;Gm13841;Gm8210 60S ribosomal protein L29
                IPI00124499 Tax_Id=10090 Gene_Symbol=Krt79 Keratin, type II cytoskeletal 79
                IPI00113410 Tax_Id=10090 Gene_Symbol=Hapln2 Hyaluronan and proteoglycan link protein 2
                IPI00223714 Tax_Id=10090 Gene_Symbol=Hist1h1e Histone H1.4
                IPI00136703 Tax_Id=10090 Gene_Symbol=Ckb Creatine kinase B-type
                IPI00229598 Tax_Id=10090 Gene_Symbol=Cnp Isoform CNPI of 2',3'-cyclic-nucleotide 3'-phosphodiesterase
                IPI00123176 Tax_Id=10090 Gene_Symbol=Gm6316 Glyceraldehyde-3-phosphate dehydrogenase
```

	IPI_mouse	**Decoy**	**False discovery rate**
Peptide matches above identity threshold	229	0	0.00 %
Peptide matches above homology or identity threshold	245	2	0.82 %

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 > 37 indicate identity or extensive homology (p<0.01).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.

Score Distribution

Peptide Summary Report

[Format As] Peptide Summary Help

Significance threshold p< 0.01 Max. number of hits AUTO

Standard scoring ○ MudPIT scoring ● Ions score or expect cut-off 0 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. IPI00621806 **Mass:** 54651 **Score:** 3316 **Queries matched:** 156 **emPAI:** 1.55
Tax_Id=10090 Gene_Symbol=Camk2a Isoform Alpha CaMKII of Calcium/calmodulin-dependent protein kinase type II 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
☑	5	445.2779	444.2706	444.2696	2.25	0	(7)	29	1	K.GAAVK.L
☑	6	445.2791	444.2718	444.2696	4.95	0	8	27	1	K.GAAVK.L
☑	11	602.3611	601.3538	601.3435	17.2	0	12	12	1	K.DLINK.M

☑	49	432.7308	863.4470	863.4501	-3.56	0	(24)	0.43	1	R.SGAPSVLPH.-
☑	50	432.7333	863.4520	863.4501	2.23	0	(14)	3.8	1	R.SGAPSVLPH.-
☑	51	432.7336	863.4526	863.4501	2.93	0	26	0.24	1	R.SGAPSVLPH.-
☑	69	452.2506	902.4866	902.4895	-3.18	0	33	0.049	1	K.MLTINPSK.R
☑	70	452.2533	902.4920	902.4895	2.80	0	(10)	10	1	K.MLTINPSK.R
☑	72	461.2145	920.4144	920.4199	-5.95	0	23	0.31	1	R.TAQSEETR.V
☑	116	525.2833	1048.5520	1048.5553	-3.09	0	(49)	0.0012	1	K.VLAGQEYAAK.I
☑	117	525.2841	1048.5536	1048.5553	-1.56	0	(33)	0.044	1	K.VLAGQEYAAK.I
☑	118	525.2841	1048.5536	1048.5553	-1.56	0	(45)	0.0028	1	K.VLAGQEYAAK.I
☑	119	525.2849	1048.5552	1048.5553	-0.03	0	52	0.00048	1	K.VLAGQEYAAK.I
☑	120	525.2850	1048.5554	1048.5553	0.16	0	(52)	0.00049	1	K.VLAGQEYAAK.I
☑	121	525.2855	1048.5564	1048.5553	1.11	0	(45)	0.0028	1	K.VLAGQEYAAK.I
☑	125	530.2988	1058.5830	1058.5906	-7.15	1	(38)	0.012	1	K.MLTINPSKR.I
☑	126	530.2988	1058.5830	1058.5906	-7.15	1	(14)	3.6	1	K.MLTINPSKR.I
☑	127	530.2996	1058.5846	1058.5906	-5.64	1	(48)	0.0014	1	K.MLTINPSKR.I
☑	128	530.2996	1058.5846	1058.5906	-5.64	1	(49)	0.0012	1	K.MLTINPSKR.I
☑	129	530.3013	1058.5880	1058.5906	-2.43	1	(46)	0.0019	1	K.MLTINPSKR.I
☑	130	530.3015	1058.5884	1058.5906	-2.05	1	(38)	0.013	1	K.MLTINPSKR.I
☑	131	530.3017	1058.5888	1058.5906	-1.68	1	52	0.00042	1	K.MLTINPSKR.I
☑	132	530.3019	1058.5892	1058.5906	-1.30	1	(43)	0.0033	1	K.MLTINPSKR.I
☑	133	530.3021	1058.5896	1058.5906	-0.92	1	(33)	0.041	1	K.MLTINPSKR.I
☑	134	530.3024	1058.5902	1058.5906	-0.35	1	(40)	0.0077	1	K.MLTINPSKR.I
☑	135	530.3027	1058.5908	1058.5906	0.21	1	(49)	0.001	1	K.MLTINPSKR.I
☑	136	530.3054	1058.5962	1058.5906	5.31	1	(41)	0.006	1	K.MLTINPSKR.I
	144	538.2992	1074.5838	1074.5855	-1.58	1	(21)	0.68	2	K.MLTINPSKR.I + Oxidation (M)
	145	538.2996	1074.5846	1074.5855	-0.83	1	(7)	16	10	K.MLTINPSKR.I + Oxidation (M)
☑	146	538.3000	1074.5854	1074.5855	-0.09	1	(47)	0.0018	1	K.MLTINPSKR.I + Oxidation (M)
☑	147	538.3003	1074.5860	1074.5855	0.47	1	(23)	0.42	1	K.MLTINPSKR.I + Oxidation (M)
☑	197	574.3211	1146.6276	1146.6431	-13.45	0	(62)	4.1e-005	1	K.GAILTTMLATR.N
☑	198	574.3234	1146.6322	1146.6431	-9.43	0	(38)	0.011	1	K.GAILTTMLATR.N
☑	199	574.3245	1146.6344	1146.6431	-7.52	0	(45)	0.002	1	K.GAILTTMLATR.N
☑	200	574.3247	1146.6348	1146.6431	-7.17	0	(54)	0.00025	1	K.GAILTTMLATR.N
☑	201	574.3251	1146.6356	1146.6431	-6.47	0	(52)	0.00036	1	K.GAILTTMLATR.N
☑	202	574.3251	1146.6356	1146.6431	-6.47	0	(38)	0.011	1	K.GAILTTMLATR.N
☑	203	574.3258	1146.6370	1146.6431	-5.25	0	(64)	2.4e-005	1	K.GAILTTMLATR.N
☑	204	574.3258	1146.6370	1146.6431	-5.25	0	(59)	8.2e-005	1	K.GAILTTMLATR.N
☑	205	574.3262	1146.6378	1146.6431	-4.55	0	(59)	7.9e-005	1	K.GAILTTMLATR.N
☑	206	574.3262	1146.6378	1146.6431	-4.55	0	(43)	0.0032	1	K.GAILTTMLATR.N
☑	207	574.3263	1146.6380	1146.6431	-4.38	0	(57)	0.00014	1	K.GAILTTMLATR.N
☑	208	574.3271	1146.6396	1146.6431	-2.98	0	(48)	0.00088	1	K.GAILTTMLATR.N
☑	209	574.3272	1146.6398	1146.6431	-2.81	0	(46)	0.0013	1	K.GAILTTMLATR.N
☑	210	574.3275	1146.6404	1146.6431	-2.28	0	(41)	0.0049	1	K.GAILTTMLATR.N
☑	211	574.3278	1146.6410	1146.6431	-1.76	0	(58)	8.4e-005	1	K.GAILTTMLATR.N
☑	212	574.3279	1146.6412	1146.6431	-1.59	0	(59)	7.2e-005	1	K.GAILTTMLATR.N
☑	213	574.3279	1146.6412	1146.6431	-1.59	0	(59)	7.1e-005	1	K.GAILTTMLATR.N
☑	214	574.3279	1146.6412	1146.6431	-1.59	0	(59)	7.1e-005	1	K.GAILTTMLATR.N
☑	215	574.3281	1146.6416	1146.6431	-1.24	0	(63)	3e-005	1	K.GAILTTMLATR.N
☑	216	574.3281	1146.6416	1146.6431	-1.24	0	78	9.7e-007	1	K.GAILTTMLATR.N
☑	217	574.3283	1146.6420	1146.6431	-0.89	0	(50)	0.00053	1	K.GAILTTMLATR.N
☑	218	574.3287	1146.6428	1146.6431	-0.19	0	(49)	0.00065	1	K.GAILTTMLATR.N
☑	219	574.3294	1146.6442	1146.6431	1.03	0	(56)	0.00015	1	K.GAILTTMLATR.N
☑	220	574.3297	1146.6448	1146.6431	1.55	0	(31)	0.048	1	K.GAILTTMLATR.N
☑	221	574.3318	1146.6490	1146.6431	5.22	0	(42)	0.0029	1	K.GAILTTMLATR.N
☑	261	631.3007	1260.5868	1260.5927	-4.68	0	(35)	0.02	1	R.FYFENLWSR.N
☑	262	631.3032	1260.5918	1260.5927	-0.71	0	(37)	0.012	1	R.FYFENLWSR.N
☑	263	631.3038	1260.5930	1260.5927	0.24	0	(48)	0.001	1	R.FYFENLWSR.N
☑	264	631.3044	1260.5942	1260.5927	1.19	0	(35)	0.021	1	R.FYFENLWSR.N
☑	265	631.3046	1260.5946	1260.5927	1.51	0	(51)	0.00059	1	R.FYFENLWSR.N
☑	266	631.3048	1260.5950	1260.5927	1.83	0	(48)	0.0011	1	R.FYFENLWSR.N
☑	267	631.3051	1260.5956	1260.5927	2.30	0	(38)	0.0099	1	R.FYFENLWSR.N
☑	268	631.3055	1260.5964	1260.5927	2.94	0	(48)	0.0011	1	R.FYFENLWSR.N
☑	269	631.3056	1260.5966	1260.5927	3.10	0	(51)	0.0006	1	R.FYFENLWSR.N
☑	270	631.3056	1260.5966	1260.5927	3.10	0	(36)	0.016	1	R.FYFENLWSR.N
☑	271	631.3060	1260.5974	1260.5927	3.73	0	(51)	0.0006	1	R.FYFENLWSR.N
☑	272	631.3065	1260.5984	1260.5927	4.53	0	51	0.00061	1	R.FYFENLWSR.N
☑	292	652.3373	1302.6600	1302.6932	-25.44	0	(54)	0.00031	1	R.ITQYLDAGGIPR.T
☑	293	652.3430	1302.6714	1302.6932	-16.69	0	(75)	2.6e-006	1	R.ITQYLDAGGIPR.T
☑	294	652.3467	1302.6788	1302.6932	-11.01	0	(73)	4e-006	1	R.ITQYLDAGGIPR.T
☑	295	652.3514	1302.6882	1302.6932	-3.80	0	(59)	0.0001	1	R.ITQYLDAGGIPR.T
☑	296	652.3551	1302.6956	1302.6932	1.89	0	(77)	1.4e-006	1	R.ITQYLDAGGIPR.T
☑	297	652.3551	1302.6956	1302.6932	1.89	0	79	9.7e-007	1	R.ITQYLDAGGIPR.T
☑	298	652.3563	1302.6980	1302.6932	3.73	0	(52)	0.0004	1	R.ITQYLDAGGIPR.T
☑	308	670.8843	1339.7540	1339.7711	-12.71	0	(4)	18	1	R.DLKPENLLLASK.L
☑	309	670.8865	1339.7584	1339.7711	-9.42	0	(20)	0.47	1	R.DLKPENLLLASK.L
☑	310	670.8892	1339.7638	1339.7711	-5.39	0	(27)	0.088	1	R.DLKPENLLLASK.L
☑	311	670.8903	1339.7660	1339.7711	-3.75	0	(52)	0.00028	1	R.DLKPENLLLASK.L
☑	312	670.8908	1339.7670	1339.7711	-3.00	0	(33)	0.018	1	R.DLKPENLLLASK.L
☑	313	670.8910	1339.7674	1339.7711	-2.70	0	(35)	0.012	1	R.DLKPENLLLASK.L
☑	314	670.8913	1339.7680	1339.7711	-2.26	0	(53)	0.00019	1	R.DLKPENLLLASK.L
☑	315	670.8915	1339.7684	1339.7711	-1.96	0	(60)	3.6e-005	1	R.DLKPENLLLASK.L
☑	316	670.8926	1339.7706	1339.7711	-0.32	0	(58)	6.1e-005	1	R.DLKPENLLLASK.L

☑	317	670.8928	1339.7710	1339.7711	-0.02	0	(23)	0.17	1	R.DLKPENLLLASK.L
☑	318	670.8931	1339.7716	1339.7711	0.43	0	(37)	0.0077	1	R.DLKPENLLLASK.L
☑	319	670.8934	1339.7722	1339.7711	0.88	0	(61)	3e-005	1	R.DLKPENLLLASK.L
☑	320	670.8937	1339.7728	1339.7711	1.33	0	(66)	8.4e-006	1	R.DLKPENLLLASK.L
☑	321	670.8940	1339.7734	1339.7711	1.77	0	82	2.1e-007	1	R.DLKPENLLLASK.L
☑	322	670.8940	1339.7734	1339.7711	1.77	0	(67)	6.9e-006	1	R.DLKPENLLLASK.L
☑	323	670.8940	1339.7734	1339.7711	1.77	0	(63)	1.7e-005	1	R.DLKPENLLLASK.L
☑	324	670.8945	1339.7744	1339.7711	2.52	0	(51)	0.00028	1	R.DLKPENLLLASK.L
☑	325	670.8946	1339.7746	1339.7711	2.67	0	(70)	3.2e-006	1	R.DLKPENLLLASK.L
☑	326	670.8951	1339.7756	1339.7711	3.42	0	(63)	1.6e-005	1	R.DLKPENLLLASK.L
☑	327	670.8954	1339.7762	1339.7711	3.86	0	(63)	1.6e-005	1	R.DLKPENLLLASK.L
☑	328	670.8955	1339.7764	1339.7711	4.01	0	(59)	4.4e-005	1	R.DLKPENLLLASK.L
☑	398	816.8909	1631.7672	1631.7719	-2.84	0	(62)	4.1e-005	1	R.FTEEYQLFEELGK.G
☑	399	816.8932	1631.7718	1631.7719	-0.02	0	(54)	0.00023	1	R.FTEEYQLFEELGK.G
☑	400	816.8936	1631.7726	1631.7719	0.47	0	(60)	6.7e-005	1	R.FTEEYQLFEELGK.G
☑	401	816.8937	1631.7728	1631.7719	0.59	0	(59)	8.6e-005	1	R.FTEEYQLFEELGK.G
☑	402	816.8939	1631.7732	1631.7719	0.84	0	(54)	0.00024	1	R.FTEEYQLFEELGK.G
☑	403	816.8940	1631.7734	1631.7719	0.96	0	(64)	2.3e-005	1	R.FTEEYQLFEELGK.G
☑	404	816.8947	1631.7748	1631.7719	1.82	0	(64)	2.6e-005	1	R.FTEEYQLFEELGK.G
☑	405	816.8948	1631.7750	1631.7719	1.94	0	(64)	2.4e-005	1	R.FTEEYQLFEELGK.G
☑	406	816.8949	1631.7752	1631.7719	2.06	0	70	6.7e-006	1	R.FTEEYQLFEELGK.G
☑	407	816.8950	1631.7754	1631.7719	2.19	0	(58)	0.00011	1	R.FTEEYQLFEELGK.G
☑	408	816.8951	1631.7756	1631.7719	2.31	0	(66)	1.7e-005	1	R.FTEEYQLFEELGK.G
☑	409	816.8952	1631.7758	1631.7719	2.43	0	(63)	3e-005	1	R.FTEEYQLFEELGK.G
☑	410	816.8953	1631.7760	1631.7719	2.55	0	(59)	7.2e-005	1	R.FTEEYQLFEELGK.G
☑	411	816.8957	1631.7768	1631.7719	3.04	0	(64)	2.6e-005	1	R.FTEEYQLFEELGK.G
☑	412	816.8958	1631.7770	1631.7719	3.17	0	(61)	4.7e-005	1	R.FTEEYQLFEELGK.G
☑	413	816.8960	1631.7774	1631.7719	3.41	0	(61)	4.9e-005	1	R.FTEEYQLFEELGK.G
☑	414	816.8961	1631.7776	1631.7719	3.53	0	(53)	0.00032	1	R.FTEEYQLFEELGK.G
☑	415	816.8961	1631.7776	1631.7719	3.53	0	(56)	0.00017	1	R.FTEEYQLFEELGK.G
☑	416	816.8962	1631.7778	1631.7719	3.66	0	(67)	1.4e-005	1	R.FTEEYQLFEELGK.G
☑	417	816.8962	1631.7778	1631.7719	3.66	0	(60)	6.2e-005	1	R.FTEEYQLFEELGK.G
☑	418	816.8970	1631.7794	1631.7719	4.64	0	(57)	0.00013	1	R.FTEEYQLFEELGK.G
☑	419	816.8971	1631.7796	1631.7719	4.76	0	(26)	0.15	1	R.FTEEYQLFEELGK.G
☑	420	816.8973	1631.7800	1631.7719	5.00	0	(51)	0.0005	1	R.FTEEYQLFEELGK.G
☑	421	816.8973	1631.7800	1631.7719	5.00	0	(68)	1.1e-005	1	R.FTEEYQLFEELGK.G
☑	422	816.8975	1631.7804	1631.7719	5.25	0	(62)	4e-005	1	R.FTEEYQLFEELGK.G
☑	423	816.8977	1631.7808	1631.7719	5.50	0	(61)	5.2e-005	1	R.FTEEYQLFEELGK.G
☑	424	816.8977	1631.7808	1631.7719	5.50	0	(55)	0.0002	1	R.FTEEYQLFEELGK.G
☑	425	816.8979	1631.7812	1631.7719	5.74	0	(57)	0.00013	1	R.FTEEYQLFEELGK.G
☑	426	816.8990	1631.7834	1631.7719	7.09	0	(54)	0.00024	1	R.FTEEYQLFEELGK.G
☑	477	680.9728	2039.8966	2039.9131	-8.10	1	103	1.4e-009	1	K.ESSESTNTTIEDEDTKVR.K
☑	478	680.9773	2039.9101	2039.9131	-1.48	1	(102)	2.3e-009	1	K.ESSESTNTTIEDEDTKVR.K
☑	483	1040.9476	2079.8806	2079.9426	-29.76	0	(74)	8.8e-007	1	K.AGAYDFPSPEWDTVTPEAK.D
☑	484	1040.9493	2079.8840	2079.9426	-28.13	0	(58)	3.7e-005	1	K.AGAYDFPSPEWDTVTPEAK.D
☑	485	1040.9618	2079.9090	2079.9426	-16.11	0	(57)	5.8e-005	1	K.AGAYDFPSPEWDTVTPEAK.D
☑	486	694.3159	2079.9259	2079.9426	-8.02	0	(70)	3.7e-006	1	K.AGAYDFPSPEWDTVTPEAK.D
☑	487	694.3180	2079.9322	2079.9426	-4.99	0	90	3.7e-008	1	K.AGAYDFPSPEWDTVTPEAK.D
☑	488	1040.9735	2079.9324	2079.9426	-4.86	0	(42)	0.0023	1	K.AGAYDFPSPEWDTVTPEAK.D
☑	489	1040.9767	2079.9388	2079.9426	-1.78	0	(64)	1.7e-005	1	K.AGAYDFPSPEWDTVTPEAK.D
☑	490	1040.9814	2079.9482	2079.9426	2.74	0	(62)	2.8e-005	1	K.AGAYDFPSPEWDTVTPEAK.D
☑	491	1040.9825	2079.9504	2079.9426	3.80	0	(75)	1.4e-006	1	K.AGAYDFPSPEWDTVTPEAK.D
☑	498	715.3460	2143.0162	2143.0321	-7.42	0	(71)	4.1e-006	1	K.VTEQLIEAISNGDFESYTK.M
☑	499	715.3465	2143.0177	2143.0321	-6.72	0	102	3.4e-009	1	K.VTEQLIEAISNGDFESYTK.M
☑	500	1072.5264	2143.0382	2143.0321	2.88	0	(93)	2.6e-008	1	K.VTEQLIEAISNGDFESYTK.M
☑	501	1072.5287	2143.0428	2143.0321	5.03	0	(77)	1e-006	1	K.VTEQLIEAISNGDFESYTK.M
☑	558	888.7586	2663.2540	2663.2755	-8.08	1	(47)	0.00081	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
☑	559	888.7591	2663.2555	2663.2755	-7.52	1	(71)	3.1e-006	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
☑	560	888.7594	2663.2564	2663.2755	-7.18	1	(90)	4e-008	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
☑	561	888.7601	2663.2585	2663.2755	-6.39	1	(59)	4.9e-005	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
☑	562	888.7601	2663.2585	2663.2755	-6.39	1	97	8.5e-009	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
☑	563	888.7603	2663.2591	2663.2755	-6.17	1	(78)	7e-007	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
☑	564	888.7603	2663.2591	2663.2755	-6.17	1	(79)	5.1e-007	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
☑	565	888.7603	2663.2591	2663.2755	-6.17	1	(78)	7e-007	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
☑	566	888.7608	2663.2606	2663.2755	-5.60	1	(74)	1.5e-006	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
☑	567	888.7608	2663.2606	2663.2755	-5.60	1	(52)	0.00027	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
☑	568	888.7616	2663.2630	2663.2755	-4.70	1	(32)	0.03	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
☑	569	888.7617	2663.2633	2663.2755	-4.59	1	(26)	0.11	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
☑	570	888.7621	2663.2645	2663.2755	-4.14	1	(79)	4.8e-007	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
☑	571	888.7621	2663.2645	2663.2755	-4.14	1	(67)	7.6e-006	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
☑	572	888.7629	2663.2669	2663.2755	-3.24	1	(78)	6e-007	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
☑	573	888.7650	2663.2732	2663.2755	-0.87	1	(12)	2.6	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M

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2. IPI00474502 **Mass:** 61164 **Score:** 2503 **Queries matched:** 106 **emPAI:** 1.85
Tax_Id=10090 Gene_Symbol=Camk2b Calcium/calmodulin-dependent protein kinase type II subunit 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
5	445.2779	444.2706	444.2696	2.25	0	(7)	29	1	K.GAAVK.L
6	445.2791	444.2718	444.2696	4.95	0	8	27	1	K.GAAVK.L
71	452.7382	903.4618	903.4661	-4.75	0	51	0.0009	1	K.NSSAITSPK.G

☑										
☑	188	572.8056	1143.5966	1143.5964	0.20	0	21	0.77	1	R.FYFENLLAK.N
☑	189	572.8057	1143.5968	1143.5964	0.37	0	(19)	1.1	1	R.FYFENLLAK.N
☑	190	572.8067	1143.5988	1143.5964	2.12	0	(11)	6.9	1	R.FYFENLLAK.N
☑	191	572.8068	1143.5990	1143.5964	2.30	0	(19)	1.1	1	R.FYFENLLAK.N
☑	193	572.8070	1143.5994	1143.5964	2.65	0	(7)	18	1	R.FYFENLLAK.N
☑	194	572.8076	1143.6006	1143.5964	3.70	0	(15)	2.5	1	R.FYFENLLAK.N
	195	572.8080	1143.6014	1143.5964	4.40	0	(4)	32	3	R.FYFENLLAK.N
	197	574.3211	1146.6276	1146.6431	-13.45	0	(62)	4.1e-005	1	K.GAILTTMLATR.N
	198	574.3234	1146.6322	1146.6431	-9.43	0	(38)	0.011	1	K.GAILTTMLATR.N
	199	574.3245	1146.6344	1146.6431	-7.52	0	(45)	0.002	1	K.GAILTTMLATR.N
	200	574.3247	1146.6348	1146.6431	-7.17	0	(54)	0.00025	1	K.GAILTTMLATR.N
	201	574.3251	1146.6356	1146.6431	-6.47	0	(52)	0.00036	1	K.GAILTTMLATR.N
	202	574.3251	1146.6356	1146.6431	-6.47	0	(38)	0.011	1	K.GAILTTMLATR.N
	203	574.3258	1146.6370	1146.6431	-5.25	0	(64)	2.4e-005	1	K.GAILTTMLATR.N
	204	574.3258	1146.6370	1146.6431	-5.25	0	(59)	8.2e-005	1	K.GAILTTMLATR.N
	205	574.3262	1146.6378	1146.6431	-4.55	0	(59)	7.9e-005	1	K.GAILTTMLATR.N
	206	574.3262	1146.6378	1146.6431	-4.55	0	(43)	0.0032	1	K.GAILTTMLATR.N
	207	574.3263	1146.6380	1146.6431	-4.38	0	(57)	0.00014	1	K.GAILTTMLATR.N
	208	574.3271	1146.6396	1146.6431	-2.98	0	(48)	0.00088	1	K.GAILTTMLATR.N
	209	574.3272	1146.6398	1146.6431	-2.81	0	(46)	0.0013	1	K.GAILTTMLATR.N
	210	574.3275	1146.6404	1146.6431	-2.28	0	(41)	0.0049	1	K.GAILTTMLATR.N
	211	574.3278	1146.6410	1146.6431	-1.76	0	(58)	8.4e-005	1	K.GAILTTMLATR.N
	212	574.3279	1146.6412	1146.6431	-1.59	0	(59)	7.2e-005	1	K.GAILTTMLATR.N
	213	574.3279	1146.6412	1146.6431	-1.59	0	(59)	7.1e-005	1	K.GAILTTMLATR.N
	214	574.3279	1146.6412	1146.6431	-1.59	0	(59)	7.1e-005	1	K.GAILTTMLATR.N
	215	574.3281	1146.6416	1146.6431	-1.24	0	(63)	3e-005	1	K.GAILTTMLATR.N
	216	574.3281	1146.6416	1146.6431	-1.24	0	78	9.7e-007	1	K.GAILTTMLATR.N
	217	574.3283	1146.6420	1146.6431	-0.89	0	(50)	0.00053	1	K.GAILTTMLATR.N
	218	574.3287	1146.6428	1146.6431	-0.19	0	(49)	0.00065	1	K.GAILTTMLATR.N
	219	574.3294	1146.6442	1146.6431	1.03	0	(56)	0.00015	1	K.GAILTTMLATR.N
	220	574.3297	1146.6448	1146.6431	1.55	0	(31)	0.048	1	K.GAILTTMLATR.N
	221	574.3318	1146.6490	1146.6431	5.22	0	(42)	0.0029	1	K.GAILTTMLATR.N
	308	670.8843	1339.7540	1339.7711	-12.71	0	(4)	18	1	R.DLKPENLLLASK.C
	309	670.8865	1339.7584	1339.7711	-9.42	0	(20)	0.47	1	R.DLKPENLLLASK.C
	310	670.8892	1339.7638	1339.7711	-5.39	0	(27)	0.088	1	R.DLKPENLLLASK.C
	311	670.8903	1339.7660	1339.7711	-3.75	0	(52)	0.00028	1	R.DLKPENLLLASK.C
	312	670.8908	1339.7670	1339.7711	-3.00	0	(33)	0.018	1	R.DLKPENLLLASK.C
	313	670.8910	1339.7674	1339.7711	-2.70	0	(35)	0.012	1	R.DLKPENLLLASK.C
	314	670.8913	1339.7680	1339.7711	-2.26	0	(53)	0.00019	1	R.DLKPENLLLASK.C
	315	670.8915	1339.7684	1339.7711	-1.96	0	(60)	3.6e-005	1	R.DLKPENLLLASK.C
	316	670.8926	1339.7706	1339.7711	-0.32	0	(58)	6.1e-005	1	R.DLKPENLLLASK.C
	317	670.8928	1339.7710	1339.7711	-0.02	0	(23)	0.17	1	R.DLKPENLLLASK.C
	318	670.8931	1339.7716	1339.7711	0.43	0	(37)	0.0077	1	R.DLKPENLLLASK.C
	319	670.8934	1339.7722	1339.7711	0.88	0	(61)	3e-005	1	R.DLKPENLLLASK.C
	320	670.8937	1339.7728	1339.7711	1.33	0	(66)	8.4e-006	1	R.DLKPENLLLASK.C
	321	670.8940	1339.7734	1339.7711	1.77	0	82	2.1e-007	1	R.DLKPENLLLASK.C
	322	670.8940	1339.7734	1339.7711	1.77	0	(67)	6.9e-006	1	R.DLKPENLLLASK.C
	323	670.8940	1339.7734	1339.7711	1.77	0	(63)	1.7e-005	1	R.DLKPENLLLASK.C
	324	670.8945	1339.7744	1339.7711	2.52	0	(51)	0.00028	1	R.DLKPENLLLASK.C
	325	670.8946	1339.7746	1339.7711	2.67	0	(70)	3.2e-006	1	R.DLKPENLLLASK.C
	326	670.8951	1339.7756	1339.7711	3.42	0	(63)	1.6e-005	1	R.DLKPENLLLASK.C
	327	670.8954	1339.7762	1339.7711	3.86	0	(63)	1.6e-005	1	R.DLKPENLLLASK.C
	328	670.8955	1339.7764	1339.7711	4.01	0	(59)	4.4e-005	1	R.DLKPENLLLASK.C
☑	346	468.5799	1402.7179	1402.7317	-9.86	0	(50)	0.00069	1	R.LTQYIDGQGRPR.T
☑	347	468.5800	1402.7182	1402.7317	-9.65	0	(51)	0.00053	1	R.LTQYIDGQGRPR.T
☑	348	468.5803	1402.7191	1402.7317	-9.01	0	(52)	0.00046	1	R.LTQYIDGQGRPR.T
☑	349	468.5805	1402.7197	1402.7317	-8.58	0	(38)	0.011	1	R.LTQYIDGQGRPR.T
☑	350	468.5811	1402.7215	1402.7317	-7.30	0	59	8.4e-005	1	R.LTQYIDGQGRPR.T
☑	351	702.3745	1402.7344	1402.7317	1.96	0	(53)	0.00035	1	R.LTQYIDGQGRPR.T
☑	352	702.3751	1402.7356	1402.7317	2.81	0	(39)	0.0085	1	R.LTQYIDGQGRPR.T
☑	353	702.3760	1402.7374	1402.7317	4.09	0	(43)	0.0035	1	R.LTQYIDGQGRPR.T
☑	354	702.3771	1402.7396	1402.7317	5.66	0	(18)	0.99	1	R.LTQYIDGQGRPR.T
☑	355	702.3782	1402.7418	1402.7317	7.23	0	(26)	0.17	1	R.LTQYIDGQGRPR.T
☑	360	735.4061	1468.7976	1468.8071	-6.47	0	75	1.8e-006	1	K.NLINQMLTINPAK.R
☑	361	735.4121	1468.8096	1468.8071	1.70	0	(71)	4.1e-006	1	K.NLINQMLTINPAK.R
☑	362	735.4124	1468.8102	1468.8071	2.11	0	(41)	0.0041	1	K.NLINQMLTINPAK.R
☑	363	735.4127	1468.8108	1468.8071	2.52	0	(70)	4.3e-006	1	K.NLINQMLTINPAK.R
☑	364	735.4138	1468.8130	1468.8071	4.02	0	(71)	3.5e-006	1	K.NLINQMLTINPAK.R
☑	394	810.8770	1619.7394	1619.7355	2.43	0	70	5.6e-006	1	R.FTDEYQLYEDIGK.G
☑	395	810.8795	1619.7444	1619.7355	5.52	0	(65)	1.8e-005	1	R.FTDEYQLYEDIGK.G
☑	396	810.8807	1619.7468	1619.7355	7.00	0	(51)	0.00047	1	R.FTDEYQLYEDIGK.G
☑	397	542.6334	1624.8784	1624.9082	-18.39	1	45	0.0014	1	K.NLINQMLTINPAKR.I
☑	443	871.3691	1740.7236	1740.7173	3.62	0	90	2.1e-008	1	K.ESSDSTNTTIEDEDAK.A
☑	475	656.9542	1967.8408	1967.8556	-7.51	1	94	8.8e-009	1	K.ESSDSTNTTIEDEDAKAR.K
	483	1040.9476	2079.8806	2079.9426	-29.76	0	(74)	8.8e-007	1	K.AGAYDFPSPEWDTVTPEAK.N
	484	1040.9493	2079.8840	2079.9426	-28.13	0	(58)	3.7e-005	1	K.AGAYDFPSPEWDTVTPEAK.N
	485	1040.9618	2079.9090	2079.9426	-16.11	0	(57)	5.8e-005	1	K.AGAYDFPSPEWDTVTPEAK.N
	486	694.3159	2079.9259	2079.9426	-8.02	0	(70)	3.7e-006	1	K.AGAYDFPSPEWDTVTPEAK.N
	487	694.3180	2079.9322	2079.9426	-4.99	0	90	3.7e-008	1	K.AGAYDFPSPEWDTVTPEAK.N
	488	1040.9735	2079.9324	2079.9426	-4.86	0	(42)	0.0023	1	K.AGAYDFPSPEWDTVTPEAK.N
	489	1040.9767	2079.9388	2079.9426	-1.78	0	(64)	1.7e-005	1	K.AGAYDFPSPEWDTVTPEAK.N
	490	1040.9814	2079.9482	2079.9426	2.74	0	(62)	2.8e-005	1	K.AGAYDFPSPEWDTVTPEAK.N
	491	1040.9825	2079.9504	2079.9426	3.80	0	(75)	1.4e-006	1	K.AGAYDFPSPEWDTVTPEAK.N
☑	494	705.0025	2111.9857	2112.0011	-7.30	0	(66)	1.3e-005	1	K.TTEQLIEAVNNGDFEAYAK.I
☑	495	705.0052	2111.9938	2112.0011	-3.47	0	(65)	1.5e-005	1	K.TTEQLIEAVNNGDFEAYAK.I
☑	496	1057.0114	2112.0082	2112.0011	3.38	0	94	1.8e-008	1	K.TTEQLIEAVNNGDFEAYAK.I

☑	540	779.7122	2336.1148	2336.1325	-7.58	1	(13)	2.4	1	R.FTDEYQLYEDIGKGAFSVVR.R
☑	541	779.7162	2336.1268	2336.1325	-2.44	1	73	2.3e-006	1	R.FTDEYQLYEDIGKGAFSVVR.R
☑	542	785.0447	2352.1123	2352.1301	-7.58	0	(87)	8.1e-008	1	R.QTTAPATMSTAASGTTMGLVEQAK.S
☑	543	785.0452	2352.1138	2352.1301	-6.95	0	(108)	6.7e-010	1	R.QTTAPATMSTAASGTTMGLVEQAK.S
☑	544	1177.0774	2352.1402	2352.1301	4.31	0	(60)	4.2e-005	1	R.QTTAPATMSTAASGTTMGLVEQAK.S
☑	545	1177.0776	2352.1406	2352.1301	4.48	0	(71)	3.7e-006	1	R.QTTAPATMSTAASGTTMGLVEQAK.S
☑	546	1177.0782	2352.1418	2352.1301	4.99	0	130	4.7e-012	1	R.QTTAPATMSTAASGTTMGLVEQAK.S
☑	547	785.4210	2353.2412	2353.2642	-9.77	0	(34)	0.015	1	K.GSLPPAALEPQTTVIHNPVDGIK.E
☑	548	785.4226	2353.2460	2353.2642	-7.73	0	89	4.7e-008	1	K.GSLPPAALEPQTTVIHNPVDGIK.E
☑	549	785.4229	2353.2469	2353.2642	-7.35	0	(70)	3.4e-006	1	K.GSLPPAALEPQTTVIHNPVDGIK.E
☑	550	785.4230	2353.2472	2353.2642	-7.22	0	(82)	2.1e-007	1	K.GSLPPAALEPQTTVIHNPVDGIK.E
☑	551	785.4232	2353.2478	2353.2642	-6.96	0	(80)	3.1e-007	1	K.GSLPPAALEPQTTVIHNPVDGIK.E
☑	552	785.4244	2353.2514	2353.2642	-5.43	0	(71)	2.8e-006	1	K.GSLPPAALEPQTTVIHNPVDGIK.E
☑	553	790.3778	2368.1116	2368.1250	-5.68	0	(88)	6.5e-008	1	R.QTTAPATMSTAASGTTMGLVEQAK.S + Oxidation (M)
☑	554	790.3788	2368.1146	2368.1250	-4.42	0	(111)	3.2e-010	1	R.QTTAPATMSTAASGTTMGLVEQAK.S + Oxidation (M)
☑	555	1185.0740	2368.1334	2368.1250	3.55	0	(88)	6.7e-008	1	R.QTTAPATMSTAASGTTMGLVEQAK.S + Oxidation (M)
☑	556	1185.0802	2368.1458	2368.1250	8.79	0	(72)	2.9e-006	1	R.QTTAPATMSTAASGTTMGLVEQAK.S + Oxidation (M)

Proteins matching the same set of peptides:
IPI00875723 **Mass:** 68686 **Score:** 2503 **Queries matched:** 106
Tax_Id=10090 Gene_Symbol=Camk2b 68 kDa protein

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3. IPI00406790 **Mass:** 60593 **Score:** 1774 **Queries matched:** 91 **emPAI:** 0.70
Tax_Id=10090 Gene_Symbol=Camk2d Isoform 4 of Calcium/calmodulin-dependent protein kinase type II subunit 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
	5	445.2779	444.2706	444.2696	2.25	0	(7)	29	1	K.GAAVK.L
	6	445.2791	444.2718	444.2696	4.95	0	8	27	1	K.GAAVK.L
	11	602.3611	601.3538	601.3435	17.2	0	12	12	1	K.DLINK.M
☑	149	539.2814	1076.5482	1076.5502	-1.81	0	44	0.0034	1	K.IPTGQEYAAK.I
	161	556.8326	1111.6506	1111.6349	14.1	1	(3)	16	6	K.KPDGVKINNK.A
	163	556.8347	1111.6548	1111.6349	17.9	1	(1)	24	7	K.KPDGVKINNK.A
	166	556.8363	1111.6580	1111.6349	20.8	1	(2)	21	3	K.KPDGVKINNK.A
☑	167	556.8364	1111.6582	1111.6349	21.0	1	5	9.5	1	K.KPDGVKINNK.A
	168	556.8366	1111.6586	1111.6349	21.3	1	(3)	16	2	K.KPDGVKINNK.A
☑	174	559.7805	1117.5464	1117.5444	1.84	0	(22)	0.52	1	R.FYFENALSK.S
☑	175	559.7811	1117.5476	1117.5444	2.92	0	27	0.16	1	R.FYFENALSK.S
☑	176	559.7817	1117.5488	1117.5444	3.99	0	(26)	0.2	1	R.FYFENALSK.S
☑	177	559.7820	1117.5494	1117.5444	4.53	0	(20)	0.76	1	R.FYFENALSK.S
	197	574.3211	1146.6276	1146.6431	-13.45	0	(62)	4.1e-005	1	K.GAILTTMLATR.N
	198	574.3234	1146.6322	1146.6431	-9.43	0	(38)	0.011	1	K.GAILTTMLATR.N
	199	574.3245	1146.6344	1146.6431	-7.52	0	(45)	0.002	1	K.GAILTTMLATR.N
	200	574.3247	1146.6348	1146.6431	-7.17	0	(54)	0.00025	1	K.GAILTTMLATR.N
	201	574.3251	1146.6356	1146.6431	-6.47	0	(52)	0.00036	1	K.GAILTTMLATR.N
	202	574.3251	1146.6356	1146.6431	-6.47	0	(38)	0.011	1	K.GAILTTMLATR.N
	203	574.3258	1146.6370	1146.6431	-5.25	0	(64)	2.4e-005	1	K.GAILTTMLATR.N
	204	574.3258	1146.6370	1146.6431	-5.25	0	(59)	8.2e-005	1	K.GAILTTMLATR.N
	205	574.3262	1146.6378	1146.6431	-4.55	0	(59)	7.9e-005	1	K.GAILTTMLATR.N
	206	574.3262	1146.6378	1146.6431	-4.55	0	(43)	0.0032	1	K.GAILTTMLATR.N
	207	574.3263	1146.6380	1146.6431	-4.38	0	(57)	0.00014	1	K.GAILTTMLATR.N
	208	574.3271	1146.6396	1146.6431	-2.98	0	(48)	0.00088	1	K.GAILTTMLATR.N
	209	574.3272	1146.6398	1146.6431	-2.81	0	(46)	0.0013	1	K.GAILTTMLATR.N
	210	574.3275	1146.6404	1146.6431	-2.28	0	(41)	0.0049	1	K.GAILTTMLATR.N
	211	574.3278	1146.6410	1146.6431	-1.76	0	(58)	8.4e-005	1	K.GAILTTMLATR.N
	212	574.3279	1146.6412	1146.6431	-1.59	0	(59)	7.2e-005	1	K.GAILTTMLATR.N
	213	574.3279	1146.6412	1146.6431	-1.59	0	(59)	7.1e-005	1	K.GAILTTMLATR.N
	214	574.3279	1146.6412	1146.6431	-1.59	0	(59)	7.1e-005	1	K.GAILTTMLATR.N
	215	574.3281	1146.6416	1146.6431	-1.24	0	(63)	3e-005	1	K.GAILTTMLATR.N
	216	574.3281	1146.6416	1146.6431	-1.24	0	78	9.7e-007	1	K.GAILTTMLATR.N
	217	574.3283	1146.6420	1146.6431	-0.89	0	(50)	0.00053	1	K.GAILTTMLATR.N
	218	574.3287	1146.6428	1146.6431	-0.19	0	(49)	0.00065	1	K.GAILTTMLATR.N
	219	574.3294	1146.6442	1146.6431	1.03	0	(56)	0.00015	1	K.GAILTTMLATR.N
	220	574.3297	1146.6448	1146.6431	1.55	0	(31)	0.048	1	K.GAILTTMLATR.N
	221	574.3318	1146.6490	1146.6431	5.22	0	(42)	0.0029	1	K.GAILTTMLATR.N
☑	303	664.3068	1326.5990	1326.5948	3.20	0	(52)	0.0003	1	R.LTQYMDGSGMPK.T
☑	304	664.3070	1326.5994	1326.5948	3.50	0	(60)	4.5e-005	1	R.LTQYMDGSGMPK.T
☑	305	664.3091	1326.6036	1326.5948	6.67	0	71	3.9e-006	1	R.LTQYMDGSGMPK.T
	308	670.8843	1339.7540	1339.7711	-12.71	0	(4)	18	1	R.DLKPENLLLASK.S
	309	670.8865	1339.7584	1339.7711	-9.42	0	(20)	0.47	1	R.DLKPENLLLASK.S
	310	670.8892	1339.7638	1339.7711	-5.39	0	(27)	0.088	1	R.DLKPENLLLASK.S
	311	670.8903	1339.7660	1339.7711	-3.75	0	(52)	0.00028	1	R.DLKPENLLLASK.S
	312	670.8908	1339.7670	1339.7711	-3.00	0	(33)	0.018	1	R.DLKPENLLLASK.S
	313	670.8910	1339.7674	1339.7711	-2.70	0	(35)	0.012	1	R.DLKPENLLLASK.S
	314	670.8913	1339.7680	1339.7711	-2.26	0	(53)	0.00019	1	R.DLKPENLLLASK.S
	315	670.8915	1339.7684	1339.7711	-1.96	0	(60)	3.6e-005	1	R.DLKPENLLLASK.S
	316	670.8926	1339.7706	1339.7711	-0.32	0	(58)	6.1e-005	1	R.DLKPENLLLASK.S
	317	670.8928	1339.7710	1339.7711	-0.02	0	(23)	0.17	1	R.DLKPENLLLASK.S
	318	670.8931	1339.7716	1339.7711	0.43	0	(37)	0.0077	1	R.DLKPENLLLASK.S
	319	670.8934	1339.7722	1339.7711	0.88	0	(61)	3e-005	1	R.DLKPENLLLASK.S
	320	670.8937	1339.7728	1339.7711	1.33	0	(66)	8.4e-006	1	R.DLKPENLLLASK.S
	321	670.8940	1339.7734	1339.7711	1.77	0	82	2.1e-007	1	R.DLKPENLLLASK.S
	322	670.8940	1339.7734	1339.7711	1.77	0	(67)	6.9e-006	1	R.DLKPENLLLASK.S
	323	670.8940	1339.7734	1339.7711	1.77	0	(63)	1.7e-005	1	R.DLKPENLLLASK.S
	324	670.8945	1339.7744	1339.7711	2.52	0	(51)	0.00028	1	R.DLKPENLLLASK.S
	325	670.8946	1339.7746	1339.7711	2.67	0	(70)	3.2e-006	1	R.DLKPENLLLASK.S

	326	670.8951	1339.7756	1339.7711	3.42	0	(63)	1.6e-005	1	R.DLKPENLLLASK.S
	327	670.8954	1339.7762	1339.7711	3.86	0	(63)	1.6e-005	1	R.DLKPENLLLASK.S
	328	670.8955	1339.7764	1339.7711	4.01	0	(59)	4.4e-005	1	R.DLKPENLLLASK.S
☑	329	**672.3059**	**1342.5972**	**1342.5897**	**5.61**	**0**	**(54)**	**0.00014**	**1**	**R.LTQYMDGSGMPK.T + Oxidation (M)**
☑	390	**809.8870**	**1617.7594**	**1617.7562**	**1.98**	**0**	**(55)**	**0.00018**	**1**	**R.FTDEYQLFEELGK.G**
☑	391	**809.8891**	**1617.7636**	**1617.7562**	**4.58**	**0**	**66**	**1.5e-005**	**1**	**R.FTDEYQLFEELGK.G**
☑	392	**809.8947**	**1617.7748**	**1617.7562**	**11.5**	**0**	**(60)**	**6.7e-005**	**1**	**R.FTDEYQLFEELGK.G**
	483	1040.9476	2079.8806	2079.9426	-29.76	0	(74)	8.8e-007	1	K.AGAYDFPSPEWDTVTPEAK.D
	484	1040.9493	2079.8840	2079.9426	-28.13	0	(58)	3.7e-005	1	K.AGAYDFPSPEWDTVTPEAK.D
	485	1040.9618	2079.9090	2079.9426	-16.11	0	(57)	5.8e-005	1	K.AGAYDFPSPEWDTVTPEAK.D
	486	694.3159	2079.9259	2079.9426	-8.02	0	(70)	3.7e-006	1	K.AGAYDFPSPEWDTVTPEAK.D
	487	694.3180	2079.9322	2079.9426	-4.99	0	90	3.7e-008	1	K.AGAYDFPSPEWDTVTPEAK.D
	488	1040.9735	2079.9324	2079.9426	-4.86	0	(42)	0.0023	1	K.AGAYDFPSPEWDTVTPEAK.D
	489	1040.9767	2079.9388	2079.9426	-1.78	0	(64)	1.7e-005	1	K.AGAYDFPSPEWDTVTPEAK.D
	490	1040.9814	2079.9482	2079.9426	2.74	0	(62)	2.8e-005	1	K.AGAYDFPSPEWDTVTPEAK.D
	491	1040.9825	2079.9504	2079.9426	3.80	0	(75)	1.4e-006	1	K.AGAYDFPSPEWDTVTPEAK.D
	558	888.7586	2663.2540	2663.2755	-8.08	1	(47)	0.00081	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
	559	888.7591	2663.2555	2663.2755	-7.52	1	(71)	3.1e-006	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
	560	888.7594	2663.2564	2663.2755	-7.18	1	(90)	4e-008	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
	561	888.7601	2663.2585	2663.2755	-6.39	1	(59)	4.9e-005	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
	562	888.7601	2663.2585	2663.2755	-6.39	1	97	8.5e-009	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
	563	888.7603	2663.2591	2663.2755	-6.17	1	(78)	7e-007	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
	564	888.7603	2663.2591	2663.2755	-6.17	1	(79)	5.1e-007	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
	565	888.7603	2663.2591	2663.2755	-6.17	1	(78)	7e-007	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
	566	888.7608	2663.2606	2663.2755	-5.60	1	(74)	1.5e-006	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
	567	888.7608	2663.2606	2663.2755	-5.60	1	(52)	0.00027	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
	568	888.7616	2663.2630	2663.2755	-4.70	1	(32)	0.03	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
	569	888.7617	2663.2633	2663.2755	-4.59	1	(26)	0.11	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
	570	888.7621	2663.2645	2663.2755	-4.14	1	(79)	4.8e-007	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
	571	888.7621	2663.2645	2663.2755	-4.14	1	(67)	7.6e-006	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
	572	888.7629	2663.2669	2663.2755	-3.24	1	(78)	6e-007	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M
	573	888.7650	2663.2732	2663.2755	-0.87	1	(12)	2.6	1	K.AGAYDFPSPEWDTVTPEAKDLINK.M

Proteins matching the same set of peptides:
IPI00858128 **Mass:** 58283 **Score:** 1774 **Queries matched:** 91
Tax_Id=10090 Gene_Symbol=Camk2d calcium/calmodulin-dependent protein kinase type II subunit delta isoform 1

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4. IPI00124695 **Mass:** 60254 **Score:** 1126 **Queries matched:** 53 **emPAI:** 0.61
Tax_Id=10090 Gene_Symbol=Camk2g Isoform 1 of Calcium/calmodulin-dependent protein kinase type II 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
	5	445.2779	444.2706	444.2696	2.25	0	(7)	29	1	K.GAAVK.L
	6	445.2791	444.2718	444.2696	4.95	0	8	27	1	K.GAAVK.L
☑	230	**580.8067**	**1159.5988**	**1159.5913**	**6.48**	**0**	**22**	**0.52**	**1**	**K.FYFENLLSK.N**
☑	231	**580.8068**	**1159.5990**	**1159.5913**	**6.65**	**0**	**(22)**	**0.52**	**1**	**K.FYFENLLSK.N**
	308	670.8843	1339.7540	1339.7711	-12.71	0	(4)	18	1	R.DLKPENLLLASK.C
	309	670.8865	1339.7584	1339.7711	-9.42	0	(20)	0.47	1	R.DLKPENLLLASK.C
	310	670.8892	1339.7638	1339.7711	-5.39	0	(27)	0.088	1	R.DLKPENLLLASK.C
	311	670.8903	1339.7660	1339.7711	-3.75	0	(52)	0.00028	1	R.DLKPENLLLASK.C
	312	670.8908	1339.7670	1339.7711	-3.00	0	(33)	0.018	1	R.DLKPENLLLASK.C
	313	670.8910	1339.7674	1339.7711	-2.70	0	(35)	0.012	1	R.DLKPENLLLASK.C
	314	670.8913	1339.7680	1339.7711	-2.26	0	(53)	0.00019	1	R.DLKPENLLLASK.C
	315	670.8915	1339.7684	1339.7711	-1.96	0	(60)	3.6e-005	1	R.DLKPENLLLASK.C
	316	670.8926	1339.7706	1339.7711	-0.32	0	(58)	6.1e-005	1	R.DLKPENLLLASK.C
	317	670.8928	1339.7710	1339.7711	-0.02	0	(23)	0.17	1	R.DLKPENLLLASK.C
	318	670.8931	1339.7716	1339.7711	0.43	0	(37)	0.0077	1	R.DLKPENLLLASK.C
	319	670.8934	1339.7722	1339.7711	0.88	0	(61)	3e-005	1	R.DLKPENLLLASK.C
	320	670.8937	1339.7728	1339.7711	1.33	0	(66)	8.4e-006	1	R.DLKPENLLLASK.C
	321	670.8940	1339.7734	1339.7711	1.77	0	82	2.1e-007	1	R.DLKPENLLLASK.C
	322	670.8940	1339.7734	1339.7711	1.77	0	(67)	6.9e-006	1	R.DLKPENLLLASK.C
	323	670.8940	1339.7734	1339.7711	1.77	0	(63)	1.7e-005	1	R.DLKPENLLLASK.C
	324	670.8945	1339.7744	1339.7711	2.52	0	(51)	0.00028	1	R.DLKPENLLLASK.C
	325	670.8946	1339.7746	1339.7711	2.67	0	(70)	3.2e-006	1	R.DLKPENLLLASK.C
	326	670.8951	1339.7756	1339.7711	3.42	0	(63)	1.6e-005	1	R.DLKPENLLLASK.C
	327	670.8954	1339.7762	1339.7711	3.86	0	(63)	1.6e-005	1	R.DLKPENLLLASK.C
	328	670.8955	1339.7764	1339.7711	4.01	0	(59)	4.4e-005	1	R.DLKPENLLLASK.C
	346	468.5799	1402.7179	1402.7317	-9.86	0	(50)	0.00069	1	R.LTQYIDGQGRPR.T
	347	468.5800	1402.7182	1402.7317	-9.65	0	(51)	0.00053	1	R.LTQYIDGQGRPR.T
	348	468.5803	1402.7191	1402.7317	-9.01	0	(52)	0.00046	1	R.LTQYIDGQGRPR.T
	349	468.5805	1402.7197	1402.7317	-8.58	0	(38)	0.011	1	R.LTQYIDGQGRPR.T
	350	468.5811	1402.7215	1402.7317	-7.30	0	59	8.4e-005	1	R.LTQYIDGQGRPR.T
	351	702.3745	1402.7344	1402.7317	1.96	0	(53)	0.00035	1	R.LTQYIDGQGRPR.T
	352	702.3751	1402.7356	1402.7317	2.81	0	(39)	0.0085	1	R.LTQYIDGQGRPR.T
	353	702.3760	1402.7374	1402.7317	4.09	0	(43)	0.0035	1	R.LTQYIDGQGRPR.T
	354	702.3771	1402.7396	1402.7317	5.66	0	(18)	0.99	1	R.LTQYIDGQGRPR.T
	355	702.3782	1402.7418	1402.7317	7.23	0	(26)	0.17	1	R.LTQYIDGQGRPR.T
	360	735.4061	1468.7976	1468.8071	-6.47	0	75	1.8e-006	1	K.NLINQMLTINPAK.R
	361	735.4121	1468.8096	1468.8071	1.70	0	(71)	4.1e-006	1	K.NLINQMLTINPAK.R
	362	735.4124	1468.8102	1468.8071	2.11	0	(41)	0.0041	1	K.NLINQMLTINPAK.R
	363	735.4127	1468.8108	1468.8071	2.52	0	(70)	4.3e-006	1	K.NLINQMLTINPAK.R
	364	735.4138	1468.8130	1468.8071	4.02	0	(71)	3.5e-006	1	K.NLINQMLTINPAK.R
☑	385	**802.8809**	**1603.7472**	**1603.7406**	**4.14**	**0**	**70**	**5.2e-006**	**1**	**R.FTDDYQLFEELGK.G**
☑	386	**802.8814**	**1603.7482**	**1603.7406**	**4.77**	**0**	**(60)**	**5.5e-005**	**1**	**R.FTDDYQLFEELGK.G**
☑	387	**802.8885**	**1603.7624**	**1603.7406**	**13.6**	**0**	**(59)**	**7.2e-005**	**1**	**R.FTDDYQLFEELGK.G**
	397	542.6334	1624.8784	1624.9082	-18.39	1	45	0.0014	1	K.NLINQMLTINPAKR.I
	483	1040.9476	2079.8806	2079.9426	-29.76	0	(74)	8.8e-007	1	K.AGAYDFPSPEWDTVTPEAK.N
	484	1040.9493	2079.8840	2079.9426	-28.13	0	(58)	3.7e-005	1	K.AGAYDFPSPEWDTVTPEAK.N
	485	1040.9618	2079.9090	2079.9426	-16.11	0	(57)	5.8e-005	1	K.AGAYDFPSPEWDTVTPEAK.N

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   486   694.3159  2079.9259  2079.9426   -8.02   0   (70) 3.7e-006   1   K.AGAYDFPSPEWDTVTPEAK.N
   487   694.3180  2079.9322  2079.9426   -4.99   0    90  3.7e-008   1   K.AGAYDFPSPEWDTVTPEAK.N
   488  1040.9735  2079.9324  2079.9426   -4.86   0   (42)   0.0023   1   K.AGAYDFPSPEWDTVTPEAK.N
   489  1040.9767  2079.9388  2079.9426   -1.78   0   (64) 1.7e-005   1   K.AGAYDFPSPEWDTVTPEAK.N
   490  1040.9814  2079.9482  2079.9426    2.74   0   (62) 2.8e-005   1   K.AGAYDFPSPEWDTVTPEAK.N
   491  1040.9825  2079.9504  2079.9426    3.80   0   (75) 1.4e-006   1   K.AGAYDFPSPEWDTVTPEAK.N


  Proteins matching the same set of peptides:
  IPI00228044     Mass: 59013    Score: 1126    Queries matched: 53
  Tax_Id=10090 Gene_Symbol=Camk2g Isoform 2 of Calcium/calmodulin-dependent protein kinase type II subunit gamma
  IPI00228045     Mass: 56610    Score: 1126    Queries matched: 53
  Tax_Id=10090 Gene_Symbol=Camk2g Isoform 3 of Calcium/calmodulin-dependent protein kinase type II subunit gamma

5.    IPI00169463     Mass: 50255    Score: 246    Queries matched: 13    emPAI: 0.21
      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
       148  539.2706   1076.5266   1076.5250   1.49   1    13       4.6    2    K.IREEYPDR.I
  ☑    301  660.3567   1318.6988   1318.6955   2.53   0    80  7.9e-007    1    R.IMNTFSVVPSPK.V
  ☑    302  660.3600   1318.7054   1318.6955   7.54   0   (80) 7.5e-007    1    R.IMNTFSVVPSPK.V
  ☑    382  801.4147   1600.8148   1600.8131   1.11   0   (76) 1.4e-006    1    R.AVLVDLEPGTMDSVR.S
  ☑    383  801.4150   1600.8154   1600.8131   1.49   0    87  1.2e-007    1    R.AVLVDLEPGTMDSVR.S
  ☑    384  801.4154   1600.8162   1600.8131   1.99   0   (43)   0.0028    1    R.AVLVDLEPGTMDSVR.S
  ☑    432  846.4415   1690.8684   1690.8600   5.00   0    46    0.0016    1    R.ALTVPELTQQMFDAK.N
  ☑    434  848.9237   1695.8328   1695.8257   4.24   0   (20)     0.63    1    K.NSSYFVEWIPNNVK.T
  ☑    435  848.9244   1695.8342   1695.8257   5.07   0    26      0.15    1    K.NSSYFVEWIPNNVK.T
       439  854.4377   1706.8608   1706.8549   3.47   0   (13)      3.4    2    R.ALTVPELTQQMFDAK.N + Oxidation (M)
  ☑    584  933.4465   2797.3177   2797.3361  -6.60   0   (22)     0.23    1    R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
  ☑    585  933.4496   2797.3270   2797.3361  -3.27   0   (18)     0.54    1    R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
  ☑    586  933.4506   2797.3300   2797.3361  -2.20   0    27     0.073    1    R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G

6.    IPI00110850     Mass: 42052    Score: 234    Queries matched: 7    emPAI: 0.25
      Tax_Id=10090 Gene_Symbol=Actb Actin, cytoplasmic 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
  ☑    233  581.3168   1160.6190   1160.6111    6.86   0    35     0.025    1    K.EITALAPSTMK.I
  ☑    452  895.9521   1789.8896   1789.8846    2.80   0    96  1.4e-008    1    K.SYELPDGQVITIGNER.F
  ☑    453  895.9536   1789.8926   1789.8846    4.48   0   (87) 1.1e-007    1    K.SYELPDGQVITIGNER.F
  ☑    468  652.0190   1953.0352   1953.0571  -11.23   0   (56)  0.00011    1    R.VAPEEHPVLLTEAPLNPK.A
       469  652.0204   1953.0394   1953.0571   -9.08   0   (30)    0.044    2    R.VAPEEHPVLLTEAPLNPK.A
  ☑    470  652.0221   1953.0445   1953.0571   -6.46   0    63  2.1e-005    1    R.VAPEEHPVLLTEAPLNPK.A
  ☑    471  652.0244   1953.0514   1953.0571   -2.93   0   (60) 4.2e-005    1    R.VAPEEHPVLLTEAPLNPK.A


  Proteins matching the same set of peptides:
  IPI00136929     Mass: 44029    Score: 234    Queries matched: 7
  Tax_Id=10090 Gene_Symbol=Actg1 Gamma actin-like protein
  IPI00473320     Mass: 42115    Score: 234    Queries matched: 7
  Tax_Id=10090 Gene_Symbol=Actb Putative uncharacterized protein
  IPI00652436     Mass: 42053    Score: 234    Queries matched: 7
  Tax_Id=10090 Gene_Symbol=Actg1 Putative uncharacterized protein
  IPI00874482     Mass: 42108    Score: 234    Queries matched: 7
  Tax_Id=10090 Gene_Symbol=Actg1 Actin, cytoplasmic 2

7.    IPI00115546     Mass: 40524    Score: 208    Queries matched: 3    emPAI: 0.17
      Tax_Id=10090 Gene_Symbol=Gnao1 Isoform Alpha-2 of Guanine nucleotide-binding protein G(o) 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
  ☑    431  838.4230   1674.8314   1674.8213   6.06   0    99    8e-009    1    R.IGAGDYQPTEQDILR.T
  ☑    472  979.4432   1956.8718   1956.8631   4.48   0   (86) 9.3e-008    1    R.MEDTEPFSAELLSAMMR.L
  ☑    473  979.4452   1956.8758   1956.8631   6.52   0    92  2.4e-008    1    R.MEDTEPFSAELLSAMMR.L


  Proteins matching the same set of peptides:
  IPI00230192     Mass: 40629    Score: 208    Queries matched: 3
  Tax_Id=10090 Gene_Symbol=Gnao1 Isoform Alpha-1 of Guanine nucleotide-binding protein G(o) subunit alpha
  IPI00969970     Mass: 20777    Score: 208    Queries matched: 3
  Tax_Id=10090 Gene_Symbol=Gnao1 Uncharacterized protein

8.    IPI00221528     Mass: 42319    Score: 172    Queries matched: 6    emPAI: 0.16
      Tax_Id=10090 Gene_Symbol=Actbl2 Beta-actin-like 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
       452  895.9521   1789.8896   1789.8846    2.80   0    96  1.4e-008    1    R.SYELPDGQVITIGNER.F
       453  895.9536   1789.8926   1789.8846    4.48   0   (87) 1.1e-007    1    R.SYELPDGQVITIGNER.F
       468  652.0190   1953.0352   1953.0571  -11.23   0    48   0.00078    2    R.VAPDEHPILLTEAPLNPK.I
  ☑    469  652.0204   1953.0394   1953.0571   -9.08   0   (31)    0.035    1    R.VAPDEHPILLTEAPLNPK.I
       470  652.0221   1953.0445   1953.0571   -6.46   0   (43)   0.0023    2    R.VAPDEHPILLTEAPLNPK.I
       471  652.0244   1953.0514   1953.0571   -2.93   0   (32)    0.028    2    R.VAPDEHPILLTEAPLNPK.I
```

9. IPI00112251 **Mass:** 50842 **Score:** 162 **Queries matched:** 8 **emPAI:** 0.21
Tax_Id=10090 Gene_Symbol=Tubb3 Tubulin beta-3 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
	301	660.3567	1318.6988	1318.6955	2.53	0	80	7.9e-007	1	R.IMNTFSVVPSPK.V
	302	660.3600	1318.7054	1318.6955	7.54	0	(80)	7.5e-007	1	R.IMNTFSVVPSPK.V
☑	388	**808.4205**	**1614.8264**	**1614.8287**	**-1.40**	**0**	**(38)**	**0.011**	**1**	**R.AILVDLEPGTMDSVR.S**
☑	389	**808.4229**	**1614.8312**	**1614.8287**	**1.57**	**0**	**52**	**0.00045**	**1**	**R.AILVDLEPGTMDSVR.S**
	432	846.4415	1690.8684	1690.8600	5.00	0	46	0.0016	1	R.ALTVPELTQQMFDAK.N
	434	848.9237	1695.8328	1695.8257	4.24	0	(20)	0.63	1	K.NSSYFVEWIPNNVK.V
	435	848.9244	1695.8342	1695.8257	5.07	0	26	0.15	1	K.NSSYFVEWIPNNVK.V
	439	854.4377	1706.8608	1706.8549	3.47	0	(13)	3.4	2	R.ALTVPELTQQMFDAK.N + Oxidation (M)

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10. IPI00323571 **Mass:** 35901 **Score:** 147 **Queries matched:** 8 **emPAI:** 0.42
Tax_Id=10090 Gene_Symbol=Apoe Apolipoprotein E
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	92	**484.7768**	**967.5390**	**967.5451**	**-6.23**	**0**	**(56)**	**0.00011**	**1**	**R.LGPLVEQGR.Q**
☑	93	**484.7803**	**967.5460**	**967.5451**	**1.01**	**0**	**57**	**8.5e-005**	**1**	**R.LGPLVEQGR.Q**
☑	144	538.2992	1074.5838	1074.5822	1.56	0	46	0.0024	1	R.LQAEIFQAR.L
☑	145	538.2996	1074.5846	1074.5822	2.31	0	(43)	0.0043	1	R.LQAEIFQAR.L
	147	538.3003	1074.5860	1074.5822	3.61	0	(14)	3	2	R.LQAEIFQAR.L
☑	234	**581.7838**	**1161.5530**	**1161.5448**	**7.10**	**0**	**42**	**0.0054**	**1**	**K.MEEQTQQIR.L**
☑	381	**800.4018**	**1598.7890**	**1598.7787**	**6.44**	**0**	**74**	**2.7e-006**	**1**	**K.ELEEQLGPVAEETR.A**
☑	476	**997.5348**	**1993.0550**	**1993.0480**	**3.53**	**0**	**13**	**2.7**	**1**	**K.IQASVATNPIITPVAQENQ.-**

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11. IPI00117352 **Mass:** 50095 **Score:** 141 **Queries matched:** 11 **emPAI:** 0.14
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
	148	539.2706	1076.5266	1076.5250	1.49	1	13	4.6	2	K.IREEYPDR.I
	301	660.3567	1318.6988	1318.6955	2.53	0	80	7.9e-007	1	R.IMNTFSVVPSPK.V
	302	660.3600	1318.7054	1318.6955	7.54	0	(80)	7.5e-007	1	R.IMNTFSVVPSPK.V
	388	808.4205	1614.8264	1614.8287	-1.40	0	(38)	0.011	1	R.AILVDLEPGTMDSVR.S
	389	808.4229	1614.8312	1614.8287	1.57	0	52	0.00045	1	R.AILVDLEPGTMDSVR.S
☑	429	**830.4437**	**1658.8728**	**1658.8879**	**-9.10**	**0**	**20**	**0.54**	**1**	**R.ALTVPELTQQVFDAK.N**
	434	848.9237	1695.8328	1695.8257	4.24	0	(20)	0.63	1	K.NSSYFVEWIPNNVK.T
	435	848.9244	1695.8342	1695.8257	5.07	0	26	0.15	1	K.NSSYFVEWIPNNVK.T
	584	933.4465	2797.3177	2797.3361	-6.60	0	(22)	0.23	1	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
	585	933.4496	2797.3270	2797.3361	-3.27	0	(18)	0.54	1	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
	586	933.4506	2797.3300	2797.3361	-2.20	0	27	0.073	1	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G

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12. IPI00138892 **Mass:** 15004 **Score:** 133 **Queries matched:** 4 **emPAI:** 0.23
Tax_Id=10090 Gene_Symbol=Uba52 Ubiquitin-60S ribosomal protein L40
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	448	**894.4662**	**1786.9178**	**1786.9200**	**-1.21**	**0**	**(47)**	**0.0012**	**1**	**K.TITLEVEPSDTIENVK.A**
☑	449	**894.4691**	**1786.9236**	**1786.9200**	**2.03**	**0**	**(65)**	**2.1e-005**	**1**	**K.TITLEVEPSDTIENVK.A**
☑	450	**894.4700**	**1786.9254**	**1786.9200**	**3.04**	**0**	**71**	**4.7e-006**	**1**	**K.TITLEVEPSDTIENVK.A**
☑	451	**894.4707**	**1786.9268**	**1786.9200**	**3.83**	**0**	**(53)**	**0.00033**	**1**	**K.TITLEVEPSDTIENVK.A**

Proteins matching the same set of peptides:
IPI00470152 **Mass:** 18282 **Score:** 133 **Queries matched:** 4
Tax_Id=10090 Gene_Symbol=Rps27a Ubiquitin-40S ribosomal protein S27a
IPI00895319 **Mass:** 22277 **Score:** 133 **Queries matched:** 4
Tax_Id=10090 Gene_Symbol=2810422J05Rik 22 kDa protein
IPI00895479 **Mass:** 27181 **Score:** 133 **Queries matched:** 4
Tax_Id=10090 Gene_Symbol=2810422J05Rik 27 kDa protein
IPI00918763 **Mass:** 11021 **Score:** 133 **Queries matched:** 4
Tax_Id=10090 Gene_Symbol=Uba52 Ubiqutin subunit 1
IPI00750889 **Mass:** 22822 **Score:** 133 **Queries matched:** 4
Tax_Id=10090 Gene_Symbol=Ubc Ubc protein
IPI00923013 **Mass:** 26603 **Score:** 133 **Queries matched:** 4
Tax_Id=10090 Gene_Symbol=Ubb Ubiquitin B
IPI00923037 **Mass:** 22578 **Score:** 133 **Queries matched:** 4
Tax_Id=10090 Gene_Symbol=Ubc Putative uncharacterized protein
IPI00139518 **Mass:** 34348 **Score:** 133 **Queries matched:** 4
Tax_Id=10090 Gene_Symbol=Ubb Polyubiquitin-B
IPI00755916 **Mass:** 82614 **Score:** 133 **Queries matched:** 4
Tax_Id=10090 Gene_Symbol=Ubc ubiquitin
IPI00969323 **Mass:** 82603 **Score:** 133 **Queries matched:** 4
Tax_Id=10090 Gene_Symbol=Ubc Polyubiquitin-C

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13. IPI00755181 **Mass:** 57178 **Score:** 132 **Queries matched:** 5 **emPAI:** 0.12
Tax_Id=10090 Gene_Symbol=Krt10 keratin, type I cytoskeletal 10
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	154	**545.7697**	**1089.5248**	**1089.5237**	**1.07**	**0**	**(46)**	**0.002**	**1**	**K.VTMQNLNDR.L**

☑	155	545.7701	1089.5256	1089.5237	1.80	0	64	3.4e-005	1	K.VTMQNLNDR.L
☑	156	545.7711	1089.5276	1089.5237	3.64	0	(62)	5.4e-005	1	K.VTMQNLNDR.L
☑	334	691.3312	1380.6478	1380.6408	5.08	0	(52)	0.00036	1	R.ALEESNYELEGK.I
☑	335	691.3317	1380.6488	1380.6408	5.80	0	61	4.3e-005	1	R.ALEESNYELEGK.I

Proteins matching the same set of peptides:
IPI00798492 **Mass:** 57906 **Score:** 132 **Queries matched:** 5
Tax_Id=10090 Gene_Symbol=Krt10 Isoform 1 of Keratin, type I cytoskeletal 10
IPI00828744 **Mass:** 57197 **Score:** 132 **Queries matched:** 5
Tax_Id=10090 Gene_Symbol=Krt10 Isoform 2 of Keratin, type I cytoskeletal 10

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14. IPI00122094 **Mass:** 85656 **Score:** 123 **Queries matched:** 2 **emPAI:** 0.04
Tax_Id=10090 Gene_Symbol=Dlg4 Isoform 2 of Disks large homolog 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
☑	441	857.9645	1713.9144	1713.9090	3.18	0	83	2.7e-007	1	R.VIEDLSGPYIWVPAR.E
☑	442	857.9650	1713.9154	1713.9090	3.76	0	(68)	8e-006	1	R.VIEDLSGPYIWVPAR.E

Proteins matching the same set of peptides:
IPI00622720 **Mass:** 80765 **Score:** 123 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=Dlg4 Isoform 1 of Disks large homolog 4
IPI00626797 **Mass:** 80395 **Score:** 123 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=Dlg4 Isoform 3 of Disks large homolog 4

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15. IPI00131366 **Mass:** 60627 **Score:** 114 **Queries matched:** 4 **emPAI:** 0.05
Tax_Id=10090 Gene_Symbol=Krt6b Keratin, type II cytoskeletal 6B
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	288	651.8555	1301.6964	1301.7078	-8.74	0	(30)	0.072	1	R.SLDLDSIIAEVK.A
☑	289	651.8582	1301.7018	1301.7078	-4.59	0	(45)	0.0022	1	R.SLDLDSIIAEVK.A
☑	290	651.8605	1301.7064	1301.7078	-1.06	0	(60)	6.3e-005	1	R.SLDLDSIIAEVK.A
☑	291	651.8612	1301.7078	1301.7078	0.02	0	67	1.3e-005	1	R.SLDLDSIIAEVK.A

Proteins matching the same set of peptides:
IPI00131368 **Mass:** 59641 **Score:** 114 **Queries matched:** 4
Tax_Id=10090 Gene_Symbol=Krt6a Keratin, type II cytoskeletal 6A
IPI00139301 **Mass:** 61957 **Score:** 114 **Queries matched:** 4
Tax_Id=10090 Gene_Symbol=Krt5 Keratin, type II cytoskeletal 5
IPI00221797 **Mass:** 59932 **Score:** 114 **Queries matched:** 4
Tax_Id=10090 Gene_Symbol=Krt75 Keratin, type II cytoskeletal 75
IPI00330480 **Mass:** 35315 **Score:** 114 **Queries matched:** 4
Tax_Id=10090 Gene_Symbol=- 35 kDa protein
IPI00470126 **Mass:** 60553 **Score:** 114 **Queries matched:** 4
Tax_Id=10090 Gene_Symbol=Krt5 Uncharacterized protein
IPI00762364 **Mass:** 50641 **Score:** 114 **Queries matched:** 4
Tax_Id=10090 Gene_Symbol=Krt6a Uncharacterized protein
IPI00785403 **Mass:** 59832 **Score:** 114 **Queries matched:** 4
Tax_Id=10090 Gene_Symbol=Krt6b keratin, type II cytoskeletal 6B

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16. IPI00134997 **Mass:** 106777 **Score:** 112 **Queries matched:** 1 **emPAI:** 0.03
Tax_Id=10090 Gene_Symbol=Dlgap3 Disks large-associated protein 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
☑	369	751.8735	1501.7324	1501.7274	3.39	0	112	4.7e-010	1	R.GPAGPGPGPGSGAAPEAR.S

Proteins matching the same set of peptides:
IPI00648401 **Mass:** 105576 **Score:** 112 **Queries matched:** 1
Tax_Id=10090 Gene_Symbol=Dlgap3 Discs, large (Drosophila) homolog-associated protein 3

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17. IPI00122928 **Mass:** 50514 **Score:** 97 **Queries matched:** 6 **emPAI:** 0.13
Tax_Id=10090 Gene_Symbol=Tubb6 Tubulin beta-6 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
	148	539.2706	1076.5266	1076.5250	1.49	1	13	4.6	2	K.IREEYPDR.I
☑	331	676.3433	1350.6720	1350.6676	3.31	0	78	1.2e-006	1	R.IMNTFSVMPSPK.V
	432	846.4415	1690.8684	1690.8600	5.00	0	46	0.0016	1	R.ALTVPELTQQMFDAK.N
	434	848.9237	1695.8328	1695.8257	4.24	0	(20)	0.63	1	K.NSSYFVEWIPNNVK.V
	435	848.9244	1695.8342	1695.8257	5.07	0	26	0.15	1	K.NSSYFVEWIPNNVK.V
	439	854.4377	1706.8608	1706.8549	3.47	0	(13)	3.4	2	R.ALTVPELTQQMFDAK.N + Oxidation (M)

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18. IPI00109061 **Mass:** 50377 **Score:** 96 **Queries matched:** 10 **emPAI:** 0.14
Tax_Id=10090 Gene_Symbol=Tubb2b Tubulin beta-2B 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
	148	539.2706	1076.5266	1076.5250	1.49	1	13	4.6	2	K.IREEYPDR.I
	331	676.3433	1350.6720	1350.6676	3.31	0	78	1.2e-006	1	R.IMNTFSVMPSPK.V
	388	808.4205	1614.8264	1614.8287	-1.40	0	(38)	0.011	1	R.AILVDLEPGTMDSVR.S
	389	808.4229	1614.8312	1614.8287	1.57	0	52	0.00045	1	R.AILVDLEPGTMDSVR.S

```
     434  848.9237  1695.8328  1695.8257   4.24   0  (20)      0.63   1   K.NSSYFVEWIPNNVK.T
     435  848.9244  1695.8342  1695.8257   5.07   0   26       0.15   1   K.NSSYFVEWIPNNVK.T
  ☑  439  854.4377  1706.8608  1706.8549   3.47   0   20       0.61   1   R.ALTVPELTQQMFDSK.N
     584  933.4465  2797.3177  2797.3361  -6.60   0  (22)      0.23   1   R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
     585  933.4496  2797.3270  2797.3361  -3.27   0  (18)      0.54   1   R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
     586  933.4506  2797.3300  2797.3361  -2.20   0   27      0.073   1   R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G


    Proteins matching the same set of peptides:
    IPI00338039     Mass: 50274     Score: 96     Queries matched: 10
    Tax_Id=10090 Gene_Symbol=Tubb2a Tubulin beta-2A chain
```

```
19. IPI00462140     Mass: 61379     Score: 94     Queries matched: 3    emPAI: 0.05
    Tax_Id=10090 Gene_Symbol=Krt77 Keratin, type II cytoskeletal 1b
 ☐  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  532.2756  1062.5366  1062.5709  -32.26   0     6      21    1   R.AQYEIIAQK.S
  ☑  367  738.3973  1474.7800  1474.7780    1.40   0   (61)  5e-005   1   R.FLEQQNQVLQTK.W
  ☑  368  738.3973  1474.7800  1474.7780    1.40   0    63   3e-005   1   R.FLEQQNQVLQTK.W
```

```
20. IPI00420970     Mass: 55340     Score: 94     Queries matched: 3    emPAI: 0.06
    Tax_Id=10090 Gene_Symbol=Krt74 Keratin, type II cytoskeletal 74
 ☐  Check to include this hit in error tolerant search or archive report

    Query  Observed    Mr(expt)    Mr(calc)    ppm  Miss Score Expect Rank  Peptide
     111  519.2660  1036.5174  1036.5189  -1.41   0     5      24    5   R.YEVEITQR.T
     367  738.3973  1474.7800  1474.7780   1.40   0   (61)  5e-005   1   R.FLEQQNQVLQTK.W
     368  738.3973  1474.7800  1474.7780   1.40   0    63   3e-005   1   R.FLEQQNQVLQTK.W
```

```
21. IPI00131209     Mass: 52420     Score: 94     Queries matched: 4    emPAI: 0.06
    Tax_Id=10090 Gene_Symbol=Krt16 Keratin intermediate filament 16a
 ☐  Check to include this hit in error tolerant search or archive report

    Query  Observed    Mr(expt)    Mr(calc)    ppm  Miss Score    Expect  Rank  Peptide
     154  545.7697  1089.5248  1089.5237   1.07   0   (46)     0.002   1   K.VTMQNLNDR.L
     155  545.7701  1089.5256  1089.5237   1.80   0    64   3.4e-005   1   K.VTMQNLNDR.L
     156  545.7711  1089.5276  1089.5237   3.64   0   (62)  5.4e-005   1   K.VTMQNLNDR.L
     227  577.7924  1153.5702  1153.5220   41.9   0     7         13   2   R.MSSILAGGSCR.A + Oxidation (M)


    Proteins matching the same set of peptides:
    IPI00227140     Mass: 53176     Score: 94     Queries matched: 4
    Tax_Id=10090 Gene_Symbol=Krt14 Keratin, type I cytoskeletal 14
    IPI00874585     Mass: 51973     Score: 94     Queries matched: 4
    Tax_Id=10090 Gene_Symbol=Krt16 Keratin, type I cytoskeletal 16
```

```
22. IPI00348328     Score: 90     Queries matched: 3
    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
     222  577.2903  1152.5660  1152.5234   37.0   0     2         44   4   R.EYGGQVTMPR.G + Oxidation (M)
  ☑  336  692.3635  1382.7124  1382.6830   21.3   0    63   3.1e-005   1   R.SLNNQFASFIDK.V
  ☑  337  692.3693  1382.7240  1382.6830   29.7   0   (58)   0.00011   1   R.SLNNQFASFIDK.V
```

```
23. IPI00322209     Mass: 54531     Score: 90     Queries matched: 2    emPAI: 0.06
    Tax_Id=10090 Gene_Symbol=Krt8 Keratin, type II cytoskeletal 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
     336  692.3635  1382.7124  1382.7194  -5.02   1    63   3.1e-005   1   K.SLNNKFASFIDK.V
     337  692.3693  1382.7240  1382.7194   3.37   1   (58)   0.00011   1   K.SLNNKFASFIDK.V
```

```
24. IPI00119063     Mass: 523342     Score: 88     Queries matched: 4    emPAI: 0.01
    Tax_Id=10090 Gene_Symbol=Lrp1 Prolow-density lipoprotein receptor-related 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
  ☑   91  479.2393   956.4640   956.4676   -3.67   0     8        9.8   1   R.AGTSPGTPNR.I
     128  530.2996  1058.5846  1058.5356    46.3   0     2         55   8   R.EDVVTNGIGR.V
     258  626.3500  1250.6854  1250.7347  -39.36   0     0         51   2   R.GVAGAPPTVTLLR.S
  ☑  306  665.3570  1328.6994  1328.6976    1.38   0    88   1.2e-007   1   K.GPVGLAIDFPESK.L
```

```
25. IPI00121038     Mass: 368613     Score: 78     Queries matched: 1    emPAI: 0.01
    Tax_Id=10090 Gene_Symbol=Vcan Isoform V0 of Versican core 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
  ☑  474  656.6594  1966.9564  1966.9670  -5.42   0    78   9.3e-007   1   R.VSVPTHPDDVGDASLTMVK.L


    Proteins matching the same set of peptides:
```

IPI00230441 **Mass:** 264594 **Score:** 78 **Queries matched:** 1
Tax_Id=10090 Gene_Symbol=Vcan Isoform V1 of Versican core protein
IPI00469172 **Mass:** 76209 **Score:** 78 **Queries matched:** 1
Tax_Id=10090 Gene_Symbol=Vcan versican core protein isoform 4
IPI00469565 **Mass:** 180325 **Score:** 78 **Queries matched:** 1
Tax_Id=10090 Gene_Symbol=Vcan versican core protein isoform 3
IPI00473932 **Mass:** 41850 **Score:** 78 **Queries matched:** 1
Tax_Id=10090 Gene_Symbol=Vcan versican core protein isoform 5
IPI00656277 **Mass:** 41758 **Score:** 78 **Queries matched:** 1
Tax_Id=10090 Gene_Symbol=Vcan Versican
IPI00875672 **Mass:** 368720 **Score:** 78 **Queries matched:** 1
Tax_Id=10090 Gene_Symbol=Vcan versican core protein isoform 1

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26. IPI00122048 **Mass:** 113045 **Score:** 76 **Queries matched:** 2 **emPAI:** 0.03
Tax_Id=10090 Gene_Symbol=Atp1a3 Sodium/potassium-transporting ATPase subunit alpha-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
☑	253	618.8558	1235.6970	1235.6986	-1.26	0	(43)	0.0019	1	R.LNIPVSQVNPR.D
☑	254	618.8574	1235.7002	1235.6986	1.33	0	64	1.7e-005	1	R.LNIPVSQVNPR.D

Proteins matching the same set of peptides:
IPI00420569 **Mass:** 113457 **Score:** 76 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=Atp1a2 Sodium/potassium-transporting ATPase subunit alpha-2
IPI00752412 **Mass:** 117548 **Score:** 76 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=Atp1a3 ATPase, Na+/K+ transporting, alpha 3 polypeptide, isoform CRA_c
IPI00762871 **Mass:** 104717 **Score:** 76 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=Atp1a2 Uncharacterized protein

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27. IPI00120793 **Mass:** 28131 **Score:** 70 **Queries matched:** 6 **emPAI:** 0.25
Tax_Id=10090 Gene_Symbol=Prnp Major prion 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
☑	150	544.7386	1087.4626	1087.4570	5.17	0	40	0.0024	1	K.ESQAYYDGR.R
☑	186	570.2647	1138.5148	1138.5142	0.54	0	56	0.00012	1	K.GENFTETDVK.M
☑	187	570.2665	1138.5184	1138.5142	3.70	0	(32)	0.032	1	K.GENFTETDVK.M
☑	255	622.7899	1243.5652	1243.5581	5.72	1	(13)	2.6	1	K.ESQAYYDGRR.S
☑	256	622.7908	1243.5670	1243.5581	7.17	1	24	0.2	1	K.ESQAYYDGRR.S
☑	257	622.7933	1243.5720	1243.5581	11.2	1	(7)	12	1	K.ESQAYYDGRR.S

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28. IPI00136402 **Mass:** 111559 **Score:** 55 **Queries matched:** 1 **emPAI:** 0.03
Tax_Id=10090 Gene_Symbol=Dlgap1 Isoform 1 of Disks large-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
☑	370	757.4081	1512.8016	1512.8035	-1.24	0	55	0.00018	1	R.SLDSLDPAGLLTSPK.F

Proteins matching the same set of peptides:
IPI00473783 **Mass:** 106407 **Score:** 55 **Queries matched:** 1
Tax_Id=10090 Gene_Symbol=Dlgap1 Uncharacterized protein
IPI00648461 **Mass:** 60639 **Score:** 55 **Queries matched:** 1
Tax_Id=10090 Gene_Symbol=Dlgap1 Isoform 5 of Disks large-associated protein 1
IPI00649710 **Mass:** 110576 **Score:** 55 **Queries matched:** 1
Tax_Id=10090 Gene_Symbol=Dlgap1 Isoform 2 of Disks large-associated protein 1
IPI00650032 **Mass:** 108461 **Score:** 55 **Queries matched:** 1
Tax_Id=10090 Gene_Symbol=Dlgap1 Isoform 3 of Disks large-associated protein 1
IPI00653701 **Mass:** 71554 **Score:** 55 **Queries matched:** 1
Tax_Id=10090 Gene_Symbol=Dlgap1 disks large-associated protein 1 isoform 4
IPI00918030 **Mass:** 76735 **Score:** 55 **Queries matched:** 1
Tax_Id=10090 Gene_Symbol=Dlgap1 disks large-associated protein 1 isoform 3
IPI00918186 **Mass:** 74905 **Score:** 55 **Queries matched:** 1
Tax_Id=10090 Gene_Symbol=Dlgap1 Uncharacterized protein
IPI00918416 **Mass:** 77718 **Score:** 55 **Queries matched:** 1
Tax_Id=10090 Gene_Symbol=Dlgap1 Uncharacterized protein

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29. IPI00222548 **Mass:** 17633 **Score:** 55 **Queries matched:** 1 **emPAI:** 0.19
Tax_Id=10090 Gene_Symbol=Rpl29;Gm13841;Gm8210 60S ribosomal protein L29
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	112	520.2804	1038.5462	1038.5458	0.45	0	55	0.00021	1	K.AQASAPAQAPK.G

Proteins matching the same set of peptides:
IPI00461500 **Mass:** 17603 **Score:** 55 **Queries matched:** 1
Tax_Id=10090 Gene_Symbol=Rpl29-ps2 Uncharacterized protein
IPI00662684 **Mass:** 17663 **Score:** 55 **Queries matched:** 1
Tax_Id=10090 Gene_Symbol=Gm6344 Uncharacterized protein
IPI00762791 **Mass:** 17693 **Score:** 55 **Queries matched:** 1
Tax_Id=10090 Gene_Symbol=Gm10709 Uncharacterized protein
IPI00849210 **Mass:** 17678 **Score:** 55 **Queries matched:** 1
Tax_Id=10090 Gene_Symbol=Gm5561 similar to ribosomal protein
IPI00849550 **Mass:** 28730 **Score:** 55 **Queries matched:** 1

Tax_Id=10090 Gene_Symbol=Gm12508 similar to ribosomal protein
IPI00850168 **Mass:** 22613 **Score:** 55 **Queries matched:** 1
Tax_Id=10090 Gene_Symbol=Gm5218 similar to ribosomal protein
IPI00874437 **Mass:** 17127 **Score:** 55 **Queries matched:** 1
Tax_Id=10090 Gene_Symbol=- Uncharacterized protein

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30. IPI00124499 **Mass:** 57802 **Score:** 50 **Queries matched:** 2 **emPAI:** 0.06
Tax_Id=10090 Gene_Symbol=Krt79 Keratin, type II cytoskeletal 79
☐ 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	532.2756	1062.5366	1062.5709	-32.26	0	6	21	1	K.AQYELIAQK.S
☑	307	**665.3589**	**1328.7032**	**1328.7187**	**-11.64**	**0**	**50**	**0.00068**	**1**	**R.NLDLDSIIAEVK.A**

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31. IPI00113410 **Mass:** 38586 **Score:** 50 **Queries matched:** 1 **emPAI:** 0.09
Tax_Id=10090 Gene_Symbol=Hapln2 Hyaluronan and proteoglycan link 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
☑	342	**696.3721**	**1390.7296**	**1390.7245**	**3.70**	**0**	**50**	**0.00072**	**1**	**R.LEGVVFPYQPSR.G**

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32. IPI00223714 **Mass:** 21964 **Score:** 47 **Queries matched:** 1 **emPAI:** 0.15
Tax_Id=10090 Gene_Symbol=Hist1h1e Histone H1.4
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	250	**614.8409**	**1227.6672**	**1227.6711**	**-3.11**	**0**	**47**	**0.0013**	**1**	**K.TSGPPVSELITK.A**

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33. IPI00136703 **Mass:** 42971 **Score:** 46 **Queries matched:** 2 **emPAI:** 0.08
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
☑	299	**652.3648**	**1302.7150**	**1302.7183**	**-2.51**	**0**	**(36)**	**0.016**	**1**	**K.VLTPELYAELR.A**
☑	300	**652.3654**	**1302.7162**	**1302.7183**	**-1.59**	**0**	**46**	**0.0016**	**1**	**K.VLTPELYAELR.A**

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34. IPI00229598 **Mass:** 45025 **Score:** 40 **Queries matched:** 1 **emPAI:** 0.07
Tax_Id=10090 Gene_Symbol=Cnp Isoform CNPI of 2',3'-cyclic-nucleotide 3'-phosphodiesterase
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	260	**628.8149**	**1255.6152**	**1255.6157**	**-0.34**	**0**	**40**	**0.0062**	**1**	**K.GGSQGEAVGELPR.G**

Proteins matching the same set of peptides:
IPI00319602 **Mass:** 47493 **Score:** 40 **Queries matched:** 1
Tax_Id=10090 Gene_Symbol=Cnp Isoform CNPII of 2',3'-cyclic-nucleotide 3'-phosphodiesterase

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35. IPI00123176 **Mass:** 36804 **Score:** 39 **Queries matched:** 2 **emPAI:** 0.09
Tax_Id=10090 Gene_Symbol=Gm6316 Glyceraldehyde-3-phosphate dehydrogenase
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	332	**685.3768**	**1368.7390**	**1368.7361**	**2.15**	**0**	**39**	**0.0067**	**1**	**R.GAAQNIIPASTGAAK.A**
☑	333	**685.3788**	**1368.7430**	**1368.7361**	**5.08**	**0**	**(33)**	**0.031**	**1**	**R.GAAQNIIPASTGAAK.A**

Proteins matching the same set of peptides:
IPI00135284 **Mass:** 36092 **Score:** 39 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=Gm16374 Glyceraldehyde-3-phosphate dehydrogenase
IPI00229201 **Mass:** 16676 **Score:** 39 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=3000002C10Rik Putative uncharacterized protein
IPI00271869 **Mass:** 36293 **Score:** 39 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=- 36 kDa protein
IPI00273646 **Mass:** 36072 **Score:** 39 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=Gapdh;LOC100042025 Glyceraldehyde-3-phosphate dehydrogenase
IPI00622795 **Mass:** 36074 **Score:** 39 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=- 36 kDa protein
IPI00625893 **Mass:** 36205 **Score:** 39 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=Gm6981 Glyceraldehyde-3-phosphate dehydrogenase
IPI00752289 **Mass:** 36308 **Score:** 39 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=Gm10290 Glyceraldehyde-3-phosphate dehydrogenase
IPI00848801 **Mass:** 36100 **Score:** 39 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=- 36 kDa protein
IPI00849045 **Mass:** 36072 **Score:** 39 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=- 36 kDa protein
IPI00850337 **Mass:** 44633 **Score:** 39 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=LOC100048117 similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) isoform 1
IPI00850377 **Mass:** 35975 **Score:** 39 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=- 36 kDa protein
IPI00850779 **Mass:** 36076 **Score:** 39 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=- 36 kDa protein
IPI00874682 **Mass:** 36038 **Score:** 39 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=- 36 kDa protein

IPI00874964 **Mass:** 36512 **Score:** 39 **Queries matched:** 2
Tax_Id=10090 Gene_Symbol=- 36 kDa protein

Peptide matches not assigned to protein hits: (no details means no match)

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	235	582.7992	1163.5838	1163.5757	6.99	0	34	0.036	1	QMIGEFLGNR
☑	157	551.8046	1101.5946	1101.5778	15.3	1	28	0.13	1	EEEGRITIR
☑	48	428.7658	855.5170	855.4814	41.7	0	26	0.14	1	LGAETLPR
☑	30	408.2383	814.4620	814.4661	-4.97	1	24	0.43	1	GTVAPSKR
☑	34	408.2388	814.4630	814.4661	-3.74	1	24	0.45	1	GTVAPSKR
☑	461	912.9987	1823.9828	1823.9782	2.57	0	23	0.19	1	VGINYQPPTVVPGGDLAK
☑	53	435.7717	869.5288	869.5446	-18.17	1	20	0.39	1	ERLLAIR
☑	344	699.8972	1397.7798	1397.8493	-49.71	1	20	0.5	1	LNKLEDTIVLIK
☑	274	634.3542	1266.6938	1266.7084	-11.52	1	19	0.6	1	YLYGIRVEVR
☑	47	428.7636	855.5126	855.5542	-48.53	0	19	0.62	1	TLAVLALR
☑	276	634.3552	1266.6958	1266.7084	-9.94	1	19	0.68	1	YLYGIRVEVR
☑	437	851.4508	1700.8870	1700.8985	-6.74	0	18	0.89	1	AVFVDLEPTVIDEVR
☑	38	408.2404	814.4662	814.4661	0.19	1	17	1.9	1	GTVAPSKR
☑	275	634.3550	1266.6954	1266.7084	-10.25	1	17	0.95	1	YLYGIRVEVR
☑	172	557.7983	1113.5820	1113.5891	-6.30	1	17	1.6	1	SSPLRGPGTSR
☑	32	408.2387	814.4628	814.4661	-3.99	1	17	2.1	1	GTVAPSKR
☑	246	595.8132	1189.6118	1189.6489	-31.12	1	17	2	1	KTNIIDSMLR
☑	345	699.8976	1397.7806	1397.8493	-49.14	1	16	1.2	1	LNKLEDTIVLIK
☑	35	408.2389	814.4632	814.4661	-3.50	1	16	2.6	1	GTVAPSKR
☑	170	557.7947	1113.5748	1113.5891	-12.77	1	16	2.1	1	SSPLRGPGTSR
☑	171	557.7957	1113.5768	1113.5891	-10.97	1	16	2.2	1	SSPLRGPGTSR
☑	228	578.8077	1155.6008	1155.5897	9.62	1	16	1.9	1	SSWTGHGLRR
☑	41	413.6995	825.3844	825.4093	-30.13	0	15	1.3	1	HQDVATR
☑	140	531.2813	1060.5480	1060.5665	-17.41	0	15	2.6	1	YLLASNAPGR
☑	36	408.2390	814.4634	814.4661	-3.23	1	15	3.1	1	KISPNTR
☑	31	408.2386	814.4626	814.4661	-4.23	1	15	3.3	1	GTVAPSKR
☑	29	408.2381	814.4616	814.4661	-5.44	1	15	3	1	KISPNTR
☑	12	602.3666	601.3593	601.3435	26.3	0	15	5.6	1	SSPALK
☑	19	343.7292	685.4438	685.4235	29.7	1	15	1.8	1	KGAAALR
☑	37	408.2393	814.4640	814.4661	-2.49	1	15	3.3	1	KISPNTR
☑	45	423.2270	844.4394	844.4515	-14.24	1	15	3.9	1	AIRENSR
☑	180	565.3195	1128.6244	1128.6754	-45.16	0	14	2.7	1	QLITDLVISK
☑	225	577.2920	1152.5694	1152.6251	-48.29	1	14	2.6	1	EGVHAGTINKK
☑	227	577.7924	1153.5702	1153.5840	-11.89	1	14	2.7	1	KLHDSNDGLR
☑	40	412.7514	823.4882	823.4817	7.98	0	14	1.1	1	RPWLPR
☑	138	531.2780	1060.5414	1060.5665	-23.63	0	14	3.6	1	YLLASNAPGR
☑	39	412.7500	823.4854	823.5028	-21.08	1	14	1	1	VPSRLPR
☑	223	577.2915	1152.5684	1152.6251	-49.16	1	14	3	1	EGVHAGTINKK
☑	33	408.2388	814.4630	814.4661	-3.74	1	14	4.6	1	GTVAPSKR
☑	148	539.2706	1076.5266	1076.5098	15.6	0	13	3.7	1	SSLDGESGGIR
☑	143	533.2622	1064.5098	1064.5138	-3.72	0	13	3.3	1	AQYEDIAQK
☑	61	450.7198	899.4250	899.4461	-23.38	1	13	2.3	1	REPEDVR
☑	111	519.2660	1036.5174	1036.5011	15.7	0	13	4.2	1	VLPYMENR + Oxidation (M)
☑	28	408.2372	814.4598	814.4661	-7.67	1	12	5.7	1	GTVAPSKR
☑	195	572.8080	1143.6014	1143.6546	-46.49	1	12	5.2	1	QAMLRQLLR + Oxidation (M)
☑	104	508.2908	1014.5670	1014.5709	-3.83	0	12	5.1	1	DVNAAIATIK
☑	229	578.8155	1155.6164	1155.6611	-38.68	1	12	4.4	1	DAVSSLPLAKR
☑	94	487.3005	972.5864	972.5869	-0.46	0	12	2.7	1	VPGHLPVVR
☑	52	435.7706	869.5266	869.4858	46.9	0	12	2.8	1	VSGVEVPLA
☑	285	645.8337	1289.6528	1289.6054	36.8	1	11	5.8	1	GGDYWRFHPR
☑	159	556.8300	1111.6454	1111.6713	-23.25	1	11	2.6	1	LRAELLELR
☑	139	531.2795	1060.5444	1060.5665	-20.80	0	11	6.9	1	YLLASNAPGR
☑	95	491.7284	981.4422	981.4879	-46.56	0	11	3.3	1	EPAPQGQAGK
☑	239	595.3087	1188.6028	1188.6285	-21.58	1	11	7.2	1	SPTIRDMVVR + Oxidation (M)
☑	248	606.8034	1211.5922	1211.6371	-37.01	1	10	5.8	1	GSRGDLGLQGPR
☑	114	520.7663	1039.5180	1039.5062	11.4	1	10	5.8	1	KFPFCWR
☑	173	558.2787	1114.5428	1114.5731	-27.11	1	10	7	1	KSASSHIETR
☑	179	565.3195	1128.6244	1128.6502	-22.85	1	10	7.4	1	KLELEATVAR
☑	73	464.7799	927.5452	927.5501	-5.27	1	10	6.1	1	LNLTSPKR
☑	82	464.7838	927.5530	927.5138	42.3	1	10	5.6	1	DVPVQSKR
☑	358	728.8514	1455.6882	1455.7027	-9.96	0	10	6	1	DAMELKPNGGAEPK
☑	57	444.2293	886.4440	886.4695	-28.67	1	10	10	1	KVMGPSPR + Oxidation (M)
☑	108	517.2664	1032.5182	1032.4724	44.5	0	10	9.5	1	VLDEEGSER
☑	27	399.7258	797.4370	797.4759	-48.75	1	9	6	1	IPVKGER
☑	152	545.2901	1088.5656	1088.5397	23.9	0	9	11	1	MGSADRPALR + Oxidation (M)
☑	280	643.3559	1284.6972	1284.7190	-16.91	1	9	7.9	1	NQKWLEILNK
☑	153	545.2922	1088.5698	1088.5978	-25.71	1	9	11	1	KDFTVNLPR
☑	240	595.3089	1188.6032	1188.5887	12.2	0	9	10	1	FVPPQTSSGNR
☑	142	532.2774	1062.5402	1062.5128	25.9	1	9	11	1	KMEEQQVR + Oxidation (M)
☑	81	464.7831	927.5516	927.5250	28.7	1	9	6.7	1	QSPLATRR
☑	273	631.8077	1261.6008	1261.5826	14.4	0	9	9	1	EALEVDWSGEK
☑	446	885.9580	1769.9014	1769.9271	-14.51	1	9	8.1	1	ELEAERQIVASQLER
☑	243	595.3099	1188.6052	1188.6285	-19.56	1	9	11	1	SPTIRDMVVR + Oxidation (M)
☑	76	464.7814	927.5482	927.5501	-2.02	1	9	7.7	1	LKAESKPR
☑	105	514.8010	1027.5874	1027.5597	27.0	1	9	8.2	1	MLSKAVSHR
☑	85	470.7675	939.5204	939.5515	-33.03	1	9	7.2	1	LRPGWRR

☑	137	530.7860	1059.5574	1059.5924	-32.98	0	9	15	1	TASLAELISR
☑	241	595.3092	1188.6038	1188.5887	12.7	0	9	11	1	FVPPQTSSGNR
☑	279	643.3487	1284.6828	1284.6357	36.7	1	8	9.9	1	GRAGVCDPALNR
☑	113	520.7655	1039.5164	1039.5121	4.23	0	8	8.9	1	SGMLSYGLGR
☑	79	464.7817	927.5488	927.5501	-1.38	1	8	8.5	1	LKAESKPR
☑	169	557.7910	1113.5674	1113.6005	-29.66	1	8	11	1	MTAFFKTLR
☑	465	948.9885	1895.9624	1895.9516	5.71	0	8	9.3	1	TITFEQFQEALEELAK
☑	182	565.3201	1128.6256	1128.6754	-44.09	0	8	11	1	QLITDLVISK
☑	226	577.2932	1152.5718	1152.6251	-46.19	1	8	12	1	EGKLEHTLAR
☑	58	449.7471	897.4796	897.4556	26.8	0	8	11	1	DAETPLPR
☑	181	565.3198	1128.6250	1128.6503	-22.33	0	8	12	1	TKPVLSSLER
☑	43	415.2015	828.3884	828.4276	-47.26	0	8	6.5	1	IHGSMLR + Oxidation (M)
☑	97	496.2269	990.4392	990.4883	-49.50	0	8	8.1	1	AFSSHSSLR
☑	445	885.9568	1769.8990	1769.8995	-0.27	1	8	11	1	LQFRDVNGEMVAVHR
☑	80	464.7817	927.5488	927.5138	37.8	1	8	10	1	DVPVQSKR
☑	77	464.7814	927.5482	927.5138	37.2	1	8	10	1	DVPVQSKR
☑	330	672.8422	1343.6698	1343.6681	1.32	1	7	12	1	AQGDEQEAQLKK
☑	222	577.2903	1152.5660	1152.5420	20.9	0	7	13	1	AGGLAAMPYMR + Oxidation (M)
☑	100	506.2394	1010.4642	1010.4781	-13.71	1	7	10	1	DYDRSLSR
☑	74	464.7807	927.5468	927.5138	35.7	1	7	12	1	DVPVQSKR
☑	338	692.3942	1382.7738	1382.7630	7.86	1	7	10	1	QSASPLRLQLDR
☑	99	500.2558	998.4970	998.4491	48.0	0	7	14	1	TMSNFLDR + Oxidation (M)
☑	283	645.8325	1289.6504	1289.6054	34.9	1	7	17	1	GGDYWRFHPR
☑	42	415.2015	828.3884	828.4276	-47.26	0	7	8.7	1	IHGSMLR + Oxidation (M)
☑	64	450.7218	899.4290	899.4324	-3.68	0	7	11	1	FMFNGLR + Oxidation (M)
☑	244	595.3101	1188.6056	1188.5887	14.2	0	7	18	1	FVPPQTSSGNR
☑	103	506.2436	1010.4726	1010.5145	-41.43	0	7	12	1	EGTQAPGVPR
☑	96	496.2260	990.4374	990.4487	-11.39	1	7	10	1	ASMSRHMR + Oxidation (M)
☑	438	852.4293	1702.8440	1702.8989	-32.20	0	6	15	1	VLSTSTDLEAAVADALK
☑	286	645.8344	1289.6542	1289.6054	37.9	1	6	18	1	GGDYWRFHPR
☑	59	450.2231	898.4316	898.4695	-42.09	0	6	11	1	MSVVPPNR
☑	196	572.8097	1143.6048	1143.6546	-43.52	1	6	20	1	QAMLRQLLR + Oxidation (M)
☑	192	572.8068	1143.5990	1143.6546	-48.59	1	6	20	1	QAMLRQLLR + Oxidation (M)
☑	161	556.8326	1111.6506	1111.5985	46.9	1	6	8.1	1	SKSHPASLASK
☑	151	545.2896	1088.5646	1088.5978	-30.49	1	6	22	1	KDFTVNLPR
☑	98	499.2703	996.5260	996.5141	12.0	1	6	16	1	EGYFRAVR
☑	184	565.3227	1128.6308	1128.6754	-39.49	0	6	17	1	QLITDLVISK
☑	75	464.7812	927.5478	927.5138	36.7	1	6	14	1	DVPVQSKR
☑	343	699.8953	1397.7760	1397.7990	-16.45	1	6	12	1	TGNDVLKALALGAR
☑	78	464.7816	927.5486	927.5501	-1.59	1	6	14	1	LKAESKPR
☑	242	595.3098	1188.6050	1188.6285	-19.71	1	6	22	1	AALKDVVACSR
☑	124	529.2703	1056.5260	1056.5087	16.4	0	6	18	1	KPETGEDPGK
☑	359	730.9042	1459.7938	1459.7453	33.3	1	6	15	1	VDILENRVMDTR
☑	278	643.3486	1284.6826	1284.6357	36.5	1	6	19	1	GRAGVCDPALNR
☑	232	581.3160	1160.6174	1160.6587	-35.53	1	6	25	1	TELSILRAMK
☑	224	577.2915	1152.5684	1152.5420	23.0	0	5	21	1	MTLNTMTWR
☑	282	645.8323	1289.6500	1289.6054	34.6	1	5	25	1	GGDYWRFHPR
☑	277	636.8104	1271.6062	1271.6357	-23.17	0	5	17	1	LLDAESEDRPK
☑	88	470.7690	939.5234	939.5515	-29.84	1	5	16	1	LRPGWRR
☑	185	565.3278	1128.6410	1128.6251	14.1	1	5	21	1	AGLSDLELRR
☑	55	441.2665	880.5184	880.5355	-19.36	1	5	9	1	SPRLRPR
☑	168	556.8366	1111.6586	1111.6462	11.2	1	5	9.8	1	SPRISRPTAK
☑	249	612.3348	1222.6550	1222.6346	16.7	0	5	22	1	LDGNAIFFQAK
☑	284	645.8327	1289.6508	1289.6054	35.2	1	5	27	1	GGDYWRFHPR
☑	462	612.9324	1835.7754	1835.7858	-5.70	1	5	6.7	1	DESLVSRAMEYMFGW + Oxidation (M)
☑	247	597.3036	1192.5926	1192.5724	17.0	1	5	28	1	KEGTEWSQTK
☑	183	565.3204	1128.6262	1128.6503	-21.27	0	5	26	1	TKPVLSSLER
☑	56	441.2668	880.5190	880.4879	35.4	1	5	9.6	1	GLDGRHVK
☑	115	523.7672	1045.5198	1045.5152	4.45	1	5	35	1	QEQESARAK
☑	160	556.8324	1111.6502	1111.5985	46.5	1	4	12	1	SKSHPASLASK
☑	502	1073.0221	2144.0296	2144.0498	-9.39	1	4	18	1	KLQNSIQESTQNFDDHLK
☑	84	470.7674	939.5202	939.5614	-43.77	1	4	20	1	NRLPIATR
☑	90	475.7499	949.4852	949.5089	-24.87	1	4	32	1	LCMSLKAK
☑	520	747.3844	2239.1314	2239.2259	-42.22	1	4	18	1	GAFTGLHSLKVLMLQNNQLR
☑	54	435.7731	869.5316	869.5123	22.2	0	4	15	1	VSLWLPR
☑	163	556.8347	1111.6548	1111.6462	7.80	1	4	12	1	KPQLDTRVR
☑	83	470.7668	939.5190	939.5515	-34.52	1	4	21	1	LRPGWRR
☑	236	586.7966	1171.5786	1171.6271	-41.33	0	4	26	1	MNLPSPVISSK
☑	67	450.7224	899.4302	899.4032	30.1	0	4	19	1	HSGCAVNR
☑	365	735.9140	1469.8134	1469.7435	47.6	1	4	18	1	TTLLQEEYAKMK + Oxidation (M)
☑	522	747.3883	2239.1431	2239.1346	3.80	1	4	18	1	VSQSGGTGHANPTFKLQTPQGK
☑	281	645.8319	1289.6492	1289.6292	15.5	1	4	32	1	TKEFWSTYTK
☑	109	517.2719	1032.5292	1032.5564	-26.28	0	4	35	1	VSQGSTVISR
☑	467	650.9503	1949.8291	1949.9001	-36.40	0	4	9.3	1	EGGGTELVGTVMTSNTPER + Oxidation (M)
☑	238	595.3069	1188.5992	1188.6285	-24.60	1	4	33	1	SPTIRDMVVR + Oxidation (M)
☑	164	556.8352	1111.6558	1111.6462	8.70	1	4	14	1	KPQLDTRVR
☑	44	422.2433	842.4720	842.4610	13.1	0	4	37	1	VAVEGNVR
☑	178	561.2647	1120.5148	1120.5625	-42.53	1	3	32	1	GAFSNNERVK
☑	251	616.8057	1231.5968	1231.5680	23.4	1	3	33	1	EENEAEKVER
☑	258	626.3500	1250.6854	1250.6329	42.0	0	3	25	1	YLPTCLDTLR
☑	123	529.2694	1056.5242	1056.5352	-10.40	0	3	30	1	NGFVLHENK

☑	427	552.5915	1654.7527	1654.7708	-10.97	1	3	20	1	MRGPCQLFDFTGAR
☑	87	470.7683	939.5220	939.5250	-3.15	1	3	23	1	PRAVPSGTR
☑	158	556.7419	1111.4692	1111.5121	-38.51	1	3	12	1	WKMEFDTR
☑	503	1073.0231	2144.0316	2144.0233	3.89	0	3	25	1	KPDLENVSSEGGGGTLDNLDK
☑	24	370.6898	739.3650	739.3357	39.7	0	3	23	1	MTMGLR + 2 Oxidation (M)
☑	245	595.3107	1188.6068	1188.5631	36.8	0	3	42	1	LDMPQGMIPR + 2 Oxidation (M)
☑	20	349.2049	696.3952	696.3629	46.5	0	3	18	1	MVIYR + Oxidation (M)
☑	66	450.7223	899.4300	899.4726	-47.29	1	3	25	1	HFPSTRR
☑	10	577.2819	576.2746	576.2867	-21.00	0	3	46	1	SSAQGK
☑	455	897.9139	1793.8132	1793.7699	24.2	1	3	26	1	MSYLKTTMEDEESSK + Oxidation (M)
☑	576	916.4275	2746.2607	2746.2996	-14.16	1	3	17	1	QAPPQYTFIGELNSMGIWYRMGR + 2 Oxidation (M)
☑	62	450.7201	899.4256	899.4647	-43.42	0	3	24	1	SLQHMLR + Oxidation (M)
☑	13	323.1536	644.2926	644.3242	-48.93	0	3	16	1	GAASPSR
☑	86	470.7677	939.5208	939.5548	-36.18	1	3	28	1	MRKPRPR
☑	89	470.7696	939.5246	939.5515	-28.56	1	3	25	1	LRPGWRR
☑	166	556.8363	1111.6580	1111.6423	14.1	1	3	18	1	MKPKASLPPK + Oxidation (M)
☑	17	325.1857	648.3568	648.3377	29.5	1	3	42	1	MAAGKR + Oxidation (M)
☑	63	450.7214	899.4282	899.4647	-40.53	0	2	28	1	SLQHMLR + Oxidation (M)
☑	357	728.3519	1454.6892	1454.7617	-49.78	1	2	34	1	VVSSTSLFESSGKK
☑	68	450.7227	899.4308	899.4686	-41.92	1	2	30	1	GAAAGGRGGAR
☑	60	450.7193	899.4240	899.4647	-45.20	0	2	26	1	LNTHLMR + Oxidation (M)
☑	165	556.8359	1111.6572	1111.6713	-12.66	1	2	19	1	GVKALIQDIR
☑	454	897.9121	1793.8096	1793.7699	22.2	1	2	28	1	MSYLKTTMEDEESSK + Oxidation (M)
☑	101	506.2419	1010.4692	1010.4525	16.6	1	2	32	1	RMDMDTVK + Oxidation (M)
☑	162	556.8341	1111.6536	1111.5986	49.6	1	2	21	1	QPLSGTPKER
☑	532	762.0566	2283.1480	2283.2620	-49.94	1	2	29	1	EKSLVAQLAAAQLELQMTALR
☑	65	450.7219	899.4292	899.4647	-39.42	0	2	31	1	SLQHMLR + Oxidation (M)
☑	107	516.3027	1030.5908	1030.5593	30.6	0	2	42	1	LMTGAGNVLR
☑	521	747.3854	2239.1344	2239.0625	32.1	1	2	32	1	VACSGGAPGAGGRGGAGGAAAAGAGAAGR
☑	106	516.2996	1030.5846	1030.5407	42.7	1	2	47	1	ELDTLRER
☑	9	575.3143	574.3070	574.2962	18.8	1	2	1.1e+002	1	KDLEA
☑	252	618.2717	1234.5288	1234.5724	-35.29	1	2	24	1	ADTSQPSARMR + Oxidation (M)
☑	430	838.3983	1674.7820	1674.8246	-25.43	1	2	41	1	ALDGLQREAMEELGK + Oxidation (M)
☑	525	762.0536	2283.1390	2283.1894	-22.10	0	1	33	1	EEVIDFSKPFMSLGISIMIK
☑	526	762.0540	2283.1402	2283.1190	9.26	1	1	33	1	KGTTTNATATSTSTASTAVADAQK
☑	480	688.3133	2061.9181	2061.9426	-11.89	1	1	26	1	SKGSQGTSPFPMSPPSPDSR + Oxidation (M)
☑	380	795.3489	1588.6832	1588.7515	-42.96	1	1	19	1	TPEEVICERSQNK
☑	479	688.3128	2061.9166	2061.9426	-12.61	1	1	25	1	SKGSQGTSPFPMSPPSPDSR + Oxidation (M)
☑	259	627.2626	1252.5106	1252.5587	-38.34	0	1	12	1	VWNYFSYMK + Oxidation (M)
☑	8	562.3096	561.3023	561.3122	-17.64	0	1	84	1	TLGSGK
☑	14	647.3585	646.3512	646.3438	11.4	0	1	93	1	LYSHK
☑	530	762.0560	2283.1462	2283.1205	11.2	0	1	39	1	DWDPGLPIIDNLMQSINQSK
☑	444	882.9548	1763.8950	1763.8889	3.46	1	1	54	1	NIPWRCVVIDEAHR
☑	537	767.0458	2298.1156	2298.1525	-16.07	1	1	39	1	MSLSLEVATYRTLLEAENSR + Oxidation (M)
☑	587	1414.1199	2826.2252	2826.3139	-31.38	1	1	16	1	HGRAGVPMEVMGLMLGEFVDDYTVR + 3 Oxidation (M)
☑	102	506.2426	1010.4706	1010.4855	-14.70	0	1	45	1	SCLEFSLR
☑	26	396.7331	791.4516	791.4177	42.8	0	0	55	1	EFIGAQK
☑	18	325.1862	648.3578	648.3629	-7.74	1	0	73	1	GLGMKK + Oxidation (M)
☑	504	546.7143	2182.8281	2182.8329	-2.22	0	0	4.1	1	CFPCPDQGCPQMGHYADK + Oxidation (M)
☑	339	692.3972	1382.7798	1382.7154	46.6	1	0	45	1	KDPSQTSPLGTPR
☑	1	*369.8990*	*368.8917*							
☑	2	*412.8516*	*411.8443*							
☑	3	*429.1010*	*428.0937*							
☑	4	*445.1302*	*444.1229*							
☑	7	*460.2643*	*459.2570*							
☑	15	*325.1771*	*648.3396*							
☑	16	*325.1830*	*648.3514*							
☑	21	*350.1520*	*698.2894*							
☑	22	*360.7044*	*719.3942*							
☑	23	*360.7065*	*719.3984*							
☑	25	*396.7322*	*791.4498*							
☑	46	*423.7246*	*845.4346*							
☑	110	*519.1532*	*1036.2918*							
☑	122	*528.3091*	*1054.6036*							
☑	237	*588.3435*	*1174.6724*							
☑	287	*648.3742*	*1294.7338*							
☑	340	*692.8701*	*1383.7256*							
☑	341	*692.8714*	*1383.7282*							
☑	356	*720.3672*	*1438.7198*							
☑	366	*736.4177*	*1470.8208*							
☑	371	*757.8600*	*1513.7054*							
☑	372	*766.3796*	*1530.7446*							
☑	373	*766.3809*	*1530.7472*							
☑	374	*775.8672*	*1549.7198*							
☑	375	*785.8416*	*1569.6686*							
☑	376	*785.8436*	*1569.6726*							
☑	377	*785.8450*	*1569.6754*							
☑	378	*785.8463*	*1569.6780*							
☑	379	*785.8502*	*1569.6858*							
☑	393	*810.3764*	*1618.7382*							
☑	428	*828.4725*	*1654.9304*							

☑	433	*847.4376*	*1692.8606*
☑	436	*849.4251*	*1696.8356*
☑	440	*855.4716*	*1708.9286*
☑	447	*444.8585*	*1775.4049*
☑	456	*897.9154*	*1793.8162*
☑	457	*897.9534*	*1793.8922*
☑	458	*906.4670*	*1810.9194*
☑	459	*906.4675*	*1810.9204*
☑	460	*906.4682*	*1810.9218*
☑	463	*924.9924*	*1847.9702*
☑	464	*617.9799*	*1850.9179*
☑	466	*948.9913*	*1895.9680*
☑	481	*1036.4299*	*2070.8452*
☑	482	*1038.5869*	*2075.1592*
☑	492	*701.6434*	*2101.9084*
☑	493	*701.6444*	*2101.9114*
☑	497	*1062.4862*	*2122.9578*
☑	505	*1093.5850*	*2185.1554*
☑	506	*737.6982*	*2210.0728*
☑	507	*737.6986*	*2210.0740*
☑	508	*737.6988*	*2210.0746*
☑	509	*737.6998*	*2210.0776*
☑	510	*737.7000*	*2210.0782*
☑	511	*737.7000*	*2210.0782*
☑	512	*737.7003*	*2210.0791*
☑	513	*737.7007*	*2210.0803*
☑	514	*737.7010*	*2210.0812*
☑	515	*737.7013*	*2210.0821*
☑	516	*737.7016*	*2210.0830*
☑	517	*737.7018*	*2210.0836*
☑	518	*737.7018*	*2210.0836*
☑	519	*737.7036*	*2210.0890*
☑	523	*761.7198*	*2282.1376*
☑	524	*761.7235*	*2282.1487*
☑	527	*762.0549*	*2283.1429*
☑	528	*762.0551*	*2283.1435*
☑	529	*762.0555*	*2283.1447*
☑	531	*762.0562*	*2283.1468*
☑	533	*762.0594*	*2283.1564*
☑	534	*1144.1368*	*2286.2590*
☑	535	*767.0423*	*2298.1051*
☑	536	*767.0435*	*2298.1087*
☑	538	*779.0403*	*2334.0991*
☑	539	*1168.5659*	*2335.1172*
☑	557	*1259.6788*	*2517.3430*
☑	574	*916.4235*	*2746.2487*
☑	575	*916.4275*	*2746.2607*
☑	577	*917.0772*	*2748.2098*
☑	578	*917.0789*	*2748.2149*
☑	579	*917.0808*	*2748.2206*
☑	580	*917.0855*	*2748.2347*
☑	581	*922.4243*	*2764.2511*
☑	582	*927.0934*	*2778.2584*
☑	583	*927.7480*	*2780.2222*
☑	588	*1414.1230*	*2826.2314*
☑	589	*1415.1056*	*2828.1966*
☑	590	*1415.1093*	*2828.2040*
☑	591	*975.8646*	*2924.5720*
☑	592	*1015.5191*	*3043.5355*
☑	593	*1179.7867*	*4715.1177*
☑	594	*1572.7246*	*4715.1520*

Search Parameters

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Type of search         : MS/MS Ion Search
Enzyme                 : Trypsin
Fixed modifications    : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values            : Monoisotopic
Protein Mass           : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages   : 1
Instrument type        : ESI-QUAD-TOF
Number of queries      : 594
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Mascot: http://www.matrixscience.com/