Supplementary Table S2 – 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.

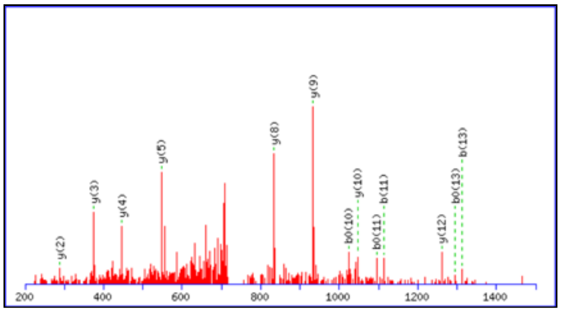
Mascot Search Results

Peptide View

MS/MS Fragmentation of **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)

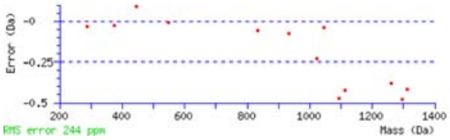
Match to Query 1650: 1486.872284 from(744.443418,2+)
Title: Arrell12290819 scan 3266 3266 (Arrell12290819.3266.3266.2.dta)
Data file Arrell12290819.mgf

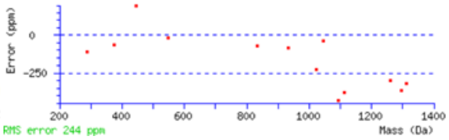
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1486.8719
Ions Score: 58 **Expect:** 2.4e-06
Matches (Bold Red): 13/142 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	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
57.8	1486.8719	0.0004	LISQIVSSITASLR

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

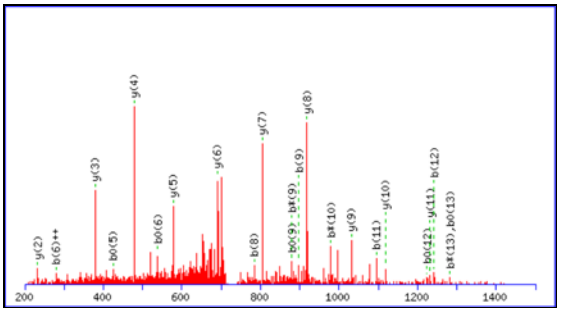
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGANSLLDLVVFGR**
Found in **DHSA_MOUSE**, Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial precursor (EC 1.3.5.1) (Fp) (Flavoprotein subunit of complex II) - Mus musculus (Mouse) (Q8K2B3)

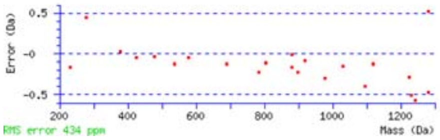
Match to Query 781: 1472.837924 from(737.426238,2+)
Title: Arrell12290802 scan 2107 2109 (Arrell12290802.2107.2109.2.dta)
Data file Arrell12290802.mgf

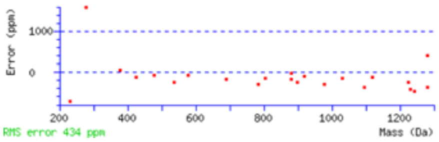
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1472.8351
Ions Score: 64 **Expect:** 4.9e-06
Matches (Bold Red): 23/130 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	171.1128	86.0600					G	1360.7583	680.8828	1343.7318	672.3695	1342.7478	671.8775	13
3	242.1499	121.5786					A	1303.7369	652.3721	1286.7103	643.8588	1285.7263	643.3668	12
4	356.1928	178.6001	339.1663	170.0868			N	**1232.6997**	616.8535	1215.6732	608.3402	1214.6892	607.8482	11
5	443.2249	222.1161	426.1983	213.6028	**425.2143**	213.1108	S	**1118.6568**	559.8320	1101.6303	551.3188	1100.6463	550.8268	10
6	556.3089	**278.6581**	539.2824	270.1448	**538.2984**	269.6528	L	**1031.6248**	516.3160	1014.5982	507.8028	1013.6142	507.3108	9
7	669.3930	335.2001	652.3665	326.6869	651.3824	326.1949	L	**918.5407**	459.7740	901.5142	451.2607	900.5302	450.7687	8
8	**784.4199**	392.7136	767.3934	384.2003	766.4094	383.7083	D	**805.4567**	403.2320	788.4301	394.7187	787.4461	394.2267	7
9	**897.5040**	449.2556	**880.4775**	440.7424	**879.4934**	440.2504	L	**690.4297**	345.7185	673.4032	337.2052			6
10	996.5724	498.7898	**979.5459**	490.2766	978.5619	489.7846	V	**577.3457**	289.1765	560.3191	280.6632			5
11	**1095.6408**	548.3241	1078.6143	539.8108	1077.6303	539.3188	V	**478.2772**	239.6423	461.2507	231.1290			4
12	**1242.7093**	621.8583	1225.6827	613.3450	**1224.6987**	612.8530	F	**379.2088**	190.1081	362.1823	181.5948			3
13	1299.7307	650.3690	**1282.7042**	641.8557	**1281.7201**	641.3637	G	**232.1404**	116.5738	215.1139	108.0606			2
14							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
63.8	1472.8351	0.0028	LGANSLLDLVVFGR

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

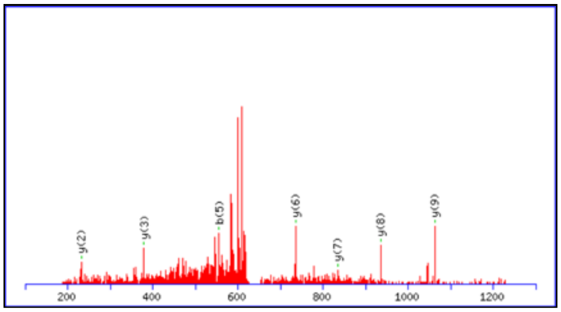
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VQQTVQDLFGR**
Found in **GRP75_MOUSE**, Stress-70 protein, mitochondrial precursor (75 kDa glucose-regulated protein) (GRP 75) (Heat shock 70 kDa protein 9) (Peptide-binding protein 74) (PBP74) (P66 MOT) (Mortalin) - Mus musculus (Mouse) (P38647)

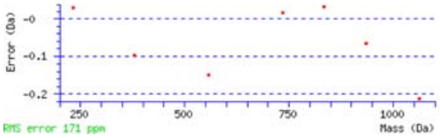
Match to Query 716: 1289.674044 from(645.844298,2+)
Title: Arrell12290802 scan 1212 1214 (Arrell12290802.1212.1214.2.dta)
Data file Arrell12290802.mgf

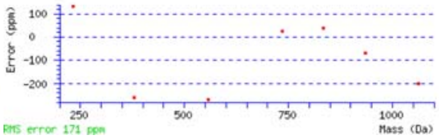
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1289.6728
Ions Score: 33 **Expect:** 0.0047
Matches (Bold Red): 7/104 fragment ions using 22 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							11
2	228.1343	114.5708	211.1077	106.0575			Q	1191.6117	596.3095	1174.5851	587.7962	1173.6011	587.3042	10
3	356.1928	178.6001	339.1663	170.0868			Q	**1063.5531**	532.2802	1046.5265	523.7669	1045.5425	523.2749	9
4	457.2405	229.1239	440.2140	220.6106	439.2300	220.1186	T	**935.4945**	468.2509	918.4680	459.7376	917.4839	459.2456	8
5	**556.3089**	278.6581	539.2824	270.1448	538.2984	269.6528	V	**834.4468**	417.7271	817.4203	409.2138	816.4363	408.7218	7
6	684.3675	342.6874	667.3410	334.1741	666.3570	333.6821	Q	**735.3784**	368.1928	718.3519	359.6796	717.3678	359.1876	6
7	799.3945	400.2009	782.3679	391.6876	781.3839	391.1956	D	607.3198	304.1636	590.2933	295.6503	589.3093	295.1583	5
8	912.4785	456.7429	895.4520	448.2296	894.4680	447.7376	L	492.2929	246.6501	475.2663	238.1368			4
9	1059.5469	530.2771	1042.5204	521.7638	1041.5364	521.2718	F	**379.2088**	190.1081	362.1823	181.5948			3
10	1116.5684	558.7878	1099.5419	550.2746	1098.5578	549.7826	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 VQQTVQDLFGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.4	1289.6728	0.0012	VQQTVQDLFGR

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

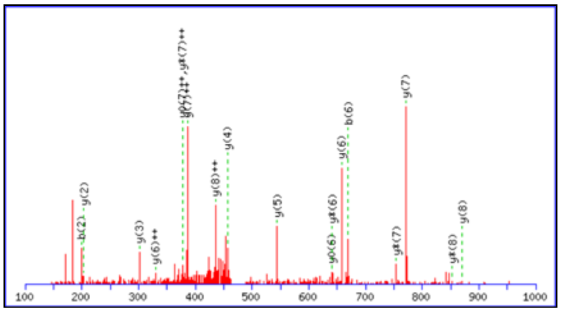
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVLNSRPGK**
Found in **ZADH1_MOUSE**, Zinc-binding alcohol dehydrogenase domain-containing protein 1 (EC 1.-.-.-) - Mus musculus (Mouse) (Q8VDQ1)

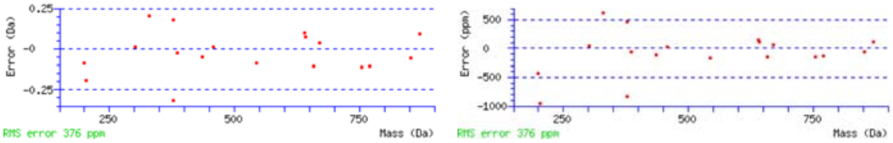
Match to Query 352: 968.575904 from(485.295228,2+)
Title: Arrell12290833 scan 348 348 (Arrell12290833.348.348.2.dta)
Data file Arrell12290833.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 968.5767
Ions Score: 43 **Expect:** 0.00015
Matches (Bold Red): 18/74 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	100.0757	50.5415					V							9
2	**199.1441**	100.0757					V	**870.5156**	**435.7614**	**853.4890**	427.2482	852.5050	426.7561	8
3	312.2282	156.6177					L	**771.4472**	**386.2272**	**754.4206**	**377.7139**	753.4366	**377.2219**	7
4	426.2711	213.6392	409.2445	205.1259			N	**658.3631**	**329.6852**	**641.3365**	321.1719	**640.3525**	320.6799	6
5	513.3031	257.1552	496.2766	248.6419	495.2926	248.1499	S	**544.3202**	272.6637	527.2936	264.1504	526.3096	263.6584	5
6	**669.4042**	335.2058	652.3777	326.6925	651.3937	326.2005	R	**457.2881**	229.1477	440.2616	220.6344			4
7	766.4570	383.7321	749.4304	375.2189	748.4464	374.7269	P	**301.1870**	151.0972	284.1605	142.5839			3
8	823.4785	412.2429	806.4519	403.7296	805.4679	403.2376	G	**204.1343**	102.5708	187.1077	94.0575			2
9							K	147.1128	74.0600	130.0863	65.5468			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
43.4	968.5767	-0.0008	VVLNSRPGK
1.1	968.5767	-0.0008	RLSPVSLR

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

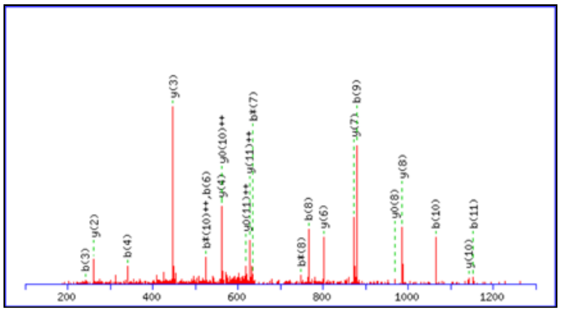
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALGVLAQLIWSR**
Found in **CISY_MOUSE**, Citrate synthase, mitochondrial precursor (EC 2.3.3.1) - Mus musculus (Mouse) (Q9CZU6)

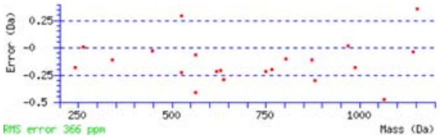
Match to Query 916: 1325.782994 from(663.898773,2+)
Title: Arrell12300839 scan 2285 2287 (Arrell12300839.2285.2287.2.dta)
Data file Arrell12300839.mgf

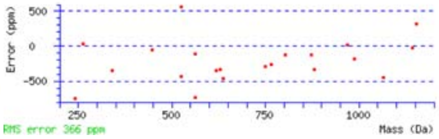
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1325.7819
Ions Score: 51 **Expect:** 2.1e-05
Matches (Bold Red): 21/98 fragment ions using 41 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							12
2	185.1285	93.0679					L	1255.7521	**628.3797**	1238.7256	619.8664	1237.7416	**619.3744**	11
3	**242.1499**	121.5786					G	**1142.6681**	571.8377	1125.6415	563.3244	1124.6575	**562.8324**	10
4	**341.2183**	171.1128					V	1085.6466	543.3269	1068.6200	534.8137	1067.6360	534.3217	9
5	454.3024	227.6548					L	**986.5782**	493.7927	969.5516	485.2795	**968.5676**	484.7874	8
6	**525.3395**	263.1734					A	**873.4941**	437.2507	856.4676	428.7374	855.4835	428.2454	7
7	653.3981	327.2027	**636.3715**	318.6894			Q	**802.4570**	401.7321	785.4305	393.2189	784.4464	392.7269	6
8	**766.4822**	383.7447	**749.4556**	375.2314			L	674.3984	337.7028	657.3719	329.1896	656.3879	328.6976	5
9	**879.5662**	440.2867	862.5397	431.7735			I	**561.3144**	281.1608	544.2878	272.6475	543.3038	272.1555	4
10	**1065.6455**	533.3264	1048.6190	**524.8131**			W	**448.2303**	224.6188	431.2037	216.1055	430.2197	215.6135	3
11	**1152.6776**	576.8424	1135.6510	568.3291	1134.6670	567.8371	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 ALGVLAQLIWSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
50.6	1325.7819	0.0011	ALGVLAQLIWSR

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

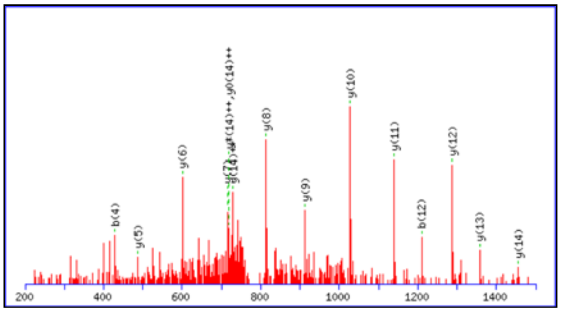
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IPAFLNVVDIAGLVK**
Found in **GTPB9_MOUSE**, Putative GTP-binding protein 9 - Mus musculus (Mouse) (Q9CZ30)

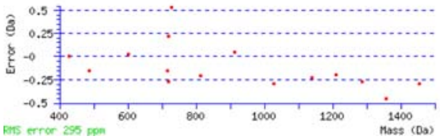
Match to Query 894: 1567.935334 from(784.974943,2+)
Title: Arrell12300840 scan 2117 2119 (Arrell12300840.2117.2119.2.dta)
Data file Arrell12300840.mgf

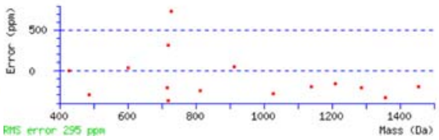
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range



```
Monoisotopic mass of neutral peptide Mr(calc): 1567.9338
Ions Score: 64  Expect: 3.5e-07
Matches (Bold Red): 15/130 fragment ions using 30 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							15
2	211.1441	106.0757					P	**1455.8570**	**728.4321**	1438.8304	**719.9189**	1437.8464	**719.4268**	14
3	282.1812	141.5942					A	**1358.8042**	679.9057	1341.7777	671.3925	1340.7936	670.9005	13
4	**429.2496**	215.1285					F	**1287.7671**	644.3872	1270.7406	635.8739	1269.7565	635.3819	12
5	542.3337	271.6705					L	**1140.6987**	570.8530	1123.6721	562.3397	1122.6881	561.8477	11
6	656.3766	328.6919	639.3501	320.1787			N	**1027.6146**	514.3109	1010.5881	505.7977	1009.6041	505.3057	10
7	755.4450	378.2262	738.4185	369.7129			V	**913.5717**	457.2895	896.5451	448.7762	895.5611	448.2842	9
8	854.5135	427.7604	837.4869	419.2471			V	**814.5033**	407.7553	797.4767	399.2420	796.4927	398.7500	8
9	969.5404	485.2738	952.5138	476.7606	951.5298	476.2686	D	**715.4349**	358.2211	698.4083	349.7078	697.4243	349.2158	7
10	1082.6245	541.8159	1065.5979	533.3026	1064.6139	532.8106	I	**600.4079**	300.7076	583.3814	292.1943			6
11	1153.6616	577.3344	1136.6350	568.8211	1135.6510	568.3291	A	**487.3239**	244.1656	470.2973	235.6523			5
12	**1210.6830**	605.8452	1193.6565	597.3319	1192.6725	596.8399	G	416.2867	208.6470	399.2602	200.1337			4
13	1323.7671	662.3872	1306.7406	653.8739	1305.7565	653.3819	L	359.2653	180.1363	342.2387	171.6230			3
14	1422.8355	711.9214	1405.8090	703.4081	1404.8249	702.9161	V	246.1812	123.5942	229.1547	115.0810			2
15							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
64.1	1567.9338	0.0016	IPAFLNVVDIAGLVK

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

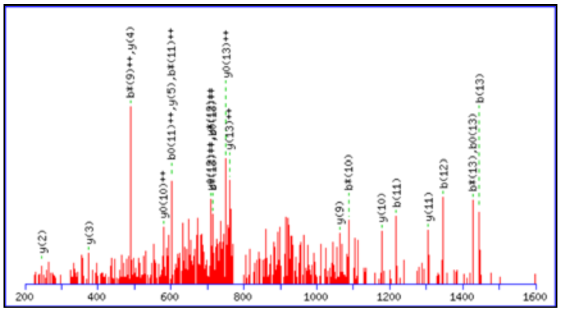
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ASQQDFENALNQVK**
Found in **PECI_MOUSE**, Peroxisomal 3,2-trans-enoyl-CoA isomerase (EC 5.3.3.8) (Dodecenoyl-CoA isomerase) (Delta(3),delta(2)-enoyl-CoA isomerase) (D3,D2-enoyl-CoA isomerase) - Mus musculus (Mouse) (Q9WUR2)

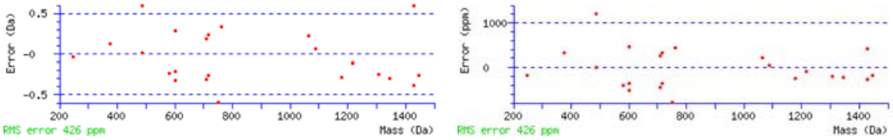
Match to Query 865: 1590.763764 from(796.389158,2+)
Title: Arrell12300842 scan 1082 1082 (Arrell12300842.1082.1082.2.dta)
Data file Arrell12300842.mgf

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): 1590.7638
Ions Score: 39 **Expect:** 0.001
Matches (Bold Red): 23/136 fragment ions using 30 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	159.0764	80.0418			141.0659	71.0366	S	1520.7340	**760.8706**	1503.7074	752.3573	1502.7234	**751.8653**	13
3	287.1350	144.0711	270.1084	135.5579	269.1244	135.0659	Q	1433.7019	717.3546	1416.6754	**708.8413**	1415.6914	**708.3493**	12
4	415.1936	208.1004	398.1670	199.5872	397.1830	199.0951	Q	**1305.6434**	653.3253	1288.6168	644.8120	1287.6328	644.3200	11
5	530.2205	265.6139	513.1940	257.1006	512.2100	256.6086	D	**1177.5848**	589.2960	1160.5582	580.7828	1159.5742	**580.2907**	10
6	677.2889	339.1481	660.2624	330.6348	659.2784	330.1428	F	**1062.5578**	531.7826	1045.5313	523.2693	1044.5473	522.7773	9
7	806.3315	403.6694	789.3050	395.1561	788.3210	394.6641	E	915.4894	458.2483	898.4629	449.7351	897.4789	449.2431	8
8	920.3745	460.6909	903.3479	452.1776	902.3639	451.6856	N	786.4468	393.7271	769.4203	385.2138			7
9	991.4116	496.2094	974.3850	**487.6961**	973.4010	487.2041	A	672.4039	336.7056	655.3774	328.1923			6
10	1104.4956	552.7515	**1087.4691**	544.2382	1086.4851	543.7462	L	**601.3668**	301.1870	584.3402	292.6738			5
11	**1218.5386**	609.7729	1201.5120	**601.2596**	1200.5280	**600.7676**	N	**488.2827**	244.6450	471.2562	236.1317			4
12	**1346.5971**	673.8022	1329.5706	665.2889	1328.5866	664.7969	Q	**374.2398**	187.6235	357.2132	179.1103			3
13	**1445.6655**	723.3364	**1428.6390**	**714.8231**	**1427.6550**	**714.3311**	V	**246.1812**	123.5942	229.1547	115.0810			2
14							K	147.1128	74.0600	130.0863	65.5468			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.2	1590.7638	-0.0000	ASQQDFENALNQVK

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

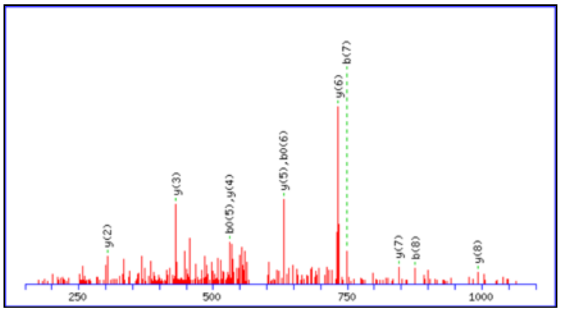
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GEFITTVQQR**
Found in **MDHC_MOUSE**, Malate dehydrogenase, cytoplasmic (EC 1.1.1.37) (Cytosolic malate dehydrogenase) - Mus musculus (Mouse) (P14152)

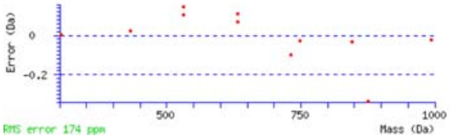
Match to Query 479: 1177.610574 from(589.812563,2+)
Title: Arrell12300843 scan 639 639 (Arrell12300843.639.639.2.dta)
Data file Arrell12300843.mgf

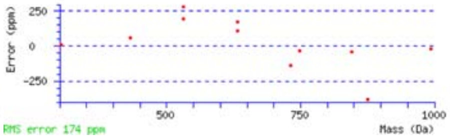
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1100 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1177.6091
Ions Score: 61 **Expect:** 9e-06
Matches (Bold Red): 11/84 fragment ions using 15 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							10
2	187.0713	94.0393			169.0608	85.0340	E	1121.5950	561.3011	1104.5684	552.7878	1103.5844	552.2958	9
3	334.1397	167.5735			316.1292	158.5682	F	**992.5524**	496.7798	975.5258	488.2665	974.5418	487.7745	8
4	447.2238	224.1155			429.2132	215.1103	I	**845.4839**	423.2456	828.4574	414.7323	827.4734	414.2403	7
5	548.2715	274.6394			**530.2609**	265.6341	T	**732.3999**	366.7036	715.3733	358.1903	714.3893	357.6983	6
6	649.3192	325.1632			**631.3086**	316.1579	T	**631.3522**	316.1797	614.3257	307.6665	613.3416	307.1745	5
7	**748.3876**	374.6974			730.3770	365.6921	V	**530.3045**	265.6559	513.2780	257.1426			4
8	**876.4462**	438.7267	859.4196	430.2134	858.4356	429.7214	Q	**431.2361**	216.1217	414.2096	207.6084			3
9	1004.5047	502.7560	987.4782	494.2427	986.4942	493.7507	Q	**303.1775**	152.0924	286.1510	143.5791			2
10							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
61.4	1177.6091	0.0014	GEFITTVQQR
5.8	1177.6125	-0.0019	GTEMVITKSGR
1.9	1177.6125	-0.0019	AGSSAMKLLER

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

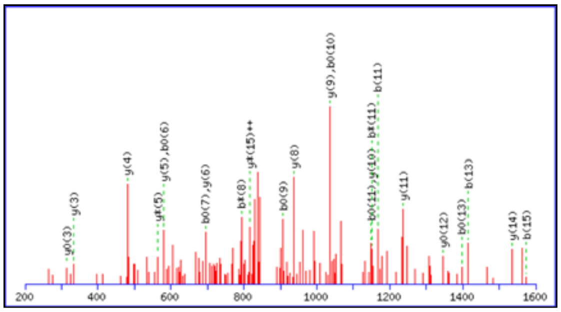
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VIGNQSLVNELTFSAR**
Found in **ECH1_MOUSE**, Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial precursor (EC 5.3.3.-) - Mus musculus (Mouse) (O35459)

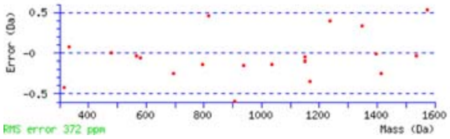
Match to Query 657: 1746.929294 from(874.471923,2+)
Title: Arrell12300844 scan 1231 1231 (Arrell12300844.1231.1231.2.dta)
Data file Arrell12300844.mgf

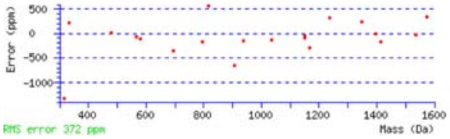
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1746.9264
Ions Score: 59 **Expect:** 4.8e-06
Matches (Bold Red): 24/160 fragment ions using 34 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	213.1598	107.0835					I	1648.8653	824.9363	1631.8388	**816.4230**	1630.8547	815.9310	15
3	270.1812	135.5942					G	**1535.7812**	768.3943	1518.7547	759.8810	1517.7707	759.3890	14
4	384.2241	192.6157	367.1976	184.1024			N	1478.7598	739.8835	1461.7332	731.3703	1460.7492	730.8782	13
5	512.2827	256.6450	495.2562	248.1317			Q	1364.7169	682.8621	1347.6903	674.3488	**1346.7063**	673.8568	12
6	599.3148	300.1610	582.2882	291.6477	**581.3042**	291.1557	S	**1236.6583**	618.8328	1219.6317	610.3195	1218.6477	609.8275	11
7	712.3988	356.7030	695.3723	348.1898	**694.3883**	347.6978	L	**1149.6262**	575.3168	1132.5997	566.8035	1131.6157	566.3115	10
8	811.4672	406.2373	**794.4407**	397.7240	793.4567	397.2320	V	**1036.5422**	518.7747	1019.5156	510.2615	1018.5316	509.7694	9
9	925.5102	463.2587	908.4836	454.7454	**907.4996**	454.2534	N	**937.4738**	469.2405	920.4472	460.7272	919.4632	460.2352	8
10	1054.5527	527.7800	1037.5262	519.2667	**1036.5422**	518.7747	E	823.4308	412.2191	806.4043	403.7058	805.4203	403.2138	7
11	**1167.6368**	584.3220	**1150.6103**	575.8088	**1149.6262**	575.3168	L	**694.3883**	347.6978	677.3617	339.1845	676.3777	338.6925	6
12	1268.6845	634.8459	1251.6579	626.3326	1250.6739	625.8406	T	**581.3042**	291.1557	**564.2776**	282.6425	563.2936	282.1504	5
13	**1415.7529**	708.3801	1398.7264	699.8668	**1397.7423**	699.3748	F	**480.2565**	240.6319	463.2300	232.1186	462.2459	231.6266	4
14	1502.7849	751.8961	1485.7584	743.3828	1484.7744	742.8908	S	**333.1881**	167.0977	316.1615	158.5844	**315.1775**	158.0924	3
15	**1573.8220**	787.4147	1556.7955	778.9014	1555.8115	778.4094	A	246.1561	123.5817	229.1295	115.0684			2
16							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
59.2	1746.9264	0.0029	VIGNQSLVNELTFSAR

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

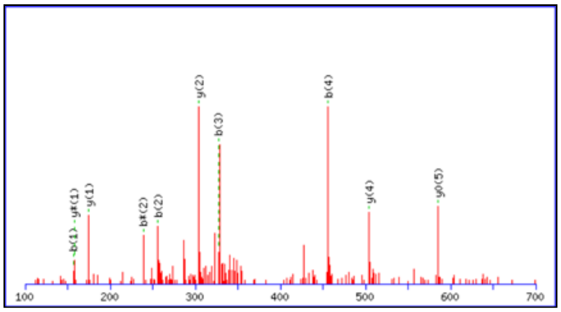
Mascot Search Results

Peptide View

MS/MS Fragmentation of **RVAEER**
Found in **MAP7_MOUSE**, Ensconsin (Microtubule-associated protein 7) (Epithelial microtubule-associated protein of 115 kDa) (E-MAP-115) - Mus musculus (Mouse) (O88735)

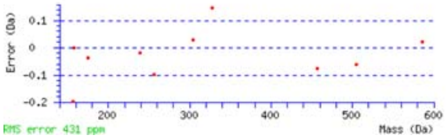
Match to Query 22: 758.403174 from(380.208863,2+)
Title: Arrell12290805 scan 268 268 (Arrell12290805.268.268.2.dta)
Data file Arrell12290805.mgf

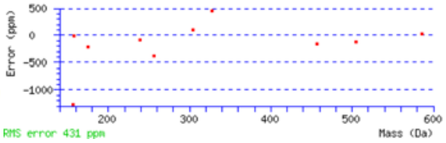
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 700 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 758.4035
Ions Score: 34 **Expect:** 0.0068
Matches (Bold Red): 11/52 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	**157.1084**	79.0578	140.0818	70.5446			R							6
2	**256.1768**	128.5920	**239.1503**	120.0788			V	603.3097	302.1585	586.2831	293.6452	**585.2991**	293.1532	5
3	**327.2139**	164.1106	310.1874	155.5973			A	**504.2413**	252.6243	487.2147	244.1110	486.2307	243.6190	4
4	**456.2565**	228.6319	439.2300	220.1186	438.2459	219.6266	E	433.2041	217.1057	416.1776	208.5924	415.1936	208.1004	3
5	**585.2991**	293.1532	568.2726	284.6399	567.2885	284.1479	E	**304.1615**	152.5844	287.1350	144.0711	286.1510	143.5791	2
6							R	**175.1190**	88.0631	**158.0924**	79.5498			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.0	758.4035	-0.0003	RVAEER
21.9	758.4035	-0.0003	RVEAER
17.7	758.4035	-0.0003	RGIEER
14.7	758.4035	-0.0003	REVAER
13.8	758.4109	-0.0077	MATALPR
13.8	758.4035	-0.0003	TTPRER
10.9	758.4035	-0.0003	DALRER
10.9	758.4035	-0.0003	EVARER
10.9	758.3936	0.0096	FRGHSR
10.9	758.4035	-0.0003	IDARER

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

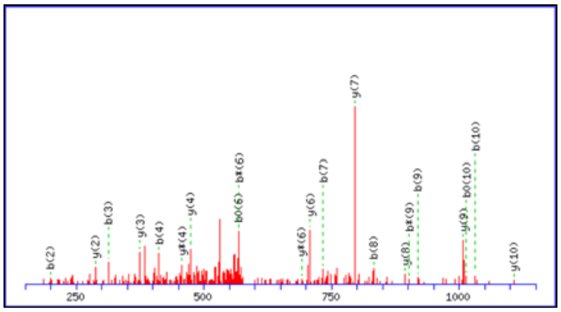
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVNVSSMVSLR**
Found in **CBR1_MOUSE**, Carbonyl reductase [NADPH] 1 (EC 1.1.1.184) (NADPH-dependent carbonyl reductase 1) - Mus musculus (Mouse) (P48758)

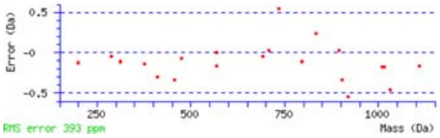
Match to Query 756: 1205.647064 from(603.830808,2+)
Title: Arrell01100950 scan 662 662 (Arrell01100950.662.662.2.dta)
Data file Arrell01100950.mgf

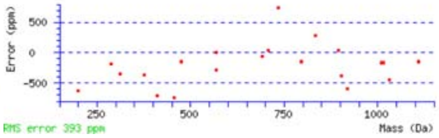
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1150 Da Full range



```
Monoisotopic mass of neutral peptide Mr(calc): 1205.6438
Variable modifications:
M7     : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 50  Expect: 0.00011
Matches (Bold Red): 21/164 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	100.0757	50.5415					V							11
2	**199.1441**	100.0757					V	**1107.5827**	554.2950	1090.5561	545.7817	1089.5721	545.2897	10
3	**313.1870**	157.0972	296.1605	148.5839			N	**1008.5143**	504.7608	991.4877	496.2475	990.5037	495.7555	9
4	**412.2554**	206.6314	395.2289	198.1181			V	**894.4713**	447.7393	877.4448	439.2260	876.4608	438.7340	8
5	499.2875	250.1474	482.2609	241.6341	481.2769	241.1421	S	**795.4029**	398.2051	778.3764	389.6918	777.3924	389.1998	7
6	586.3195	293.6634	**569.2930**	285.1501	**568.3089**	284.6581	S	**708.3709**	354.6891	**691.3443**	346.1758	690.3603	345.6838	6
7	**733.3549**	367.1811	716.3284	358.6678	715.3443	358.1758	M	621.3389	311.1731	604.3123	302.6598	603.3283	302.1678	5
8	**832.4233**	416.7153	815.3968	408.2020	814.4128	407.7100	V	**474.3035**	237.6554	**457.2769**	229.1421	456.2929	228.6501	4
9	**919.4553**	460.2313	**902.4288**	451.7180	901.4448	451.2260	S	**375.2350**	188.1212	358.2085	179.6079	357.2245	179.1159	3
10	**1032.5394**	516.7733	1015.5129	508.2601	**1014.5288**	507.7681	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 VVNVSSMVSLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
50.2	1205.6438	0.0032	VVNVSSMVSLR
0.4	1205.6438	0.0033	KTIGECSLSLR

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

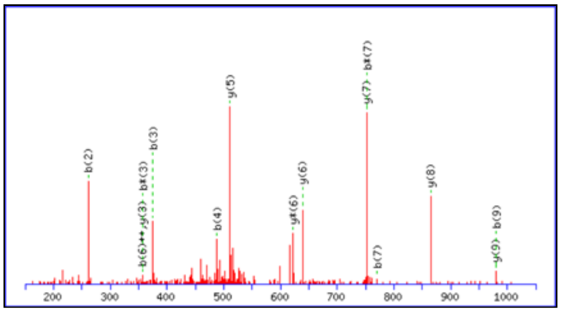
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FNIIQPGPIK**
Found in **DECR_MOUSE**, 2,4-dienoyl-CoA reductase, mitochondrial precursor (EC 1.3.1.34) (2,4-dienoyl-CoA reductase [NADPH]) (4-enoyl-CoA reductase [NADPH]) - Mus musculus (Mouse) (Q9CQ62)

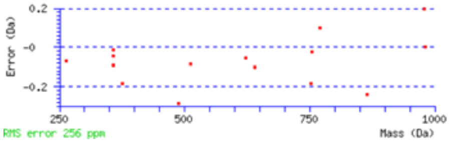
Match to Query 682: 1125.654024 from(563.834288,2+)
Title: Arrell01100950 scan 1133 1133 (Arrell01100950.1133.1133.2.dta)
Data file Arrell01100950.mgf

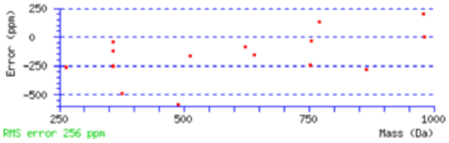
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1050 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1125.6546
Ions Score: 51 **Expect:** 4e-05
Matches (Bold Red): 15/70 fragment ions using 22 most intense peaks

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	148.0757	74.5415			F					10
2	**262.1186**	131.5629	245.0921	123.0497	N	**979.5935**	490.3004	962.5669	481.7871	9
3	**375.2027**	188.1050	**358.1761**	179.5917	I	**865.5506**	433.2789	848.5240	424.7656	8
4	**488.2867**	244.6470	471.2602	236.1337	I	**752.4665**	376.7369	735.4400	368.2236	7
5	616.3453	308.6763	599.3188	300.1630	Q	**639.3824**	320.1949	**622.3559**	311.6816	6
6	713.3981	**357.2027**	696.3715	348.6894	P	**511.3239**	256.1656	494.2973	247.6523	5
7	**770.4196**	385.7134	**753.3930**	377.2001	G	414.2711	207.6392	397.2445	199.1259	4
8	867.4723	434.2398	850.4458	425.7265	P	**357.2496**	179.1285	340.2231	170.6152	3
9	**980.5564**	490.7818	963.5298	482.2686	I	260.1969	130.6021	243.1703	122.0888	2
10					K	147.1128	74.0600	130.0863	65.5468	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
50.5	1125.6546	-0.0006	FNIIQPGPIK
9.9	1125.6618	-0.0078	SKPVPSRLSR

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

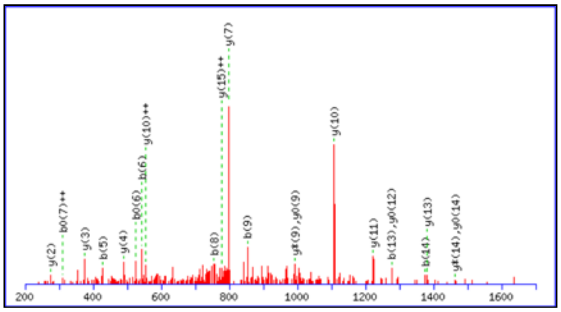
Mascot Search Results

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)

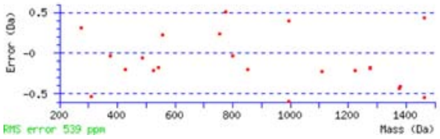
Match to Query 634: 1649.910374 from(825.962463,2+)
Title: Arrell12300855 scan 974 974 (Arrell12300855.974.974.2.dta)
Data file Arrell12300855.mgf

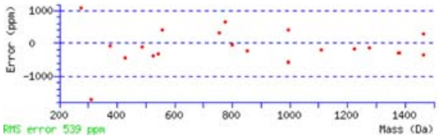
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range



`Monoisotopic mass of neutral peptide Mr(calc): 1649.9101`
`Ions Score: 37  Expect: 0.00064`
`Matches (Bold Red): 22/158 fragment ions using 40 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
36.7	1649.9101	0.0003	VAVSADPNVPNVIVTR

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

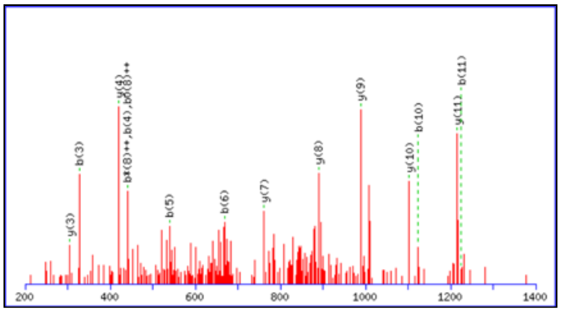
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NVLIVEDIIDTGK**
Found in **HPRT_MOUSE**, Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8) (HGPRT) (HGPRTase) (HPRT B) - Mus musculus (Mouse) (P00493)

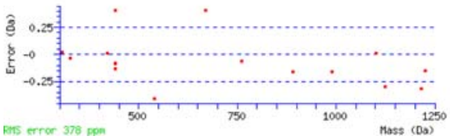
Match to Query 679: 1427.788424 from(714.901488,2+)
Title: Arrell12300857 scan 1717 1717 (Arrell12300857.1717.1717.2.dta)
Data file Arrell12300857.mgf

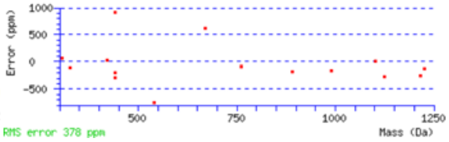
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1427.7872
Ions Score: 64 **Expect:** 2.5e-06
Matches (Bold Red): 15/130 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	115.0502	58.0287	98.0237	49.5155			N							13
2	214.1186	107.5629	197.0921	99.0497			V	1314.7515	657.8794	1297.7250	649.3661	1296.7409	648.8741	12
3	**327.2027**	164.1050	310.1761	155.5917			L	**1215.6831**	608.3452	1198.6565	599.8319	1197.6725	599.3399	11
4	**440.2867**	220.6470	423.2602	212.1337			I	**1102.5990**	551.8032	1085.5725	543.2899	1084.5885	542.7979	10
5	**539.3552**	270.1812	522.3286	261.6679			V	**989.5150**	495.2611	972.4884	486.7478	971.5044	486.2558	9
6	**668.3978**	334.7025	651.3712	326.1892	650.3872	325.6972	E	**890.4466**	445.7269	873.4200	437.2136	872.4360	436.7216	8
7	783.4247	392.2160	766.3981	383.7027	765.4141	383.2107	D	**761.4040**	381.2056	744.3774	372.6923	743.3934	372.2003	7
8	896.5088	448.7580	879.4822	**440.2447**	878.4982	**439.7527**	I	646.3770	323.6921	629.3505	315.1789	628.3665	314.6869	6
9	1009.5928	505.3000	992.5663	496.7868	991.5823	496.2948	I	533.2930	267.1501	516.2664	258.6368	515.2824	258.1448	5
10	**1124.6198**	562.8135	1107.5932	554.3002	1106.6092	553.8082	D	**420.2089**	210.6081	403.1823	202.0948	402.1983	201.6028	4
11	**1225.6674**	613.3374	1208.6409	604.8241	1207.6569	604.3321	T	**305.1819**	153.0946	288.1554	144.5813	287.1714	144.0893	3
12	1282.6889	641.8481	1265.6624	633.3348	1264.6783	632.8428	G	204.1343	102.5708	187.1077	94.0575			2
13							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
63.8	1427.7872	0.0013	NVLIVEDIIDTGK

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

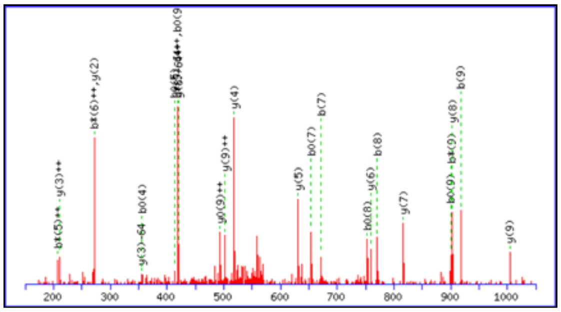
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GQTSGQIVMPR**
Found in **ITPA_MOUSE**, Inosine triphosphate pyrophosphatase (EC 3.6.1.19) (ITPase) (Inosine triphosphatase) - Mus musculus (Mouse) (Q9D892)

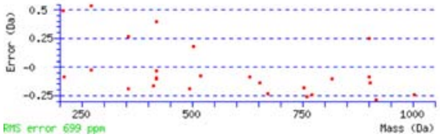
Match to Query 464: 1188.592194 from(595.303373,2+)
Title: Arrell12300868 scan 334 336 (Arrell12300868.334.336.2.dta)
Data file Arrell12300868.mgf

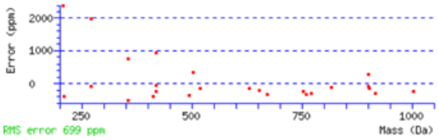
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1050 Da Full range



```
Monoisotopic mass of neutral peptide Mr(calc): 1188.5921
Variable modifications:
M9     : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 70  Expect: 1.1e-06
Matches (Bold Red): 26/150 fragment ions using 32 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							11
2	186.0873	93.5473	169.0608	85.0340			Q	1132.5779	566.7926	1115.5514	558.2793	1114.5674	557.7873	10
3	287.1350	144.0711	270.1084	135.5579	269.1244	135.0659	T	**1004.5193**	**502.7633**	987.4928	494.2500	986.5088	**493.7580**	9
4	374.1670	187.5872	357.1405	179.0739	**356.1565**	178.5819	S	**903.4717**	452.2395	886.4451	443.7262	885.4611	443.2342	8
5	431.1885	216.0979	414.1619	**207.5846**	**413.1779**	207.0926	G	**816.4396**	408.7235	799.4131	400.2102			7
6	559.2471	280.1272	542.2205	**271.6139**	541.2365	271.1219	Q	**759.4182**	380.2127	742.3916	371.6995			6
7	**672.3311**	336.6692	655.3046	328.1559	**654.3206**	327.6639	I	**631.3596**	316.1834	614.3330	307.6702			5
8	**771.3995**	386.2034	754.3730	377.6901	**753.3890**	377.1981	V	**518.2755**	259.6414	501.2490	251.1281			4
9	**918.4349**	459.7211	**901.4084**	451.2078	**900.4244**	450.7158	M	**419.2071**	**210.1072**	402.1806	201.5939			3
10	1015.4877	508.2475	998.4612	499.7342	997.4771	499.2422	P	**272.1717**	136.5895	255.1452	128.0762			2
11							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
69.5	1188.5921	0.0001	GQTSGQIVMPR
2.6	1188.5887	0.0035	GGDETRLPFR
0.7	1188.5986	-0.0064	ISATDEAQVQK

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

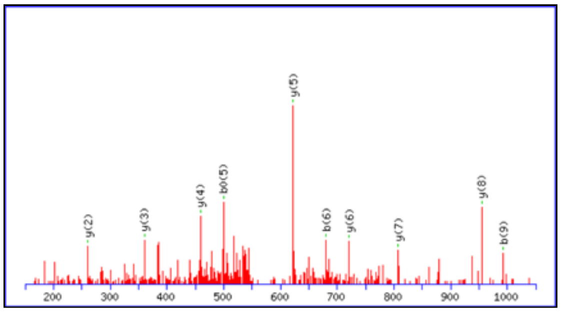
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **AIFSVYVVNK**
Found in **TPPC4_MOUSE**, Trafficking protein particle complex subunit 4 (Synbindin) (TRS23 homolog) - Mus musculus (Mouse) (Q9ES56)

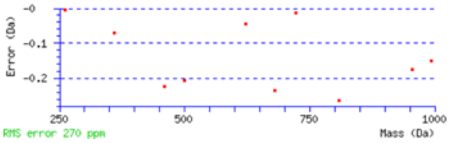
Match to Query 388: 1138.638214 from(570.326383,2+)
Title: Arrell12300879 scan 1037 1039 (Arrell12300879.1037.1039.2.dta)
Data file Arrell12300879.mgf

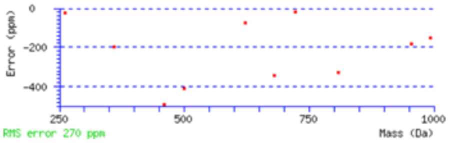
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1050 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1138.6386
Ions Score: 60 **Expect:** 5e-06
Matches (Bold Red): 10/74 fragment ions using 11 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							10
2	185.1285	93.0679					I	1068.6088	534.8080	1051.5823	526.2948	1050.5982	525.8028	9
3	332.1969	166.6021					F	**955.5247**	478.2660	938.4982	469.7527	937.5142	469.2607	8
4	419.2289	210.1181			401.2183	201.1128	S	**808.4563**	404.7318	791.4298	396.2185	790.4458	395.7265	7
5	518.2973	259.6523			**500.2867**	250.6470	V	**721.4243**	361.2158	704.3978	352.7025			6
6	**681.3606**	341.1840			663.3501	332.1787	Y	**622.3559**	311.6816	605.3293	303.1683			5
7	780.4291	390.7182			762.4185	381.7129	V	**459.2926**	230.1499	442.2660	221.6366			4
8	879.4975	440.2524			861.4869	431.2471	V	**360.2241**	180.6157	343.1976	172.1024			3
9	**993.5404**	497.2738	976.5138	488.7606	975.5298	488.2686	N	**261.1557**	131.0815	244.1292	122.5682			2
10							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of AIFSVYVVNK
(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	1138.6386	-0.0004	AIFSVYVVNK
3.3	1137.6441	0.9941	LRCIHVVNK
1.4	1138.6346	0.0036	QPSKPEIVNK

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

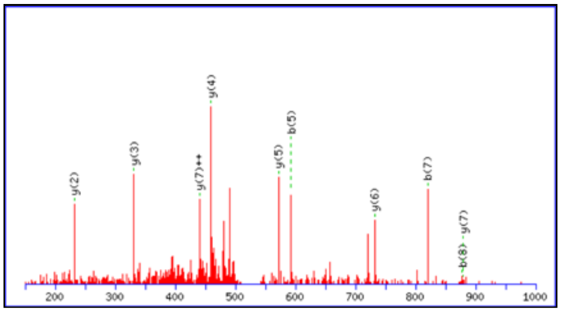
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GDFCIQVGR**
Found in **NDKA_MOUSE**, Nucleoside diphosphate kinase A (EC 2.7.4.6) (NDK A) (NDP kinase A) (Tumor metastatic process-associated protein) (Metastasis inhibition factor NM23) (NDPK-A) (nm23-M1) - Mus musculus (Mouse) (P15532)

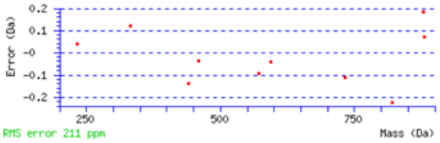
Match to Query 454: 1050.490204 from(526.252378,2+)
Title: Arrell12300881 scan 926 928 (Arrell12300881.926.928.2.dta)
Data file Arrell12300881.mgf

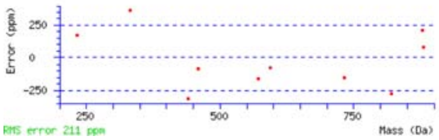
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1000 Da Full range



```
Monoisotopic mass of neutral peptide Mr(calc): 1050.4917
Variable modifications:
C4     : Carbamidomethyl (C)
Ions Score: 40  Expect: 0.0011
Matches (Bold Red): 10/70 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	58.0287	29.5180					G							9
2	173.0557	87.0315			155.0451	78.0262	D	994.4775	497.7424	977.4509	489.2291	976.4669	488.7371	8
3	320.1241	160.5657			302.1135	151.5604	F	**879.4505**	**440.2289**	862.4240	431.7156			7
4	480.1548	240.5810			462.1442	231.5757	C	**732.3821**	366.6947	715.3556	358.1814			6
5	**593.2388**	297.1230			575.2283	288.1178	I	**572.3515**	286.6794	555.3249	278.1661			5
6	721.2974	361.1523	704.2708	352.6391	703.2868	352.1471	Q	**459.2674**	230.1373	442.2409	221.6241			4
7	**820.3658**	410.6865	803.3393	402.1733	802.3552	401.6813	V	**331.2088**	166.1081	314.1823	157.5948			3
8	**877.3873**	439.1973	860.3607	430.6840	859.3767	430.1920	G	**232.1404**	116.5738	215.1139	108.0606			2
9							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.8	1050.4917	-0.0015	GDFCIQVGR

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

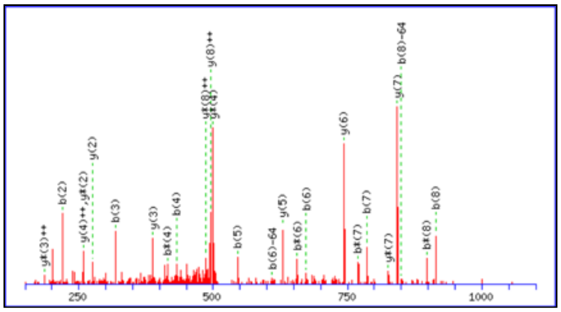
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AMVNLQIQK**
Found in **ZCD1_MOUSE**, Zinc finger CDGSH domain-containing protein 1 - Mus musculus (Mouse) (Q91WS0)

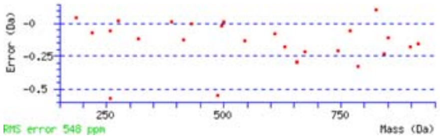
Match to Query 377: 1059.574194 from(530.794373,2+)
Title: Arrell12300884 scan 655 655 (Arrell12300884.655.655.2.dta)
Data file Arrell12300884.mgf

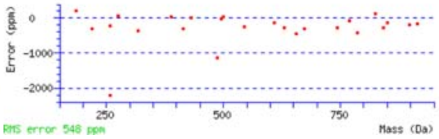
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1100 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1059.5746
Variable modifications:
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 35 **Expect:** 0.0045
Matches (Bold Red): 25/86 fragment ions using 56 most intense peaks

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	72.0444	36.5258			A					9
2	**219.0798**	110.0435			M	989.5448	**495.2761**	972.5183	**486.7628**	8
3	**318.1482**	159.5777			V	**842.5094**	421.7584	**825.4829**	413.2451	7
4	**432.1911**	216.5992	**415.1646**	208.0859	N	**743.4410**	372.2241	726.4145	363.7109	6
5	**545.2752**	273.1412	528.2486	264.6280	L	**629.3981**	315.2027	612.3715	306.6894	5
6	**673.3338**	337.1705	**656.3072**	328.6573	Q	516.3140	**258.6607**	**499.2875**	250.1474	4
7	**786.4178**	393.7126	**769.3913**	385.1993	I	**388.2554**	194.6314	371.2289	**186.1181**	3
8	**914.4764**	457.7418	**897.4499**	449.2286	Q	**275.1714**	138.0893	**258.1448**	129.5761	2
9					K	147.1128	74.0600	130.0863	65.5468	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.7	1059.5746	-0.0005	AMVNLQIQK
3.3	1059.5746	-0.0005	SPMQNVLKK

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

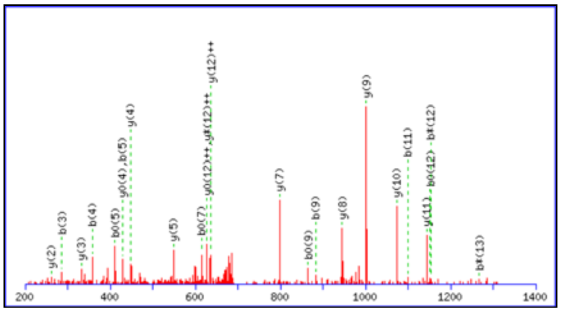
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TGQAAGFSYTDANK**
Found in **CYC_MOUSE**, Cytochrome c, somatic OS=Mus musculus GN=Cycs PE=1 SV=2 (sp) (P62897)

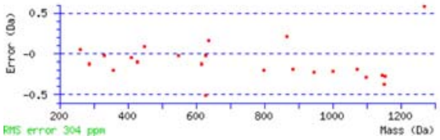
Match to Query 598: 1429.647924 from(715.831238,2+)
Title: Arrell12300884 scan 560 560 (Arrell12300884.560.560.2.dta)
Data file Arrell12300884.mgf

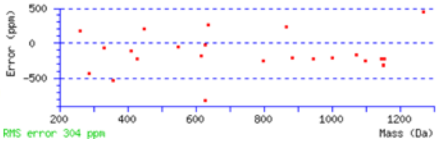
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1429.6474
Ions Score: 56 **Expect:** 0.00016
Matches (Bold Red): 24/146 fragment ions using 41 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							14
2	159.0764	80.0418			141.0659	71.0366	G	1329.6070	665.3071	1312.5804	656.7938	1311.5964	656.3018	13
3	**287.1350**	144.0711	270.1084	135.5579	269.1244	135.0659	Q	1272.5855	**636.7964**	1255.5590	**628.2831**	1254.5749	**627.7911**	12
4	**358.1721**	179.5897	341.1456	171.0764	340.1615	170.5844	A	**1144.5269**	572.7671	1127.5004	564.2538	1126.5164	563.7618	11
5	**429.2092**	215.1083	412.1827	206.5950	**411.1987**	206.1030	A	**1073.4898**	537.2485	1056.4633	528.7353	1055.4793	528.2433	10
6	486.2307	243.6190	469.2041	235.1057	468.2201	234.6137	G	**1002.4527**	501.7300	985.4262	493.2167	984.4421	492.7247	9
7	633.2991	317.1532	616.2726	308.6399	**615.2885**	308.1479	F	**945.4312**	473.2193	928.4047	464.7060	927.4207	464.2140	8
8	720.3311	360.6692	703.3046	352.1559	702.3206	351.6639	S	**798.3628**	399.6851	781.3363	391.1718	780.3523	390.6798	7
9	**883.3945**	442.2009	866.3679	433.6876	**865.3839**	433.1956	Y	711.3308	356.1690	694.3042	347.6558	693.3202	347.1638	6
10	984.4421	492.7247	967.4156	484.2114	966.4316	483.7194	T	**548.2675**	274.6374	531.2409	266.1241	530.2569	265.6321	5
11	**1099.4691**	550.2382	1082.4425	541.7249	1081.4585	541.2329	D	**447.2198**	224.1135	430.1932	215.6003	**429.2092**	215.1082	4
12	1170.5062	585.7567	**1153.4796**	577.2435	**1152.4956**	576.7515	A	**332.1928**	166.6001	315.1663	158.0868			3
13	1284.5491	642.7782	**1267.5226**	634.2649	1266.5386	633.7729	N	**261.1557**	131.0815	244.1292	122.5682			2
14							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.6	1429.6474	0.0006	TGQAAGFSYTDANK
12.9	1428.6490	0.9989	GPVCAGETPPVSCR
2.2	1429.6482	-0.0003	AIFDDRFVCCNK
0.7	1429.6404	0.0076	FMKVAEMGMPNK

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