

MASCOT Mascot Search Results

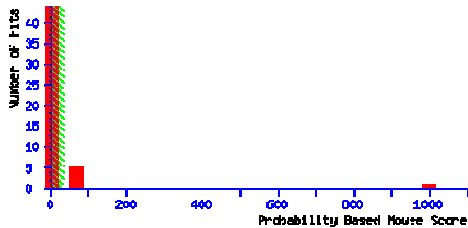
User : Bob
 Email : rdenglis@utmb.edu
 Search title : 11081913.raw #2271 acetylation
 MS data file : tempfile
 Database : NCBI nr 20110707 (14481393 sequences; 4958963357 residues)
 Taxonomy : Mus musculus (house mouse) (143921 sequences)
 Timestamp : 24 Aug 2011 at 15:46:26 GMT
 Protein hits : [gi|124248512](#) carbamoyl-phosphate synthase [ammonia], mitochondrial precursor [Mus musculus]
[gi|14917005](#) RecName: Full=Stress-70 protein, mitochondrial; AltName: Full=75 kDa glucose-regulated protein; Short=GRP-75;
[gi|84781771](#) trypsin 10 [Mus musculus]
[gi|12843914](#) unnamed protein product [Mus musculus]
[gi|12838381](#) unnamed protein product [Mus musculus]
[gi|3093758](#) cyclic AMP specific phosphodiesterase PDE4D5A [Mus musculus]

NCBI nr [Decoy](#) False discovery rate

Peptide matches above identity threshold 33 3 9.09 %
 Peptide matches above homology or identity threshold 37 3 8.11 %

Probability Based Mowse Score

Ions score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event. Individual ions scores > 32 indicate identity or extensive homology (p<0.05). Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Peptide Summary Report

Format As [Help](#)

Significance threshold p< Max. number of hits

Standard scoring MudPIT scoring Ions score or expect cut-off Show sub-sets

Show pop-ups Suppress pop-ups Sort unassigned Require bold red

1. [gi|124248512](#) Mass: 164514 Score: 999 Queries matched: 34 emPAI: 0.63
 carbamoyl-phosphate synthase [ammonia], mitochondrial precursor [Mus musculus]
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Score	Expect	Rank	Peptide
b 3	406.2201	810.4257	810.4276	-0.0019	0	30	0.14	1	R.SFPFVSK.T
b 4	406.2204	810.4263	810.4276	-0.0013	0	(12)	8.5	1	R.SFPFVSK.T
b 21	453.2571	904.4996	904.5018	-0.0022	0	(38)	0.024	1	K.LFAEAVQK.S
b 22	453.2573	904.4999	904.5018	-0.0019	0	51	0.0011	1	K.LFAEAVQK.S
b 24	495.2783	988.5421	988.5441	-0.0020	0	58	0.00074	1	K.ETLIDLGTK.A
b 26	508.2394	1014.4642	1014.4658	-0.0016	0	30	0.064	1	R.TFEESFQK.A
b 27	508.8016	1015.5887	1015.5914	-0.0027	0	41	0.0079	1	K.GTTITSVLPK.P
b 30	518.7695	1035.5245	1035.5237	0.0009	0	43	0.0088	1	K.EIEYEVVR.D
b 32	545.7971	1089.5796	1089.5819	-0.0023	0	46	0.0042	1	K.VPAIYGVDR.M
b 33	551.8077	1101.6009	1101.6030	-0.0021	0	65	5e-005	1	K.QNLIAEVSTK.D
b 34	568.7777	1135.5408	1135.5431	-0.0023	0	63	5.7e-005	1	K.VMIGESIDEX.R + Oxidation (M)
b 36	582.3725	1162.7305	1162.7325	-0.0020	0	52	3.1e-005	1	K.IALGIPLPEIK.N
b 41	609.3103	1216.6059	1216.6088	-0.0028	0	60	0.00016	1	K.SLGLQWQEEK.V
b 43	611.3385	1220.6624	1220.6652	-0.0029	0	64	3.9e-005	1	R.SIFSVALDELK.V
b 44	611.8440	1221.6735	1221.6757	-0.0022	0	51	0.00061	1	K.ATGYPLAFIAK.I
b 46	623.8258	1245.6370	1245.6387	-0.0017	0	56	0.00039	1	K.IMGTSPLQIDR.A + Oxidation (M)
b 49	639.8492	1277.6838	1277.6867	-0.0029	0	72	7.3e-006	1	K.TLGVDFIDVATK.V
b 50	649.8332	1297.6517	1297.6554	-0.0036	0	57	0.00023	1	K.LYFEELSLEK.I
b 54	661.8407	1321.6668	1321.6700	-0.0032	0	60	0.00011	1	K.AADTIGYFVPIR.S + Oxidation (M)
b 60	677.3660	1352.7174	1352.7160	0.0014	0	68	1.7e-005	1	R.GQNQPVLNITNR.Q
b 65	704.8631	1407.7116	1407.7180	-0.0064	0	(51)	0.00088	1	K.AFAMTNQILVER.S + Oxidation (M)
b 66	704.8696	1407.7246	1407.7180	0.0066	0	73	5.1e-006	1	K.AFAMTNQILVER.S + Oxidation (M)
b 68	710.8476	1419.6806	1419.6841	-0.0035	0	84	4.7e-007	1	K.GLNDSVTEETLR.K
b 74	760.3725	1518.7304	1518.7348	-0.0044	0	72	5.9e-006	1	K.ALENNMSLDEIVR.L + Oxidation (M)

b	82	526.6109	1576.8108	1576.8096	0.0012	1	19	1.3	1	R.QLFSDKLNINEK.I
b	84	530.2740	1587.8003	1587.8045	-0.0042	0	16	2.6	1	R.FLGVAEQLHNEGFK.L
b	86	812.3974	1622.7803	1622.7861	-0.0058	0	86	2.5e-007	1	K.IAPSFVAVESMEDALK.A + Oxidation (M)
b	87	812.4010	1622.7875	1622.7822	0.0054	0	120	1e-010	1	K.VLGTSVESIMATEDR.Q + Oxidation (M)
b	88	812.4048	1622.7949	1622.7861	0.0088	0	(71)	7.6e-006	1	K.IAPSFVAVESMEDALK.A + Oxidation (M)
b	96	862.4102	1722.8059	1722.8101	-0.0042	0	80	6.5e-007	1	K.IEFEGQSVDFVDPNK.Q
b	97	863.9507	1725.8868	1725.8897	-0.0029	0	79	9.3e-007	1	R.DGSIDLVLINLNNNTK.F
b	98	576.6102	1726.8089	1726.8083	0.0006	1	17	1.3	1	R.DELGLNKYMESDGK.V + Oxidation (M)
b	111	682.0283	2043.0632	2043.0670	-0.0039	0	56	0.00013	1	K.TVLMNPNIASVQTNEVGLK.Q + Oxidation (M)
b	151	936.4723	2806.3952	2806.4025	-0.0073	1	59	3.5e-005	1	K.IEFEGQSVDFVDPNKQLIAEVSTK.D

2. [gi|14917005](#) Mass: 73483 Score: 99 Queries matched: 1 emPAI: 0.04
 RecName: Full=Stress-70 protein, mitochondrial; AltName: Full=75 kDa glucose-regulated protein; Short=GRP-75; AltName: Full=Heat shock
 e Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide	
b	108	904.9530	1807.8915	1807.8952	-0.0037	0	99	9.1e-009	1	K.SQVFSTAADGQTQVEIK.V

Proteins matching the same set of peptides:
[gi|74204605](#) Mass: 73446 Score: 99 Queries matched: 1
 unnamed protein product [Mus musculus]
[gi|74205924](#) Mass: 63924 Score: 99 Queries matched: 1
 unnamed protein product [Mus musculus]
[gi|74225724](#) Mass: 73431 Score: 99 Queries matched: 1
 unnamed protein product [Mus musculus]
[gi|162461907](#) Mass: 73416 Score: 99 Queries matched: 1
 stress-70 protein, mitochondrial [Mus musculus]

3. [gi|84781771](#) Mass: 26204 Score: 94 Queries matched: 3 emPAI: 0.26
 trypsin 10 [Mus musculus]
 e Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide	
b	37	588.3176	1174.6207	1174.6267	-0.0061	0	(62)	0.0001	1	K.TLNDNDIMLIK.L
b	39	596.3170	1190.6195	1190.6217	-0.0021	0	63	8.2e-005	1	K.TLNDNDIMLIK.L + Oxidation (M)
b	52	655.3216	1308.6286	1308.6206	0.0079	0	5	35	9	K.NMICVGFLEGGK.D + Acetyl (K)

4. [gi|12843914](#) Mass: 29993 Score: 79 Queries matched: 1 emPAI: 0.11
 unnamed protein product [Mus musculus]
 e Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide	
b	51	651.8597	1301.7048	1301.7078	-0.0031	0	79	1.4e-006	1	R.SLDDLSIIAEVK.A

Proteins matching the same set of peptides:
[gi|13272554](#) Mass: 42357 Score: 79 Queries matched: 1
 cytokeratin KRT2-6HF [Mus musculus]
[gi|16303309](#) Mass: 61743 Score: 79 Queries matched: 1
 type II keratin 5 [Mus musculus]
[gi|20911031](#) Mass: 61729 Score: 79 Queries matched: 1
 keratin, type II cytoskeletal 5 [Mus musculus]
[gi|29789317](#) Mass: 59704 Score: 79 Queries matched: 1
 keratin, type II cytoskeletal 75 [Mus musculus]
[gi|54607171](#) Mass: 59299 Score: 79 Queries matched: 1
 keratin, type II cytoskeletal 6A [Mus musculus]
[gi|59798479](#) Mass: 60285 Score: 79 Queries matched: 1
 RecName: Full=Keratin, type II cytoskeletal 6B; AltName: Full=Cytokeratin-6B; Short=CK-6B; AltName: Full=Keratin-6-beta; Short=mK6-bet
[gi|110645788](#) Mass: 60236 Score: 79 Queries matched: 1
 Krt6b protein [Mus musculus]
[gi|113195684](#) Mass: 59490 Score: 79 Queries matched: 1
 keratin, type II cytoskeletal 6B [Mus musculus]
[gi|116063325](#) Mass: 60154 Score: 79 Queries matched: 1
 Krt6b protein [Mus musculus]
[gi|148672084](#) Mass: 34775 Score: 79 Queries matched: 1
 mCG17577 [Mus musculus]
[gi|148672085](#) Mass: 38119 Score: 79 Queries matched: 1
 mCG144996 [Mus musculus]
[gi|148672089](#) Mass: 62241 Score: 79 Queries matched: 1
 keratin 75 [Mus musculus]

5. [gi|12838381](#) Mass: 29379 Score: 40 Queries matched: 2 emPAI: 0.11
 unnamed protein product [Mus musculus]
 e Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
21	453.2571	904.4996	904.5018	-0.0022	1	(31)	0.12	2	R.IFAQEKK.L + Acetyl (K)
22	453.2573	904.4999	904.5018	-0.0018	1	40	0.015	2	R.IFAQEKK.L + Acetyl (K)

Proteins matching the same set of peptides:

[gi|148705305](#) Mass: 16801 Score: 40 Queries matched: 2
 mCG11633, isoform CRA_d [Mus musculus]
[gi|188219642](#) Mass: 29451 Score: 40 Queries matched: 2
 dnaI homolog subfamily B member 6 isoform b [Mus musculus]

6. [gi|3093758](#) Mass: 23890 Score: 36 Queries matched: 1 emPAI: 0.13
 cyclic AMP specific phosphodiesterase PDE4D5A [Mus musculus]
 e Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
b 17	434.7656	867.5166	867.5178	-0.0011	0	36	0.013	1	K.LSPVISPR.N

Proteins matching the same set of peptides:

[gi|148686495](#) Mass: 79441 Score: 36 Queries matched: 1
 phosphodiesterase 4D, cAMP specific, isoform CRA_c [Mus musculus]

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

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
b 11	421.7575	841.5005	841.4810	0.0195	0	30	0.15	1	LGTWLPR
b 9	421.7574	841.5003	841.4810	0.0193	0	28	0.25	1	LGTWLPR
b 8	421.7567	841.4988	841.4810	0.0177	0	25	0.46	1	LGTWLPR
b 80	783.8719	1565.7292	1565.7184	0.0108	1	25	0.25	1	EKDFQGMLEYHK + Acetyl (K)
b 10	421.7575	841.5004	841.4810	0.0194	0	25	0.52	1	LGTWLPR
b 12	421.7579	841.5013	841.5021	-0.0008	1	23	0.77	1	VKTSLPR + Acetyl (K)
b 42	611.3076	1220.6007	1220.6037	-0.0030	0	23	0.73	1	FEGAQSVVQEK
b 13	421.7586	841.5025	841.5021	0.0004	1	23	0.85	1	VKTSLPR + Acetyl (K)
b 77	769.3227	1536.6309	1536.6258	0.0050	1	21	0.1	1	MVSSGMYKMDNGK + Acetyl (Protein N-term); 3 Oxidation (M)
b 62	688.8440	1375.6734	1375.6700	0.0034	1	21	0.96	1	RMMEVAADVQR
b 118	737.7040	2210.0902	2210.0967	-0.0065	0	21	0.43	1	LGEHNINLVLEGNEQFIDAAK
b 119	737.7041	2210.0904	2210.0967	-0.0063	0	20	0.51	1	LGEHNINLVLEGNEQFIDAAK
b 90	820.3950	1638.7755	1638.7745	0.0009	1	20	0.78	1	IQMEKFKMAANPSK + Oxidation (M)
b 79	780.8968	1559.7790	1559.7654	0.0137	0	19	1.3	1	QWELLCDDLEQDK
b 124	737.7048	2210.0925	2210.0967	-0.0042	0	19	0.68	1	LGEHNINLVLEGNEQFIDAAK
b 85	804.8985	1607.7824	1607.7825	-0.0001	1	18	1.5	1	QKQDETQTISLTK
b 53	655.8552	1309.6958	1309.6878	0.0080	1	18	1.5	1	KGSALDPEPQVK + Acetyl (K)
b 92	837.3882	1672.7618	1672.7693	-0.0075	0	18	0.94	1	DSEGDTPSLINWFSR
b 122	737.7043	2210.0912	2210.0967	-0.0055	0	18	0.89	1	LGEHNINLVLEGNEQFIDAAK
b 35	570.2702	1138.5259	1138.5189	0.0069	1	18	1.7	1	GMAEAEERGF + Oxidation (M)
b 31	536.3229	1070.6311	1070.6196	0.0115	1	18	1.2	1	DLQLRVTAR
b 45	617.3082	1232.6018	1232.6149	-0.0131	1	17	2.6	1	KSEAPGAFQTR + Acetyl (K)
b 15	428.7647	855.5148	855.5178	-0.0029	0	17	2.2	1	EAAALIALR
b 52	655.3216	1308.6286	1308.6271	0.0015	0	17	2	1	MELGELLYNK + Acetyl (K); Acetyl (Protein N-term); Oxidation
b 57	669.8388	1337.6631	1337.6616	0.0016	0	17	2.4	1	GFPGLPGSPGEGK + Acetyl (K)
b 47	625.3053	1248.5960	1248.6020	-0.0060	1	16	2.8	1	LKSGMSPQSK + Acetyl (K); Oxidation (M)
b 117	737.7030	2210.0872	2210.0967	-0.0095	0	16	1.5	1	LGEHNINLVLEGNEQFIDAAK
b 23	459.2761	916.5377	916.5382	-0.0004	1	15	2.5	1	GKAFGLLK + 2 Acetyl (K)
b 16	428.7670	855.5193	855.5112	0.0081	1	15	3.3	1	ALRMLPR
b 38	595.3264	1188.6383	1188.6462	-0.0080	1	15	3.7	1	ITDTISDRLR
b 28	510.7709	1019.5273	1019.5321	-0.0048	1	15	5.4	1	VAKMTVSGK + 2 Acetyl (K); Oxidation (M)
b 121	737.7043	2210.0912	2210.0967	-0.0055	0	14	2.2	1	LGEHNINLVLEGNEQFIDAAK
b 100	864.4420	1726.8694	1726.8638	0.0055	1	14	4.4	1	GLEWIGRIDPNDGGTK
b 123	737.7047	2210.0924	2210.0967	-0.0043	0	13	2.3	1	LGEHNINLVLEGNEQFIDAAK
b 125	737.7051	2210.0934	2210.0967	-0.0033	0	13	2.5	1	LGEHNINLVLEGNEQFIDAAK
b 40	597.7979	1193.5813	1193.5863	-0.0050	0	13	6.9	1	MDASLGNLFAR
b 67	710.8361	1419.6577	1419.6453	0.0125	0	13	4.5	1	LESSGCSGGVNWPK
b 48	631.8247	1261.6349	1261.6277	0.0072	1	13	7.9	1	LYGSFNFRMK
b 18	435.7731	869.5316	869.5123	0.0193	0	11	7.1	1	VSLWLPR
b 64	701.3595	1400.7044	1400.6936	0.0108	0	11	10	1	DEVTWVAGDVIR + Acetyl (Protein N-term)
b 70	712.8628	1423.7110	1423.7129	-0.0019	1	11	8.1	1	SMPSLDFSGRLSK
b 99	864.4410	1726.8674	1726.8638	0.0035	1	11	9	1	GLEWIGRIDPNDGGTK
b 59	673.8514	1345.6883	1345.6734	0.0150	1	10	13	1	MLQDVQMPQK + Acetyl (K)
b 19	435.7740	869.5335	869.5334	0.0001	1	10	9	1	VVVVEKR + Acetyl (K)
b 120	737.7041	2210.0906	2210.0967	-0.0061	0	9	7	1	LGEHNINLVLEGNEQFIDAAK
b 126	738.0335	2211.0785	2211.0920	-0.0135	0	9	6.9	1	LGEHNINLVLEGNEQFVNSAK
b 78	774.8640	1547.7135	1547.7137	-0.0002	0	8	11	1	QLEDAIEDCTNAVK
b 91	830.9283	1659.8421	1659.8250	0.0171	1	8	13	1	TSVHQETKSMLLDR + Oxidation (M)
b 102	882.8930	1763.7713	1763.7616	0.0098	1	8	5.3	1	MQMPWNSNPMCKTR + Acetyl (K); Oxidation (M)
b 63	696.8414	1391.6683	1391.6867	-0.0184	0	8	20	1	GTILPASNFDMAR
b 25	505.2683	1008.5220	1008.5136	0.0083	0	7	24	1	MVSGFIPMK
b 76	768.3708	1534.7269	1534.7376	-0.0106	0	7	17	1	AELPNGHAQSLGK + Acetyl (K)
b 73	752.8660	1503.7174	1503.7317	-0.0143	1	7	21	1	DGIQTKEHPNPGK + 2 Acetyl (K)
b 29	512.2384	1022.4623	1022.4629	-0.0005	0	7	21	1	SVENGSSSTR
b 69	711.3399	1420.6653	1420.6722	-0.0069	1	6	21	1	SKDSSPSYLPK + 2 Acetyl (K)
b 127	738.0386	2211.0940	2211.0742	0.0197	1	6	12	1	VESGFHQHGLSELRAMDK + Acetyl (K); Oxidation (M)

b	106	897.9082	1793.8019	1793.8036	-0.0017	1	6	12	1	KMAECLSESHAQSTTR + Oxidation (M)
b	142	762.7132	2285.1177	2285.1301	-0.0124	1	5	16	1	DPAGHRAAAILHGGSPDFVGNK + Acetyl (K)
b	75	760.8651	1519.7157	1519.7197	-0.0039	1	5	26	1	VCAETHCSMLLK + Acetyl (K); Oxidation (M)
b	89	820.3943	1638.7740	1638.7606	0.0133	1	5	26	1	PLCGSDGRTYAQICR
b	83	790.8885	1579.7625	1579.7776	-0.0152	1	4	39	1	SFVSVALQKQNNMR + Acetyl (K); Oxidation (M)
b	139	762.0572	2283.1499	2283.1442	0.0057	1	4	18	1	QTSSKSQVNIVTSTLLTSTSDS
b	103	887.9500	1773.8854	1773.8819	0.0036	1	4	38	1	KGDLLDAINSCVTVDK + 2 Acetyl (K)
b	114	732.0281	2193.0626	2193.0711	-0.0085	0	3	23	1	EMPVQFQVVELPSGHHLCK + Oxidation (M)
b	149	767.7172	2300.1298	2300.1156	0.0143	1	3	27	1	ECYPRAMHCIFVGAQSLFLK + Oxidation (M)
b	94	559.9082	1676.7028	1676.7022	0.0007	0	3	8.6	1	MDDCHSALEQLTEK + Acetyl (Protein N-term); Oxidation (M)
b	6	412.7524	823.4903	823.4916	-0.0013	0	2	26	1	AVLSHGLK
b	109	970.9696	1939.9246	1939.9230	0.0016	1	2	35	1	LMEMEQLTSSLRETEK + Oxidation (M)
b	95	857.4052	1712.7959	1712.7981	-0.0021	0	2	37	1	FENDAAMVQSWFR
b	132	742.7034	2225.0885	2225.0787	0.0099	1	2	37	1	VWTFPPQEELMDLQKDR + Oxidation (M)
b	129	742.3740	2224.1001	2224.0933	0.0069	1	1	42	1	SSGQKISAEMSLYPSLEDLK + Acetyl (K)
b	143	574.2677	2293.0419	2293.0329	0.0090	1	1	29	1	YKPVNCQVECHPYLNQMK + 2 Acetyl (K); Oxidation (M)
b	113	729.0346	2184.0819	2184.0741	0.0078	1	1	44	1	ACIESRVNMVTASYITPAMK
b	146	767.3894	2299.1463	2299.1513	-0.0051	0	0	50	1	NMQMMSIEILTLFTELAK + Acetyl (K); 2 Oxidation (M)
b	7	412.7531	823.4917	823.4916	0.0001	0	0	38	1	TVAPALPR
b	141	762.3864	2284.1375	2284.1279	0.0096	1	0	46	1	YGRHPLMELPLMINPTGCAR + Oxidation (M)
b	56	668.8388	1335.6631	1335.6670	-0.0039	0	0	1.1e+002	1	IENLEEYFGLR
b	1	362.2217	722.4287							
b	2	384.2344	766.4542							
b	5	406.2475	810.4804							
b	14	428.2606	854.5067							
b	20	450.2733	898.5321							
b	55	664.8316	1327.6487							
b	58	448.2180	1341.6323							
b	61	459.5363	1375.5870							
b	71	488.2188	1461.6346							
b	72	492.2074	1473.6005							
b	81	525.2239	1572.6499							
b	93	559.9062	1676.6966							
b	101	878.3738	1754.7330							
b	104	890.8900	1779.7654							
b	105	594.2753	1779.8041							
b	107	904.9407	1807.8668							
b	110	665.6211	1993.8414							
b	112	1042.0058	2081.9970							
b	115	737.3604	2209.0593							
b	116	737.3670	2209.0793							
b	128	742.0317	2223.0734							
b	130	742.3742	2224.1007							
b	131	742.3753	2224.1040							
b	133	746.3762	2236.1068							
b	134	747.0466	2238.1179							
b	135	563.0173	2248.0400							
b	136	567.0099	2264.0103							
b	137	567.5066	2265.9974							
b	138	758.3397	2271.9973							
b	140	762.3857	2284.1353							
b	144	766.7296	2297.1669							
b	145	767.3891	2299.1454							
b	147	767.7166	2300.1279							
b	148	767.7168	2300.1287							
b	150	772.0613	2313.1620							

Search Parameters

Type of search : MS/MS Ion Search
 Enzyme : Trypsin/P
 Variable modifications : Acetyl (K),Acetyl (Protein N-term),Oxidation (M)
 Mass values : Monoisotopic
 Protein Mass : Unrestricted
 Peptide Mass Tolerance : ± 0.02 Da
 Fragment Mass Tolerance : ± 0.3 Da
 Max Missed Cleavages : 1
 Instrument type : ESI-TRAP
 Number of queries : 151

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

Mascot Search Results

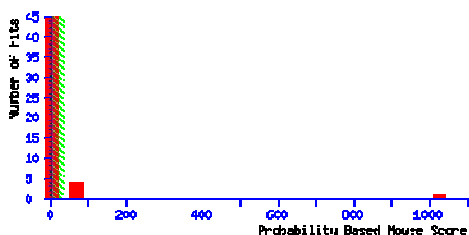
User : Bob
 Email : rdenglis@utmb.edu
 Search title : 11081913.raw #2271 phospho
 MS data file : tempfile
 Database : NCBI nr 20110707 (14481393 sequences; 4958963357 residues)
 Taxonomy : Mus musculus (house mouse) (143921 sequences)
 Timestamp : 24 Aug 2011 at 15:44:25 GMT
 Protein hits : [gi|124248512](#) carbamoyl-phosphate synthase [ammonia], mitochondrial precursor [Mus musculus]
[gi|14917005](#) RecName: Full=Stress-70 protein, mitochondrial; AltName: Full=75 kDa glucose-regulated protein; Short=GRP-75;
[gi|51092303](#) Try10-like trypsinogen [Mus musculus]
[gi|12843914](#) unnamed protein product [Mus musculus]
[gi|3093758](#) cyclic AMP specific phosphodiesterase PDE4D5A [Mus musculus]

NCBI nr [Decoy](#) False discovery rate

Peptide matches above identity threshold 33 3 9.09 %
 Peptide matches above homology or identity threshold 36 4 11.11 %

Probability Based Mowse Score

Ions score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event. Individual ions scores > 32 indicate identity or extensive homology (p<0.05). Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Peptide Summary Report

Format As [Help](#)
 Significance threshold p< Max. number of hits
 Standard scoring MudPIT scoring Ions score or expect cut-off Show sub-sets
 Show pop-ups Suppress pop-ups Sort unassigned Require bold red

1. [gi|124248512](#) Mass: 164514 Score: 1027 Queries matched: 34 emPAI: 0.63
 carbamoyl-phosphate synthase [ammonia], mitochondrial precursor [Mus musculus]
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Score	Expect	Rank	Peptide
b 3	406.2201	810.4257	810.4276	-0.0019	0	30	0.1	1	R.SFPFVSK.T
b 4	406.2204	810.4263	810.4276	-0.0013	0	(12)	6.3	1	R.SFPFVSK.T
b 21	453.2571	904.4996	904.5018	-0.0022	0	(38)	0.015	1	K.LFAEAVQK.S
b 22	453.2573	904.4999	904.5018	-0.0019	0	51	0.00067	1	K.LFAEAVQK.S
b 24	495.2783	988.5421	988.5441	-0.0020	0	58	0.00061	1	K.ETLIDLGTK.A
b 26	508.2394	1014.4642	1014.4658	-0.0016	0	30	0.12	1	R.TFEESFQK.A
b 27	508.8016	1015.5887	1015.5914	-0.0027	0	41	0.0045	1	K.GTTITSVLPK.P
b 30	518.7695	1035.5245	1035.5237	0.0009	0	43	0.0059	1	K.EIEYEVVR.D
b 32	545.7971	1089.5796	1089.5819	-0.0023	0	46	0.0024	1	K.VPAIYVDTR.M
b 33	551.8077	1101.6009	1101.6030	-0.0021	0	65	2.8e-005	1	K.QNLAEVSTK.D
b 34	568.7777	1135.5408	1135.5431	-0.0023	0	63	5.6e-005	1	K.VMIGESIDEK.R + Oxidation (M)
b 36	582.3725	1162.7305	1162.7325	-0.0020	0	52	2.6e-005	1	K.IALGIPLPEIK.N
b 41	609.3103	1216.6059	1216.6088	-0.0028	0	60	0.00012	1	K.SLQWLQEEK.V
b 43	611.3385	1220.6624	1220.6652	-0.0029	0	64	2.6e-005	1	R.SIFSAVLDELK.V
b 44	611.8440	1221.6735	1221.6757	-0.0022	0	51	0.00044	1	K.ATGYPLAFLAAK.I
b 46	623.8258	1245.6370	1245.6387	-0.0017	0	56	0.00024	1	K.IMGTSPLQIDR.A + Oxidation (M)
b 49	639.8492	1277.6838	1277.6867	-0.0029	0	72	4.7e-006	1	K.TLGVDFIDVATK.V
b 50	649.8332	1297.6517	1297.6554	-0.0036	0	57	0.0002	1	K.LYFEELSLSR.I
b 54	661.8407	1321.6668	1321.6700	-0.0032	0	60	9.8e-005	1	K.AADTIGYFVPMIR.S + Oxidation (M)
b 60	677.3660	1352.7174	1352.7160	0.0014	0	68	1.1e-005	1	R.GQNQPVLNITNR.Q
b 65	704.8631	1407.7116	1407.7180	-0.0064	0	(51)	0.00082	1	K.AFAMTNQILVER.S + Oxidation (M)
b 66	704.8696	1407.7246	1407.7180	0.0066	0	73	4.7e-006	1	K.AFAMTNQILVER.S + Oxidation (M)
b 68	710.8476	1419.6806	1419.6841	-0.0035	0	84	4.4e-007	1	K.GLNSDSVTEETLR.K
b 74	760.3725	1518.7304	1518.7348	-0.0044	0	72	6.2e-006	1	K.ALENNMSLDEIVR.L + Oxidation (M)
b 82	526.6109	1576.8108	1576.8096	0.0012	1	19	0.99	1	R.QLFSDKLNINEIK.I

b	84	530.2740	1587.8003	1587.8045	-0.0042	0	16	2.8	1	R.FLGVAEQLHNEGFK.L
b	86	812.3974	1622.7803	1622.7861	-0.0058	0	86	2.6e-007	1	K.IAPSF AVESIM EDALK.A + Oxidation (M)
b	87	812.4010	1622.7875	1622.7822	0.0054	0	120	1e-010	1	K.VLGT SVESIM ATEDR.Q + Oxidation (M)
b	88	812.4048	1622.7949	1622.7861	0.0088	0	(71)	7.2e-006	1	K.IAPSF AVESIM EDALK.A + Oxidation (M)
b	96	862.4102	1722.8059	1722.8101	-0.0042	0	80	9.7e-007	1	K.IEFEGQSVDFVDPNK.Q
b	97	863.9507	1725.8868	1725.8897	-0.0029	0	79	7.3e-007	1	R.DGSIDLVINL PNNNTK .F
b	98	576.6102	1726.8089	1726.8083	0.0006	1	17	2.2	1	R.DLGLN KYMESD GK.V + Oxidation (M)
b	111	682.0283	2043.0632	2043.0670	-0.0039	0	56	9.7e-005	1	K.TVL MNPNIASVQ TNEVGLK.Q + Oxidation (M)
b	151	936.4723	2806.3952	2806.4025	-0.0073	1	59	4e-005	1	K.IEFEGQSVDFVDPNK QLIAEV STK.D

2. [gi|14917005](#) Mass: 73483 Score: 99 Queries matched: 1 emPAI: 0.04
 RecName: Full=Stress-70 protein, mitochondrial; AltName: Full=75 kDa glucose-regulated protein; Short=GRP-75; AltName: Full=Heat shock
 e Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide	
b	108	904.9530	1807.8915	1807.8952	-0.0037	0	99	8.6e-009	1	K.SQV FSTAADG TQVEIK.V

Proteins matching the same set of peptides:
[gi|74204605](#) Mass: 73446 Score: 99 Queries matched: 1
 unnamed protein product [Mus musculus]
[gi|74205924](#) Mass: 63924 Score: 99 Queries matched: 1
 unnamed protein product [Mus musculus]
[gi|74225724](#) Mass: 73431 Score: 99 Queries matched: 1
 unnamed protein product [Mus musculus]
[gi|162461907](#) Mass: 73416 Score: 99 Queries matched: 1
 stress-70 protein, mitochondrial [Mus musculus]

3. [gi|51092303](#) Mass: 26514 Score: 97 Queries matched: 2 emPAI: 0.25
 Try10-like trypsinogen [Mus musculus]
 e Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide	
b	37	588.3176	1174.6207	1174.6267	-0.0061	0	(62)	5.8e-005	1	K.TLDNDI MLIK .L
b	39	596.3170	1190.6195	1190.6217	-0.0021	0	63	4.8e-005	1	K.TLDNDI MLIK .L + Oxidation (M)

Proteins matching the same set of peptides:
[gi|84781771](#) Mass: 26204 Score: 97 Queries matched: 2
 trypsin 10 [Mus musculus]

4. [gi|12843914](#) Mass: 29993 Score: 79 Queries matched: 1 emPAI: 0.11
 unnamed protein product [Mus musculus]
 e Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide	
b	51	651.8597	1301.7048	1301.7078	-0.0031	0	79	8.4e-007	1	R.SLDL DSIAEVK .A

Proteins matching the same set of peptides:
[gi|13272554](#) Mass: 42357 Score: 79 Queries matched: 1
 cytokeratin KRT2-6HF [Mus musculus]
[gi|16303309](#) Mass: 61743 Score: 79 Queries matched: 1
 type II keratin 5 [Mus musculus]
[gi|20911031](#) Mass: 61729 Score: 79 Queries matched: 1
 keratin, type II cytoskeletal 5 [Mus musculus]
[gi|29789317](#) Mass: 59704 Score: 79 Queries matched: 1
 keratin, type II cytoskeletal 75 [Mus musculus]
[gi|54607171](#) Mass: 59299 Score: 79 Queries matched: 1
 keratin, type II cytoskeletal 6A [Mus musculus]
[gi|59798479](#) Mass: 60285 Score: 79 Queries matched: 1
 RecName: Full=Keratin, type II cytoskeletal 6B; AltName: Full=Cytokeratin-6B; Short=CK-6B; AltName: Full=Keratin-6-beta; Short=mK6-bet
[gi|110645788](#) Mass: 60236 Score: 79 Queries matched: 1
 Krt6b protein [Mus musculus]
[gi|113195684](#) Mass: 59490 Score: 79 Queries matched: 1
 keratin, type II cytoskeletal 6B [Mus musculus]
[gi|116063325](#) Mass: 60154 Score: 79 Queries matched: 1
 Krt6b protein [Mus musculus]
[gi|148672084](#) Mass: 34775 Score: 79 Queries matched: 1
 mCG17577 [Mus musculus]
[gi|148672085](#) Mass: 38119 Score: 79 Queries matched: 1
 mCG144996 [Mus musculus]
[gi|148672089](#) Mass: 62241 Score: 79 Queries matched: 1
 keratin 75 [Mus musculus]

5. [gi|3093758](#) Mass: 23890 Score: 36 Queries matched: 1 emPAI: 0.13
 cyclic AMP specific phosphodiesterase PDE4D5A [Mus musculus]
 e Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide	
b	17	434.7656	867.5166	867.5178	-0.0011	0	36	0.0069	1	K.LSPVIS PR .N

Proteins matching the same set of peptides:

gi|148686495 Mass: 79441 Score: 36 Queries matched: 1
 phosphodiesterase 4D, cAMP specific, isoform CRA_c [Mus musculus]

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

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
b 11	421.7575	841.5005	841.4810	0.0195	0	30	0.06	1	LGTWLPR
b 9	421.7574	841.5003	841.4810	0.0193	0	28	0.1	1	LGTWLPR
b 8	421.7567	841.4988	841.4810	0.0177	0	25	0.19	1	LGTWLPR
b 10	421.7575	841.5004	841.4810	0.0194	0	25	0.21	1	LGTWLPR
b 42	611.3076	1220.6007	1220.6037	-0.0030	0	23	0.56	1	FEGAQSVVQEK
b 62	688.8440	1375.6734	1375.6700	0.0034	1	21	0.85	1	RMMEVAADVQR
b 118	737.7040	2210.0902	2210.0967	-0.0065	0	21	0.5	1	LGEHNINVLGNEQFIDAAK
b 119	737.7041	2210.0904	2210.0967	-0.0063	0	20	0.59	1	LGEHNINVLGNEQFIDAAK
b 63	696.8414	1391.6683	1391.6810	-0.0127	0	20	1.2	1	QGSLLIQVPSVER + Phospho (ST)
b 90	820.3950	1638.7755	1638.7745	0.0009	1	20	0.94	1	IQMEEFMAANPSK + Oxidation (M)
b 79	780.8968	1559.7790	1559.7654	0.0137	0	19	1.1	1	QWGLLCDLLEQDK
b 124	737.7048	2210.0925	2210.0967	-0.0042	0	19	0.81	1	LGEHNINVLGNEQFIDAAK
b 47	625.3053	1248.5960	1248.5825	0.0135	1	18	1.8	1	MSLSLKFKEK + Phospho (ST)
b 85	804.8985	1607.7824	1607.7825	-0.0001	1	18	1.6	1	QKQDQTQTISLTK
b 92	837.3882	1672.7618	1672.7693	-0.0075	0	18	1.8	1	DSEGDTPSLINWPSR
b 122	737.7043	2210.0912	2210.0967	-0.0055	0	18	1	1	LGEHNINVLGNEQFIDAAK
b 35	570.2702	1138.5259	1138.5189	0.0069	1	18	2.4	1	GMAEAERGFR + Oxidation (M)
b 31	536.3229	1070.6311	1070.6196	0.0115	1	18	0.78	1	DLQLRVTAR
b 15	428.7647	855.5148	855.5178	-0.0029	0	17	1.1	1	EAALIALR
b 57	669.8388	1337.6631	1337.6452	0.0179	1	16	2.7	1	RASQSIGGIPSR + Phospho (ST)
b 117	737.7030	2210.0872	2210.0967	-0.0095	0	16	1.6	1	LGEHNINVLGNEQFIDAAK
b 45	617.3082	1232.6018	1232.6183	-0.0165	0	15	3.3	1	LSGGAVPSASMTK
b 16	428.7670	855.5193	855.5112	0.0081	1	15	1.5	1	ALRMLPR
b 38	595.3264	1188.6383	1188.6462	-0.0080	1	15	2.2	1	ITDITSDRLR
b 12	421.7579	841.5013	841.5134	-0.0121	1	15	2	1	LGLRLDR
b 70	712.8628	1423.7110	1423.7072	0.0039	1	14	3.1	1	AENSSLNLIGKAK + Phospho (ST)
b 28	510.7709	1019.5273	1019.5182	0.0091	1	14	4.3	1	MRDLGVASR + Oxidation (M)
b 121	737.7043	2210.0912	2210.0967	-0.0055	0	14	2.5	1	LGEHNINVLGNEQFIDAAK
b 100	864.4420	1726.8694	1726.8638	0.0055	1	14	3.1	1	GLEWIGRIDPNDGGTK
b 95	857.4052	1712.7959	1712.8056	-0.0096	1	14	4.3	1	TSPLKILANADTMK + Oxidation (M); Phospho (ST)
b 123	737.7047	2210.0924	2210.0967	-0.0043	0	13	2.8	1	LGEHNINVLGNEQFIDAAK
b 67	710.8361	1419.6577	1419.6759	-0.0182	1	13	5.1	1	QDGLQLRDLSPV + Phospho (ST)
b 13	421.7586	841.5025	841.5021	0.0004	0	13	3	1	LSVALSPR
b 125	737.7051	2210.0934	2210.0967	-0.0033	0	13	2.9	1	LGEHNINVLGNEQFIDAAK
b 40	597.7979	1193.5813	1193.5863	-0.0050	0	13	6.6	1	MDASLGNLFAR
b 53	655.8552	1309.6958	1309.6812	0.0145	1	13	3.3	1	VGM DYRTSILR
b 48	631.8247	1261.6349	1261.6277	0.0072	1	13	5.7	1	LYGSFNFRMK
b 106	897.9082	1793.8019	1793.8059	-0.0041	1	12	5.6	1	EFLGTTQTASFCGPKK + Phospho (ST)
b 80	783.8719	1565.7292	1565.7169	0.0123	1	12	7.1	1	VSETSGGKTSGEDANK
b 73	752.8660	1503.7174	1503.7275	-0.0101	1	12	6.6	1	FFKEIWSAAR + Phospho (ST)
b 64	701.3595	1400.7044	1400.7139	-0.0095	0	11	7.1	1	MVFITVIEILR + Phospho (ST)
b 18	435.7731	869.5316	869.5123	0.0193	0	11	3.3	1	VSLWLPR
b 101	878.3738	1754.7330	1754.7334	-0.0004	1	11	7.5	1	SVTPPKVSLFEPK + 3 Phospho (ST)
b 59	673.8514	1345.6883	1345.6723	0.0160	0	11	6.5	1	FEELYPFLK + Phospho (Y)
b 136	567.0099	2264.0103	2264.0087	0.0016	1	11	7.5	1	ARALLASTAISTAVDNSGSGDK + 2 Phospho (ST)
b 99	864.4410	1726.8674	1726.8638	0.0035	1	11	6.8	1	GLEWIGRIDPNDGGTK
b 52	655.3216	1308.6286	1308.6098	0.0187	0	10	11	1	GNFIPYANEER
b 120	737.7041	2210.0906	2210.0967	-0.0061	0	9	8.2	1	LGEHNINVLGNEQFIDAAK
b 81	525.2239	1572.6499	1572.6529	-0.0030	1	9	11	1	SSENSSEGNALRR + Phospho (ST)
b 126	738.0335	2211.0785	2211.0920	-0.0135	0	9	8.7	1	LGEHNINVLGNEQFVNSAK
b 78	774.8640	1547.7135	1547.7137	-0.0002	0	8	16	1	QLEDAIEDCTNAVK
b 91	830.9283	1659.8421	1659.8250	0.0171	1	8	11	1	TSVHQETKSMLLDR + Oxidation (M)
b 89	820.3943	1638.7740	1638.7800	-0.0061	1	8	14	1	GQLASKSTILCSHK + Phospho (ST)
b 25	505.2683	1008.5220	1008.5136	0.0083	0	7	21	1	MVSGFIFMK
b 76	768.3708	1534.7269	1534.7207	0.0063	1	7	20	1	ACRPSWLCLCEVR
b 103	887.9500	1773.8854	1773.8662	0.0192	1	7	16	1	LIDTSHLSSEVTKK + Phospho (ST)
b 29	512.2384	1022.4623	1022.4798	-0.0174	0	7	19	1	TAPLSTTPR + Phospho (ST)
b 132	742.7034	2225.0885	2225.0970	-0.0085	1	7	12	1	SVIQRQSGALGPIISVTPSGR + 2 Phospho (ST)
b 23	459.2761	916.5377	916.5229	0.0148	0	7	12	1	LNTSELIK
b 69	711.3399	1420.6653	1420.6516	0.0136	1	7	22	1	GLSNRNLIIY + Phospho (ST); Phospho (Y)
b 83	790.8885	1579.7625	1579.7503	0.0122	1	6	29	1	TKYLQILTSMR + Oxidation (M); Phospho (ST)
b 114	732.0281	2193.0626	2193.0541	0.0085	1	5	21	1	TEVHKVVNSFLCLVPDDAK + Phospho (ST)
b 113	729.0346	2184.0819	2184.0690	0.0129	0	5	18	1	MTGLESLSWSEVLQLPFR + Phospho (ST)
b 75	760.8651	1519.7157	1519.7163	-0.0005	1	5	36	1	LKSVDTAMYCAR
b 110	665.6211	1993.8414	1993.8564	-0.0150	0	5	30	1	GDIVLTQSPATLSVTPR + 3 Phospho (ST)
b 19	435.7740	869.5335	869.5487	-0.0152	0	4	16	1	LWVALLR
b 105	594.2753	1779.8041	1779.7957	0.0084	1	4	40	1	TSFQDELIRAITAR + 2 Phospho (ST)
b 139	762.0572	2283.1499	2283.1442	0.0057	1	4	21	1	QTSKSKQVNIIVSTLLSTSDS

b	93	559.9062	1676.6966	1676.6882	0.0085	0	3	43	1	QGLSTMP E IEA S V R + 2 Phospho (ST)
b	109	970.9696	1939.9246	1939.9054	0.0192	1	3	38	1	IQGLTGNVQFDHYGRR + Phospho (ST)
b	149	767.7172	2300.1298	2300.1156	0.0143	1	3	26	1	ECYPKAMHCIFVGAQSLFLK + Oxidation (M)
b	129	742.3740	2224.1001	2224.0889	0.0112	1	3	30	1	LQGVLEGLTNSKTYDTLHR + Phospho (ST)
b	128	742.0317	2223.0734	2223.0784	-0.0050	1	3	37	1	SLDTLQNVSVQLEGLERDK + Phospho (ST)
b	102	882.8930	1763.7713	1763.7892	-0.0179	1	3	56	1	NMSYMEKGTMTGAALK + 2 Oxidation (M)
b	133	746.3762	2236.1068	2236.0979	0.0088	0	3	39	1	LVGLLMLAVVNSITLDIR + Oxidation (M); 2 Phospho (ST)
b	94	559.9082	1676.7028	1676.6938	0.0090	0	3	54	1	IAMALSDLV I Y T K + 2 Phospho (ST); Phospho (Y)
b	104	890.8900	1779.7654	1779.7515	0.0139	1	2	59	1	RIPSV E EMS Q T S LK + Oxidation (M); 2 Phospho (ST)
b	6	412.7524	823.4903	823.4916	-0.0013	0	2	17	1	AVLSHGLK
b	142	762.7132	2285.1177	2285.1362	-0.0185	0	2	34	1	SATLMVVEDVVQIVSGFQGAR + Oxidation (M)
b	134	747.0466	2238.1179	2238.1158	0.0021	0	2	30	1	DTHSLPPAQILGIQSGQGIAR + Phospho (ST)
b	77	769.3227	1536.6309	1536.6110	0.0199	0	2	72	1	I S TGGGETGETLQK + 2 Phospho (ST)
b	144	766.7296	2297.1669	2297.1533	0.0136	1	2	26	1	LCMPGLT V LRLCMPGLT V LRL + 2 Oxidation (M); Phospho (ST)
b	55	664.8316	1327.6487	1327.6537	-0.0050	1	1	68	1	RTATY L PEVAK + Phospho (Y)
b	72	492.2074	1473.6005	1473.6171	-0.0166	0	1	71	1	SQEATEG T MATLR + Phospho (ST)
b	143	574.2677	2293.0419	2293.0304	0.0115	0	0	71	1	LEWVATISGGGNTYYFDSVK + Phospho (ST)
b	145	767.3891	2299.1454	2299.1501	-0.0047	1	0	42	1	AKFDGIFESLLFPVNGLLSGDK + Phospho (ST)
b	7	412.7531	823.4917	823.4916	0.0001	0	0	24	1	TVAPALPR
b	112	1042.0058	2081.9970	2081.9857	0.0114	0	0	67	1	DV T LHVSASN P AMLLYQK + Oxidation (M); Phospho (ST)
b	141	762.3864	2284.1375	2284.1279	0.0096	1	0	41	1	YGRHPLMELPLMINPTGCAR + Oxidation (M)
b	147	767.7166	2300.1279	2300.1354	-0.0076	1	0	49	1	QPSGKGL E WLLHILW N DSK + Phospho (ST)
b	56	668.8388	1335.6631	1335.6670	-0.0039	0	0	1e+002	1	IENLEEYTG L R
b	127	738.0386	2211.0940	2211.1101	-0.0162	1	0	63	1	SAPEIKYNSMVLICALMGSGK
b	1	362.2217	722.4287							
b	2	384.2344	766.4542							
b	5	406.2475	810.4804							
b	14	428.2606	854.5067							
b	20	450.2733	898.5321							
b	58	448.2180	1341.6323							
b	61	459.5363	1375.5870							
b	71	488.2188	1461.6346							
b	107	904.9407	1807.8668							
b	115	737.3604	2209.0593							
b	116	737.3670	2209.0793							
b	130	742.3742	2224.1007							
b	131	742.3753	2224.1040							
b	135	563.0173	2248.0400							
b	137	567.5066	2265.9974							
b	138	758.3397	2271.9973							
b	140	762.3857	2284.1353							
b	146	767.3894	2299.1463							
b	148	767.7168	2300.1287							
b	150	772.0613	2313.1620							

Search Parameters

Type of search : MS/MS Ion Search
 Enzyme : Trypsin/P
 Variable modifications : Oxidation (M),Phospho (ST),Phospho (Y)
 Mass values : Monoisotopic
 Protein Mass : Unrestricted
 Peptide Mass Tolerance : ± 0.02 Da
 Fragment Mass Tolerance : ± 0.3 Da
 Max Missed Cleavages : 1
 Instrument type : ESI-TRAP
 Number of queries : 151

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

MASCOT Mascot Search Results

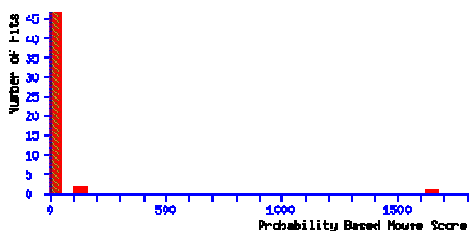
User : Bob
 Email : rdenglis@utmb.edu
 Search title : 11081915.raw #2289 acetylation
 MS data file : tempfile
 Database : NCBI nr 20110707 (14481393 sequences; 4958963357 residues)
 Taxonomy : Mus musculus (house mouse) (143921 sequences)
 Timestamp : 24 Aug 2011 at 16:25:11 GMT
 Protein hits : [gi|124248512](#) carbamoyl-phosphate synthase [ammonia], mitochondrial precursor [Mus musculus]
[gi|7638398](#) epidermal keratin 10 [Mus musculus]
[gi|12843914](#) unnamed protein product [Mus musculus]
[gi|9910294](#) keratin, type II cytoskeletal 71 [Mus musculus]
[gi|51092303](#) Try10-like trypsinogen [Mus musculus]

NCBI nr [Decoy](#) False discovery rate

Peptide matches above identity threshold 32 1 3.13 %
 Peptide matches above homology or identity threshold 38 1 2.63 %

Probability Based Mowse Score

Ions score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event. Individual ions scores > 32 indicate identity or extensive homology (p<0.05). Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Peptide Summary Report

Format As [Help](#)

Significance threshold p< Max. number of hits

Standard scoring MudPIT scoring Ions score or expect cut-off Show sub-sets

Show pop-ups Suppress pop-ups Sort unassigned Require bold red

Error tolerant

1. [gi|124248512](#) Mass: 164514 Score: 1647 Queries matched: 32 emPAI: 0.69
 carbamoyl-phosphate synthase [ammonia], mitochondrial precursor [Mus musculus]
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Score	Expect	Rank	Peptide
b 3	406.2209	810.4273	810.4276	-0.0003	0	18	2.1	1	R.SFPFVSK.T
b 4	406.2210	810.4274	810.4276	-0.0002	0	(18)	2.5	1	R.SFPFVSK.T
b 20	453.2577	904.5008	904.5018	-0.0010	0	51	0.00089	1	K.LFAEAVQK.S
b 22	495.2792	988.5438	988.5441	-0.0003	0	64	0.00018	1	K.ETLIDLGTK.A
b 24	508.2386	1014.4626	1014.4658	-0.0032	0	34	0.029	1	R.TFEESFQK.A
b 25	508.8025	1015.5904	1015.5914	-0.0010	0	36	0.019	1	K.GTTITSVLPK.P
b 28	518.7687	1035.5228	1035.5237	-0.0008	0	42	0.0094	1	K.EIEYEVVR.D
b 29	545.7978	1089.5810	1089.5819	-0.0009	0	52	0.0011	1	K.VPAIYGVDT.R.M
b 30	551.8083	1101.6020	1101.6030	-0.0009	0	63	7.7e-005	1	K.QNLIAEVSTK.D
b 33	568.7786	1135.5427	1135.5431	-0.0004	0	68	2.3e-005	1	K.VMIGESIDEK.R + Oxidation (M)
b 35	582.3728	1162.7311	1162.7325	-0.0014	0	46	0.00012	1	K.IALGIPLPEIK.N
b 39	609.3110	1216.6075	1216.6088	-0.0013	0	56	0.00034	1	K.SLGLWQEEK.V
b 40	611.3398	1220.6651	1220.6652	-0.0001	0	64	3.5e-005	1	R.SIFSVALDELK.V
b 41	611.8448	1221.6750	1221.6757	-0.0007	0	43	0.0039	1	K.ATGYPLAFIAK.I
b 43	623.8305	1245.6463	1245.6387	0.0076	0	55	0.00058	1	K.IMGTSPLQIDR.A + Oxidation (M)
b 45	639.8505	1277.6864	1277.6867	-0.0003	0	55	0.0003	1	K.TLGVDFIDVATK.V
b 46	649.8343	1297.6540	1297.6554	-0.0013	0	57	0.00021	1	K.LYFEELSLEK.I
b 50	661.8425	1321.6705	1321.6700	0.0005	0	56	0.00031	1	K.AADTIGYVPMIR.S + Oxidation (M)
b 52	677.3653	1352.7161	1352.7160	0.0001	0	68	1.7e-005	1	R.GQNQPVLTNTR.Q
b 57	704.8639	1407.7132	1407.7180	-0.0049	0	(50)	0.0011	1	K.AFAMTNQILVER.S + Oxidation (M)
b 58	704.8662	1407.7178	1407.7180	-0.0003	0	65	3.2e-005	1	K.AFAMTNQILVER.S + Oxidation (M)
b 60	710.8537	1419.6928	1419.6841	0.0087	0	85	3.6e-007	1	K.GLNDSVTEETLR.K
b 65	760.3782	1518.7418	1518.7348	0.0071	0	72	7e-006	1	K.ALENNMSLDEIVR.L + Oxidation (M)
b 71	526.6100	1576.8082	1576.8096	-0.0014	1	30	0.094	1	R.QLFSDKLINEK.I
b 73	530.2751	1587.8035	1587.8045	-0.0010	0	12	5.9	1	R.FLGVAEQLHNEGFK.L
b 76	812.3998	1622.7850	1622.7861	-0.0012	0	74	3.5e-006	1	K.IAPFAVESMEDALK.A + Oxidation (M)

[gi|47059013](#) Mass: 58875 Score: 71 Queries matched: 1
 keratin, type II cytoskeletal 73 [Mus musculus]
[gi|51092293](#) Mass: 61322 Score: 71 Queries matched: 1
 keratin, type II cytoskeletal 1b [Mus musculus]
[gi|81891697](#) Mass: 54712 Score: 71 Queries matched: 1
 RecName: Full=Keratin, type II cytoskeletal 74; AltName: Full=Keratin-74; Short=K74; AltName: Full=Type-II keratin Kb37
[gi|115528975](#) Mass: 61265 Score: 71 Queries matched: 1
 Keratin 77 [Mus musculus]
[gi|126116585](#) Mass: 65565 Score: 71 Queries matched: 1
 keratin, type II cytoskeletal 1 [Mus musculus]
[gi|148672081](#) Mass: 43429 Score: 71 Queries matched: 1
 mCG17589, isoform CRA_b [Mus musculus]

5. [gi|51092303](#) Mass: 26514 Score: 66 Queries matched: 2 emPAI: 0.25

Try10-like trypsinogen [Mus musculus]

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

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
b 36	588.3192	1174.6239	1174.6267	-0.0028	0	66	3.3e-005	1	K.TLNDI MLIK .L
b 38	596.3189	1190.6233	1190.6217	0.0017	0	(50)	0.0017	1	K.TLNDI MLIK .L + Oxidation (M)

Proteins matching the same set of peptides:

[gi|84781771](#) Mass: 26204 Score: 66 Queries matched: 2
 trypsin 10 [Mus musculus]

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

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
b 8	421.7573	841.5001	841.4810	0.0191	0	30	0.17	1	LGTW LPR
b 13	421.7582	841.5019	841.5022	-0.0002	1	27	0.29	1	V KT TV PR + Acetyl (K)
b 34	570.2713	1138.5279	1138.5189	0.0090	1	26	0.22	1	CAT F ERE QR
b 14	421.7588	841.5031	841.5021	0.0010	1	26	0.36	1	V KT SL PR + Acetyl (K)
b 9	421.7576	841.5007	841.4810	0.0197	0	25	0.48	1	LGTW LPR
b 110	737.7051	2210.0934	2210.0967	-0.0033	0	25	0.17	1	LGEHNIN V LEGNE Q FID AAK
b 70	783.8732	1565.7318	1565.7184	0.0134	1	24	0.29	1	E K DF Q GM L EY HK + Acetyl (K)
b 11	421.7581	841.5015	841.5021	-0.0006	1	23	0.73	1	V KT SL PR + Acetyl (K)
b 15	428.7641	855.5137	855.5112	0.0024	1	23	0.6	1	AL R ML PR
b 12	421.7581	841.5015	841.5021	-0.0006	1	23	0.8	1	V KT SL PR + Acetyl (K)
b 109	737.7026	2210.0860	2210.0967	-0.0107	0	22	0.33	1	LGEHNIN V LEGNE Q FID AAK
b 51	673.8523	1345.6901	1345.7089	-0.0188	1	22	0.82	1	G S L D Q S L K D L T LK + Acetyl (K)
b 74	804.8999	1607.7852	1607.7825	0.0027	1	22	0.66	1	Q K C Q E T Q T I S S LK
b 17	434.7661	867.5177	867.5178	-0.0001	0	21	0.35	1	L S P V I S P R
b 10	421.7579	841.5013	841.5021	-0.0008	1	21	1.2	1	V KT SL PR + Acetyl (K)
b 113	737.7058	2210.0956	2210.0967	-0.0011	0	21	0.4	1	LGEHNIN V LEGNE Q FID AAK
b 80	820.3974	1638.7803	1638.7745	0.0057	1	21	0.62	1	I Q M E E K F M A N P S K + Oxidation (M)
b 111	737.7055	2210.0946	2210.0967	-0.0021	0	19	0.68	1	LGEHNIN V LEGNE Q FID AAK
b 115	737.7060	2210.0961	2210.0967	-0.0006	0	19	0.68	1	LGEHNIN V LEGNE Q FID AAK
b 16	428.7683	855.5220	855.5112	0.0107	1	18	1.7	1	AL R ML PR
b 42	617.3086	1232.6026	1232.6136	-0.0110	1	18	2.3	1	E E L D T L K E E K
b 69	780.8978	1559.7811	1559.7977	-0.0166	1	17	2.1	1	E A T A I N M K N E A L Q K
b 114	737.7059	2210.0960	2210.0967	-0.0007	0	17	1	1	LGEHNIN V LEGNE Q FID AAK
b 67	769.3233	1536.6321	1536.6258	0.0062	1	16	0.34	1	M V S S G M Y K M D N G K + Acetyl (Protein N-term); 3 Oxidation (M)
b 48	655.3226	1308.6307	1308.6271	0.0036	0	15	3.1	1	M E L G E L L Y N K + Acetyl (K); Acetyl (Protein N-term); Oxidation (1)
b 19	435.7742	869.5338	869.5222	0.0116	1	15	2.5	1	V E A V K I K + 2 Acetyl (K)
b 59	710.8391	1419.6637	1419.6816	-0.0180	0	15	3.1	1	L W E I G N M L D T G R + Oxidation (M)
b 37	595.3283	1188.6421	1188.6462	-0.0042	1	14	4.8	1	I T D T I S D R L R
b 112	737.7058	2210.0955	2210.0967	-0.0012	0	14	2.1	1	LGEHNIN V LEGNE Q FID AAK
b 81	830.9298	1659.8450	1659.8250	0.0200	1	14	3.8	1	T S V H Q E T K S M L L D R + Oxidation (M)
b 26	510.7716	1019.5287	1019.5321	-0.0034	1	13	7.9	1	V A K M T V S G K + 2 Acetyl (K); Oxidation (M)
b 49	655.8563	1309.6980	1309.6878	0.0102	1	13	4.2	1	K G S A L D P E P Q V K + Acetyl (K)
b 27	516.3026	1030.5907	1030.5733	0.0174	0	13	5	1	V M L I T D G K + Acetyl (K)
b 91	882.8944	1763.7743	1763.7616	0.0128	1	10	3	1	M Q M P P S N P M C K T R + Acetyl (K); Oxidation (M)
b 44	631.8233	1261.6321	1261.6277	0.0043	1	10	16	1	L Y S F N F R M K
b 18	435.7732	869.5318	869.5123	0.0195	0	10	10	1	V S L W L P R
b 62	712.8635	1423.7125	1423.6943	0.0182	0	10	11	1	I A E S L G S G S G S V E R
b 89	864.4429	1726.8712	1726.8638	0.0073	1	9	12	1	G L E W I G R I D P N D G G T K
b 55	696.8424	1391.6703	1391.6767	-0.0064	1	9	15	1	T Q R S Q H S Q H A R
b 32	564.2780	1126.5414	1126.5216	0.0198	0	9	12	1	I E T M D S V Y K + Acetyl (K)
b 23	505.2692	1008.5238	1008.5170	0.0068	0	9	18	1	M V G T V I M M K
b 119	738.0396	2211.0971	2211.1101	-0.0131	1	9	6.5	1	S A P E I K Y N S M V L I C A L M G S G K
b 116	737.7078	2210.1017	2210.0967	0.0050	0	8	7.2	1	LGEHNIN V LEGNE Q FID AAK
b 75	811.9078	1621.8010	1621.8208	-0.0198	0	8	13	1	G V Y L T D I M P Q G V A M K
b 61	711.3410	1420.6674	1420.6722	-0.0048	1	8	16	1	S K D D S P S Y L P T K + 2 Acetyl (K)
b 101	1006.4891	2010.9636	2010.9834	-0.0198	1	8	11	1	M Y T L L S G L Y K Y M F Q K + 2 Acetyl (K); Acetyl (Protein N-term)
b 90	864.4432	1726.8718	1726.8638	0.0080	1	7	19	1	G L E W I G R I D P N D G G T K
b 56	701.3608	1400.7071	1400.7035	0.0036	0	7	24	1	E V D L V E S G D L V K + Acetyl (Protein N-term)
b 6	412.7521	823.4896	823.4916	-0.0020	0	6	11	1	G I P V S P V R

b	7	412.7530	823.4915	823.4916	-0.0001	0	6	11	1	GIPVSPVR
b	98	970.9708	1939.9270	1939.9172	0.0098	0	6	15	1	MDQVMQFVPEPSQQFVK
b	66	760.8655	1519.7165	1519.7341	-0.0176	1	6	22	1	GGSAVGLKGYMAPAPS + Acetyl (K); Oxidation (M)
b	79	820.3954	1638.7762	1638.7606	0.0156	1	6	20	1	PLCGSDGRTYAQICR
b	82	837.3885	1672.7625	1672.7540	0.0086	0	5	16	1	QAEEAEQSNANLAK + Acetyl (K)
b	64	752.8670	1503.7194	1503.7317	-0.0123	1	5	33	1	DGIQTKEHPNPGK + 2 Acetyl (K)
b	133	762.0587	2283.1544	2283.1482	0.0062	0	5	15	1	ESSSLVQYDLIGQTVSSETIK
b	106	732.0312	2193.0718	2193.0711	0.0007	0	5	16	1	EMPVQFQVVELPSGHHLCK + Oxidation (M)
b	72	790.8900	1579.7654	1579.7776	-0.0122	1	5	38	1	SFSVALQKQNNMR + Acetyl (K); Oxidation (M)
b	118	738.0351	2211.0834	2211.0742	0.0092	1	5	18	1	VESGFHIHQGELSLRAMDK + Acetyl (K); Oxidation (M)
b	97	970.9697	1939.9249	1939.9230	0.0019	1	4	22	1	LMEMEQTLSSLRETEK + Oxidation (M)
b	117	738.0335	2211.0788	2211.0920	-0.0132	0	4	20	1	LGEHNINVLEGNQFVNSAK
b	136	762.7150	2285.1232	2285.1362	-0.0130	0	4	20	1	SATLMLVYEDVVQIVSGFQGAR + Oxidation (M)
b	95	897.9098	1793.8050	1793.8063	-0.0013	0	4	21	1	MQEGDLEMTLALEEK + Acetyl (K); Oxidation (M)
b	85	857.4066	1712.7985	1712.8006	-0.0020	1	3	27	1	INPSSGDTNYNEKFK
b	108	737.3612	2209.0618	2209.0573	0.0046	0	3	26	1	GTEEVFQALEDNQVALSTMK
b	92	887.9549	1773.8952	1773.8819	0.0134	1	3	48	1	KGDLLDAINSCTVVDK + 2 Acetyl (K)
b	78	545.9461	1634.8165	1634.8165	-0.0000	1	2	57	1	WPQDASHLLQKDR + Acetyl (K)
b	104	1042.0073	2082.0000	2081.9939	0.0061	1	2	36	1	LSSSPGKTMPTTQSFASDPK + Oxidation (M)
b	68	774.8655	1547.7165	1547.7063	0.0102	1	2	47	1	GEEELGKSSDLEDNR
b	135	762.3869	2284.1390	2284.1207	0.0183	1	2	33	1	ECYPKAMHCIFVGAQSLFLK
b	125	742.7056	2225.0948	2225.0773	0.0175	1	2	36	1	FGLDKLLSSEGSSEMEDIDLK + Acetyl (K)
b	138	767.3857	2299.1352	2299.1513	-0.0162	0	2	41	1	NMQMMSIEILLTLLFTELAKE + Acetyl (K); 2 Oxidation (M)
b	93	890.8915	1779.7684	1779.7655	0.0029	0	2	17	1	DDDIAALVVDNGSGMCK + Acetyl (Protein N-term); Oxidation (M)
b	139	767.3909	2299.1507	2299.1671	-0.0164	1	1	36	1	AHGVDKVVACTSAFLLDWPTK + Acetyl (K)
b	105	729.0345	2184.0816	2184.0741	0.0075	1	0	47	1	ACIESRVNMVTASYITPAMK
b	128	747.0480	2238.1221	2238.1236	-0.0015	1	0	47	1	SVVMGTDKDTVTTGLFGAMNVAKE + Acetyl (K); Oxidation (M)
b	1	362.2218	722.4291							
b	2	384.2350	766.4554							
b	5	406.2480	810.4814							
b	21	453.8080	905.6015							
b	31	559.7704	1117.5261							
b	53	453.8080	1358.4022							
b	83	559.9075	1676.7007							
b	84	559.9087	1676.7042							
b	94	594.2765	1779.8076							
b	96	904.9415	1807.8684							
b	99	997.4829	1992.9513							
b	100	665.6223	1993.8452							
b	103	1033.0008	2063.9870							
b	107	1104.0569	2206.0992							
b	120	742.0332	2223.0779							
b	121	742.3754	2224.1043							
b	122	742.3763	2224.1069							
b	123	742.3764	2224.1073							
b	124	742.7046	2225.0919							
b	126	746.3780	2236.1122							
b	127	747.0081	2238.0026							
b	129	563.0185	2248.0448							
b	130	567.0127	2264.0218							
b	131	567.2566	2264.9972							
b	132	570.5136	2278.0254							
b	134	762.3868	2284.1387							
b	137	766.7309	2297.1707							
b	140	767.7181	2300.1324							
b	141	772.0623	2313.1651							
b	142	580.4893	2317.9283							

Search Parameters

Type of search : MS/MS Ion Search
 Enzyme : Trypsin/P
 Variable modifications : Acetyl (K),Acetyl (Protein N-term),Oxidation (M)
 Mass values : Monoisotopic
 Protein Mass : Unrestricted
 Peptide Mass Tolerance : ± 0.02 Da
 Fragment Mass Tolerance: ± 0.3 Da
 Max Missed Cleavages : 1
 Instrument type : ESI-TRAP
 Number of queries : 143

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

MASCOT Mascot Search Results

User : Bob
 Email : rdenglis@utmb.edu
 Search title : 11081915.raw #2289 phospho
 MS data file : tempfile
 Database : NCBI nr 20110707 (14481393 sequences; 4958963357 residues)
 Taxonomy : Mus musculus (house mouse) (143921 sequences)
 Timestamp : 24 Aug 2011 at 16:23:23 GMT
 Protein hits : [gi|124248512](#) carbamoyl-phosphate synthase [ammonia], mitochondrial precursor [Mus musculus]
[gi|7638398](#) epidermal keratin 10 [Mus musculus]
[gi|12843914](#) unnamed protein product [Mus musculus]
[gi|9910294](#) keratin, type II cytoskeletal 71 [Mus musculus]
[gi|51092303](#) Try10-like trypsinogen [Mus musculus]

NCBI nr [Decoy](#) False discovery rate

Peptide matches above identity threshold 32 3 9.38 %
 Peptide matches above homology or identity threshold 37 3 8.11 %

Probability Based Mowse Score

Ions score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event. Individual ions scores > 31 indicate identity or extensive homology (p<0.05). Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.

Error: try setting browser cache to automatic.

Peptide Summary Report

Format As [Help](#)
 Significance threshold p< Max. number of hits
 Standard scoring MudPIT scoring Ions score or expect cut-off Show sub-sets
 Show pop-ups Suppress pop-ups Sort unassigned Require bold red
 Error tolerant

1. [gi|124248512](#) Mass: 164514 Score: 1653 Queries matched: 32 emPAI: 0.69
 carbamoyl-phosphate synthase [ammonia], mitochondrial precursor [Mus musculus]
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
b 3	406.2209	810.4273	810.4276	-0.0003	0	18	1.5	1	R.SFPFVSK.T
b 4	406.2210	810.4274	810.4276	-0.0002	0	(18)	1.9	1	R.SFPFVSK.T
b 20	453.2577	904.5008	904.5018	-0.0010	0	51	0.00056	1	K.LFAEAVQK.S
b 22	495.2792	988.5438	988.5441	-0.0003	0	64	0.00015	1	K.ETLIDLGTK.A
b 24	508.2386	1014.4626	1014.4658	-0.0032	0	34	0.049	1	R.TFEESFQK.A
b 25	508.8025	1015.5904	1015.5914	-0.0010	0	36	0.012	1	K.GTTITSVLPK.P
b 28	518.7687	1035.5228	1035.5237	-0.0008	0	42	0.0063	1	K.EIEYEVVR.D
b 29	545.7978	1089.5810	1089.5819	-0.0009	0	52	0.00061	1	K.VPAIYGVDTK.M
b 30	551.8083	1101.6020	1101.6030	-0.0009	0	63	4.3e-005	1	K.QNLIAEVSTK.D
b 33	568.7786	1135.5427	1135.5431	-0.0004	0	68	2.1e-005	1	K.VMIGESIDEK.R + Oxidation (M)
b 35	582.3728	1162.7311	1162.7325	-0.0014	0	46	9.8e-005	1	K.IALGIPLPEIK.N
b 39	609.3110	1216.6075	1216.6088	-0.0013	0	56	0.00025	1	K.SLGQWLQEEK.V
b 40	611.3398	1220.6651	1220.6652	-0.0001	0	64	2.1e-005	1	R.SIFSVAVLDELK.V
b 41	611.8448	1221.6750	1221.6757	-0.0007	0	43	0.0029	1	K.ATGYPLAFIAK.I
b 43	623.8305	1245.6463	1245.6387	0.0076	0	55	0.00033	1	K.IMGTSPLQIDR.A + Oxidation (M)
b 45	639.8505	1277.6864	1277.6867	-0.0003	0	55	0.00018	1	K.TLGVDFIDVATK.V
b 46	649.8343	1297.6540	1297.6554	-0.0013	0	57	0.00018	1	K.LYFEELSLEK.I
b 50	661.8425	1321.6705	1321.6700	0.0005	0	56	0.00025	1	K.AADTIGYVPMIR.S + Oxidation (M)
b 52	677.3653	1352.7161	1352.7160	0.0001	0	68	1.2e-005	1	R.GQNQPVNLITNR.Q
b 57	704.8639	1407.7132	1407.7180	-0.0049	0	(50)	0.00098	1	K.AFAMTNQILVER.S + Oxidation (M)
b 58	704.8662	1407.7178	1407.7180	-0.0003	0	65	3e-005	1	K.AFAMTNQILVER.S + Oxidation (M)
b 60	710.8537	1419.6928	1419.6841	0.0087	0	85	3.3e-007	1	K.GLNSDSVTEETLR.K
b 65	760.3782	1518.7418	1518.7348	0.0071	0	72	6.2e-006	1	K.ALENNMSLDEIVR.L + Oxidation (M)
b 71	526.6100	1576.8082	1576.8096	-0.0014	1	30	0.073	1	R.QLFSDKLNEINEK.I
b 73	530.2751	1587.8035	1587.8045	-0.0010	0	12	6.6	1	R.FLGVAEQLHNEGFK.L
b 76	812.3998	1622.7850	1622.7861	-0.0012	0	74	3.7e-006	1	K.IAPSAVESMEDALK.A + Oxidation (M)

[gi|47059013](#) Mass: 58875 Score: 71 Queries matched: 1
 keratin, type II cytoskeletal 73 [Mus musculus]
[gi|51092293](#) Mass: 61322 Score: 71 Queries matched: 1
 keratin, type II cytoskeletal 1b [Mus musculus]
[gi|81891697](#) Mass: 54712 Score: 71 Queries matched: 1
 RecName: Full=Keratin, type II cytoskeletal 74; AltName: Full=Keratin-74; Short=K74; AltName: Full=Type-II keratin Kb37
[gi|115528975](#) Mass: 61265 Score: 71 Queries matched: 1
 Keratin 77 [Mus musculus]
[gi|126116585](#) Mass: 65565 Score: 71 Queries matched: 1
 keratin, type II cytoskeletal 1 [Mus musculus]
[gi|148672081](#) Mass: 43429 Score: 71 Queries matched: 1
 mCG17589, isoform CRA_b [Mus musculus]

5. [gi|51092303](#) Mass: 26514 Score: 66 Queries matched: 2 emPAI: 0.25
 Try10-like trypsinogen [Mus musculus]
 e Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
b 36	588.3192	1174.6239	1174.6267	-0.0028	0	66	2e-005	1	K.TLDNDIMLIK.L
b 38	596.3189	1190.6233	1190.6217	0.0017	0	(50)	0.0011	1	K.TLDNDIMLIK.L + Oxidation (M)

Proteins matching the same set of peptides:

[gi|84781771](#) Mass: 26204 Score: 66 Queries matched: 2
 trypsin 10 [Mus musculus]

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

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
b 8	421.7573	841.5001	841.4810	0.0191	0	30	0.069	1	LGTWLR
b 34	570.2713	1138.5279	1138.5189	0.0090	1	26	0.29	1	CATFEREQR
b 9	421.7576	841.5007	841.4810	0.0197	0	25	0.19	1	LGTWLR
b 110	737.7051	2210.0934	2210.0967	-0.0033	0	25	0.2	1	LGEHNINLVLEGNEQFIDAAK
b 15	428.7641	855.5137	855.5112	0.0024	1	23	0.29	1	ALRMLPR
b 109	737.7026	2210.0860	2210.0967	-0.0107	0	22	0.37	1	LGEHNINLVLEGNEQFIDAAK
b 74	804.8999	1607.7852	1607.7825	0.0027	1	22	0.64	1	QKQDETQTISLK
b 17	434.7661	867.5177	867.5178	-0.0001	0	21	0.18	1	LSPVISPR
b 113	737.7058	2210.0956	2210.0967	-0.0011	0	21	0.49	1	LGEHNINLVLEGNEQFIDAAK
b 80	820.3974	1638.7803	1638.7745	0.0057	1	21	0.74	1	IQMEKFMANPSK + Oxidation (M)
b 12	421.7581	841.5015	841.5021	-0.0006	1	19	0.81	1	LKESLPR
b 111	737.7055	2210.0946	2210.0967	-0.0021	0	19	0.79	1	LGEHNINLVLEGNEQFIDAAK
b 115	737.7060	2210.0961	2210.0967	-0.0006	0	19	0.83	1	LGEHNINLVLEGNEQFIDAAK
b 11	421.7581	841.5015	841.5134	-0.0118	1	18	0.93	1	VIRALDR
b 16	428.7683	855.5220	855.5112	0.0107	1	18	0.74	1	ALRMLPR
b 42	617.3086	1232.6026	1232.6136	-0.0110	1	18	1.8	1	EELDTLKEEK
b 69	780.8978	1559.7811	1559.7977	-0.0166	1	17	1.6	1	EATAINMKNEALQK
b 14	421.7588	841.5031	841.5021	0.0010	1	17	1.2	1	LKESLPR
b 114	737.7059	2210.0960	2210.0967	-0.0007	0	17	1.3	1	LGEHNINLVLEGNEQFIDAAK
b 10	421.7579	841.5013	841.5021	-0.0008	0	15	1.8	1	LSVALSPR
b 55	696.8424	1391.6703	1391.6810	-0.0107	0	15	3.4	1	QGSLLIQVPSVER + Phospho (ST)
b 59	710.8391	1419.6637	1419.6816	-0.0180	0	15	3.6	1	LWEIGNMLDTGR + Oxidation (M)
b 37	595.3283	1188.6421	1188.6462	-0.0042	1	14	2.9	1	ITDTISDRLR
b 13	421.7582	841.5019	841.5021	-0.0002	0	14	2.4	1	LSVALSPR
b 112	737.7058	2210.0955	2210.0967	-0.0012	0	14	2.5	1	LGEHNINLVLEGNEQFIDAAK
b 51	673.8523	1345.6901	1345.6725	0.0176	0	14	3.5	1	SASQNETIEDLIK
b 56	701.3608	1400.7071	1400.7139	-0.0067	0	14	4.2	1	MVFITVIEQLR + Phospho (ST)
b 81	830.9298	1659.8450	1659.8250	0.0200	1	14	3.1	1	TSVHQETKSMLLDR + Oxidation (M)
b 62	712.8635	1423.7125	1423.7072	0.0053	1	13	4.5	1	AENSSLNLIGKAK + Phospho (ST)
b 44	631.8233	1261.6321	1261.6180	0.0141	1	12	6.1	1	AVSGLHSLKDR + Phospho (ST)
b 85	857.4066	1712.7985	1712.8056	-0.0070	1	11	7.8	1	TSDDLKILANADTMK + Oxidation (M); Phospho (ST)
b 105	729.0345	2184.0816	2184.0690	0.0126	0	11	4.6	1	MTGLESLVVGEVLQLPFR + Phospho (ST)
b 26	510.7716	1019.5287	1019.5334	-0.0047	1	11	9	1	MSLRTWAR
b 70	783.8732	1565.7318	1565.7243	0.0076	1	10	11	1	ETSELKEAMEQQK + Oxidation (M)
b 124	742.7046	2225.0919	2225.1068	-0.0149	1	10	6.4	1	SGKIQPYVMSNLPVTLWGR + Phospho (Y)
b 18	435.7732	869.5318	869.5123	0.0195	0	10	4.7	1	VSLWLR
b 82	837.3885	1672.7625	1672.7644	-0.0018	1	10	12	1	KSLFSQQSNPCNLK + Phospho (ST)
b 49	655.8563	1309.6980	1309.7159	-0.0179	1	10	6.8	1	KTLLQYVPIR + Phospho (Y)
b 89	864.4429	1726.8712	1726.8638	0.0073	1	9	8.9	1	GLEWIGRIDPDGGTK
b 32	564.2780	1126.5414	1126.5457	-0.0044	0	9	13	1	LVSCVQLASK + Phospho (ST)
b 23	505.2692	1008.5238	1008.5170	0.0068	0	9	15	1	MVGTVIMMK
b 92	887.9549	1773.8952	1773.8848	0.0104	1	9	9.7	1	TVKLPQDHATIVCAAK + Phospho (ST)
b 119	738.0396	2211.0971	2211.1101	-0.0131	1	9	8.7	1	SAPEIKYNSMVLICALMGSGK
b 27	516.3026	1030.5907	1030.6022	-0.0116	1	8	8.1	1	NKITLTVDK
b 116	737.7078	2210.1017	2210.0967	0.0050	0	8	8.1	1	LGEHNINLVLEGNEQFIDAAK
b 48	655.3226	1308.6307	1308.6198	0.0109	0	8	18	1	VGDTGDFSVLDLQK
b 68	774.8655	1547.7165	1547.7246	-0.0081	1	8	17	1	WAAGQNKQHSITK + Phospho (ST)
b 75	811.9078	1621.8010	1621.8208	-0.0198	0	8	14	1	GVYLLDIMPQGVAMK
b 99	997.4829	1992.9513	1992.9492	0.0021	1	8	13	1	MGAGSRSGVVEGLPAVPWK + Oxidation (M); Phospho (ST)

b	79	820.3954	1638.7762	1638.7800	-0.0038	1	8	14	1	GQLASKSTILSCSHK + Phospho (ST)
b	95	897.9098	1793.8050	1793.8059	-0.0009	1	8	17	1	EFLGTTQTASFCGPKK + Phospho (ST)
b	64	752.8670	1503.7194	1503.7195	-0.0000	1	8	18	1	AVRDLEAALS S HR + Phospho (ST)
b	90	864.4432	1726.8718	1726.8638	0.0080	1	7	13	1	GLEWIGRIDPNDGGTK
b	61	711.3410	1420.6674	1420.6550	0.0124	1	7	20	1	AMLA T RSASLLK + 2 Phospho (ST)
b	67	769.3233	1536.6321	1536.6230	0.0090	1	7	22	1	MKNL F SNMAL S R + Oxidation (M); 2 Phospho (ST)
b	117	738.0335	2211.0788	2211.0985	-0.0198	0	7	13	1	NWQHII M VVLA M LGVTK + Oxidation (M); Phospho (Y)
b	142	580.4893	2317.9283	2317.9416	-0.0133	1	7	20	1	S GNII N MSSVASSIKGVENR + Oxidation (M); 3 Phospho (ST)
b	130	567.0127	2264.0218	2264.0087	0.0131	1	6	20	1	ARALLA S TAL S TAVD N SGSGDK + 2 Phospho (ST)
b	6	412.7521	823.4896	823.4916	-0.0020	0	6	6.8	1	GIPVSPVR
b	72	790.8900	1579.7654	1579.7503	0.0151	1	6	27	1	TKYLQILT S MMR + Oxidation (M); Phospho (ST)
b	7	412.7530	823.4915	823.4916	-0.0001	0	6	6.8	1	GIPVSPVR
b	98	970.9708	1939.9270	1939.9172	0.0098	0	6	21	1	MDQVMQFV F EPSQQFVK
b	125	742.7056	2225.0948	2225.0970	-0.0022	1	6	15	1	S VIQRQSALGPIISVTP S GR + 2 Phospho (ST)
b	91	882.8944	1763.7743	1763.7685	0.0058	0	5	32	1	QISYPY S AQVPPVR + Phospho (ST); Phospho (Y)
b	133	762.0587	2283.1544	2283.1482	0.0062	0	5	16	1	ESSSLVQYDLIGQTVSSETIK
b	106	732.0312	2193.0718	2193.0711	0.0007	0	5	20	1	EMPVQFQV V ELPSGHHLCK + Oxidation (M)
b	97	970.9697	1939.9249	1939.9230	0.0019	1	4	30	1	LMEMEQTLS S LRETEK + Oxidation (M)
b	100	665.6223	1993.8452	1993.8340	0.0112	0	4	34	1	LNEVQSFSE T ETEMVR + Oxidation (M); Phospho (ST)
b	136	762.7150	2285.1232	2285.1362	-0.0130	0	4	21	1	SATLMVYEDV V QIVSGFQGAR + Oxidation (M)
b	128	747.0480	2238.1221	2238.1231	-0.0010	0	4	18	1	FLMQNLSL P NS T AQALLAAR + Phospho (ST)
b	66	760.8655	1519.7165	1519.7048	0.0117	1	4	42	1	ILDSSIN T LK T R + 2 Phospho (ST)
b	108	737.3612	2209.0618	2209.0573	0.0046	0	3	33	1	GTEEVQALE D NQVALSTMK
b	121	742.3754	2224.1043	2224.0889	0.0154	1	3	27	1	LQGVLEG T LNSKTYDTLHR + Phospho (ST)
b	19	435.7742	869.5338	869.5487	-0.0149	0	3	22	1	LWVALLR
b	78	545.9461	1634.8165	1634.8277	-0.0112	1	2	42	1	DHPHTAAYLRELGR
b	104	1042.0073	2082.0000	2081.9939	0.0061	1	2	41	1	LSSSPGK T MP T TSFASDPK + Oxidation (M)
b	135	762.3869	2284.1390	2284.1207	0.0183	1	2	30	1	ECYPKAMHCIFVGAQSLFLK
b	93	890.8915	1779.7684	1779.7750	-0.0066	0	1	83	1	LQSM P TSGLP E EHK + Oxidation (M); Phospho (ST)
b	139	767.3909	2299.1507	2299.1382	0.0125	1	1	41	1	GVDSILE V DV N SLK M AVVSK + Oxidation (M); Phospho (ST)
b	84	559.9087	1676.7042	1676.6994	0.0048	1	0	93	1	NLTVSS P QMR P SGK + Oxidation (M); 2 Phospho (ST)
b	122	742.3763	2224.1069	2224.0889	0.0180	1	0	54	1	LQGVLEG T LNSKTYDTLHR + Phospho (ST)
b	1	362.2218	722.4291							
b	2	384.2350	766.4554							
b	5	406.2480	810.4814							
b	21	453.8080	905.6015							
b	31	559.7704	1117.5261							
b	53	453.8080	1358.4022							
b	83	559.9075	1676.7007							
b	94	594.2765	1779.8076							
b	96	904.9415	1807.8684							
b	101	1006.4891	2010.9636							
b	103	1033.0008	2063.9870							
b	107	1104.0569	2206.0992							
b	118	738.0351	2211.0834							
b	120	742.0332	2223.0779							
b	123	742.3764	2224.1073							
b	126	746.3780	2236.1122							
b	127	747.0081	2238.0026							
b	129	563.0185	2248.0448							
b	131	567.2566	2264.9972							
b	132	570.5136	2278.0254							
b	134	762.3868	2284.1387							
b	137	766.7309	2297.1707							
b	138	767.3857	2299.1352							
b	140	767.7181	2300.1324							
b	141	772.0623	2313.1651							

Search Parameters

Type of search : MS/MS Ion Search
 Enzyme : Trypsin/P
 Variable modifications : Oxidation (M),Phospho (ST),Phospho (Y)
 Mass values : Monoisotopic
 Protein Mass : Unrestricted
 Peptide Mass Tolerance : ± 0.02 Da
 Fragment Mass Tolerance: ± 0.3 Da
 Max Missed Cleavages : 1
 Instrument type : ESI-TRAP
 Number of queries : 143

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

MASCOT SCIENCE Mascot Search Results

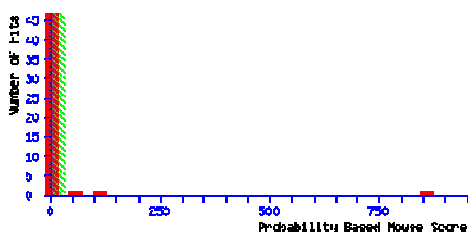
User : Bob
 Email : rdenglis@utmb.edu
 Search title : 11081916.raw #2298 acetylation
 MS data file : tempfile
 Database : NCBI nr 20110707 (14481393 sequences; 4958963357 residues)
 Taxonomy : Mus musculus (house mouse) (143921 sequences)
 Timestamp : 24 Aug 2011 at 16:29:25 GMT
 Protein hits : [gi|124248512](#) carbamoyl-phosphate synthase [ammonia], mitochondrial precursor [Mus musculus]
 [gi|51092303](#) Try10-like trypsinogen [Mus musculus]
 [gi|3093758](#) cyclic AMP specific phosphodiesterase PDE4D5A [Mus musculus]

NCBI nr [Decoy](#) False discovery rate

Peptide matches above identity threshold 28 1 3.57 %
 Peptide matches above homology or identity threshold 29 2 6.90 %

Probability Based Mowse Score

Ions score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event. Individual ions scores > 32 indicate identity or extensive homology (p<0.05). Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Peptide Summary Report

Format As [Help](#)

Significance threshold p< Max. number of hits

Standard scoring MudPIT scoring Ions score or expect cut-off Show sub-sets

Show pop-ups Suppress pop-ups Sort unassigned Require bold red

Error tolerant

1. [gi|124248512](#) Mass: 164514 Score: 857 Queries matched: 28 emPAI: 0.63
 carbamoyl-phosphate synthase [ammonia], mitochondrial precursor [Mus musculus]
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Score	Expect	Rank	Peptide
b 23	406.2211	810.4277	810.4276	0.0001	0	17	2.6	1	R.SFPFVSK.T
b 23	453.2581	904.5017	904.5018	-0.0001	0	54	0.00043	1	K.LFAEAVQK.S
b 26	495.2793	988.5440	988.5441	-0.0000	0	45	0.014	1	K.ETLIDLGTK.A
b 28	508.2387	1014.4629	1014.4658	-0.0029	0	35	0.025	1	R.TFEESFQK.A
b 29	508.8030	1015.5914	1015.5914	-0.0000	0	45	0.0024	1	K.GTTTISVLPK.P
b 32	518.7715	1035.5284	1035.5237	0.0048	0	53	0.00084	1	K.EIEYEVVR.D
b 34	545.7982	1089.5819	1089.5819	0.0000	0	55	0.00051	1	K.VPAIYGVDT.R.M
b 35	551.8089	1101.6031	1101.6030	0.0002	0	40	0.016	1	K.QNLIAEVSTK.D
b 37	568.7791	1135.5437	1135.5431	0.0006	0	60	0.00014	1	K.VMIGESIDEK.R + Oxidation (M)
b 40	582.3737	1162.7329	1162.7325	0.0004	0	41	0.00032	1	K.IALGIPLPEIK.N
b 44	609.3116	1216.6087	1216.6088	-0.0001	0	60	0.00016	1	K.SLQWQLQEEK.V
b 45	611.3386	1220.6626	1220.6652	-0.0026	0	64	3.7e-005	1	R.SIFSAVLDELK.V
b 46	611.8452	1221.6758	1221.6757	0.0001	0	48	0.001	1	K.ATGYPLAFIAAK.I
b 47	623.8266	1245.6386	1245.6387	-0.0001	0	58	0.00025	1	K.IMGTSPLQIDR.A + Oxidation (M)
b 49	639.8508	1277.6870	1277.6867	0.0002	0	66	2.4e-005	1	K.TLGVDFIDVATK.V
b 50	649.8349	1297.6552	1297.6554	-0.0002	0	55	0.0003	1	K.LYFEELSLEK.I
b 52	661.8428	1321.6710	1321.6700	0.0010	0	64	4.9e-005	1	K.AADTIGYPMVIR.S + Oxidation (M)
b 54	677.3659	1352.7172	1352.7160	0.0012	0	83	5.8e-007	1	R.GQNQPVLNITNR.Q
b 57	704.8664	1407.7183	1407.7180	0.0003	0	67	2.2e-005	1	K.AFAMTNQILVER.S + Oxidation (M)
b 59	710.8495	1419.6844	1419.6841	0.0003	0	85	3.4e-007	1	K.GLNSDSVTEETLR.K
b 63	760.3750	1518.7354	1518.7348	0.0007	0	72	6.6e-006	1	K.ALENNMSLDEIVR.L + Oxidation (M)
b 68	526.6110	1576.8112	1576.8096	0.0015	1	15	3.1	1	R.QLFSDKLNEINEK.I
b 70	530.2754	1587.8043	1587.8045	-0.0003	0	24	0.33	1	R.FLGVAEQLHNEGFK.L
b 73	812.3985	1622.7825	1622.7822	0.0003	0	117	1.9e-010	1	K.VLGTSVESIMATEDR.Q + Oxidation (M)
b 74	812.3997	1622.7848	1622.7861	-0.0013	0	79	1.2e-006	1	K.IAPSFVAVSMDALK.A + Oxidation (M)
b 80	862.4119	1722.8092	1722.8101	-0.0009	0	74	2.8e-006	1	K.IEFEGQSVDFVDPNK.Q
b 81	863.9518	1725.8891	1725.8897	-0.0006	0	70	7.5e-006	1	R.DGSIDLVINLPNNNTK.F

b [144](#) 936.4748 2806.4025 2806.4025 0.0000 1 53 0.00014 1 K.IEFEGQSVDFVDPNKQNLIAEVSTK.D

2. [gi|51092303](#) Mass: 26514 Score: 94 Queries matched: 2 emPAI: 0.25

Try10-like trypsinogen [Mus musculus]

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

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
b 41	588.3195	1174.6244	1174.6267	-0.0024	0	(49)	0.0019	1	K.TLDNDIMLIK.L
b 43	596.3178	1190.6211	1190.6217	-0.0006	0	76	3.7e-006	1	K.TLDNDIMLIK.L + Oxidation (M)

Proteins matching the same set of peptides:

[gi|84781771](#) Mass: 26204 Score: 94 Queries matched: 2
trypsin 10 [Mus musculus]

3. [gi|3093758](#) Mass: 23890 Score: 38 Queries matched: 1 emPAI: 0.13

cyclic AMP specific phosphodiesterase PDE4D5A [Mus musculus]

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

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
b 18	434.7655	867.5164	867.5178	-0.0014	0	38	0.0083	1	K.LSPVISPR.N

Proteins matching the same set of peptides:

[gi|148686495](#) Mass: 79441 Score: 38 Queries matched: 1
phosphodiesterase 4D, cAMP specific, isoform CRA_c [Mus musculus]

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

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
b 8	421.7574	841.5002	841.4810	0.0192	0	30	0.15	1	LGTWLP
b 7	421.7572	841.4998	841.4810	0.0188	0	30	0.17	1	LGTWLP
b 12	421.7584	841.5023	841.5021	0.0002	1	27	0.31	1	VKTSLPR + Acetyl (K)
b 67	783.8735	1565.7324	1565.7184	0.0140	1	25	0.26	1	EKDFQGMLEYHK + Acetyl (K)
b 10	421.7583	841.5021	841.5021	-0.0001	1	23	0.72	1	VKTSLPR + Acetyl (K)
b 11	421.7584	841.5022	841.5021	0.0001	1	23	0.78	1	VKTSLPR + Acetyl (K)
b 13	421.7586	841.5025	841.5021	0.0004	1	23	0.8	1	VKTSLPR + Acetyl (K)
b 9	421.7582	841.5019	841.5021	-0.0002	1	23	0.8	1	VKTSLPR + Acetyl (K)
b 100	737.7061	2210.0964	2210.0967	-0.0003	0	22	0.33	1	LGEHNINVLEGNEQFIDAAK
b 17	428.7655	855.5165	855.5112	0.0052	1	21	0.91	1	ALRMLPR
b 99	737.7060	2210.0961	2210.0967	-0.0006	0	21	0.38	1	LGEHNINVLEGNEQFIDAAK
b 97	737.7046	2210.0919	2210.0967	-0.0048	0	21	0.39	1	LGEHNINVLEGNEQFIDAAK
b 102	737.7062	2210.0969	2210.0967	0.0001	0	20	0.47	1	LGEHNINVLEGNEQFIDAAK
b 53	673.8529	1345.6913	1345.7089	-0.0176	1	19	1.7	1	GSLDQSLKDTLK + Acetyl (K)
b 33	536.3241	1070.6337	1070.6196	0.0141	1	18	0.86	1	DLQLRVTR
b 66	780.8984	1559.7822	1559.7654	0.0168	0	18	1.9	1	QWGLLCDLLEQDK
b 16	428.7649	855.5153	855.5178	-0.0025	0	17	2.3	1	EAALIALR
b 20	435.7759	869.5372	869.5222	0.0150	1	17	1.6	1	VEAVKIK + 2 Acetyl (K)
b 101	737.7061	2210.0965	2210.0967	-0.0002	0	16	1.1	1	LGEHNINVLEGNEQFIDAAK
b 42	595.3272	1188.6399	1188.6462	-0.0063	1	16	2.9	1	ITDTISDRLR
b 14	427.7583	853.5020	853.4844	0.0176	1	16	1.7	1	LQVMGHK + Acetyl (K)
b 76	820.3979	1638.7812	1638.7745	0.0067	1	15	2.1	1	IQMEEKFMAANPSK + Oxidation (M)
b 51	655.3228	1308.6309	1308.6271	0.0038	0	15	3.4	1	MELGELLYNK + Acetyl (K); Acetyl (Protein N-term); Oxidation (I)
b 71	804.9005	1607.7865	1607.7825	0.0041	1	15	3.2	1	QKQDETQTISLK
b 85	894.9596	1787.9046	1787.8975	0.0072	1	14	2.9	1	SLESMLSKNALDPTK + Acetyl (K); Oxidation (M)
b 31	512.2410	1022.4674	1022.4491	0.0183	0	14	3.8	1	STMNWNTK + Acetyl (K)
b 30	510.7715	1019.5285	1019.5182	0.0103	1	14	7.3	1	MRDLGVASR + Oxidation (M)
b 88	961.9653	1921.9160	1921.9356	-0.0195	1	13	2.8	1	MEWQLKAQELDPAGHK + Acetyl (K)
b 48	631.8241	1261.6336	1261.6277	0.0059	1	13	7.3	1	LYGSFNFRMK
b 82	864.4433	1726.8721	1726.8638	0.0083	1	13	5.8	1	GLEWIGRIDPNDGGTK
b 104	737.7064	2210.0974	2210.0967	0.0007	0	12	2.8	1	LGEHNINVLEGNEQFIDAAK
b 98	737.7051	2210.0936	2210.0967	-0.0032	0	11	3.6	1	LGEHNINVLEGNEQFIDAAK
b 64	769.3238	1536.6331	1536.6258	0.0072	1	11	1.2	1	MVSSGMYKMDNGK + Acetyl (Protein N-term); 3 Oxidation (M)
b 58	710.8386	1419.6627	1419.6783	-0.0155	1	11	7	1	QNGGWEDGFYK + Acetyl (K)
b 105	738.0345	2211.0818	2211.0920	-0.0102	0	11	3.9	1	LGEHNINVLEGNEQFVNSAK
b 103	737.7064	2210.0973	2210.0967	0.0006	0	10	4.4	1	LGEHNINVLEGNEQFIDAAK
b 83	887.9523	1773.8900	1773.8819	0.0081	1	10	8.4	1	KGDLLDAINSCTVTDK + 2 Acetyl (K)
b 27	505.2693	1008.5241	1008.5170	0.0071	0	10	14	1	MVGTVIMMK
b 25	478.2537	954.4928	954.5062	-0.0134	0	10	12	1	ILTFEYK + Acetyl (K)
b 55	696.8427	1391.6709	1391.6767	-0.0057	1	9	14	1	TQRSQHSQHR
b 131	767.3872	2299.1397	2299.1513	-0.0116	0	9	6.8	1	NMQMSTIEILLTFELAK + Acetyl (K); 2 Oxidation (M)
b 61	712.8639	1423.7132	1423.7129	0.0003	1	9	13	1	SMPSLDFSGRLSK
b 89	970.9707	1939.9268	1939.9172	0.0096	0	9	7.9	1	MDQVMQFVPSQQFVK
b 21	448.7168	895.4190	895.4143	0.0047	1	9	15	1	TMEKMEK
b 36	564.2791	1126.5436	1126.5328	0.0108	0	8	18	1	LSSYSACVQK + Acetyl (K)
b 94	732.0304	2193.0695	2193.0711	-0.0016	0	8	7.9	1	EMPVQFQVVELPSGHHLCK + Oxidation (M)
b 72	811.9081	1621.8017	1621.8208	-0.0191	0	8	16	1	GVYLEDIMPQGVAMK
b 78	837.3901	1672.7657	1672.7693	-0.0036	0	7	10	1	DSEGDTPSLINWPSR

b	62	752.8684	1503.7223	1503.7317	-0.0094	1	7	21	1	DGIQTKEHPNPGK + 2 Acetyl (K)
b	56	701.3612	1400.7078	1400.7048	0.0030	0	7	25	1	VQDGHLLITTYGR + Acetyl (Protein N-term)
b	119	1133.0131	2264.0116	2264.0300	-0.0184	1	7	5.6	1	ALMPSTEDAAAEVPSRDTMEK + Oxidation (M)
b	60	711.3410	1420.6675	1420.6722	-0.0047	1	7	21	1	SKDDSPSYLPTK + 2 Acetyl (K)
b	69	790.8905	1579.7664	1579.7776	-0.0112	1	6	25	1	DRAYLEGACVQSLR
b	106	738.0368	2211.0886	2211.0742	0.0143	1	6	11	1	VESGFHQHGELSLRAMDK + Acetyl (K); Oxidation (M)
b	19	435.7739	869.5333	869.5222	0.0111	0	6	23	1	DAIVLAVK + Acetyl (K)
b	133	767.3899	2299.1478	2299.1444	0.0034	0	6	15	1	AVNDSGHLIAITGYDGNLGLGK
b	134	767.3904	2299.1494	2299.1513	-0.0019	0	5	18	1	NMQMMSIEILLTLFTELAK + Acetyl (K); 2 Oxidation (M)
b	128	762.7215	2285.1428	2285.1362	0.0066	0	4	20	1	SATLMVYEDVVQIVSGFQGAR + Oxidation (M)
b	108	738.0411	2211.1013	2211.0920	0.0093	0	4	20	1	LGEHNINVLEGNEQFVNSAK
b	137	767.7184	2300.1334	2300.1156	0.0178	1	4	20	1	ECYPKAMHCIFVGAQSLFLK + Oxidation (M)
b	107	738.0407	2211.1002	2211.1101	-0.0099	1	4	20	1	SAPEIKYNSMVLICALMGSGK
b	96	737.3625	2209.0657	2209.0586	0.0071	1	4	23	1	GFMVQTGDPPTGTGRGSSSIWAK
b	65	774.8665	1547.7185	1547.7225	-0.0040	1	4	34	1	KTAQGGHLCYNPML + Oxidation (M)
b	116	746.3798	2236.1176	2236.1020	0.0155	1	3	26	1	SPKFCQFPQEIVLQMVVER + Acetyl (K); Oxidation (M)
b	92	1042.0088	2082.0030	2082.0164	-0.0133	1	3	29	1	RSPPLLAGAEEGMSQAPPEAR + Oxidation (M)
b	77	830.9302	1659.8459	1659.8329	0.0130	1	3	41	1	KNVYSSQIGHQGSK
b	5	412.7528	823.4911	823.4803	0.0108	1	2	23	1	KTPGLPK + 2 Acetyl (K)
b	118	563.2700	2249.0509	2249.0456	0.0052	1	2	29	1	KHQELQAMQMLQSPYK + 2 Oxidation (M)
b	124	762.0604	2283.1593	2283.1564	0.0029	0	2	27	1	NMQMMSIEILLTLFTELAK + Acetyl (K); Oxidation (M)
b	125	762.0604	2283.1594	2283.1529	0.0065	1	2	28	1	AEEHLQRDVLSDLTNCTVK
b	136	767.7161	2300.1263	2300.1147	0.0116	1	2	35	1	LTSYLVREVDVVFVSMGYHK + Acetyl (K)
b	86	897.9106	1793.8066	1793.8036	0.0030	1	1	35	1	KMAECLSESHAQSTTR + Oxidation (M)
b	139	772.3906	2314.1500	2314.1481	0.0018	1	1	38	1	EPTFFGVSSKSNPGTVGIFSSK + Acetyl (K)
b	91	1033.0023	2063.9900	2063.9986	-0.0085	1	1	44	1	NAHDVLFMSYAEELKQAK + 2 Acetyl (K); Oxidation (M)
b	79	857.4072	1712.7998	1712.7981	0.0017	0	1	46	1	FENDAAVMIQSWFR
b	1	384.2351	766.4556							
b	2	772.7244	771.7171							
b	4	406.2485	810.4824							
b	6	412.7538	823.4930							
b	15	428.2617	854.5088							
b	22	450.2746	898.5346							
b	24	472.2876	942.5607							
b	38	574.2686	1146.5227							
b	39	581.7801	1161.5457							
b	75	820.3959	1638.7773							
b	84	890.8921	1779.7696							
b	87	904.9432	1807.8718							
b	90	665.6227	1993.8461							
b	93	729.0349	2184.0828							
b	95	1104.0580	2206.1014							
b	109	741.7061	2222.0964							
b	110	742.0328	2223.0766							
b	111	742.3769	2224.1090							
b	112	742.3769	2224.1090							
b	113	742.3774	2224.1104							
b	114	742.7052	2225.0937							
b	115	559.5206	2234.0535							
b	117	747.0477	2238.1213							
b	120	567.0126	2264.0211							
b	121	567.2571	2264.9995							
b	122	762.0545	2283.1416							
b	123	762.0590	2283.1551							
b	126	762.3839	2284.1300							
b	127	762.3886	2284.1438							
b	129	766.7296	2297.1669							
b	130	766.7337	2297.1794							
b	132	767.3895	2299.1466							
b	135	767.3905	2299.1498							
b	138	772.0624	2313.1653							
b	140	585.5232	2338.0635							
b	141	585.5268	2338.0780							
b	142	589.5259	2354.0747							
b	143	843.4239	2527.2499							

Search Parameters

Type of search : MS/MS Ion Search
 Enzyme : Trypsin/P
 Variable modifications : Acetyl (K),Acetyl (Protein N-term),Oxidation (M)
 Mass values : Monoisotopic
 Protein Mass : Unrestricted
 Peptide Mass Tolerance : ± 0.02 Da
 Fragment Mass Tolerance: ± 0.3 Da
 Max Missed Cleavages : 1
 Instrument type : ESI-TRAP

Number of queries : 144

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

MASCOT **SCIENCE** Mascot Search Results

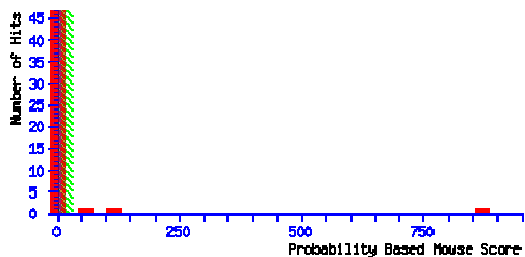
User : Bob
 Email : rdenglis@utmb.edu
 Search title : 11081916.raw #2298 phospho
 MS data file : tempfile
 Database : NCBI nr 20110707 (14481393 sequences; 4958963357 residues)
 Taxonomy : Mus musculus (house mouse) (143921 sequences)
 Timestamp : 24 Aug 2011 at 16:27:55 GMT
 Protein hits : [gi|124248512](#) carbamoyl-phosphate synthase [ammonia], mitochondrial precursor [Mus musculus]
 [gi|51092303](#) Try10-like trypsinogen [Mus musculus]
 [gi|3093758](#) cyclic AMP specific phosphodiesterase PDE4D5A [Mus musculus]

NCBI nr [Decoy](#) False discovery rate

Peptide matches above identity threshold 28 1 3.57 %
 Peptide matches above homology or identity threshold 30 3 10.00 %

Probability Based Mowse Score

Ions score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event. Individual ions scores > 31 indicate identity or extensive homology ($p < 0.05$). Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Peptide Summary Report

Format As [Help](#)

Significance threshold $p <$ Max. number of hits

Standard scoring MudPIT scoring Ions score or expect cut-off Show sub-sets

Show pop-ups Suppress pop-ups Sort unassigned Require bold red

 Error tolerant

1. [gi|124248512](#) Mass: 164514 Score: 870 Queries matched: 28 emPAI: 0.66
 carbamoyl-phosphate synthase [ammonia], mitochondrial precursor [Mus musculus]
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Score	Expect	Rank	Peptide
b 3	406.2211	810.4277	810.4276	0.0001	0	17	1.9	1	R.SFFVSK.T
b 23	453.2581	904.5017	904.5018	-0.0001	0	54	0.00027	1	K.LFAEAVQK.S
b 26	495.2793	988.5440	988.5441	-0.0000	0	45	0.012	1	K.ETLIDLGTK.A
b 28	508.2387	1014.4629	1014.4658	-0.0029	0	35	0.042	1	R.TFEESFQK.A
b 29	508.8030	1015.5914	1015.5914	-0.0000	0	45	0.0015	1	K.GTTITSVLPK.P
b 32	518.7715	1035.5284	1035.5237	0.0048	0	53	0.00061	1	K.EIEYEVVR.D
b 34	545.7982	1089.5819	1089.5819	0.0000	0	55	0.00029	1	K.VPAIYVDTR.M
b 35	551.8089	1101.6031	1101.6030	0.0002	0	40	0.0089	1	K.QNLIAEVSTK.D
b 37	568.7791	1135.5437	1135.5431	0.0006	0	60	0.00013	1	K.VMIGESIDEK.R + Oxidation (M)
b 40	582.3737	1162.7329	1162.7325	0.0004	0	41	0.00026	1	K.IALGIPLPEIK.N
b 44	609.3116	1216.6087	1216.6088	-0.0001	0	60	0.00012	1	K.SLGQWLQEEK.V
b 45	611.3386	1220.6626	1220.6652	-0.0026	0	64	2.5e-005	1	R.SIFSAVLDELK.V
b 46	611.8452	1221.6758	1221.6757	0.0001	0	48	0.00075	1	K.ATGYPLAFIAK.I
b 47	623.8266	1245.6386	1245.6387	-0.0001	0	58	0.00015	1	K.IMGTSPLQIDR.A + Oxidation (M)
b 49	639.8508	1277.6870	1277.6867	0.0002	0	66	1.4e-005	1	K.TLGVDFIDVATK.V
b 50	649.8349	1297.6552	1297.6554	-0.0002	0	55	0.00026	1	K.LYFEELSLEK.I
b 52	661.8428	1321.6710	1321.6700	0.0010	0	64	4.1e-005	1	K.AADTIGYPVMIR.S + Oxidation (M)
b 54	677.3659	1352.7172	1352.7160	0.0012	0	83	3.9e-007	1	R.GQNQPVLNITNR.Q
b 57	704.8664	1407.7183	1407.7180	0.0003	0	67	2.1e-005	1	K.AFAMTNQILVER.S + Oxidation (M)

b	59	710.8495	1419.6844	1419.6841	0.0003	0	85	3.1e-007	1	K.GLNDSVTEETLR.K
b	63	760.3750	1518.7354	1518.7348	0.0007	0	72	6e-006	1	K.ALENNMSLDEIVR.L + Oxidation (M)
b	68	526.6110	1576.8112	1576.8096	0.0015	1	15	2.3	1	R.QLFSDKLEINEK.I
b	70	530.2754	1587.8043	1587.8045	-0.0003	0	24	0.37	1	R.FLGVAEQLEHNEGFK.L
b	73	812.3985	1622.7825	1622.7822	0.0003	0	117	2.1e-010	1	K.VLGTSVESIMATEDR.Q + Oxidation (M)
b	74	812.3997	1622.7848	1622.7861	-0.0013	0	79	1.2e-006	1	K.IAPSFVAVESMEDALK.A + Oxidation (M)
b	80	862.4119	1722.8092	1722.8101	-0.0009	0	74	3.9e-006	1	K.IEFEGQSVDFVDPNK.Q
b	81	863.9518	1725.8891	1725.8897	-0.0006	0	70	5.9e-006	1	R.DGSDILVINLPNNNTK.F
b	144	936.4748	2806.4025	2806.4025	0.0000	1	53	0.00015	1	K.IEFEGQSVDFVDPNKQNLIAEVSTK.D

2. [gi|51092303](#) Mass: 26514 Score: 95 Queries matched: 2 emPAI: 0.25

Try10-like trypsinogen [Mus musculus]

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

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide	
b	41	588.3195	1174.6244	1174.6267	-0.0024	0	(49)	0.0011	1	K.TLDNDIMLIK.L
b	43	596.3178	1190.6211	1190.6217	-0.0006	0	76	2.2e-006	1	K.TLDNDIMLIK.L + Oxidation (M)

Proteins matching the same set of peptides:

[gi|84781771](#) Mass: 26204 Score: 95 Queries matched: 2
trypsin 10 [Mus musculus]

3. [gi|3093758](#) Mass: 23890 Score: 38 Queries matched: 1 emPAI: 0.13

cyclic AMP specific phosphodiesterase PDE4D5A [Mus musculus]

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

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide	
b	18	434.7655	867.5164	867.5178	-0.0014	0	38	0.0044	1	K.LSPVISPR.N

Proteins matching the same set of peptides:

[gi|148686495](#) Mass: 79441 Score: 38 Queries matched: 1
phosphodiesterase 4D, cAMP specific, isoform CRA_c [Mus musculus]

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

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide	
b	8	421.7574	841.5002	841.4810	0.0192	0	30	0.06	1	LGTWLPR
b	7	421.7572	841.4998	841.4810	0.0188	0	30	0.07	1	LGTWLPR
b	100	737.7061	2210.0964	2210.0967	-0.0003	0	22	0.4	1	LGEHNINVLEGNEQFIDAAK
b	17	428.7655	855.5165	855.5112	0.0052	1	21	0.43	1	ALRMLPR
b	99	737.7060	2210.0961	2210.0967	-0.0006	0	21	0.46	1	LGEHNINVLEGNEQFIDAAK
b	97	737.7046	2210.0919	2210.0967	-0.0048	0	21	0.47	1	LGEHNINVLEGNEQFIDAAK
b	102	737.7062	2210.0969	2210.0967	0.0001	0	20	0.58	1	LGEHNINVLEGNEQFIDAAK
b	25	478.2537	954.4928	954.4787	0.0141	1	19	0.96	1	LLSAKDTK + Phospho (ST)
b	33	536.3241	1070.6337	1070.6196	0.0141	1	18	0.56	1	DLQLRVTR
b	66	780.8984	1559.7822	1559.7654	0.0168	0	18	1.5	1	QWGLLCDLLEQDK
b	12	421.7584	841.5023	841.5021	0.0002	1	18	1.1	1	LKESLPR
b	16	428.7649	855.5153	855.5178	-0.0025	0	17	1.1	1	EAALIALR
b	101	737.7061	2210.0965	2210.0967	-0.0002	0	16	1.3	1	LGEHNINVLEGNEQFIDAAK
b	42	595.3272	1188.6399	1188.6462	-0.0063	1	16	1.7	1	ITDTISDRLR
b	10	421.7583	841.5021	841.5134	-0.0113	1	16	1.5	1	LGLRLDR
b	76	820.3979	1638.7812	1638.7745	0.0067	1	15	2.5	1	IQMEEKFMAANPSK + Oxidation (M)
b	13	421.7586	841.5025	841.5021	0.0004	0	15	1.9	1	LSVALSPR
b	14	427.7583	853.5020	853.5021	-0.0001	0	15	1.4	1	VQLELPR
b	71	804.9005	1607.7865	1607.7825	0.0041	1	15	3.2	1	QKCQDETQTISLK
b	61	712.8639	1423.7132	1423.7072	0.0061	1	15	3	1	AENSSLNLIGKAK + Phospho (ST)
b	11	421.7584	841.5022	841.5021	0.0001	1	14	2.5	1	ITKPLDR
b	30	510.7715	1019.5285	1019.5182	0.0103	1	14	4.6	1	MRDLGVASR + Oxidation (M)
b	9	421.7582	841.5019	841.5021	-0.0002	0	13	2.9	1	LSVALSPR
b	21	448.7168	895.4190	895.4164	0.0025	0	13	6.7	1	LGTTTAPR + Phospho (ST)
b	53	673.8529	1345.6913	1345.6941	-0.0028	1	13	4.2	1	MAAPLRHTLLK + Oxidation (M); Phospho (ST)
b	48	631.8241	1261.6336	1261.6277	0.0059	1	13	5.2	1	LYGSFNFRMK
b	82	864.4433	1726.8721	1726.8638	0.0083	1	13	4.1	1	GLEWIGRIDPNDGGTK
b	104	737.7064	2210.0974	2210.0967	0.0007	0	12	3.4	1	LGEHNINVLEGNEQFIDAAK
b	67	783.8735	1565.7324	1565.7169	0.0155	1	12	7.4	1	VSETSGGKTSGEDANK
b	78	837.3901	1672.7657	1672.7604	0.0053	1	12	7.6	1	MGNSTSGQTVRQALK + Oxidation (M); Phospho (ST)
b	98	737.7051	2210.0936	2210.0967	-0.0032	0	11	4.1	1	LGEHNINVLEGNEQFIDAAK
b	55	696.8427	1391.6709	1391.6671	0.0039	1	11	8.3	1	SSGGAARGAVPAVGR + Phospho (ST)

b	105	738.0345	2211.0818	2211.0920	-0.0102	0	11	4.9	1	LGEHNINVLGNEQFVNSAK
b	79	857.4072	1712.7998	1712.8056	-0.0058	1	11	8.2	1	TSDPLKILANADTMK + Oxidation (M); Phospho (ST)
b	103	737.7064	2210.0973	2210.0967	0.0006	0	10	5.4	1	LGEHNINVLGNEQFIDAAK
b	27	505.2693	1008.5241	1008.5170	0.0071	0	10	12	1	MVGTVIMMK
b	56	701.3612	1400.7078	1400.6887	0.0191	1	10	11	1	LSFCEKNVILR + Phospho (ST)
b	125	762.0604	2283.1594	2283.1399	0.0195	1	9	5.3	1	EPPGKPKGAEALSITPQLLK + Phospho (ST)
b	36	564.2791	1126.5436	1126.5424	0.0012	0	9	15	1	LIGSHPDVLP + Phospho (ST)
b	134	767.3904	2299.1494	2299.1501	-0.0007	1	9	6.1	1	AKFDGIFESLLPVNGLLSGDK + Phospho (ST)
b	62	752.8684	1503.7223	1503.7275	-0.0052	1	9	15	1	FFKEIWSAAAR + Phospho (ST)
b	89	970.9707	1939.9268	1939.9172	0.0096	0	9	11	1	MDQVMQFVPEPSQQFVK
b	58	710.8386	1419.6627	1419.6799	-0.0172	0	8	16	1	FIASFNVVNTTK + Phospho (ST)
b	86	897.9106	1793.8066	1793.8059	0.0007	1	8	14	1	EFLGTTQTASFCGPKK + Phospho (ST)
b	92	1042.0088	2082.0030	2082.0009	0.0021	1	8	11	1	FASLFNVKDOIVMFLSR + Phospho (ST)
b	94	732.0304	2193.0695	2193.0711	-0.0016	0	8	10	1	EMPVQFQVVELPSGHHLCK + Oxidation (M)
b	72	811.9081	1621.8017	1621.8208	-0.0191	0	8	17	1	GVYLTDIMPQGVAMK
b	85	894.9596	1787.9046	1787.9087	-0.0041	1	7	13	1	ANQQLEKDLNLMEDIK + Oxidation (M)
b	119	1133.0131	2264.0116	2264.0300	-0.0184	1	7	19	1	ALMPSTEDAAAEVPSRDTMEK + Oxidation (M)
b	114	742.7052	2225.0937	2225.0970	-0.0033	1	7	13	1	SVIQRQ ³ SALGPIISVTP ³ GR + 2 Phospho (ST)
b	75	820.3959	1638.7773	1638.7800	-0.0027	1	7	18	1	QQLASKSTIL ³ C ³ SHK + Phospho (ST)
b	69	790.8905	1579.7664	1579.7776	-0.0112	1	6	25	1	DRAYLEGACVQSLR
b	77	830.9302	1659.8459	1659.8307	0.0152	1	6	16	1	IAMSSAKVVIVYGDK + Phospho (ST)
b	133	767.3899	2299.1478	2299.1444	0.0034	0	6	13	1	AVNDSGHLIAITGYDGNLGDLGK
b	60	711.3410	1420.6675	1420.6729	-0.0054	1	6	29	1	ATISCRASENVDR
b	51	655.3228	1308.6309	1308.6198	0.0112	0	5	37	1	VGDTGDFSVDLGK
b	117	747.0477	2238.1213	2238.1158	0.0055	0	5	14	1	DTHSLPPAQILGIQSGQGIAR + Phospho (ST)
b	83	887.9523	1773.8900	1773.8848	0.0052	1	5	26	1	AAML ³ SLLRYNANLTK + Oxidation (M); Phospho (ST)
b	20	435.7759	869.5372	869.5487	-0.0115	0	4	14	1	LWVALLR
b	19	435.7739	869.5333	869.5487	-0.0154	0	4	15	1	LWVALLR
b	128	762.7215	2285.1428	2285.1362	0.0066	0	4	18	1	SATLMVYEDVVQIVSGFQGAR + Oxidation (M)
b	108	738.0411	2211.1013	2211.0920	0.0093	0	4	25	1	LGEHNINVLGNEQFVNSAK
b	137	767.7184	2300.1334	2300.1156	0.0178	1	4	19	1	ECYPKAMHCIFVGAQSLFLK + Oxidation (M)
b	107	738.0407	2211.1002	2211.1101	-0.0099	1	4	26	1	SAPEIKYNSMVLICALMGSGK
b	96	737.3625	2209.0657	2209.0586	0.0071	1	4	30	1	GFMVQTGDPTGTGRGGSSIWAK
b	65	774.8665	1547.7185	1547.7225	-0.0040	1	4	49	1	KTAQGGHLCYNPML + Oxidation (M)
b	31	512.2410	1022.4674	1022.4516	0.0158	0	4	40	1	SQSTSEQEK
b	93	729.0349	2184.0828	2184.0690	0.0138	0	3	26	1	MTGLES ³ LWVSEVLQLPFR + Phospho (ST)
b	106	738.0368	2211.0886	2211.1027	-0.0142	1	3	29	1	MLPSSMNSVEVYSGANRILK + Oxidation (M)
b	118	563.2700	2249.0509	2249.0456	0.0052	1	2	49	1	KHQLQAMQ ³ MELQSPEYK + 2 Oxidation (M)
b	88	961.9653	1921.9160	1921.8985	0.0176	1	2	55	1	NLMAKVIQIATSSSTAK + 2 Phospho (ST)
b	64	769.3238	1536.6331	1536.6449	-0.0118	1	2	70	1	KHSLSSMTYVPK + Phospho (ST); Phospho (Y)
b	115	559.5206	2234.0535	2234.0409	0.0126	1	2	50	1	YRLVPYGNH ³ YLES ³ LDK + Phospho (ST)
b	124	762.0604	2283.1593	2283.1399	0.0194	1	1	34	1	EPPGKPKGAEALSITPQLLK + Phospho (ST)
b	39	581.7801	1161.5457	1161.5505	-0.0048	1	1	93	1	SEIFLKM ³ SK + Phospho (ST)
b	132	767.3895	2299.1466	2299.1501	-0.0035	1	0	46	1	AKFDGIFESLLPVNGLLSGDK + Phospho (ST)
b	1	384.2351	766.4556							
b	2	772.7244	771.7171							
b	4	406.2485	810.4824							
b	5	412.7528	823.4911							
b	6	412.7538	823.4930							
b	15	428.2617	854.5088							
b	22	450.2746	898.5346							
b	24	472.2876	942.5607							
b	38	574.2686	1146.5227							
b	84	890.8921	1779.7696							
b	87	904.9432	1807.8718							
b	90	665.6227	1993.8461							
b	91	1033.0023	2063.9900							
b	95	1104.0580	2206.1014							
b	109	741.7061	2222.0964							
b	110	742.0328	2223.0766							
b	111	742.3769	2224.1090							
b	112	742.3769	2224.1090							
b	113	742.3774	2224.1104							
b	116	746.3798	2236.1176							
b	120	567.0126	2264.0211							
b	121	567.2571	2264.9995							
b	122	762.0545	2283.1416							
b	123	762.0590	2283.1551							

b	126	762.3839	2284.1300
b	127	762.3886	2284.1438
b	129	766.7296	2297.1669
b	130	766.7337	2297.1794
b	131	767.3872	2299.1397
b	135	767.3905	2299.1498
b	136	767.7161	2300.1263
b	138	772.0624	2313.1653
b	139	772.3906	2314.1500
b	140	585.5232	2338.0635
b	141	585.5268	2338.0780
b	142	589.5259	2354.0747
b	143	843.4239	2527.2499

Search Parameters

Type of search : MS/MS Ion Search
Enzyme : Trypsin/P
Variable modifications : Oxidation (M),Phospho (ST),Phospho (Y)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 0.02 Da
Fragment Mass Tolerance: ± 0.3 Da
Max Missed Cleavages : 1
Instrument type : ESI-TRAP
Number of queries : 144

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

MASCOT Mascot Search Results

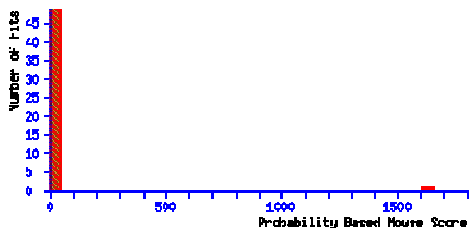
User : Bob
 Email : rdenglis@utmb.edu
 Search title : 11081917.raw #2303 acetylation
 MS data file : tempfile
 Database : NCBI nr 20110707 (14481393 sequences; 4958963357 residues)
 Taxonomy : Mus musculus (house mouse) (143921 sequences)
 Timestamp : 24 Aug 2011 at 16:33:40 GMT
 Protein hits : [gi|124248512](#) carbamoyl-phosphate synthase [ammonia], mitochondrial precursor [Mus musculus]
[gi|200246](#) pyruvate carboxylase [Mus musculus]
[gi|84781771](#) trypsin 10 [Mus musculus]
[gi|3093758](#) cyclic AMP specific phosphodiesterase PDE4D5A [Mus musculus]
[gi|148677260](#) mCG126205 [Mus musculus]

NCBI nr **Decoy** False discovery rate

Peptide matches above identity threshold 32 1 3.13 %
 Peptide matches above homology or identity threshold 35 1 2.86 %

Probability Based Mowse Score

Ions score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event. Individual ions scores > 32 indicate identity or extensive homology (p<0.05). Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Peptide Summary Report

Format As [Help](#)

Significance threshold p< Max. number of hits

Standard scoring MudPIT scoring Ions score or expect cut-off Show sub-sets

Show pop-ups Suppress pop-ups Sort unassigned Require bold red

Error tolerant

1. [gi|124248512](#) Mass: 164514 Score: 1631 Queries matched: 31 emPAI: 0.66
 carbamoyl-phosphate synthase [ammonia], mitochondrial precursor [Mus musculus]
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Score	Expect	Rank	Peptide
b 3	406.2214	810.4282	810.4276	0.0007	0	25	0.41	1	R.SFPFVSK.T
b 4	406.2214	810.4283	810.4276	0.0007	0	(18)	2.5	1	R.SFPFVSK.T
b 19	453.2583	904.5021	904.5018	0.0003	0	43	0.0059	1	K.LFAEAVQK.S
b 20	495.2797	988.5447	988.5441	0.0007	0	51	0.0033	1	K.ETLIDLGTK.A
b 22	508.2393	1014.4641	1014.4658	-0.0017	0	34	0.024	1	R.TFEESFQK.A
b 23	508.8030	1015.5914	1015.5914	-0.0000	0	38	0.012	1	K.GTTTISVLPK.P
b 25	518.7691	1035.5237	1035.5237	0.0000	0	38	0.024	1	K.EIEYEVVR.D
b 27	545.7980	1089.5815	1089.5819	-0.0004	0	46	0.0037	1	K.VPAIYGDVTR.M
b 28	551.8086	1101.6027	1101.6030	-0.0002	0	38	0.025	1	K.QNLIAEVSTK.D
b 30	568.7799	1135.5453	1135.5431	0.0022	0	67	2.8e-005	1	K.VMIGESIDEK.R + Oxidation (M)
b 31	582.3736	1162.7326	1162.7325	0.0001	0	44	0.00018	1	K.IALGIPLPEIK.N
b 35	609.3123	1216.6100	1216.6088	0.0012	0	58	0.00025	1	K.SLQWLQEEK.V
b 36	611.3392	1220.6638	1220.6652	-0.0014	0	61	7.1e-005	1	R.SIFSAVLDELK.V
b 37	611.8458	1221.6770	1221.6757	0.0013	0	52	0.00052	1	K.ATGYPLAFIAAK.I
b 38	623.8301	1245.6455	1245.6387	0.0068	0	52	0.001	1	K.IMGTSPLQIDR.A + Oxidation (M)
b 40	639.8509	1277.6872	1277.6867	0.0005	0	66	2.8e-005	1	K.TLGVDFIDVATK.V
b 41	649.8351	1297.6557	1297.6554	0.0003	0	59	0.00012	1	K.LYFEELSLEK.I
b 44	661.8426	1321.6706	1321.6700	0.0006	0	68	1.7e-005	1	K.AADTIGYVPMIR.S + Oxidation (M)
b 47	677.3656	1352.7166	1352.7160	0.0006	0	66	2.6e-005	1	R.GQNQPVLNITNR.Q
b 50	704.8641	1407.7136	1407.7180	-0.0044	0	(63)	5.2e-005	1	K.AFAMTNQILVER.S + Oxidation (M)
b 51	704.8666	1407.7186	1407.7180	0.0006	0	72	7.8e-006	1	K.AFAMTNQILVER.S + Oxidation (M)
b 53	710.8513	1419.6880	1419.6841	0.0038	0	77	2.5e-006	1	K.GLNSDSVTETELR.K
b 56	760.3773	1518.7400	1518.7348	0.0053	0	72	6.8e-006	1	K.ALENMNSLDEIVR.L + Oxidation (M)
b 62	526.6129	1576.8168	1576.8096	0.0071	1	30	0.091	1	R.QLFSDKLNEINEK.I
b 63	530.2755	1587.8046	1587.8045	0.0001	0	15	3.1	1	R.FLGVAEQLHNEGFK.L
b 66	812.3985	1622.7823	1622.7822	0.0002	0	92	5.2e-008	1	K.VLGTSVESIMATEDR.Q + Oxidation (M)

b	67	812.3998	1622.7851	1622.7861	-0.0011	0	82	5.9e-007	1	K.IAPSFVAVESMEDALK.A + Oxidation (M)
b	73	862.4122	1722.8098	1722.8101	-0.0002	0	84	2.6e-007	1	K.IEFEGQSVDFVDPNK.Q
b	74	863.9523	1725.8899	1725.8897	0.0002	0	67	1.4e-005	1	R.DGSIDLVINLPNNNTK.F
b	83	1022.5412	2043.0678	2043.0670	0.0008	0	87	8.2e-008	1	K.TVLMNPNIASVQTNEVGLK.Q + Oxidation (M)
b	132	936.4751	2806.4034	2806.4025	0.0009	1	55	7.6e-005	1	K.IEFEGQSVDFVDPNKQNLIAEVSTK.D

2. [gi|200246](#) Mass: 103041 Score: 63 Queries matched: 2 emPAI: 0.03
 pyruvate carboxylase [Mus musculus]
 e Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide	
b	45	663.8489	1325.6833	1325.6827	0.0007	0	59	0.00013	1	K.GTPLDTEVPLER.V
	61	783.8738	1565.7331	1565.7429	-0.0098	0	4	32	5	K.METVVTSPMEGTIR.K + Oxidation (M)

Proteins matching the same set of peptides:

- [gi|464506](#) Mass: 129602 Score: 63 Queries matched: 2
 RecName: Full=Pyruvate carboxylase, mitochondrial; AltName: Full=Pyruvic carboxylase; Short=PCB; Flags: Precursor
- [gi|26346581](#) Mass: 90810 Score: 63 Queries matched: 2
 unnamed protein product [Mus musculus]
- [gi|74186338](#) Mass: 129778 Score: 63 Queries matched: 2
 unnamed protein product [Mus musculus]
- [gi|74201750](#) Mass: 129650 Score: 63 Queries matched: 2
 unnamed protein product [Mus musculus]
- [gi|74215392](#) Mass: 129749 Score: 63 Queries matched: 2
 unnamed protein product [Mus musculus]
- [gi|251823978](#) Mass: 129618 Score: 63 Queries matched: 2
 pyruvate carboxylase, mitochondrial isoform 2 [Mus musculus]
- [gi|251823980](#) Mass: 129750 Score: 63 Queries matched: 2
 pyruvate carboxylase, mitochondrial isoform 1 [Mus musculus]

3. [gi|84781771](#) Mass: 26204 Score: 63 Queries matched: 3 emPAI: 0.26
 trypsin 10 [Mus musculus]
 e Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide	
b	32	588.3186	1174.6227	1174.6267	-0.0040	0	(45)	0.0044	1	K.TLDNDIMLIK.L
b	34	596.3183	1190.6220	1190.6217	0.0003	0	58	0.00024	1	K.TLDNDIMLIK.L + Oxidation (M)
	42	655.3232	1308.6318	1308.6206	0.0112	0	5	38	5	K.NMICVGFLEGCK.D + Acetyl (K)

4. [gi|3093758](#) Mass: 23890 Score: 35 Queries matched: 1 emPAI: 0.13
 cyclic AMP specific phosphodiesterase PDE4D5A [Mus musculus]
 e Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide	
b	16	434.7667	867.5189	867.5178	0.0011	0	35	0.016	1	K.LSPVISPR.N

Proteins matching the same set of peptides:

- [gi|148686495](#) Mass: 79441 Score: 35 Queries matched: 1
 phosphodiesterase 4D, cAMP specific, isoform CRA_c [Mus musculus]

5. [gi|148677260](#) Mass: 227544 Score: 32 Queries matched: 2 emPAI: 0.01
 mCG126205 [Mus musculus]
 e Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide	
b	67	812.3998	1622.7851	1622.7796	0.0055	1	(23)	0.45	2	K.IQMEEFMAANPSK.I
b	69	820.3981	1638.7817	1638.7745	0.0072	1	32	0.045	1	K.IQMEEFMAANPSK.I + Oxidation (M)

Proteins matching the same set of peptides:

- [gi|81906676](#) Mass: 227475 Score: 30 Queries matched: 2
 RecName: Full=Sodium channel protein type 5 subunit alpha; AltName: Full=Sodium channel protein cardiac muscle subunit alpha; AltName:
- [gi|84875498](#) Mass: 227559 Score: 30 Queries matched: 2
 sodium channel protein type 5 subunit alpha [Mus musculus]

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

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide	
b	8	421.7576	841.5007	841.4810	0.0197	0	30	0.17	1	LGTWLPK
b	10	421.7583	841.5021	841.5022	-0.0001	1	27	0.29	1	VKTTVPR + Acetyl (K)
b	9	421.7578	841.5010	841.5021	-0.0011	1	25	0.52	1	VKTSLPR + Acetyl (K)
b	26	536.3244	1070.6342	1070.6196	0.0145	1	24	0.25	1	DLQLRVTK
b	12	421.7584	841.5023	841.5021	0.0002	1	23	0.73	1	DGVIKLR + Acetyl (K)
b	13	421.7588	841.5030	841.5021	0.0008	1	23	0.76	1	VKTSLPR + Acetyl (K)
b	15	428.7659	855.5172	855.5112	0.0059	1	23	0.56	1	ALRMLPK
b	61	783.8738	1565.7331	1565.7184	0.0147	1	23	0.42	1	EKDPQGMLEYHK + Acetyl (K)
b	43	655.8574	1309.7003	1309.6878	0.0126	1	22	0.54	1	KGSALDPEPVK + Acetyl (K)

b	11	421.7584	841.5022	841.5022	0.0000	1	22	1	1	VKTTVPR + Acetyl (K)
b	97	737.7067	2210.0982	2210.0967	0.0015	0	21	0.39	1	LGEHNINVLEGNQFIDAAK
b	46	673.8527	1345.6909	1345.7089	-0.0180	1	21	1.1	1	GSLDQSLKDTLK + Acetyl (K)
b	92	737.7061	2210.0966	2210.0967	-0.0001	0	19	0.59	1	LGEHNINVLEGNQFIDAAK
b	96	737.7067	2210.0982	2210.0967	0.0014	0	19	0.65	1	LGEHNINVLEGNQFIDAAK
b	60	780.8987	1559.7828	1559.7654	0.0174	0	19	1.6	1	QWGLLCDLLEQDK
b	76	864.4443	1726.8740	1726.8638	0.0102	1	17	1.9	1	GLEWIGRIDPNDGGTK
b	93	737.7062	2210.0968	2210.0967	0.0001	0	17	0.95	1	LGEHNINVLEGNQFIDAAK
b	90	737.7051	2210.0934	2210.0967	-0.0033	0	17	1.1	1	LGEHNINVLEGNQFIDAAK
b	33	595.3281	1188.6416	1188.6462	-0.0046	1	16	2.9	1	ITDTISDRLR
b	94	737.7065	2210.0975	2210.0967	0.0008	0	16	1.1	1	LGEHNINVLEGNQFIDAAK
b	95	737.7065	2210.0976	2210.0967	0.0009	0	16	1.2	1	LGEHNINVLEGNQFIDAAK
b	58	769.3238	1536.6331	1536.6258	0.0073	1	15	0.48	1	MVSSGMVKMDNGK + Acetyl (Protein N-term); 3 Oxidation (M)
b	14	428.7658	855.5171	855.5112	0.0059	1	15	3.6	1	ALRMLPR
b	42	655.3232	1308.6318	1308.6271	0.0047	0	15	3.6	1	MLGLGLLYNK + Acetyl (K); Acetyl (Protein N-term); Oxidation (M)
b	39	631.8241	1261.6336	1261.6159	0.0178	0	14	5.7	1	GMTAEVGITMPR
b	24	510.7720	1019.5293	1019.5321	-0.0028	1	14	6.9	1	VAKMTVSGK + 2 Acetyl (K); Oxidation (M)
b	64	804.9007	1607.7868	1607.7825	0.0043	1	11	7.2	1	QKCQDETQTISLTK
b	52	710.8379	1419.6612	1419.6783	-0.0170	1	10	8.1	1	QNGWEDGFILK + Acetyl (K)
b	21	505.2696	1008.5247	1008.5170	0.0077	0	10	14	1	MVGTIVIMMK
b	17	435.7732	869.5319	869.5123	0.0196	0	9	11	1	VSLWLPR
b	75	864.4435	1726.8725	1726.8638	0.0086	1	9	14	1	GLEWIGRIDPNDGGTK
b	91	737.7060	2210.0961	2210.0967	-0.0006	0	9	6.7	1	LGEHNINVLEGNQFIDAAK
b	48	696.8434	1391.6722	1391.6767	-0.0045	1	9	17	1	TQRSQHSQHR
b	99	738.0352	2211.0838	2211.0639	0.0199	1	8	7.5	1	MAMNAKQPFMHPVLQEPK + Acetyl (K); Oxidation (M)
b	54	711.3414	1420.6682	1420.6722	-0.0040	1	8	17	1	SKDDSPSYLPTK + 2 Acetyl (K)
b	55	752.8687	1503.7228	1503.7317	-0.0089	1	8	18	1	DGIQTKEHPNPGK + 2 Acetyl (K)
b	98	738.0331	2211.0774	2211.0920	-0.0146	0	7	11	1	LGEHNINVLEGNQFVNSAK
b	77	887.9524	1773.8903	1773.8819	0.0084	1	7	19	1	KGDLLDLAINSCVTVDK + 2 Acetyl (K)
b	71	837.3913	1672.7681	1672.7693	-0.0012	0	6	14	1	DSEGDTPSLINWPSR
b	125	767.7175	2300.1307	2300.1147	0.0160	1	6	13	1	LTSYLVREVDVFSVMGYHK + Acetyl (K)
b	72	857.4080	1712.8014	1712.7981	0.0034	0	6	14	1	FENDAAMVQSWFR
b	79	897.9109	1793.8072	1793.8063	0.0010	0	6	13	1	MQEGDLEMTLALEEK + Acetyl (K); Oxidation (M)
b	18	435.7743	869.5340	869.5222	0.0118	0	6	25	1	DAIVLAVK + Acetyl (K)
b	81	970.9710	1939.9274	1939.9172	0.0102	0	5	17	1	MDQVMQFVPSQQFVK
b	49	701.3616	1400.7086	1400.7048	0.0038	0	5	37	1	VQDGHLLITTYGR + Acetyl (Protein N-term)
b	29	564.2776	1126.5406	1126.5328	0.0078	0	5	28	1	LSSSYACVQK + Acetyl (K)
b	59	774.8672	1547.7197	1547.7225	-0.0027	1	5	24	1	KTAQGGHLCYNPML + Oxidation (M)
b	87	732.0302	2193.0687	2193.0711	-0.0023	0	5	15	1	EMPVQFQVVELPSGHHLCK + Oxidation (M)
b	70	830.9303	1659.8461	1659.8654	-0.0193	1	4	33	1	IQNTIGIKDPSPCFK
b	120	762.7159	2285.1258	2285.1362	-0.0104	0	4	22	1	SATLMVYEDVVQIVSGFQGAR + Oxidation (M)
b	103	742.0341	2223.0806	2223.0994	-0.0188	0	4	24	1	GIEFFMADLDALSPIHTPQR + Oxidation (M)
b	121	762.7219	2285.1438	2285.1362	0.0076	0	4	22	1	SATLMVYEDVVQIVSGFQGAR + Oxidation (M)
b	57	760.8666	1519.7187	1519.7197	-0.0010	1	4	35	1	VCAETHCSMLLKK + Acetyl (K); Oxidation (M)
b	85	1042.0088	2082.0030	2082.0164	-0.0133	1	3	30	1	RSPPLLAGAEEGMSQAPPEAR + Oxidation (M)
b	65	811.9087	1621.8029	1621.7909	0.0120	1	3	46	1	KCLELFTLAEADK + 2 Acetyl (K)
b	89	737.3617	2209.0632	2209.0586	0.0045	1	3	31	1	GFMVQTGDPFGTGRGSSIWAK
b	100	738.0358	2211.0856	2211.1027	-0.0171	1	2	27	1	MLPSSMNSVEVYSGANRILK + Oxidation (M)
b	108	742.7061	2225.0964	2225.1116	-0.0153	1	2	33	1	QAKVWNTYELDLVNYQNK
b	6	412.7527	823.4908	823.4916	-0.0008	1	2	28	1	VASHIKK + Acetyl (K)
b	86	729.0353	2184.0840	2184.0741	0.0099	1	1	37	1	ACIESRVNMVTASYITPAMK
b	7	412.7536	823.4926	823.4803	0.0123	1	1	30	1	KTPGLPK + 2 Acetyl (K)
b	127	767.7215	2300.1428	2300.1432	-0.0004	1	1	38	1	IITPMCSASGIVYKVFDTK + 2 Acetyl (K); Oxidation (M)
b	112	747.0484	2238.1235	2238.1250	-0.0016	1	1	38	1	EVAMIFVNWKELIMCNK + Acetyl (K); Oxidation (M)
b	126	767.7196	2300.1370	2300.1228	0.0142	1	1	44	1	YGRHPLMELPLMINFTGAR + 2 Oxidation (M)
b	131	589.2756	2353.0734	2353.0572	0.0161	0	0	28	1	LEWMMGYISYDGTSTNPNPLK + Oxidation (M)
b	123	767.3908	2299.1505	2299.1557	-0.0052	1	0	54	1	TNGLQETNQRYPGLQEQVPK
b	124	767.3909	2299.1510	2299.1513	-0.0004	0	0	49	1	NMQMMSIEILTLFTELAK + Acetyl (K); 2 Oxidation (M)
b	117	567.5103	2266.0119	2266.0080	0.0039	1	0	27	1	HQREGMGGGAAPQCAGAGTR + Oxidation (M)
b	1	384.2357	766.4568							
b	2	772.3971	771.3899							
b	5	406.2483	810.4821							
b	68	820.3962	1638.7779							
b	78	890.8915	1779.7685							
b	80	904.9436	1807.8726							
b	82	665.6230	1993.8471							
b	84	1033.0019	2063.9892							
b	88	1104.0584	2206.1022							
b	101	738.0408	2211.1006							
b	102	738.0412	2211.1018							
b	104	742.3763	2224.1071							
b	105	742.3773	2224.1101							
b	106	742.3773	2224.1101							
b	107	742.7051	2225.0934							
b	109	745.0318	2232.0736							
b	110	559.7715	2235.0571							

b	111	746.3778	2236.1116
b	113	563.0191	2248.0472
b	114	563.2643	2249.0281
b	115	755.6789	2264.0149
b	116	567.0116	2264.0171
b	118	762.0596	2283.1569
b	119	762.3881	2284.1425
b	122	766.7318	2297.1735
b	128	772.3909	2314.1510
b	129	580.7405	2318.9330
b	130	585.2765	2337.0767

Search Parameters

Type of search : MS/MS Ion Search
Enzyme : Trypsin/P
Variable modifications : Acetyl (K),Acetyl (Protein N-term),Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : \pm 0.02 Da
Fragment Mass Tolerance: \pm 0.3 Da
Max Missed Cleavages : 1
Instrument type : ESI-TRAP
Number of queries : 132

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

Mascot Search Results

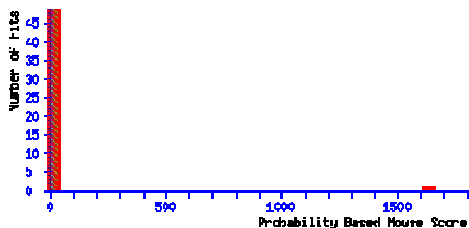
User : Bob
 Email : rdenglis@utmb.edu
 Search title : 11081917.raw #2303 Phospho
 MS data file : tempfile
 Database : NCBI nr 20110707 (14481393 sequences; 4958963357 residues)
 Taxonomy : Mus musculus (house mouse) (143921 sequences)
 Timestamp : 24 Aug 2011 at 16:32:00 GMT
 Protein hits : [gi|124248512](#) carbamoyl-phosphate synthase [ammonia], mitochondrial precursor [Mus musculus]
[gi|26346581](#) unnamed protein product [Mus musculus]
[gi|51092303](#) Try10-like trypsinogen [Mus musculus]
[gi|3093758](#) cyclic AMP specific phosphodiesterase PDE4D5A [Mus musculus]
[gi|148677260](#) mCG126205 [Mus musculus]

NCBI nr [Decoy](#) False discovery rate

Peptide matches above identity threshold 32 2 6.25 %
 Peptide matches above homology or identity threshold 35 2 5.71 %

Probability Based Mowse Score

Ions score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event. Individual ions scores > 31 indicate identity or extensive homology (p<0.05). Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Peptide Summary Report

Format As [Help](#)

Significance threshold p< Max. number of hits

Standard scoring MudPIT scoring Ions score or expect cut-off Show sub-sets

Show pop-ups Suppress pop-ups Sort unassigned Require bold red

Error tolerant

1. [gi|124248512](#) Mass: 164514 Score: 1637 Queries matched: 31 emPAI: 0.66
 carbamoyl-phosphate synthase [ammonia], mitochondrial precursor [Mus musculus]
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Score	Expect	Rank	Peptide
3	406.2214	810.4282	810.4276	0.0007	0	25	0.3	1	R.SFPFVSK.T
4	406.2214	810.4283	810.4276	0.0007	0	(18)	1.9	1	R.SFPFVSK.T
19	453.2583	904.5021	904.5018	0.0003	0	43	0.0037	1	K.LFAEAVQK.S
20	495.2797	988.5447	988.5441	0.0007	0	51	0.0027	1	K.ETLIDLGTK.A
22	508.2393	1014.4641	1014.4658	-0.0017	0	34	0.044	1	R.TFEESFQK.A
23	508.8030	1015.5914	1015.5914	-0.0000	0	38	0.0076	1	K.GTTITSVLPK.P
25	518.7691	1035.5237	1035.5237	0.0000	0	38	0.016	1	K.EIEYEVVR.D
27	545.7980	1089.5815	1089.5819	-0.0004	0	46	0.0021	1	K.VPAIYGDVTR.M
28	551.8086	1101.6027	1101.6030	-0.0002	0	38	0.014	1	K.QNLIAEVSTK.D
30	568.7799	1135.5453	1135.5431	0.0022	0	67	2.9e-005	1	K.VMIGESIDEK.R + Oxidation (M)
31	582.3736	1162.7326	1162.7325	0.0001	0	44	0.00015	1	K.IALGIPLPEIK.N
35	609.3123	1216.6100	1216.6088	0.0012	0	58	0.00018	1	K.SLQWLQEEK.V
36	611.3392	1220.6638	1220.6652	-0.0014	0	61	4.3e-005	1	R.SIFSAVLDELK.V
37	611.8458	1221.6770	1221.6757	0.0013	0	52	0.00037	1	K.ATGYPLAFIAAK.I
38	623.8301	1245.6455	1245.6387	0.0068	0	52	0.00058	1	K.IMGTSPQLIDR.A + Oxidation (M)
40	639.8509	1277.6872	1277.6867	0.0005	0	66	1.6e-005	1	K.TLGVDFIDVATK.V
41	649.8351	1297.6557	1297.6554	0.0003	0	59	0.0001	1	K.LYFEELSLEK.I
44	661.8426	1321.6706	1321.6700	0.0006	0	68	1.4e-005	1	K.AADTIGYVPMIR.S + Oxidation (M)
47	677.3656	1352.7166	1352.7160	0.0006	0	66	1.8e-005	1	R.GQNQPVLNITNR.Q
50	704.8641	1407.7136	1407.7180	-0.0044	0	(63)	4.8e-005	1	K.AFAMTNQILVER.S + Oxidation (M)
51	704.8666	1407.7186	1407.7180	0.0006	0	72	7.2e-006	1	K.AFAMTNQILVER.S + Oxidation (M)
53	710.8513	1419.6880	1419.6841	0.0038	0	77	2.3e-006	1	K.GLNSDSVTETELR.K
56	760.3773	1518.7400	1518.7348	0.0053	0	72	6.1e-006	1	K.ALENMNSLDEIVR.L + Oxidation (M)
62	526.6129	1576.8168	1576.8096	0.0071	1	30	0.074	1	R.QLFSDKLNINEK.I
63	530.2755	1587.8046	1587.8045	0.0001	0	15	3.4	1	R.FLGVAEQLHNEGFK.L
66	812.3985	1622.7823	1622.7822	0.0002	0	92	5.5e-008	1	K.VLGTSVESIMATEDR.Q + Oxidation (M)

b	67	812.3998	1622.7851	1622.7861	-0.0011	0	82	6.2e-007	1	K.IAPSFVAVESMEDALK.A + Oxidation (M)
b	73	862.4122	1722.8098	1722.8101	-0.0002	0	84	3.6e-007	1	K.IEFEGQSVDFVDPNK.Q
b	74	863.9523	1725.8899	1725.8897	0.0002	0	67	1.1e-005	1	R.DGSIDLVLINLPNNNTK.F
b	83	1022.5412	2043.0678	2043.0670	0.0008	0	87	6.2e-008	1	K.TVLMNPNIASVQTNEVGLK.Q + Oxidation (M)
b	132	936.4751	2806.4034	2806.4025	0.0009	1	55	8.4e-005	1	K.IEFEGQSVDFVDPNKQNLIAEVSTK.D

2. [gi|26346581](#) Mass: 90810 Score: 63 Queries matched: 2 emPAI: 0.03
 unnamed protein product [Mus musculus]
 e Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
b 45	663.8489	1325.6833	1325.6827	0.0007	0	59	0.0001	1	K.GTPLDTEVPLER.V
b 61	783.8738	1565.7331	1565.7429	-0.0098	0	4	48	10	K.METVVTSPMEGTIR.K + Oxidation (M)

Proteins matching the same set of peptides:

- [gi|200246](#) Mass: 103041 Score: 61 Queries matched: 2
pyruvate carboxylase [Mus musculus]
- [gi|464506](#) Mass: 129602 Score: 61 Queries matched: 2
RecName: Full=Pyruvate carboxylase, mitochondrial; AltName: Full=Pyruvic carboxylase; Short=PCB; Flags: Precursor
- [gi|74186338](#) Mass: 129778 Score: 61 Queries matched: 2
unnamed protein product [Mus musculus]
- [gi|74201750](#) Mass: 129650 Score: 61 Queries matched: 2
unnamed protein product [Mus musculus]
- [gi|74215392](#) Mass: 129749 Score: 61 Queries matched: 2
unnamed protein product [Mus musculus]
- [gi|251823978](#) Mass: 129618 Score: 61 Queries matched: 2
pyruvate carboxylase, mitochondrial isoform 2 [Mus musculus]
- [gi|251823980](#) Mass: 129750 Score: 61 Queries matched: 2
pyruvate carboxylase, mitochondrial isoform 1 [Mus musculus]

3. [gi|51092303](#) Mass: 26514 Score: 58 Queries matched: 2 emPAI: 0.25
 Try10-like trypsinogen [Mus musculus]
 e Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
b 32	588.3186	1174.6227	1174.6267	-0.0040	0	(45)	0.0027	1	K.TLDNDIMLIK.L
b 34	596.3183	1190.6220	1190.6217	0.0003	0	58	0.00014	1	K.TLDNDIMLIK.L + Oxidation (M)

Proteins matching the same set of peptides:

- [gi|84781771](#) Mass: 26204 Score: 58 Queries matched: 2
trypsin 10 [Mus musculus]

4. [gi|3093758](#) Mass: 23890 Score: 35 Queries matched: 1 emPAI: 0.13
 cyclic AMP specific phosphodiesterase PDE4D5A [Mus musculus]
 e Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
b 16	434.7667	867.5189	867.5178	0.0011	0	35	0.0083	1	K.LSPVISPR.N

Proteins matching the same set of peptides:

- [gi|148686495](#) Mass: 79441 Score: 35 Queries matched: 1
phosphodiesterase 4D, cAMP specific, isoform CRA_c [Mus musculus]

5. [gi|148677260](#) Mass: 227544 Score: 32 Queries matched: 2 emPAI: 0.01
 mCG126205 [Mus musculus]
 e Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
b 67	812.3998	1622.7851	1622.7796	0.0055	1	(23)	0.48	2	K.IQMEEFMAANPSK.I
b 69	820.3981	1638.7817	1638.7745	0.0072	1	32	0.052	1	K.IQMEEFMAANPSK.I + Oxidation (M)

Proteins matching the same set of peptides:

- [gi|81906676](#) Mass: 227475 Score: 30 Queries matched: 2
RecName: Full=Sodium channel protein type 5 subunit alpha; AltName: Full=Sodium channel protein cardiac muscle subunit alpha; AltName:
- [gi|84875498](#) Mass: 227559 Score: 30 Queries matched: 2
sodium channel protein type 5 subunit alpha [Mus musculus]

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

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
b 8	421.7576	841.5007	841.4810	0.0197	0	30	0.069	1	LGTWLPR
b 26	536.3244	1070.6342	1070.6196	0.0145	1	24	0.16	1	DLQLRV TAR
b 15	428.7659	855.5172	855.5112	0.0059	1	23	0.25	1	ALRMLPR
b 97	737.7067	2210.0982	2210.0967	0.0015	0	21	0.46	1	LGEHNINVLEGNEQFIDAAK
b 92	737.7061	2210.0966	2210.0967	-0.0001	0	19	0.72	1	LGEHNINVLEGNEQFIDAAK
b 96	737.7067	2210.0982	2210.0967	0.0014	0	19	0.76	1	LGEHNINVLEGNEQFIDAAK

b	60	780.8987	1559.7828	1559.7654	0.0174	0	19	1.2	1	QWGLLCDLLEQDK
b	9	421.7578	841.5010	841.5134	-0.0123	1	17	1.1	1	LGLRLDR
b	76	864.4443	1726.8740	1726.8638	0.0102	1	17	1.4	1	GLEWIGRIDPNDGGTK
b	93	737.7062	2210.0968	2210.0967	0.0001	0	17	1.2	1	LGEHNINVLEGNEQFIDAAK
b	72	857.4080	1712.8014	1712.8056	-0.0041	1	17	1.9	1	TSDPLKILANADTMK + Oxidation (M); Phospho (ST)
b	90	737.7051	2210.0934	2210.0967	-0.0033	0	17	1.3	1	LGEHNINVLEGNEQFIDAAK
b	10	421.7583	841.5021	841.5021	-0.0000	1	17	1.4	1	LKESLPR
b	33	595.3281	1188.6416	1188.6462	-0.0046	1	16	1.8	1	ITDTISDRLR
b	12	421.7584	841.5023	841.5021	0.0002	0	16	1.5	1	LSVALSPR
b	94	737.7065	2210.0975	2210.0967	0.0008	0	16	1.3	1	LGEHNINVLEGNEQFIDAAK
b	95	737.7065	2210.0976	2210.0967	0.0009	0	16	1.4	1	LGEHNINVLEGNEQFIDAAK
b	13	421.7588	841.5030	841.5021	0.0008	1	16	1.5	1	LKESLPR
b	64	804.9007	1607.7868	1607.8017	-0.0149	0	15	2.8	1	LLPLELFFYLLK + Phospho (ST); Phospho (Y)
b	14	428.7658	855.5171	855.5112	0.0059	1	15	1.6	1	ALRMLPR
b	11	421.7584	841.5022	841.4844	0.0178	0	14	2.3	1	NIMVLPR
b	39	631.8241	1261.6336	1261.6159	0.0178	0	14	4.1	1	GMTAEVGITMPR
b	46	673.8527	1345.6909	1345.6941	-0.0032	1	13	4.3	1	MAAPLRHTLLK + Oxidation (M); Phospho (ST)
b	24	510.7720	1019.5293	1019.5182	0.0111	1	12	6.3	1	MRLDGVASR + Oxidation (M)
b	43	655.8574	1309.7003	1309.7102	-0.0099	1	12	3.6	1	SAPQTLGGGARAPK
b	48	696.8434	1391.6722	1391.6810	-0.0088	0	12	6.9	1	QGSLIQVPSVER + Phospho (ST)
b	29	564.2776	1126.5406	1126.5424	-0.0018	0	12	7.7	1	LIGSHDPVLP + Phospho (ST)
b	52	710.8379	1419.6612	1419.6799	-0.0187	0	11	8	1	FIASFNVVNTIK + Phospho (ST)
b	61	783.8738	1565.7331	1565.7169	0.0162	1	11	9.9	1	VSETSGGKTSGEDANK
b	79	897.9109	1793.8072	1793.8059	0.0013	1	10	10	1	EFLGTTQTASFCGPKK + Phospho (ST)
b	21	505.2696	1008.5247	1008.5170	0.0077	0	10	11	1	MVGTVMKK
b	68	820.3962	1638.7779	1638.7800	-0.0021	1	10	9.5	1	GQLASKSTILCSHK + Phospho (ST)
b	17	435.7732	869.5319	869.5123	0.0196	0	9	5.2	1	VSLWLPR
b	55	752.8687	1503.7228	1503.7275	-0.0047	1	9	13	1	FFKEIWSAAAR + Phospho (ST)
b	49	701.3616	1400.7086	1400.6887	0.0199	1	9	12	1	LGFCEKNVILR + Phospho (ST)
b	75	864.4435	1726.8725	1726.8638	0.0086	1	9	9.9	1	GLEWIGRIDPNGGDTK
b	118	762.0596	2283.1569	2283.1399	0.0170	1	9	6.1	1	EPPGKPGAEALSITPQLLK + Phospho (ST)
b	91	737.7060	2210.0961	2210.0967	-0.0006	0	9	8.1	1	LGEHNINVLEGNEQFIDAAK
b	77	887.9524	1773.8903	1773.8848	0.0055	1	7	14	1	AAMLSELLRYNANLTK + Oxidation (M); Phospho (ST)
b	112	747.0484	2238.1235	2238.1158	0.0077	0	7	8.6	1	DTHSLPPAQILGIQGGGIAR + Phospho (ST)
b	98	738.0331	2211.0774	2211.0920	-0.0146	0	7	14	1	LGEHNINVLEGNEQFVNSAK
b	57	760.8666	1519.7187	1519.7048	0.0139	1	6	22	1	ILDSSINTLTKR + 2 Phospho (ST)
b	71	837.3913	1672.7681	1672.7693	-0.0012	0	6	24	1	DSEGGTSPSLINWPSR
b	86	729.0353	2184.0840	2184.0690	0.0150	0	6	13	1	MTGLESLWVSEVLQLPFR + Phospho (ST)
b	59	774.8672	1547.7197	1547.7345	-0.0147	1	6	28	1	DALEKGAVTSGPAPR + Phospho (ST)
b	81	970.9710	1939.9274	1939.9172	0.0102	0	5	22	1	MDQVMQFVPSQQFVK
b	54	711.3414	1420.6682	1420.6572	0.0109	1	5	32	1	GRSLGAPGQQSQR + Phospho (ST)
b	87	732.0302	2193.0687	2193.0711	-0.0023	0	5	20	1	EMPVQFQVVELPSGHHLCK + Oxidation (M)
b	70	830.9303	1659.8461	1659.8654	-0.0193	1	4	27	1	IQNTIGIKDPSCPFK
b	120	762.7159	2285.1258	2285.1362	-0.0104	0	4	22	1	SATLMVYEDVVQIVSGFQGAR + Oxidation (M)
b	107	742.7051	2225.0934	2225.1068	-0.0134	1	4	24	1	SGKIQFVMSNLPVTLWGR + Phospho (Y)
b	18	435.7743	869.5340	869.5487	-0.0147	0	4	16	1	LWVALLR
b	103	742.0341	2223.0806	2223.0994	-0.0188	0	4	29	1	GIEFFMADLDLSPHPTQR + Oxidation (M)
b	121	762.7219	2285.1438	2285.1362	0.0076	0	4	20	1	SATLMVYEDVVQIVSGFQGAR + Oxidation (M)
b	104	742.3763	2224.1071	2224.0889	0.0182	1	3	25	1	LQGVLEGLNSKTYDTLHR + Phospho (ST)
b	125	767.7175	2300.1307	2300.1242	0.0065	1	3	24	1	LAWTRSFDFEGSLSPVIAPK + Phospho (ST)
b	85	1042.0088	2082.0030	2082.0164	-0.0133	1	3	34	1	RSPPLLAGAEGMSQAPPEAR + Oxidation (M)
b	58	769.3238	1536.6331	1536.6313	0.0018	0	3	57	1	VTMTCVSSSVNSR + Phospho (ST)
b	65	811.9087	1621.8029	1621.7835	0.0194	1	3	50	1	ADSLDEFIEEQKAK
b	89	737.3617	2209.0632	2209.0586	0.0045	1	3	40	1	GFMVQTGDPGTGRGGSSIWAK
b	100	738.0358	2211.0856	2211.1027	-0.0171	1	2	34	1	MLPSSMNSVEVYSGANRILK + Oxidation (M)
b	108	742.7061	2225.0964	2225.1116	-0.0153	1	2	35	1	QAKVWNTYELDLVNYQNK
b	42	655.3232	1308.6318	1308.6187	0.0131	1	2	74	1	AETRAGGGVGLGK + Phospho (ST)
b	130	585.2765	2337.0767	2337.0850	-0.0082	0	2	60	1	GVVPLAGTNGETTQGLDDLSGR + Phospho (ST)
b	82	665.6230	1993.8471	1993.8414	0.0057	0	1	64	1	PYLVMCSEVLGSSAGEK + Oxidation (M); Phospho (ST)
b	123	767.3908	2299.1505	2299.1501	0.0004	1	1	34	1	AKFDGIFESLLPVNGLLSGDK + Phospho (ST)
b	126	767.7196	2300.1370	2300.1228	0.0142	1	1	42	1	YGRHPLEMLPLMINPTGCAR + 2 Oxidation (M)
b	106	742.3773	2224.1101	2224.0963	0.0138	1	1	47	1	MLELTDHISQIGYKVLER + Phospho (ST)
b	116	567.0116	2264.0171	2264.0248	-0.0076	1	1	79	1	IGSTALLYCLCDHRLGAR + 2 Phospho (ST)
b	131	589.2756	2353.0734	2353.0572	0.0161	0	0	72	1	LEWMGYISYDGTSTNYPNLSK + Oxidation (M)
b	78	890.8915	1779.7685	1779.7750	-0.0065	0	0	94	1	LQSMDTGLPEEHLK + Oxidation (M); Phospho (ST)
b	117	567.5103	2266.0119	2266.0080	0.0039	1	0	87	1	HQGREGMQGGGAAPQCPGAGAGR + Oxidation (M)
b	1	384.2357	766.4568							
b	2	772.3971	771.3899							
b	5	406.2483	810.4821							
b	6	412.7527	823.4908							
b	7	412.7536	823.4926							
b	80	904.9436	1807.8726							
b	84	1033.0019	2063.9892							
b	88	1104.0584	2206.1022							
b	99	738.0352	2211.0838							
b	101	738.0408	2211.1006							

b	102	738.0412	2211.1018
b	105	742.3773	2224.1101
b	109	745.0318	2232.0736
b	110	559.7715	2235.0571
b	111	746.3778	2236.1116
b	113	563.0191	2248.0472
b	114	563.2643	2249.0281
b	115	755.6789	2264.0149
b	119	762.3881	2284.1425
b	122	766.7318	2297.1735
b	124	767.3909	2299.1510
b	127	767.7215	2300.1428
b	128	772.3909	2314.1510
b	129	580.7405	2318.9330

Search Parameters

Type of search : MS/MS Ion Search
Enzyme : Trypsin/P
Variable modifications : Oxidation (M),Phospho (ST),Phospho (Y)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : \pm 0.02 Da
Fragment Mass Tolerance: \pm 0.3 Da
Max Missed Cleavages : 1
Instrument type : ESI-TRAP
Number of queries : 132

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