Supplementary Table S4 – MS/MS spectra of proteins identified by a single peptide match in ES(+) *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.

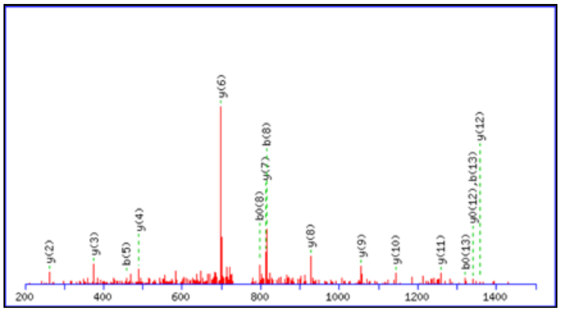
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GVVDSEDIPLNLSR**
Found in **TRAP1_MOUSE**, Heat shock protein 75 kDa, mitochondrial precursor (HSP 75) (Tumor necrosis factor type 1 receptor-associated protein) (TRAP-1) (TNFR-associated protein 1) - Mus musculus (Mouse) (Q9CQN1)

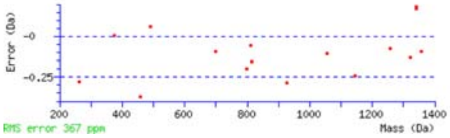
Match to Query 1371: 1512.779754 from(757.397153,2+)
Title: Arrell09040801 scan 1550 1550 (Arrell09040801.1550.1550.2.dta)
Data file Arrell09040801.mgf

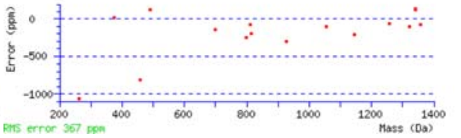
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 200 to 1500 Da [Full range]



Monoisotopic mass of neutral peptide Mr(calc): 1512.7784
Ions Score: 61 **Expect:** 6.1e-06
Matches (Bold Red): 16/128 fragment ions using 33 most intense peaks

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							14
2	157.0972	79.0522					V	1456.7642	728.8857	1439.7376	720.3725	1438.7536	719.8805	13
3	256.1656	128.5864					V	**1357.6958**	679.3515	1340.6692	670.8383	**1339.6852**	670.3462	12
4	371.1925	186.0999			353.1819	177.0946	D	**1258.6274**	629.8173	1241.6008	621.3040	1240.6168	620.8120	11
5	**458.2245**	229.6159			440.2140	220.6106	S	**1143.6004**	572.3039	1126.5739	563.7906	1125.5899	563.2986	10
6	587.2671	294.1372			569.2566	285.1319	E	**1056.5684**	528.7878	1039.5419	520.2746	1038.5578	519.7826	9
7	702.2941	351.6507			684.2835	342.6454	D	**927.5258**	464.2665	910.4993	455.7533	909.5152	455.2613	8
8	**815.3781**	408.1927			**797.3676**	399.1874	I	**812.4989**	406.7531	795.4723	398.2398	794.4883	397.7478	7
9	912.4309	456.7191			894.4203	447.7138	P	**699.4148**	350.2110	682.3882	341.6978	681.4042	341.2058	6
10	1025.5150	513.2611			1007.5044	504.2558	L	602.3620	301.6847	585.3355	293.1714	584.3515	292.6794	5
11	1139.5579	570.2826	1122.5313	561.7693	1121.5473	561.2773	N	**489.2780**	245.1426	472.2514	236.6293	471.2674	236.1373	4
12	1252.6420	626.8246	1235.6154	618.3113	1234.6314	617.8193	L	**375.2350**	188.1212	358.2085	179.6079	357.2245	179.1159	3
13	**1339.6740**	670.3406	1322.6474	661.8274	**1321.6634**	661.3353	S	**262.1510**	131.5791	245.1244	123.0659	244.1404	122.5738	2
14							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
60.8	1512.7784	0.0014	GVVDSEDIPLNLSR
60.8	1512.7784	0.0014	GVVDSEDLPLNISR

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

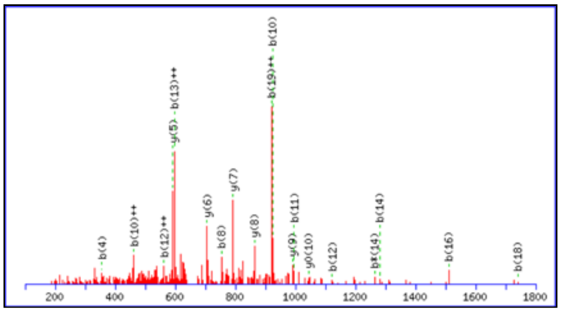
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IGIASQALGIAQASLDCAVK**
Found in **ACADS_MOUSE**, Short-chain specific acyl-CoA dehydrogenase, mitochondrial precursor (EC 1.3.99.2) (SCAD) (Butyryl-CoA dehydrogenase) - Mus musculus (Mouse) (Q07417)

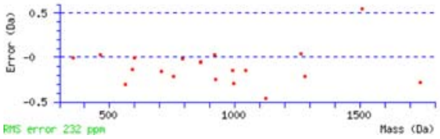
Match to Query 1669: 1985.059716 from(662.693848,3+)
Title: Arrell09040812 scan 2509 2509 (Arrell09040812.2509.2509.3.dta)
Data file Arrell09040812.mgf

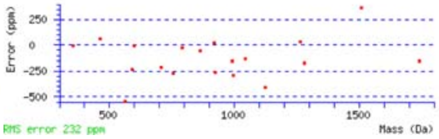
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1985.0615
Variable modifications:
C17 : Carbamidomethyl (C)
Ions Score: 41 **Expect:** 0.00024
Matches (Bold Red): 19/202 fragment ions using 37 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					I							20
2	171.1128	86.0600					G	1872.9848	936.9960	1855.9582	928.4828	1854.9742	927.9907	19
3	284.1969	142.6021					I	1815.9633	908.4853	1798.9368	899.9720	1797.9528	899.4800	18
4	**355.2340**	178.1206					A	1702.8793	851.9433	1685.8527	843.4300	1684.8687	842.9380	17
5	442.2660	221.6366			424.2554	212.6314	S	1631.8421	816.4247	1614.8156	807.9114	1613.8316	807.4194	16
6	570.3246	285.6659	553.2980	277.1527	552.3140	276.6606	Q	1544.8101	772.9087	1527.7836	764.3954	1526.7995	763.9034	15
7	641.3617	321.1845	624.3352	312.6712	623.3511	312.1792	A	1416.7515	708.8794	1399.7250	700.3661	1398.7410	699.8741	14
8	**754.4458**	377.7265	737.4192	369.2132	736.4352	368.7212	L	1345.7144	673.3608	1328.6879	664.8476	1327.7039	664.3556	13
9	811.4672	406.2373	794.4407	397.7240	793.4567	397.2320	G	1232.6304	616.8188	1215.6038	608.3055	1214.6198	607.8135	12
10	**924.5513**	**462.7793**	907.5247	454.2660	906.5407	453.7740	I	1175.6089	588.3081	1158.5823	579.7948	1157.5983	579.3028	11
11	**995.5884**	498.2978	978.5619	489.7846	977.5778	489.2926	A	1062.5248	531.7661	1045.4983	523.2528	**1044.5143**	522.7608	10
12	**1123.6470**	**562.3271**	1106.6204	553.8139	1105.6364	553.3218	Q	**991.4877**	496.2475	974.4612	487.7342	973.4771	487.2422	9
13	1194.6841	**597.8457**	1177.6576	589.3324	1176.6735	588.8404	A	**863.4291**	432.2182	846.4026	423.7049	845.4186	423.2129	8
14	**1281.7161**	641.3617	**1264.6896**	632.8484	1263.7056	632.3564	S	**792.3920**	396.6996	775.3655	388.1864	774.3815	387.6944	7
15	1394.8002	697.9037	1377.7736	689.3905	1376.7896	688.8985	L	**705.3600**	353.1836	688.3334	344.6704	687.3494	344.1784	6
16	**1509.8271**	755.4172	1492.8006	746.9039	1491.8166	746.4119	D	**592.2759**	296.6416	575.2494	288.1283	574.2654	287.6363	5
17	1669.8578	835.4325	1652.8312	826.9193	1651.8472	826.4273	C	477.2490	239.1281	460.2224	230.6149			4
18	**1740.8949**	870.9511	1723.8684	862.4378	1722.8843	861.9458	A	317.2183	159.1128	300.1918	150.5995			3
19	1839.9633	**920.4853**	1822.9368	911.9720	1821.9528	911.4800	V	246.1812	123.5942	229.1547	115.0810			2
20							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.0	1985.0615	-0.0018	IGIASQALGIAQASLDCAVK

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

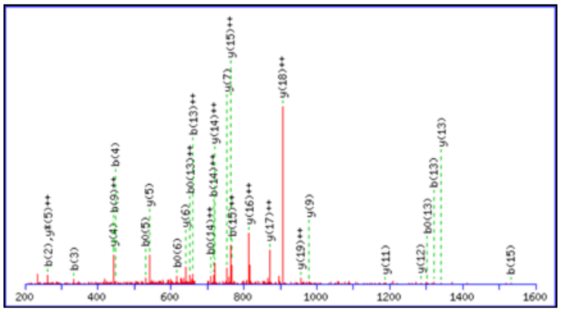
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YVALTSPGPHALLLVVPLGR**
Found in **GIMA4_MOUSE**, GTPase IMAP family member 4 (Immunity-associated protein 4) (Immunity-associated nucleotide 1 protein) - Mus musculus (Mouse) (Q99JY3)

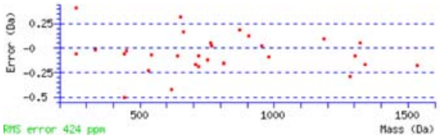
Match to Query 1730: 2072.215536 from(691.745788,3+)
Title: Arrell09040812 scan 2377 2377 (Arrell09040812.2377.2377.3.dta)
Data file Arrell09040812.mgf

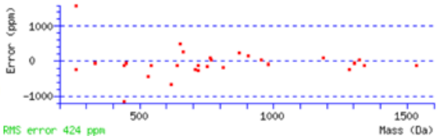
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 2072.2146
Ions Score: 45 **Expect:** 1e-05
Matches (Bold Red): 29/154 fragment ions using 65 most intense peaks

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	164.0706	82.5389			Y							20
2	**263.1390**	132.0731			V	1910.1586	**955.5829**	1893.1320	947.0697	1892.1480	946.5776	19
3	**334.1761**	167.5917			A	1811.0902	**906.0487**	1794.0636	897.5354	1793.0796	897.0434	18
4	**447.2602**	224.1337			L	1740.0531	**870.5302**	1723.0265	862.0169	1722.0425	861.5249	17
5	548.3079	274.6576	**530.2973**	265.6523	T	1626.9690	**813.9881**	1609.9424	805.4749	1608.9584	804.9828	16
6	635.3399	318.1736	**617.3293**	309.1683	S	1525.9213	**763.4643**	1508.8948	754.9510	1507.9107	754.4590	15
7	732.3927	366.7000	714.3821	357.6947	P	1438.8893	**719.9483**	1421.8627	711.4350			14
8	789.4141	395.2107	771.4036	386.2054	G	**1341.8365**	671.4219	1324.8100	662.9086			13
9	886.4669	**443.7371**	868.4563	434.7318	P	**1284.8151**	642.9112	1267.7885	634.3979			12
10	1023.5258	512.2665	1005.5152	503.2613	H	**1187.7623**	594.3848	1170.7357	585.8715			11
11	1094.5629	547.7851	1076.5524	538.7798	A	1050.7034	525.8553	1033.6768	517.3421			10
12	1207.6470	604.3271	1189.6364	595.3218	L	**979.6663**	490.3368	962.6397	481.8235			9
13	**1320.7310**	**660.8692**	**1302.7205**	**651.8639**	L	866.5822	433.7947	849.5557	425.2815			8
14	1433.8151	**717.4112**	1415.8045	**708.4059**	L	**753.4981**	377.2527	736.4716	368.7394			7
15	**1532.8835**	**766.9454**	1514.8730	757.9401	V	**640.4141**	320.7107	623.3875	312.1974			6
16	1631.9519	816.4796	1613.9414	807.4743	V	**541.3457**	271.1765	524.3191	**262.6632**			5
17	1729.0047	865.0060	1710.9941	856.0007	P	**442.2772**	221.6423	425.2507	213.1290			4
18	1842.0888	921.5480	1824.0782	912.5427	L	345.2245	173.1159	328.1979	164.6026			3
19	1899.1102	950.0588	1881.0997	941.0535	G	232.1404	116.5738	215.1139	108.0606			2
20					R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.8	2072.2146	0.0009	YVALTSPGPHALLLVVPLGR

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

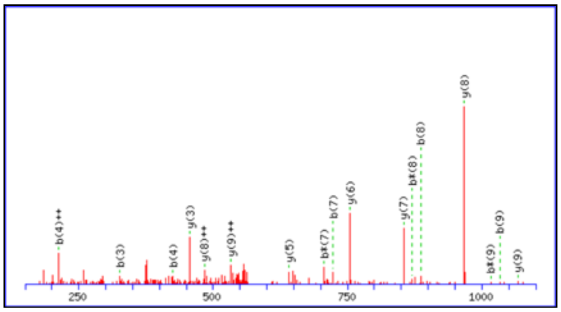
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LVLVNAIYFK**
Found in **ILEUA_MOUSE**, Leukocyte elastase inhibitor A (Serpin B1a) (Serine protease inhibitor EIA) - Mus musculus (Mouse) (Q9D154)

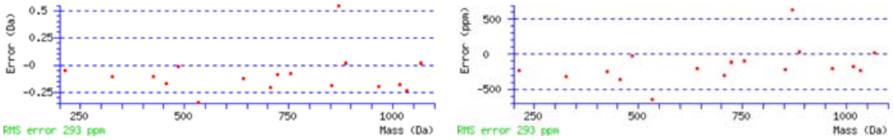
Match to Query 948: 1178.705414 from(590.359983,2+)
Title: Arrell09040812 scan 2119 2119 (Arrell09040812.2119.2119.2.dta)
Data file Arrell09040812.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1100 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1178.7063
Ions Score: 47 **Expect:** 3.5e-05
Matches (Bold Red): 18/64 fragment ions using 29 most intense peaks

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	114.0913	57.5493			L					10
2	**213.1598**	107.0835			V	**1066.6295**	**533.8184**	1049.6030	525.3051	9
3	**326.2438**	163.6255			L	**967.5611**	**484.2842**	950.5346	475.7709	8
4	**425.3122**	**213.1598**			V	**854.4771**	427.7422	837.4505	419.2289	7
5	539.3552	270.1812	522.3286	261.6679	N	**755.4087**	378.2080	738.3821	369.6947	6
6	610.3923	305.6998	593.3657	297.1865	A	**641.3657**	321.1865	624.3392	312.6732	5
7	**723.4763**	362.2418	**706.4498**	353.7285	I	570.3286	285.6679	553.3021	277.1547	4
8	**886.5397**	443.7735	**869.5131**	435.2602	Y	**457.2445**	229.1259	440.2180	220.6126	3
9	**1033.6081**	517.3077	**1016.5815**	508.7944	F	294.1812	147.5942	277.1547	139.0810	2
10					K	147.1128	74.0600	130.0863	65.5468	1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.7	1178.7063	-0.0009	LVLVNAIYFK

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

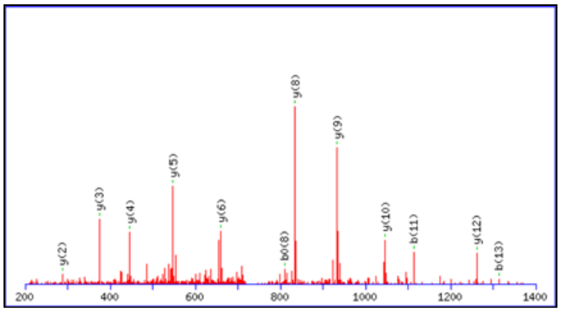
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **LISQIVSSITASLR**
Found in **TBA1B_MOUSE**, Tubulin alpha-1B chain (Tubulin alpha-2 chain) (Alpha-tubulin 2) (Alpha-tubulin isotype M-alpha-2) - Mus musculus (Mouse) (P05213)

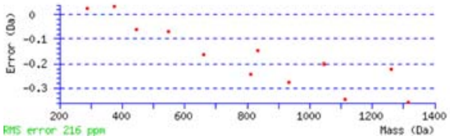
Match to Query 1371: 1486.871864 from(744.443208,2+)
Title: Arrell09050802 scan 2929 2931 (Arrell09050802.2929.2931.2.dta)
Data file Arrell09050802.mgf

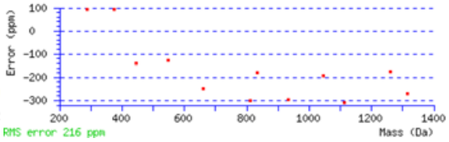
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1486.8719
Ions Score: 97 **Expect:** 3.6e-10
Matches (Bold Red): 12/142 fragment ions using 17 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					I	1374.7951	687.9012	1357.7686	679.3879	1356.7845	678.8959	13
3	314.2074	157.6074			296.1969	148.6021	S	**1261.7110**	631.3592	1244.6845	622.8459	1243.7005	622.3539	12
4	442.2660	221.6366	425.2395	213.1234	424.2554	212.6314	Q	1174.6790	587.8431	1157.6525	579.3299	1156.6684	578.8379	11
5	555.3501	278.1787	538.3235	269.6654	537.3395	269.1734	I	**1046.6204**	523.8139	1029.5939	515.3006	1028.6099	514.8086	10
6	654.4185	327.7129	637.3919	319.1996	636.4079	318.7076	V	**933.5364**	467.2718	916.5098	458.7585	915.5258	458.2665	9
7	741.4505	371.2289	724.4240	362.7156	723.4400	362.2236	S	**834.4680**	417.7376	817.4414	409.2243	816.4574	408.7323	8
8	828.4825	414.7449	811.4560	406.2316	**810.4720**	405.7396	S	747.4359	374.2216	730.4094	365.7083	729.4254	365.2163	7
9	941.5666	471.2869	924.5401	462.7737	923.5560	462.2817	I	**660.4039**	330.7056	643.3774	322.1923	642.3933	321.7003	6
10	1042.6143	521.8108	1025.5877	513.2975	1024.6037	512.8055	T	**547.3198**	274.1636	530.2933	265.6503	529.3093	265.1583	5
11	**1113.6514**	557.3293	1096.6249	548.8161	1095.6408	548.3241	A	**446.2722**	223.6397	429.2456	215.1264	428.2616	214.6344	4
12	1200.6834	600.8454	1183.6569	592.3321	1182.6729	591.8401	S	**375.2350**	188.1212	358.2085	179.6079	357.2245	179.1159	3
13	**1313.7675**	657.3874	1296.7409	648.8741	1295.7569	648.3821	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 LISQIVSSITASLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
96.8	1486.8719	-0.0000	LISQIVSSITASLR

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

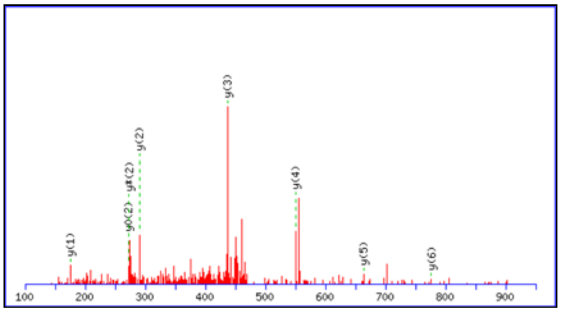
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SQLLIMDR**
Found in **STXB2_MOUSE**, Syntaxin-binding protein 2 (Unc-18 homolog 2) (Unc-18B) (MUSEC1) - Mus musculus (Mouse) (Q64324)

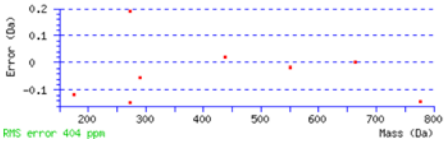
Match to Query 506: 991.514684 from(496.764618,2+)
Title: Arrell09050824 scan 2603 2603 (Arrell09050824.2603.2603.2.dta)
Data file Arrell09050824.mgf

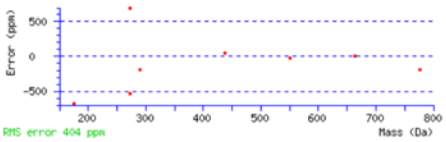
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range



```
Monoisotopic mass of neutral peptide Mr(calc): 990.5168
Variable modifications:
M6     : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 32  Expect: 0.01
Matches (Bold Red): 8/122 fragment ions using 20 most intense peaks
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							8
2	216.0979	108.5526	199.0713	100.0393	198.0873	99.5473	Q	904.4921	452.7497	887.4655	444.2364	886.4815	443.7444	7
3	329.1819	165.0946	312.1554	156.5813	311.1714	156.0893	L	**776.4335**	388.7204	759.4069	380.2071	758.4229	379.7151	6
4	442.2660	221.6366	425.2395	213.1234	424.2554	212.6314	L	**663.3494**	332.1784	646.3229	323.6651	645.3389	323.1731	5
5	555.3501	278.1787	538.3235	269.6654	537.3395	269.1734	I	**550.2654**	275.6363	533.2388	267.1230	532.2548	266.6310	4
6	702.3855	351.6964	685.3589	343.1831	684.3749	342.6911	M	**437.1813**	219.0943	420.1547	210.5810	419.1707	210.0890	3
7	817.4124	409.2098	800.3859	400.6966	799.4019	400.2046	D	**290.1459**	145.5766	**273.1193**	137.0633	**272.1353**	136.5713	2
8							R	**175.1190**	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.6	990.5168	0.9979	SQLLIMDR
19.9	990.5168	0.9979	SLQLLMDR
7.0	991.5199	-0.0052	SELITHHR
2.1	991.5087	0.0060	QAKDDFLR
0.8	990.5134	1.0013	QLAEDFLR
0.8	991.5087	0.0060	QVSAGDLFR
0.5	990.5168	0.9979	QSILAMGQK

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

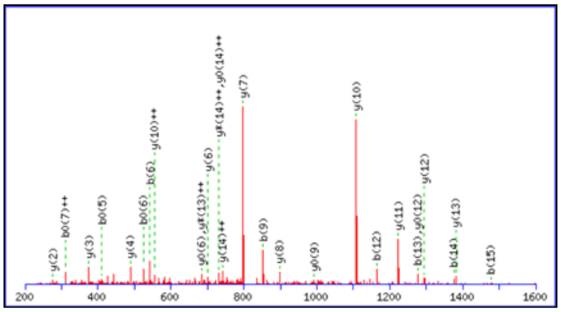
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VAVSADPNVPNVIVTR**
Found in **GDIR_MOUSE**, Rho GDP-dissociation inhibitor 1 (Rho GDI 1) (Rho-GDI alpha) (GDI-1) - Mus musculus (Mouse) (Q99PT1)

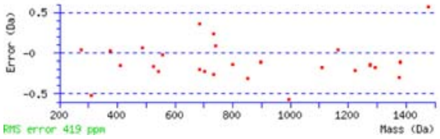
Match to Query 1694: 1649.910254 from(825.962403,2+)
Title: Arrell09050825 scan 1265 1265 (Arrell09050825.1265.1265.2.dta)
Data file Arrell09050825.mgf

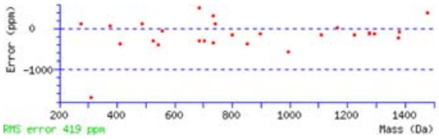
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1649.9101
Ions Score: 62 **Expect:** 1.8e-06
Matches (Bold Red): 27/158 fragment ions using 43 most intense peaks

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	100.0757	50.5415					V							16
2	171.1128	86.0600					A	1551.8489	776.4281	1534.8224	767.9148	1533.8384	767.4228	15
3	270.1812	135.5942					V	1480.8118	**740.9095**	1463.7853	**732.3963**	1462.8013	**731.9043**	14
4	357.2132	179.1103			339.2027	170.1050	S	**1381.7434**	691.3753	1364.7169	**682.8621**	1363.7328	682.3701	13
5	428.2504	214.6288			**410.2398**	205.6235	A	**1294.7114**	647.8593	1277.6848	639.3461	**1276.7008**	638.8540	12
6	**543.2773**	272.1423			**525.2667**	263.1370	D	**1223.6743**	612.3408	1206.6477	603.8275	1205.6637	603.3355	11
7	640.3301	320.6687			622.3195	**311.6634**	P	**1108.6473**	**554.8273**	1091.6208	546.3140	1090.6368	545.8220	10
8	754.3730	377.6901	737.3464	369.1769	736.3624	368.6849	N	1011.5946	506.3009	994.5680	497.7876	**993.5840**	497.2956	9
9	**853.4414**	427.2243	836.4149	418.7111	835.4308	418.2191	V	**897.5516**	449.2795	880.5251	440.7662	879.5411	440.2742	8
10	950.4942	475.7507	933.4676	467.2374	932.4836	466.7454	P	**798.4832**	399.7452	781.4567	391.2320	780.4726	390.7400	7
11	1064.5371	532.7722	1047.5105	524.2589	1046.5265	523.7669	N	**701.4305**	351.2189	684.4039	342.7056	**683.4199**	342.2136	6
12	**1163.6055**	582.3064	1146.5790	573.7931	1145.5949	573.3011	V	587.3875	294.1974	570.3610	285.6841	569.3770	285.1921	5
13	**1276.6896**	638.8484	1259.6630	630.3352	1258.6790	629.8431	I	**488.3191**	244.6632	471.2926	236.1499	470.3085	235.6579	4
14	**1375.7580**	688.3826	1358.7314	679.8694	1357.7474	679.3774	V	**375.2350**	188.1212	358.2085	179.6079	357.2245	179.1159	3
15	**1476.8057**	738.9065	1459.7791	730.3932	1458.7951	729.9012	T	**276.1666**	138.5870	259.1401	130.0737	258.1561	129.5817	2
16							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
62.1	1649.9101	0.0002	VAVSADPNVPNVIVTR

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

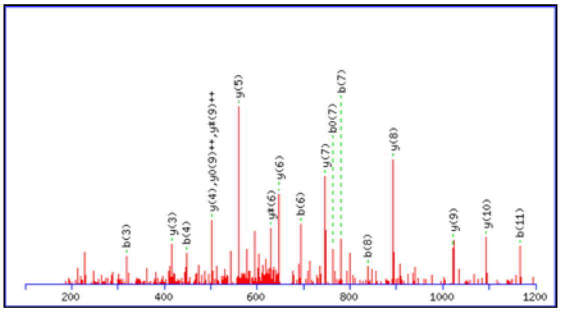
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SCAEFVSGSQLR**
Found in **ATP5H_MOUSE**, ATP synthase D chain, mitochondrial (EC 3.6.3.14) - Mus musculus (Mouse) (Q9DCX2)

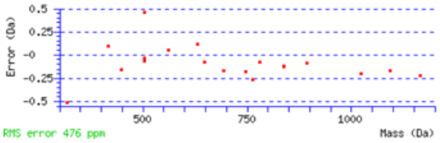
Match to Query 1191: 1339.619844 from(670.817198,2+)
Title: Arrell09050827 scan 829 829 (Arrell09050827.829.829.2.dta)
Data file Arrell09050827.mgf

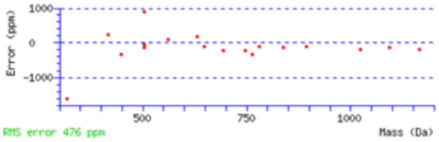
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1339.6190
Variable modifications:
C2 : Carbamidomethyl (C)
Ions Score: 60 **Expect:** 6.9e-06
Matches (Bold Red): 18/108 fragment ions using 27 most intense peaks

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							12
2	248.0700	124.5386			230.0594	115.5333	C	1253.5943	627.3008	1236.5678	618.7875	1235.5837	618.2955	11
3	**319.1071**	160.0572			301.0965	151.0519	A	**1093.5636**	547.2855	1076.5371	538.7722	1075.5531	538.2802	10
4	**448.1497**	224.5785			430.1391	215.5732	E	**1022.5265**	511.7669	1005.5000	**503.2536**	1004.5160	**502.7616**	9
5	595.2181	298.1127			577.2075	289.1074	F	**893.4839**	447.2456	876.4574	438.7323	875.4734	438.2403	8
6	**694.2865**	347.6469			676.2759	338.6416	V	**746.4155**	373.7114	729.3890	365.1981	728.4050	364.7061	7
7	**781.3185**	391.1629			**763.3080**	382.1576	S	**647.3471**	324.1772	**630.3206**	315.6639	629.3365	315.1719	6
8	**838.3400**	419.6736			820.3294	410.6683	G	**560.3151**	280.6612	543.2885	272.1479	542.3045	271.6559	5
9	925.3720	463.1896			907.3614	454.1844	S	**503.2936**	252.1504	486.2671	243.6372	485.2831	243.1452	4
10	1053.4306	527.2189	1036.4040	518.7057	1035.4200	518.2137	Q	**416.2616**	208.6344	399.2350	200.1212			3
11	**1166.5147**	583.7610	1149.4881	575.2477	1148.5041	574.7557	L	288.2030	144.6051	271.1765	136.0919			2
12							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
59.5	1339.6190	0.0008	SCAEFVSGSQLR
8.9	1339.6125	0.0073	VLPSCHAPCGSR
0.3	1338.6233	0.9965	MVTVMPLEMEK

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

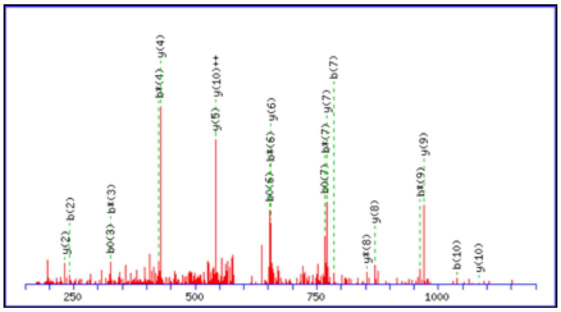
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QITVNDLPVGR**
Found in **PRDX2_MOUSE**, Peroxiredoxin-2 (EC 1.11.1.15) (Thioredoxin peroxidase 1) (Thioredoxin-dependent peroxide reductase 1) (Thiol-specific antioxidant protein) (TSA) - Mus musculus (Mouse) (Q61171)

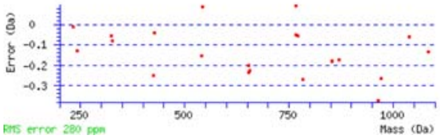
Match to Query 992: 1211.669534 from(606.842043,2+)
Title: Arrell09050827 scan 1180 1180 (Arrell09050827.1180.1180.2.dta)
Data file Arrell09050827.mgf

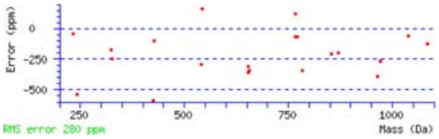
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1200 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1210.6670
Ions Score: 48 **Expect:** 0.00011
Matches (Bold Red): 21/106 fragment ions using 44 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	**242.1499**	121.5786	225.1234	113.0653			I	**1083.6157**	**542.3115**	1066.5891	533.7982	1065.6051	533.3062	10
3	343.1976	172.1024	**326.1710**	163.5892	**325.1870**	163.0972	T	**970.5316**	485.7694	953.5051	477.2562	952.5211	476.7642	9
4	442.2660	221.6366	**425.2395**	213.1234	424.2554	212.6314	V	**869.4839**	435.2456	**852.4574**	426.7323	851.4734	426.2403	8
5	556.3089	278.6581	539.2824	270.1448	538.2984	269.6528	N	**770.4155**	385.7114	753.3890	377.1981	752.4050	376.7061	7
6	671.3359	336.1716	**654.3093**	327.6583	**653.3253**	327.1663	D	**656.3726**	328.6899	639.3461	320.1767	638.3620	319.6847	6
7	**784.4199**	392.7136	**767.3934**	384.2003	**766.4094**	383.7083	L	**541.3457**	271.1765	524.3191	262.6632			5
8	881.4727	441.2400	864.4462	432.7267	863.4621	432.2347	P	**428.2616**	214.6344	411.2350	206.1212			4
9	980.5411	490.7742	**963.5146**	482.2609	962.5306	481.7689	V	331.2088	166.1081	314.1823	157.5948			3
10	**1037.5626**	519.2849	1020.5360	510.7717	1019.5520	510.2796	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 QITVNDLPVGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.6	1210.6670	1.0025	QITVNDLPVGR
6.8	1210.6670	1.0026	GAIVSEPAIQAR

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

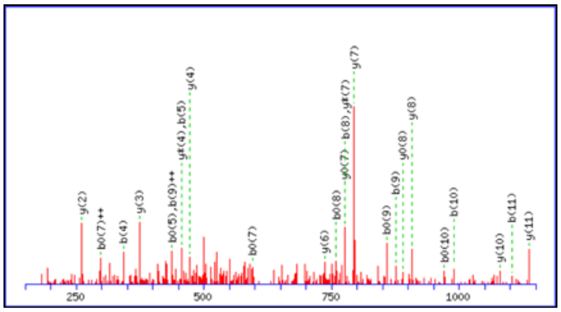
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGGDLGTYVINK**
Found in **FRDA_MOUSE**, Frataxin, mitochondrial precursor (Fxn) - Mus musculus (Mouse) (O35943)

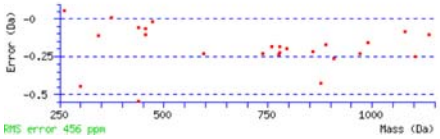
Match to Query 1009: 1248.670144 from(625.342348,2+)
Title: Arrell09050830 scan 1344 1344 (Arrell09050830.1344.1344.2.dta)
Data file Arrell09050830.mgf

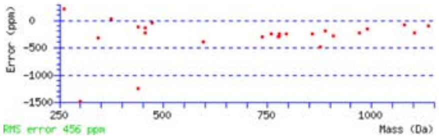
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1150 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1248.6714
Ions Score: 46 **Expect:** 0.00016
Matches (Bold Red): 25/96 fragment ions using 48 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							12
2	171.1128	86.0600					G	**1136.5946**	568.8009	1119.5681	560.2877	1118.5841	559.7957	11
3	228.1343	114.5708					G	**1079.5732**	540.2902	1062.5466	531.7769	1061.5626	531.2849	10
4	**343.1612**	172.0842			325.1506	163.0790	D	1022.5517	511.7795	1005.5251	503.2662	1004.5411	502.7742	9
5	**456.2453**	228.6263			**438.2347**	219.6210	L	**907.5247**	454.2660	890.4982	445.7527	**889.5142**	445.2607	8
6	513.2667	257.1370			495.2562	248.1317	G	**794.4407**	397.7240	**777.4141**	389.2107	**776.4301**	388.7187	7
7	614.3144	307.6608			**596.3039**	**298.6556**	T	**737.4192**	369.2132	720.3927	360.7000	719.4087	360.2080	6
8	**777.3777**	389.1925			**759.3672**	380.1872	Y	636.3715	318.6894	619.3450	310.1761			5
9	**876.4462**	**438.7267**			**858.4356**	429.7214	V	**473.3082**	237.1577	**456.2817**	228.6445			4
10	**989.5302**	495.2688			**971.5197**	486.2635	I	**374.2398**	187.6235	357.2132	179.1103			3
11	**1103.5732**	552.2902	1086.5466	543.7769	1085.5626	543.2849	N	**261.1557**	131.0815	244.1292	122.5682			2
12							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.2	1248.6714	-0.0013	LGGDLGTYVINK
7.4	1248.6747	-0.0046	TKLLLCNSALSS
1.7	1248.6722	-0.0021	MKNICWLTLK

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

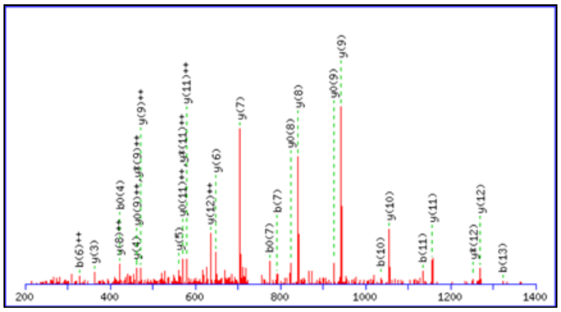
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LILTLTHGSVVSTR**
Found in **FABPH_MOUSE**, Fatty acid-binding protein, heart (H-FABP) (Heart-type fatty acid-binding protein) (Mammary-derived growth inhibitor) (MDGI) - Mus musculus (Mouse) (P11404)

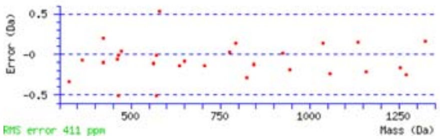
Match to Query 1375: 1495.872284 from(748.943418,2+)
Title: Arrell09050831 scan 1401 1401 (Arrell09050831.1401.1401.2.dta)
Data file Arrell09050831.mgf

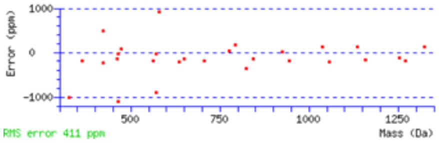
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1495.8722
Ions Score: 63 **Expect:** 1e-06
Matches (Bold Red): 28/122 fragment ions using 52 most intense peaks

#	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			I	1383.7954	692.4014	1366.7689	683.8881	1365.7849	683.3961	13
3	340.2595	170.6334			L	**1270.7114**	**635.8593**	**1253.6848**	627.3461	1252.7008	626.8540	12
4	441.3071	221.1572	**423.2966**	212.1519	T	**1157.6273**	**579.3173**	1140.6008	**570.8040**	1139.6167	**570.3120**	11
5	554.3912	277.6992	536.3806	268.6940	L	**1056.5796**	528.7935	1039.5531	520.2802	1038.5691	519.7882	10
6	655.4389	**328.2231**	637.4283	319.2178	T	**943.4956**	**472.2514**	926.4690	**463.7381**	**925.4850**	**463.2461**	9
7	**792.4978**	396.7525	**774.4872**	387.7473	H	**842.4479**	**421.7276**	825.4213	413.2143	**824.4373**	412.7223	8
8	849.5193	425.2633	831.5087	416.2580	G	**705.3890**	353.1981	688.3624	344.6849	687.3784	344.1928	7
9	936.5513	468.7793	918.5407	459.7740	S	**648.3675**	324.6874	631.3410	316.1741	630.3570	315.6821	6
10	**1035.6197**	518.3135	1017.6091	509.3082	V	**561.3355**	281.1714	544.3089	272.6581	543.3249	272.1661	5
11	**1134.6881**	567.8477	1116.6776	558.8424	V	**462.2671**	231.6372	445.2405	223.1239	444.2565	222.6319	4
12	1221.7202	611.3637	1203.7096	602.3584	S	**363.1987**	182.1030	346.1721	173.5897	345.1881	173.0977	3
13	**1322.7678**	661.8876	1304.7573	652.8823	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
14					R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
62.7	1495.8722	0.0000	LILTLTHGSVVSTR

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

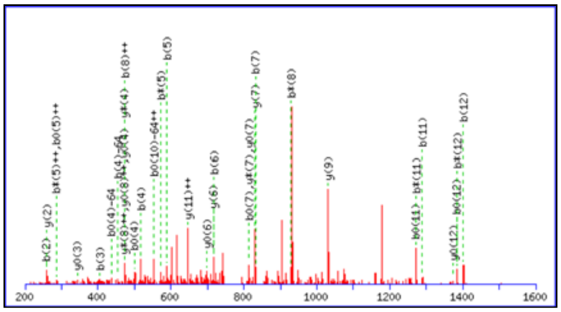
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **RTMLAENNLETLK**
Found in **CASP8_MOUSE**, Caspase-8 precursor (EC 3.4.22.61) (CASP-8) [Contains: Caspase-8 subunit p18; Caspase-8 subunit p10] - Mus musculus (Mouse) (O89110)

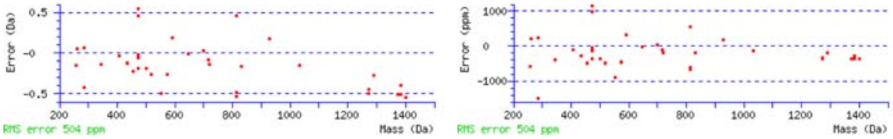
Match to Query 1246: 1547.788794 from(774.901673,2+)
Title: Arrell09050804 scan 1381 1381 (Arrell09050804.1381.1381.2.dta)
Data file Arrell09050804.mgf

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): 1547.7977
Variable modifications:
M3 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 31 **Expect:** 0.0054
Matches (Bold Red): 36/210 fragment ions using 66 most intense peaks

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	157.1084	79.0578	140.0818	70.5446			R							13
2	**258.1561**	129.5817	241.1295	121.0684	240.1455	120.5764	T	1392.7039	696.8556	1375.6774	688.3423	**1374.6933**	687.8503	12
3	**405.1915**	203.0994	388.1649	194.5861	387.1809	194.0941	M	1291.6562	**646.3318**	1274.6297	637.8185	1273.6457	637.3265	11
4	**518.2755**	259.6414	501.2490	251.1281	**500.2650**	250.6361	L	1144.6208	572.8141	1127.5943	564.3008	1126.6103	563.8088	10
5	**589.3126**	295.1600	**572.2861**	**286.6467**	571.3021	**286.1547**	A	**1031.5368**	516.2720	1014.5102	507.7587	1013.5262	507.2667	9
6	**718.3552**	359.6813	701.3287	351.1680	700.3447	350.6760	E	960.4997	480.7535	943.4731	**472.2402**	942.4891	**471.7482**	8
7	**832.3982**	416.7027	815.3716	408.1894	**814.3876**	407.6974	N	**831.4571**	416.2322	**814.4305**	407.7189	**813.4465**	407.2269	7
8	946.4411	**473.7242**	**929.4145**	465.2109	928.4305	464.7189	N	**717.4141**	359.2107	700.3876	350.6974	**699.4036**	350.2054	6
9	1059.5252	530.2662	1042.4986	521.7529	1041.5146	521.2609	L	603.3712	302.1892	586.3447	293.6760	585.3606	293.1840	5
10	1188.5678	594.7875	1171.5412	586.2742	1170.5572	585.7822	E	490.2871	245.6472	**473.2606**	237.1339	**472.2766**	236.6419	4
11	**1289.6154**	645.3114	**1272.5889**	636.7981	**1271.6049**	636.3061	T	361.2445	181.1259	344.2180	172.6126	**343.2340**	172.1206	3
12	**1402.6995**	701.8534	**1385.6729**	693.3401	**1384.6889**	692.8481	L	**260.1969**	130.6021	243.1703	122.0888			2
13							K	147.1128	74.0600	130.0863	65.5468			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
67.0	1547.7865	0.0023	DAALMVTNDGATILK
31.4	1547.7977	-0.0089	RTMLAENNLETLK

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

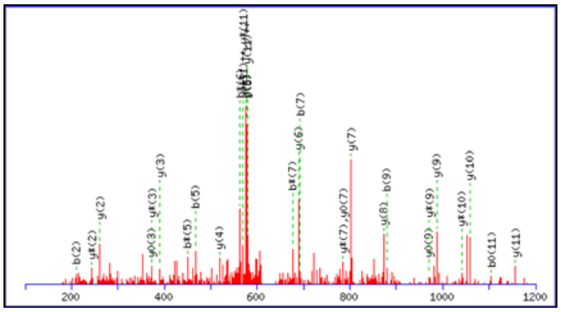
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LPANALLGEENK**
Found in **ACADL_MOUSE**, Long-chain specific acyl-CoA dehydrogenase, mitochondrial precursor (EC 1.3.99.13) (LCAD) - Mus musculus (Mouse) (P51174)

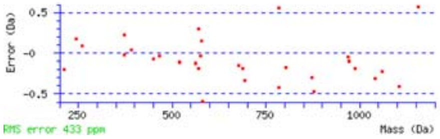
Match to Query 987: 1267.677224 from(634.845888,2+)
Title: Arrell09050808 scan 1142 1142 (Arrell09050808.1142.1142.2.dta)
Data file Arrell09050808.mgf

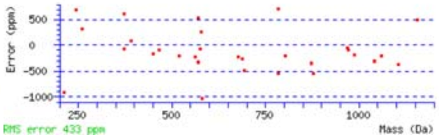
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range



```
Monoisotopic mass of neutral peptide Mr(calc): 1267.6772
Ions Score: 46  Expect: 0.00016
Matches (Bold Red): 30/106 fragment ions using 83 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							12
2	**211.1441**	106.0757					P	**1155.6004**	**578.3039**	1138.5739	**569.7906**	1137.5899	**569.2986**	11
3	282.1812	141.5942					A	**1058.5477**	529.7775	**1041.5211**	521.2642	1040.5371	520.7722	10
4	396.2241	198.6157	379.1976	190.1024			N	**987.5106**	494.2589	**970.4840**	485.7456	**969.5000**	485.2536	9
5	**467.2613**	234.1343	**450.2347**	225.6210			A	**873.4676**	437.2374	856.4411	428.7242	855.4571	428.2322	8
6	**580.3453**	290.6763	**563.3188**	282.1630			L	**802.4305**	401.7189	**785.4040**	393.2056	**784.4199**	392.7136	7
7	**693.4294**	347.2183	**676.4028**	338.7051			L	**689.3464**	345.1769	672.3199	336.6636	671.3359	336.1716	6
8	750.4509	375.7291	733.4243	367.2158			G	**576.2624**	288.6348	559.2358	280.1216	558.2518	279.6295	5
9	**879.4934**	440.2504	862.4669	431.7371	861.4829	431.2451	E	**519.2409**	260.1241	502.2144	251.6108	501.2304	251.1188	4
10	1008.5360	504.7717	991.5095	496.2584	990.5255	495.7664	E	**390.1983**	195.6028	**373.1718**	187.0895	**372.1878**	186.5975	3
11	1122.5790	561.7931	1105.5524	553.2798	**1104.5684**	552.7878	N	**261.1557**	131.0815	**244.1292**	122.5682			2
12							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.5	1267.6772	0.0001	LPANALLGEENK

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

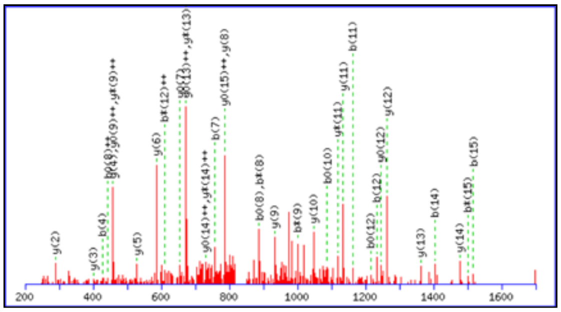
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLNVESNFISGAGILR**
Found in **TMOD1_MOUSE**, Tropomodulin-1 (Erythrocyte tropomodulin) (E-Tmod) - Mus musculus (Mouse) (P49813)

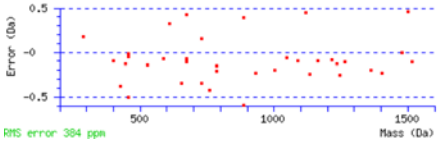
Match to Query 1487: 1689.906834 from(845.960693,2+)
Title: Arrell09050808 scan 2102 2102 (Arrell09050808.2102.2102.2.dta)
Data file Arrell09050808.mgf

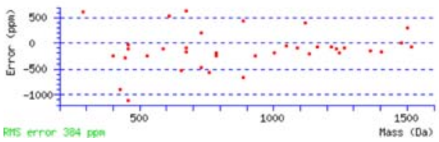
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1689.9050
Ions Score: 95 **Expect:** 1.4e-09
Matches (Bold Red): 37/164 fragment ions using 56 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							16
2	215.1390	108.0731			197.1285	99.0679	L	1589.8646	795.4359	1572.8380	786.9227	1571.8540	**786.4306**	15
3	329.1819	165.0946	312.1554	156.5813	311.1714	156.0893	N	**1476.7805**	738.8939	1459.7540	**730.3806**	1458.7700	**729.8886**	14
4	**428.2504**	214.6288	411.2238	206.1155	410.2398	205.6235	V	**1362.7376**	681.8724	1345.7110	**673.3592**	1344.7270	**672.8672**	13
5	557.2930	279.1501	540.2664	270.6368	539.2824	270.1448	E	**1263.6692**	632.3382	1246.6426	623.8250	**1245.6586**	623.3329	12
6	644.3250	322.6661	627.2984	314.1529	626.3144	313.6608	S	**1134.6266**	567.8169	**1117.6000**	559.3037	1116.6160	558.8116	11
7	**758.3679**	379.6876	741.3414	371.1743	740.3573	370.6823	N	**1047.5946**	524.3009	1030.5680	515.7876	1029.5840	515.2956	10
8	905.4363	453.2218	**888.4098**	444.7085	**887.4258**	**444.2165**	F	**933.5516**	467.2795	916.5251	**458.7662**	915.5411	**458.2742**	9
9	1018.5204	509.7638	**1001.4938**	501.2506	1000.5098	500.7585	I	**786.4832**	393.7452	769.4567	385.2320	768.4726	384.7400	8
10	1105.5524	553.2798	1088.5259	544.7666	**1087.5418**	544.2746	S	**673.3991**	337.2032	656.3726	328.6899	**655.3886**	328.1979	7
11	**1162.5739**	581.7906	1145.5473	573.2773	1144.5633	572.7853	G	**586.3671**	293.6872	569.3406	285.1739			6
12	**1233.6110**	617.3091	1216.5844	**608.7959**	**1215.6004**	608.3039	A	**529.3457**	265.1765	512.3191	256.6632			5
13	1290.6325	645.8199	1273.6059	637.3066	1272.6219	636.8146	G	**458.3085**	229.6579	441.2820	221.1446			4
14	**1403.7165**	702.3619	1386.6900	693.8486	1385.7060	693.3566	I	**401.2871**	201.1472	384.2605	192.6339			3
15	**1516.8006**	758.9039	**1499.7740**	750.3907	1498.7900	749.8986	L	**288.2030**	144.6051	271.1765	136.0919			2
16							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
94.5	1689.9050	0.0019	TLNVESNFISGAGILR
0.7	1689.9162	-0.0094	AQNNTLIFTKGNTIR

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

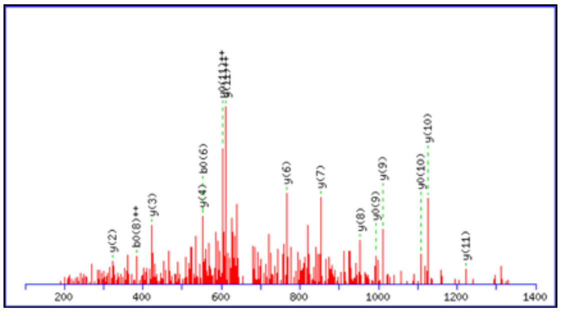
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LPDGTSLTQTFR**
Found in **SAKS1_MOUSE**, SAPK substrate protein 1 (UBA/UBX 33.3 kDa protein) (mY33K) (Protein 2B28) - Mus musculus (Mouse) (Q922Y1)

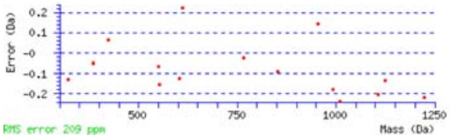
Match to Query 1108: 1334.682104 from(668.348328,2+)
Title: Arrell09050808 scan 1375 1375 (Arrell09050808.1375.1375.2.dta)
Data file Arrell09050808.mgf

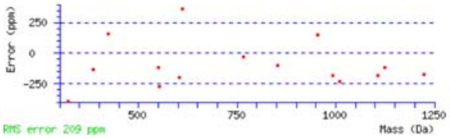
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1334.6830
Ions Score: 41 **Expect:** 0.00072
Matches (Bold Red): 15/108 fragment ions using 45 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							12
2	211.1441	106.0757					P	**1222.6062**	**611.8068**	1205.5797	603.2935	1204.5957	**602.8015**	11
3	326.1710	163.5892			308.1605	154.5839	D	**1125.5535**	563.2804	1108.5269	554.7671	**1107.5429**	554.2751	10
4	383.1925	192.0999			365.1819	183.0946	G	**1010.5265**	505.7669	993.5000	497.2536	**992.5160**	496.7616	9
5	484.2402	242.6237			466.2296	233.6185	T	**953.5051**	477.2562	936.4785	468.7429	935.4945	468.2509	8
6	571.2722	286.1397			**553.2617**	277.1345	S	**852.4574**	426.7323	835.4308	418.2191	834.4468	417.7271	7
7	684.3563	342.6818			666.3457	333.6765	L	**765.4254**	383.2163	748.3988	374.7030	747.4148	374.2110	6
8	785.4040	393.2056			767.3934	**384.2003**	T	652.3413	326.6743	635.3148	318.1610	634.3307	317.6690	5
9	913.4625	457.2349	896.4360	448.7216	895.4520	448.2296	Q	**551.2936**	276.1504	534.2671	267.6372	533.2831	267.1452	4
10	1014.5102	507.7587	997.4837	499.2455	996.4997	498.7535	T	**423.2350**	212.1212	406.2085	203.6079	405.2245	203.1159	3
11	1161.5786	581.2930	1144.5521	572.7797	1143.5681	572.2877	F	**322.1874**	161.5973	305.1608	153.0840			2
12							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.0	1334.6830	-0.0009	LPDGTSLTQTFR

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

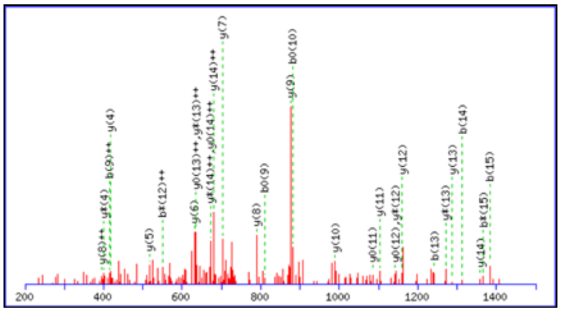
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AVAQGNLSSADVQAAK**
Found in **UQCR2_MOUSE**, Ubiquinol-cytochrome-c reductase complex core protein 2, mitochondrial precursor (EC 1.10.2.2) (Core protein II) (Complex III subunit II) - Mus musculus (Mouse) (Q9DB77)

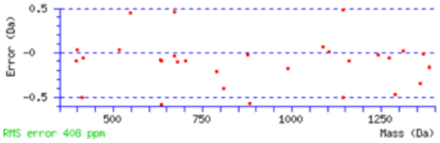
Match to Query 1344: 1528.784394 from(765.399473,2+)
Title: Arrell09050809 scan 579 579 (Arrell09050809.579.579.2.dta)
Data file Arrell09050809.mgf

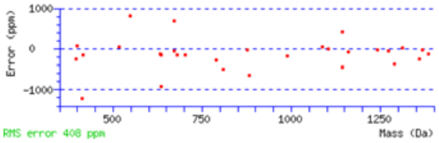
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1528.7845
Ions Score: 45 **Expect:** 0.00025
Matches (Bold Red): 30/150 fragment ions using 78 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							16
2	171.1128	86.0600					V	1458.7547	729.8810	1441.7281	721.3677	1440.7441	720.8757	15
3	242.1499	121.5786					A	**1359.6863**	**680.3468**	1342.6597	**671.8335**	1341.6757	**671.3415**	14
4	370.2085	185.6079	353.1819	177.0946			Q	**1288.6492**	644.8282	**1271.6226**	**636.3149**	1270.6386	**635.8229**	13
5	427.2300	214.1186	410.2034	205.6053			G	**1160.5906**	580.7989	**1143.5640**	572.2857	**1142.5800**	571.7937	12
6	541.2729	271.1401	524.2463	262.6268			N	**1103.5691**	552.2882	1086.5426	543.7749	**1085.5586**	543.2829	11
7	654.3570	327.6821	637.3304	319.1688			L	**989.5262**	495.2667	972.4997	486.7535	971.5156	486.2615	10
8	741.3890	371.1981	724.3624	362.6849	723.3784	362.1928	S	**876.4421**	438.7247	859.4156	430.2114	858.4316	429.7194	9
9	828.4210	**414.7141**	811.3945	406.2009	**810.4104**	405.7089	S	**789.4101**	**395.2087**	772.3836	386.6954	771.3995	386.2034	8
10	899.4581	450.2327	882.4316	441.7194	**881.4476**	441.2274	A	**702.3781**	351.6927	685.3515	343.1794	684.3675	342.6874	7
11	1014.4851	507.7462	997.4585	499.2329	996.4745	498.7409	D	**631.3410**	316.1741	614.3144	307.6608	613.3304	307.1688	6
12	1113.5535	557.2804	1096.5269	**548.7671**	1095.5429	548.2751	V	**516.3140**	258.6607	499.2875	250.1474			5
13	**1241.6121**	621.3097	1224.5855	612.7964	1223.6015	612.3044	Q	**417.2456**	209.1264	**400.2191**	200.6132			4
14	**1312.6492**	656.8282	1295.6226	648.3149	1294.6386	647.8229	A	289.1870	145.0972	272.1605	136.5839			3
15	**1383.6863**	692.3468	**1366.6597**	683.8335	1365.6757	683.3415	A	218.1499	109.5786	201.1234	101.0653			2
16							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.8	1528.7845	-0.0001	AVAQGNLSSADVQAAK

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