Supplementary Table S3 – MS/MS spectra of proteins identified by a single peptide match in Control *versus* ES(+) analysis

Proteins identified by single peptide matches required identity or extensive homology, and were considered matches when the MS/MS spectrum was of good quality with matching fragment ions above baseline noise, continuity in b- or y-ion series, and fragmentation at proline residues yielding intense y-ions.

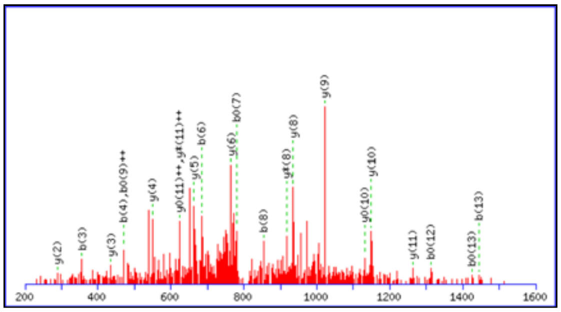
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLELQSIGTNNFLR**
Found in **LETM1_MOUSE**, Leucine zipper-EF-hand-containing transmembrane protein 1, mitochondrial precursor - Mus musculus (Mouse) (Q9Z2I0)

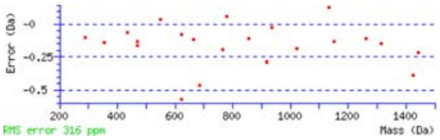
Match to Query 1207: 1616.892184 from(809.453368,2+)
Title: Arrell01090904 scan 2105 2105 (Arrell01090904.2105.2105.2.dta)
Data file Arrell01090904.mgf

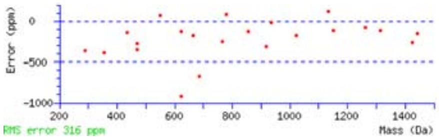
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1616.8886
Ions Score: 47 **Expect:** 8.5e-05
Matches (Bold Red): 22/134 fragment ions using 46 most intense peaks

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493					L							14
2	227.1754	114.0913					L	1504.8118	752.9095	1487.7853	744.3963	1486.8013	743.9043	13
3	**356.2180**	178.6126			338.2074	169.6074	E	1391.7278	696.3675	1374.7012	687.8542	1373.7172	687.3622	12
4	**469.3021**	235.1547			451.2915	226.1494	L	**1262.6852**	631.8462	1245.6586	**623.3329**	1244.6746	**622.8409**	11
5	597.3606	299.1840	580.3341	290.6707	579.3501	290.1787	Q	**1149.6011**	575.3042	1132.5745	566.7909	**1131.5905**	566.2989	10
6	**684.3927**	342.7000	667.3661	334.1867	666.3821	333.6947	S	**1021.5425**	511.2749	1004.5160	502.7616	1003.5320	502.2696	9
7	797.4767	399.2420	780.4502	390.7287	**779.4662**	390.2367	I	**934.5105**	467.7589	**917.4839**	459.2456	916.4999	458.7536	8
8	**854.4982**	427.7527	837.4716	419.2395	836.4876	418.7475	G	821.4264	411.2169	804.3999	402.7036	803.4159	402.2116	7
9	955.5459	478.2766	938.5193	469.7633	937.5353	**469.2713**	T	**764.4050**	382.7061	747.3784	374.1928	746.3944	373.7008	6
10	1069.5888	535.2980	1052.5623	526.7848	1051.5782	526.2928	N	**663.3573**	332.1823	646.3307	323.6690			5
11	1183.6317	592.3195	1166.6052	583.8062	1165.6212	583.3142	N	**549.3144**	275.1608	532.2878	266.6475			4
12	1330.7001	665.8537	1313.6736	657.3404	**1312.6896**	656.8484	F	**435.2714**	218.1394	418.2449	209.6261			3
13	**1443.7842**	722.3957	1426.7577	713.8825	**1425.7736**	713.3905	L	**288.2030**	144.6051	271.1765	136.0919			2
14							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of LLELQSIGTNNFLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.8	1616.8886	0.0036	LLELQSIGTNNFLR

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

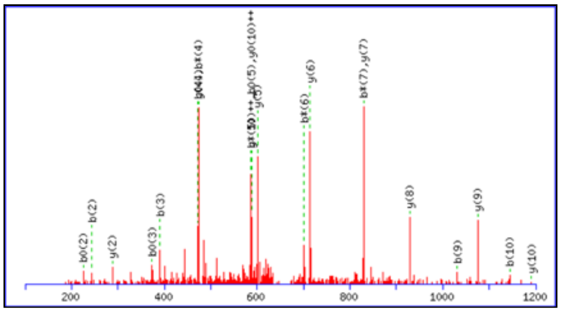
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QDFVDLQGQLR**
Found in **CACP_MOUSE**, Carnitine O-acetyltransferase OS=Mus musculus GN=Crat PE=1 SV=2 (sp) (P47934)

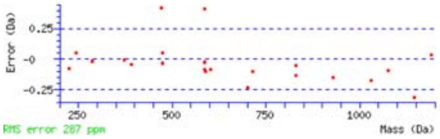
Match to Query 1090: 1317.667574 from(659.841063,2+)
Title: Arrell01090905 scan 1444 1444 (Arrell01090905.1444.1444.2.dta)
Data file Arrell01090905.mgf

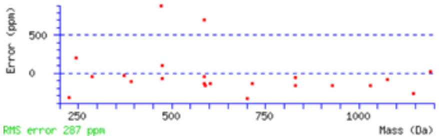
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1317.6677
Ions Score: 71 **Expect:** 1.2e-05
Matches (Bold Red): 22/106 fragment ions using 28 most intense peaks

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	129.0659	65.0366	112.0393	56.5233			Q							11
2	**244.0928**	122.5500	227.0662	114.0368	**226.0822**	113.5448	D	**1190.6164**	595.8118	1173.5899	**587.2986**	1172.6058	**586.8066**	10
3	**391.1612**	196.0842	374.1347	187.5710	**373.1506**	187.0790	F	**1075.5895**	538.2984	1058.5629	529.7851	1057.5789	529.2931	9
4	490.2296	245.6185	**473.2031**	237.1052	**472.2191**	236.6132	V	**928.5211**	464.7642	911.4945	456.2509	910.5105	455.7589	8
5	605.2566	303.1319	**588.2300**	294.6186	**587.2460**	294.1266	D	**829.4526**	415.2300	812.4261	406.7167	811.4421	406.2247	7
6	718.3406	359.6740	**701.3141**	351.1607	700.3301	350.6687	L	**714.4257**	357.7165	697.3992	349.2032			6
7	846.3992	423.7032	**829.3727**	415.1900	828.3886	414.6980	Q	**601.3416**	301.1745	584.3151	292.6612			5
8	903.4207	452.2140	886.3941	443.7007	885.4101	443.2087	G	**473.2831**	237.1452	456.2565	228.6319			4
9	**1031.4793**	516.2433	1014.4527	507.7300	1013.4687	507.2380	Q	416.2616	208.6344	399.2350	200.1212			3
10	**1144.5633**	572.7853	1127.5368	564.2720	1126.5528	563.7800	L	**288.2030**	144.6051	271.1765	136.0919			2
11							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of QDFVDLQGQLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
70.9	1317.6677	-0.0002	QDFVDLQGQLR
11.8	1317.6639	0.0037	MGILDIEVWGK
9.8	1317.6711	-0.0035	AGLETMDKAVQR
9.4	1317.6686	-0.0010	CLLAWMQQGLR
9.1	1317.6599	0.0077	MDDQLDAGVKVK
8.5	1317.6645	0.0031	MAASAARGAMALR
8.0	1317.6677	-0.0001	IDFGGKPDKEGR
7.5	1317.6664	0.0012	VESGIVEETLDK
7.2	1316.6619	1.0057	GVAESCLQRAAR
6.9	1317.6711	-0.0035	KPNMTNQVTAAK

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

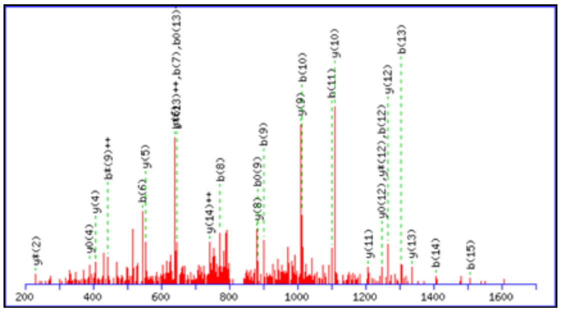
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGFAGVVQEISFGTTK**
Found in **TCPE_MOUSE**, T-complex protein 1 subunit epsilon (TCP-1-epsilon) (CCT-epsilon) - Mus musculus (Mouse) (P80316)

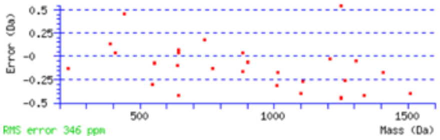
Match to Query 1295: 1652.880834 from(827.447693,2+)
Title: Arrell01090907 scan 2181 2181 (Arrell01090907.2181.2181.2.dta)
Data file Arrell01090907.mgf

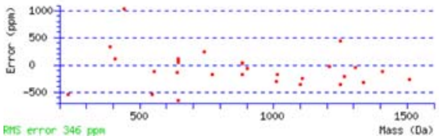
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range



```
Monoisotopic mass of neutral peptide Mr(calc): 1652.8774
Ions Score: 65  Expect: 5.6e-06
Matches (Bold Red): 28/148 fragment ions using 49 most intense peaks
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493					**L**							**16**
2	171.1128	86.0600					**G**	1540.8006	770.9039	1523.7740	762.3907	1522.7900	761.8986	**15**
3	318.1812	159.5942					**F**	1483.7791	**742.3932**	1466.7526	733.8799	1465.7686	733.3879	**14**
4	389.2183	195.1128					**A**	**1336.7107**	668.8590	1319.6842	660.3457	1318.7001	659.8537	**13**
5	446.2398	223.6235					**G**	**1265.6736**	633.3404	**1248.6470**	624.8272	**1247.6630**	624.3352	**12**
6	**545.3082**	273.1577					**V**	**1208.6521**	604.8297	1191.6256	596.3164	1190.6416	595.8244	**11**
7	**644.3766**	322.6920					**V**	**1109.5837**	555.2955	1092.5572	546.7822	1091.5732	546.2902	**10**
8	**772.4352**	386.7212	755.4087	378.2080			**Q**	**1010.5153**	505.7613	993.4888	497.2480	992.5047	496.7560	**9**
9	**901.4778**	451.2425	884.4512	**442.7293**	**883.4672**	442.2373	**E**	**882.4567**	441.7320	865.4302	433.2187	864.4462	432.7267	**8**
10	**1014.5619**	507.7846	997.5353	499.2713	996.5513	498.7793	**I**	753.4141	377.2107	736.3876	368.6974	735.4036	368.2054	**7**
11	**1101.5939**	551.3006	1084.5673	542.7873	1083.5833	542.2953	**S**	**640.3301**	320.6687	623.3035	312.1554	622.3195	311.6634	**6**
12	**1248.6623**	624.8348	1231.6358	616.3215	1230.6517	615.8295	**F**	**553.2980**	277.1527	536.2715	268.6394	535.2875	268.1474	**5**
13	**1305.6838**	653.3455	1288.6572	**644.8322**	1287.6732	**644.3402**	**G**	**406.2296**	203.6185	389.2031	195.1052	**388.2191**	194.6132	**4**
14	**1406.7314**	703.8694	1389.7049	695.3561	1388.7209	694.8641	**T**	349.2082	175.1077	332.1816	166.5944	331.1976	166.1024	**3**
15	**1507.7791**	754.3932	1490.7526	745.8799	1489.7686	745.3879	**T**	248.1605	124.5839	**231.1339**	116.0706	230.1499	115.5786	**2**
16							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of LGFAGVVQEISFGTTK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
64.7	1652.8774	0.0034	LGFAGVVQEISFGTTK
1.2	1652.8847	-0.0039	MKLPIFIADAFTTK

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

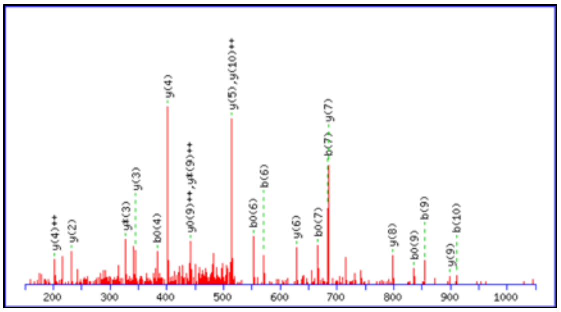
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **GETLGIIGLGR**
Found in **CTBP1_MOUSE**, C-terminal-binding protein 1 (EC 1.1.1.-) (CtBP1) - Mus musculus (Mouse) (O88712)

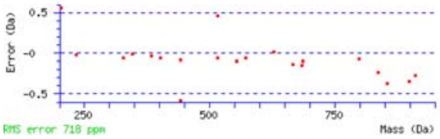
Match to Query 653: 1084.624244 from(543.319398,2+)
Title: Arrell01090915 scan 1638 1638 (Arrell01090915.1638.1638.2.dta)
Data file Arrell01090915.mgf

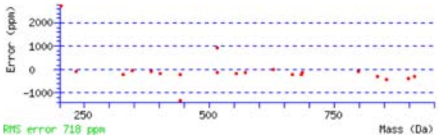
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1050 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1084.6241
Ions Score: 64 **Expect:** 8e-06
Matches (Bold Red): 21/82 fragment ions using 28 most intense peaks

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180			G							11
2	187.0713	94.0393	169.0608	85.0340	E	1028.6099	**514.8086**	1011.5833	506.2953	1010.5993	505.8033	10
3	288.1190	144.5631	270.1084	135.5579	T	**899.5673**	450.2873	882.5407	**441.7740**	881.5567	**441.2820**	9
4	401.2031	201.1052	**383.1925**	192.0999	L	**798.5196**	399.7634	781.4931	391.2502			8
5	458.2245	229.6159	440.2140	220.6106	G	**685.4355**	343.2214	668.4090	334.7081			7
6	**571.3086**	286.1579	**553.2980**	277.1527	I	**628.4141**	314.7107	611.3875	306.1974			6
7	**684.3927**	342.7000	**666.3821**	333.6947	I	**515.3300**	258.1686	498.3035	249.6554			5
8	741.4141	371.2107	723.4036	362.2054	G	**402.2459**	**201.6266**	385.2194	193.1133			4
9	**854.4982**	427.7527	**836.4876**	418.7475	L	**345.2245**	173.1159	**328.1979**	164.6026			3
10	**911.5197**	456.2635	893.5091	447.2582	G	**232.1404**	116.5738	215.1139	108.0606			2
11					R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of GETLGIIGLGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
64.5	1084.6241	0.0002	GETLGIIGLGR
17.3	1084.6240	0.0002	NASLEVALLR
14.1	1084.6240	0.0002	DTILQLNLR
7.8	1084.6215	0.0027	LKCIPLWR
7.1	1084.6240	0.0002	GLAGAVSELLR
6.4	1084.6240	0.0002	ALEEKLVGAR
6.4	1084.6175	0.0067	GLRLCTPLGR
5.7	1084.6240	0.0002	AVITANLDIR
5.6	1084.6314	-0.0072	GKPMELIIGK
4.3	1084.6240	0.0002	DLASVQALLR

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

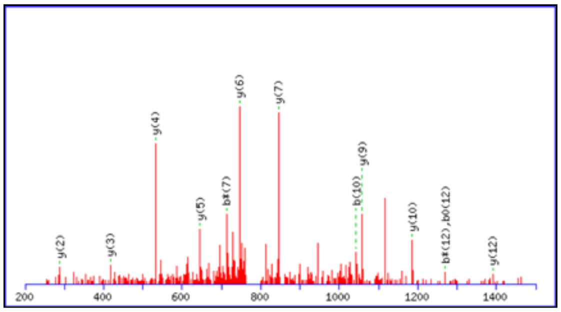
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALGFQNVVTIDELR**
Found in **CECR5_MOUSE**, Cat eye syndrome critical region protein 5 homolog precursor - Mus musculus (Mouse) (Q91WM2)

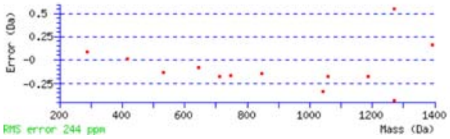
Match to Query 1121: 1573.850074 from(787.932313,2+)
Title: Arrell01090918 scan 1871 1871 (Arrell01090918.1871.1871.2.dta)
Data file Arrell01090918.mgf

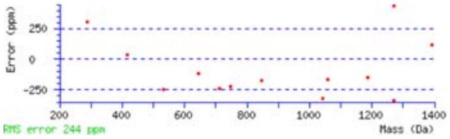
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1573.8464
Ions Score: 57 **Expect:** 4e-05
Matches (Bold Red): 13/128 fragment ions using 18 most intense peaks

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.0444	36.5258					A							14
2	185.1285	93.0679					L	1503.8166	752.4119	1486.7900	743.8986	1485.8060	743.4066	13
3	242.1499	121.5786					G	**1390.7325**	695.8699	1373.7060	687.3566	1372.7219	686.8646	12
4	389.2183	195.1128					F	1333.7110	667.3592	1316.6845	658.8459	1315.7005	658.3539	11
5	517.2769	259.1421	500.2504	250.6288			Q	**1186.6426**	593.8250	1169.6161	585.3117	1168.6321	584.8197	10
6	631.3198	316.1636	614.2933	307.6503			N	**1058.5840**	529.7957	1041.5575	521.2824	1040.5735	520.7904	9
7	730.3883	365.6978	**713.3617**	357.1845			V	944.5411	472.7742	927.5146	464.2609	926.5306	463.7689	8
8	829.4567	415.2320	812.4301	406.7187			V	**845.4727**	423.2400	828.4462	414.7267	827.4621	414.2347	7
9	930.5043	465.7558	913.4778	457.2425	912.4938	456.7505	T	**746.4043**	373.7058	729.3777	365.1925	728.3937	364.7005	6
10	**1043.5884**	522.2978	1026.5619	513.7846	1025.5778	513.2926	I	**645.3566**	323.1819	628.3301	314.6687	627.3461	314.1767	5
11	1158.6154	579.8113	1141.5888	571.2980	1140.6048	570.8060	D	**532.2726**	266.6399	515.2460	258.1266	514.2620	257.6346	4
12	1287.6579	644.3326	**1270.6314**	635.8193	**1269.6474**	635.3273	E	**417.2456**	209.1264	400.2191	200.6132	399.2350	200.1212	3
13	1400.7420	700.8746	1383.7155	692.3614	1382.7314	691.8694	L	**288.2030**	144.6051	271.1765	136.0919			2
14							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of ALGFQNVVTIDELR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.7	1573.8464	0.0037	ALGFQNVVTIDELR
0.5	1573.8563	-0.0062	TDDAEISIKIQLTK

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

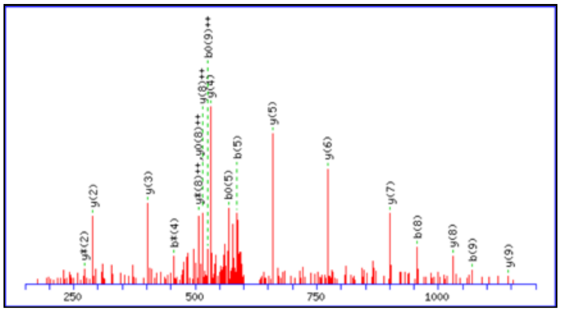
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TNQELQEINR**
Found in **ANXA2_MOUSE**, Annexin A2 (Annexin-2) (Annexin II) (Lipocortin II) (Calpactin I heavy chain) (Chromobindin-8) (p36) (Protein I) (Placental anticoagulant protein IV) (PAP-IV) - Mus musculus (Mouse) (P07356)

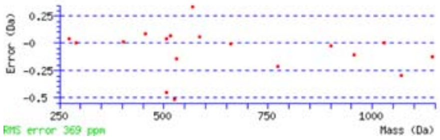
Match to Query 811: 1243.615814 from(622.815183,2+)
Title: Arrell01100927 scan 576 576 (Arrell01100927.576.576.2.dta)
Data file Arrell01100927.mgf

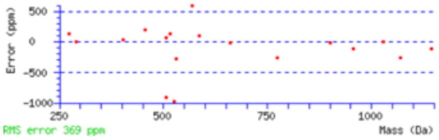
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1200 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1243.6156
Ions Score: 63 **Expect:** 1.5e-05
Matches (Bold Red): 18/100 fragment ions using 25 most intense peaks

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	T							10
2	216.0979	108.5526	199.0713	100.0393	198.0873	99.5473	N	**1143.5753**	572.2913	1126.5487	563.7780	1125.5647	563.2860	9
3	344.1565	172.5819	327.1299	164.0686	326.1459	163.5766	Q	**1029.5323**	**515.2698**	1012.5058	**506.7565**	1011.5218	**506.2645**	8
4	473.1991	237.1032	**456.1725**	228.5899	455.1885	228.0979	E	**901.4738**	451.2405	884.4472	442.7272	883.4632	442.2352	7
5	**586.2831**	293.6452	569.2566	285.1319	**568.2726**	284.6399	L	**772.4312**	386.7192	755.4046	378.2060	754.4206	377.7139	6
6	714.3417	357.6745	697.3151	349.1612	696.3311	348.6692	Q	**659.3471**	330.1772	642.3206	321.6639	641.3365	321.1719	5
7	843.3843	422.1958	826.3577	413.6825	825.3737	413.1905	E	**531.2885**	266.1479	514.2620	257.6346	513.2780	257.1426	4
8	**956.4684**	478.7378	939.4418	470.2245	938.4578	469.7325	I	**402.2459**	201.6266	385.2194	193.1133			3
9	**1070.5113**	535.7593	1053.4847	527.2460	1052.5007	**526.7540**	N	**289.1619**	145.0846	**272.1353**	136.5713			2
10							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of TNQELQEINR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
63.4	1243.6156	0.0002	TNQELQEINR
10.9	1243.6156	0.0002	EKAEGDAAALNR
7.2	1243.6231	-0.0072	TQMAEVLPSPR
2.4	1243.6244	-0.0086	GHIQMFERAR
1.6	1242.6204	0.9954	LENDQIENLR
1.5	1242.6105	1.0053	RWEQLDPSGR

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

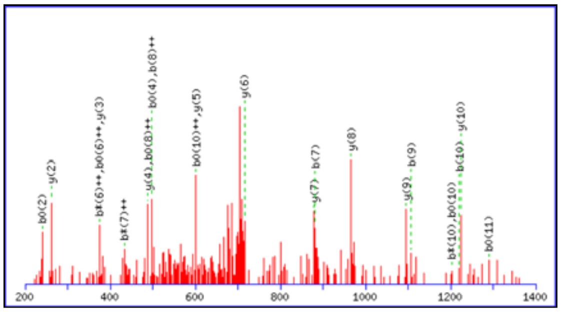
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EKEESYDLILSR**
Found in **GSTA4_MOUSE**, Glutathione S-transferase A4 (EC 2.5.1.18) (GST A4-4) (GSTA4-4) (Glutathione S-transferase 5.7) (GST 5.7) (GST class-alpha member 4) - Mus musculus (Mouse) (P24472)

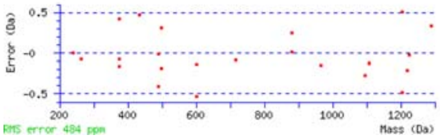
Match to Query 1025: 1480.743744 from(741.379148,2+)
Title: Arrell01100938 scan 1096 1096 (Arrell01100938.1096.1096.2.dta)
Data file Arrell01100938.mgf

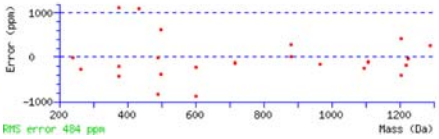
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1480.7409
Ions Score: 50 **Expect:** 0.0003
Matches (Bold Red): 23/128 fragment ions using 39 most intense peaks

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	130.0499	65.5286			112.0393	56.5233	E							12
2	258.1448	129.5761	241.1183	121.0628	**240.1343**	120.5708	K	1352.7056	676.8564	1335.6791	668.3432	1334.6951	667.8512	11
3	387.1874	194.0974	370.1609	185.5841	369.1769	185.0921	E	**1224.6107**	612.8090	1207.5841	604.2957	1206.6001	603.8037	10
4	516.2300	258.6186	499.2035	250.1054	**498.2195**	249.6134	E	**1095.5681**	548.2877	1078.5415	539.7744	1077.5575	539.2824	9
5	603.2620	302.1347	586.2355	293.6214	585.2515	293.1294	S	**966.5255**	483.7664	949.4989	475.2531	948.5149	474.7611	8
6	766.3254	383.6663	749.2988	**375.1531**	748.3148	**374.6610**	Y	**879.4934**	440.2504	862.4669	431.7371	861.4829	431.2451	7
7	**881.3523**	441.1798	864.3258	**432.6665**	863.3418	432.1745	D	**716.4301**	358.7187	699.4036	350.2054	698.4195	349.7134	6
8	994.4364	**497.7218**	977.4098	489.2086	976.4258	**488.7165**	L	**601.4032**	301.2052	584.3766	292.6919	583.3926	292.1999	5
9	**1107.5204**	554.2639	1090.4939	545.7506	1089.5099	545.2586	I	**488.3191**	244.6632	471.2926	236.1499	470.3085	235.6579	4
10	**1220.6045**	610.8059	**1203.5780**	602.2926	**1202.5939**	**601.8006**	L	**375.2350**	188.1212	358.2085	179.6079	357.2245	179.1159	3
11	1307.6365	654.3219	1290.6100	645.8086	**1289.6260**	645.3166	S	**262.1510**	131.5791	245.1244	123.0659	244.1404	122.5738	2
12							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of EKEESYDLILSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.8	1480.7409	0.0029	EKEESYDLILSR

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

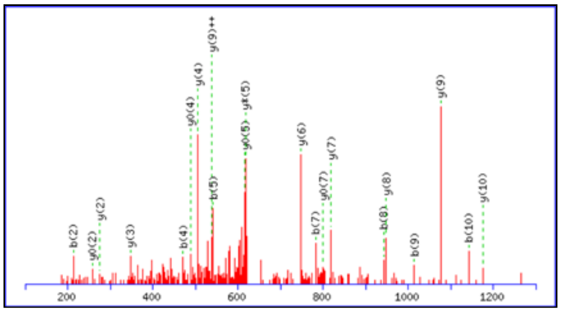
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LVEEAIQCAEK**
Found in **ECHM_MOUSE**, Enoyl-CoA hydratase, mitochondrial precursor (EC 4.2.1.17) (Short chain enoyl-CoA hydratase) (SCEH) (Enoyl-CoA hydratase 1) - Mus musculus (Mouse) (Q8BH95)

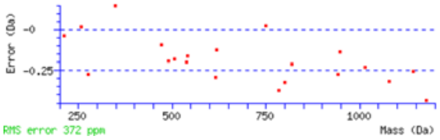
Match to Query 843: 1288.635964 from(645.325258,2+)
Title: Arrell01100939 scan 711 711 (Arrell01100939.711.711.2.dta)
Data file Arrell01100939.mgf

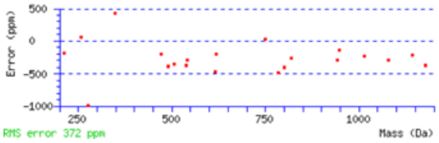
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1288.6333
Variable modifications:
C8 : Carbamidomethyl (C)
Ions Score: 55 **Expect:** 0.00011
Matches (Bold Red): 21/102 fragment ions using 36 most intense peaks

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							11
2	**213.1598**	107.0835					V	**1176.5565**	588.7819	1159.5300	580.2686	1158.5460	579.7766	10
3	342.2023	171.6048			324.1918	162.5995	E	**1077.4881**	**539.2477**	1060.4616	530.7344	1059.4775	530.2424	9
4	**471.2449**	236.1261			453.2344	227.1208	E	**948.4455**	474.7264	931.4190	466.2131	930.4349	465.7211	8
5	**542.2821**	271.6447			524.2715	262.6394	A	**819.4029**	410.2051	802.3764	401.6918	**801.3924**	401.1998	7
6	655.3661	328.1867			637.3556	319.1814	I	**748.3658**	374.6865	731.3393	366.1733	730.3552	365.6813	6
7	**783.4247**	392.2160	766.3981	383.7027	765.4141	383.2107	Q	635.2817	318.1445	**618.2552**	309.6312	**617.2712**	309.1392	5
8	**943.4554**	472.2313	926.4288	463.7180	925.4448	463.2260	C	**507.2232**	254.1152	490.1966	245.6019	**489.2126**	245.1099	4
9	**1014.4925**	507.7499	997.4659	499.2366	996.4819	498.7446	A	**347.1925**	174.0999	330.1660	165.5866	329.1819	165.0946	3
10	**1143.5351**	572.2712	1126.5085	563.7579	1125.5245	563.2659	E	**276.1554**	138.5813	259.1288	130.0681	**258.1448**	129.5761	2
11							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of LVEEAIQCAEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.4	1288.6333	0.0027	LVEEAIQCAEK
3.0	1288.6445	-0.0086	LVDCQRELEK
2.6	1288.6299	0.0061	DDIYEHIKEK
2.2	1288.6299	0.0061	LEIWDTAGQEK
1.9	1287.6241	1.0119	CGPRLSAEAAEK

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