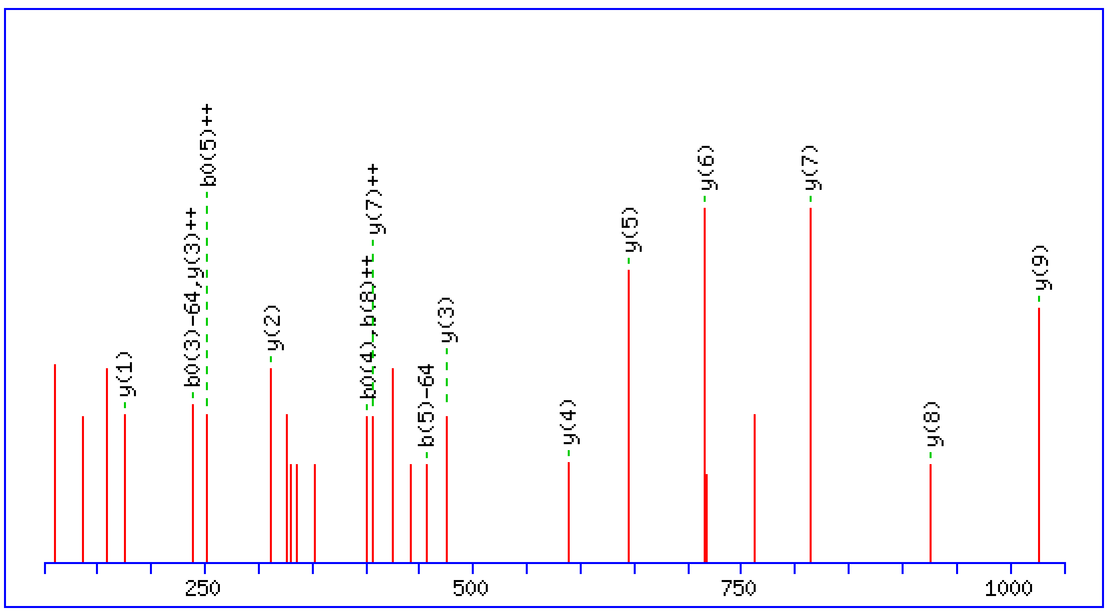
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **GDMVTLPAGIYHR**
Found in **MTND_HUMAN**, 1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase OS=Homo sapiens GN=ADI1 PE=1 SV=1

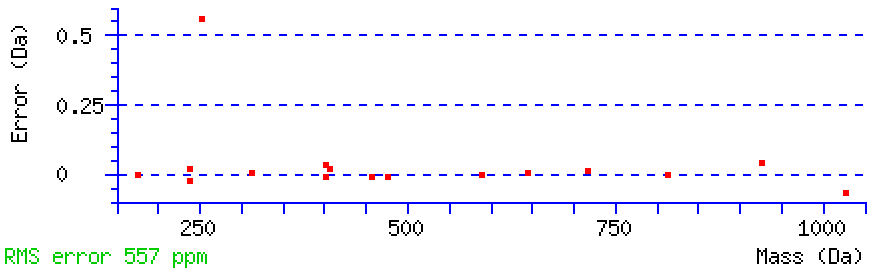
Match to Query 48218: 1444.712562 from(482.578130,3+) rtinseconds(2295) index(26457)
Title: Locus:1.1.1.2131.10
Data file 2011-11-10 - TFD - EP 4-6.mgf

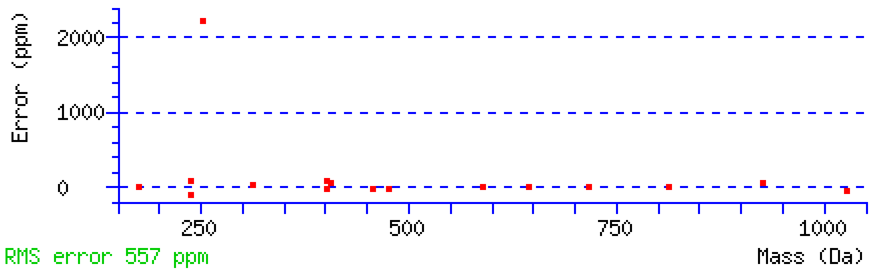
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1444.713287
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M3 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 58 **Expect:** 1.7e-005
Matches : 16/154 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008			G							13
2	173.055683	87.031479	155.045118	78.026197	D	1388.699099	694.853188	1371.672550	686.339913	1370.688534	685.847905	12
3	320.091083	160.549179	302.080518	151.543897	M	1273.672156	637.339716	1256.645607	628.826442	1255.661591	628.334434	11
4	419.159497	210.083386	401.148932	201.078104	V	1126.636756	563.822016	1109.610207	555.308742	1108.626191	554.816734	10
5	520.207176	260.607226	502.196611	251.601944	T	***1027.568342***	514.287809	1010.541793	505.774535	1009.557777	505.282527	9
6	633.291240	317.149258	615.280675	308.143976	L	***926.520663***	463.763970	909.494114	455.250695			8
7	730.344004	365.675640	712.333439	356.670358	P	***813.436599***	407.221938	796.410050	398.708663			7
8	801.381118	401.194197	783.370553	392.188915	A	***716.383835***	358.695556	699.357286	350.182281			6
9	858.402582	429.704929	840.392017	420.699647	G	***645.346721***	323.176999	628.320172	314.663724			5
10	971.486646	486.246961	953.476081	477.241679	I	***588.325257***	294.666267	571.298708	286.152992			4
11	1134.549975	567.778626	1116.539410	558.773343	Y	***475.241193***	238.124234	458.214644	229.610960			3
12	1271.608887	636.308082	1253.598322	627.302799	H	***312.177864***	156.592570	295.151315	148.079295			2
13					R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.0	1444.713287	-0.000725	GDMVTLPAGIYHR
26.5	1444.713287	-0.000725	GDMVTLPAGIYHR
11.4	1444.702072	0.010490	TGTFPETPMVPPR
9.1	1444.713272	-0.000710	ELIQGIFMGEHR
6.8	1444.702072	0.010490	TGTFPETPMVPPR
6.8	1444.702072	0.010490	TGTFPETPMVPPR
4.9	1444.721130	-0.008568	RLESFLHDSWR
4.6	1444.702072	0.010490	TGTFPETPMVPPR
2.9	1444.702072	0.010490	TGTFPETPMVPPR
1.6	1444.723801	-0.011239	YYDFKNPIIEK

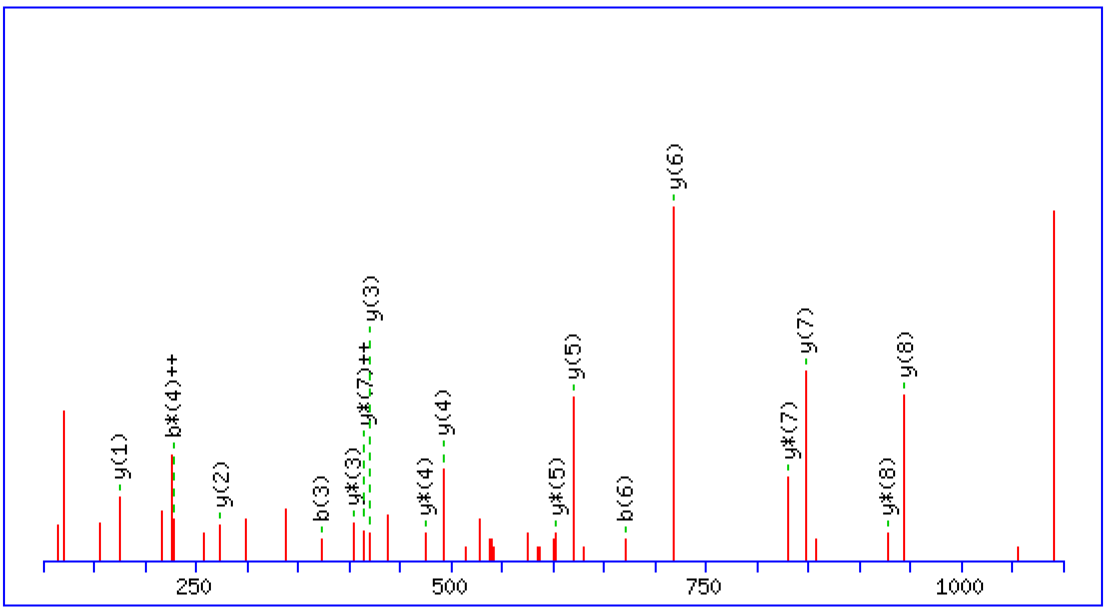
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FPQVQAFVR**
Found in **SEP15_HUMAN**, 15 kDa selenoprotein OS=Homo sapiens GN=SEP15 PE=1 SV=3

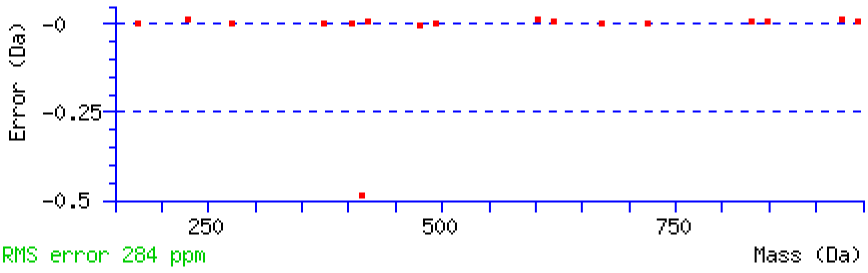
Match to Query 20790: 1090.591548 from(546.303050,2+) rtinseconds(2786) index(30005)
Title: Locus:1.1.1.2515.14
Data file 2011-11-13 - TFD - EP 7-7.mgf

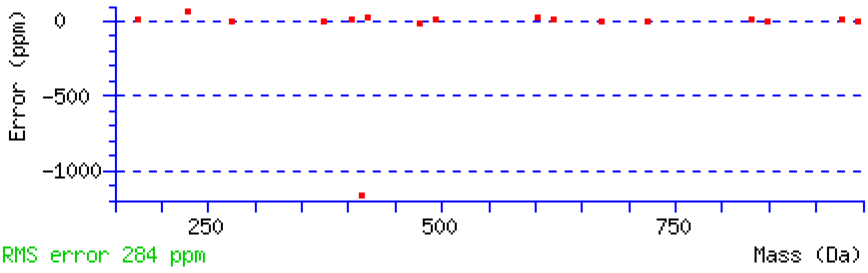
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1090.592377
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 60  Expect: 4.5e-006
Matches : 17/60 fragment ions using 33 most intense peaks   (help)
```

#	b	b^{++}	b*	b*$^{++}$	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	148.075690	74.541483			**F**					9
2	245.128454	123.067865			**P**	***944.531228***	472.769252	927.504679	464.255977	8
3	**373.187032**	187.097154	356.160483	178.583879	**Q**	***847.478464***	424.242870	830.451915	415.729595	7
4	472.255446	236.631361	455.228897	228.118087	**V**	***719.419886***	360.213581	702.393337	351.700306	6
5	600.314024	300.660650	583.287475	292.147376	**Q**	***620.351472***	310.679374	603.324923	302.166099	5
6	**671.351138**	336.179207	654.324589	327.665933	**A**	***492.292894***	246.650085	475.266345	238.136810	4
7	818.419552	409.713414	801.393003	401.200139	**F**	***421.255780***	211.131528	404.229231	202.618253	3
8	917.487966	459.247621	900.461417	450.734346	**V**	***274.187366***	137.597321	257.160817	129.084046	2
9					**R**	***175.118952***	88.063114	158.092403	79.549839	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
59.9	1090.592377	-0.000829	FPQVQAFVR
2.8	1090.588318	0.003230	NSPLYVRSR

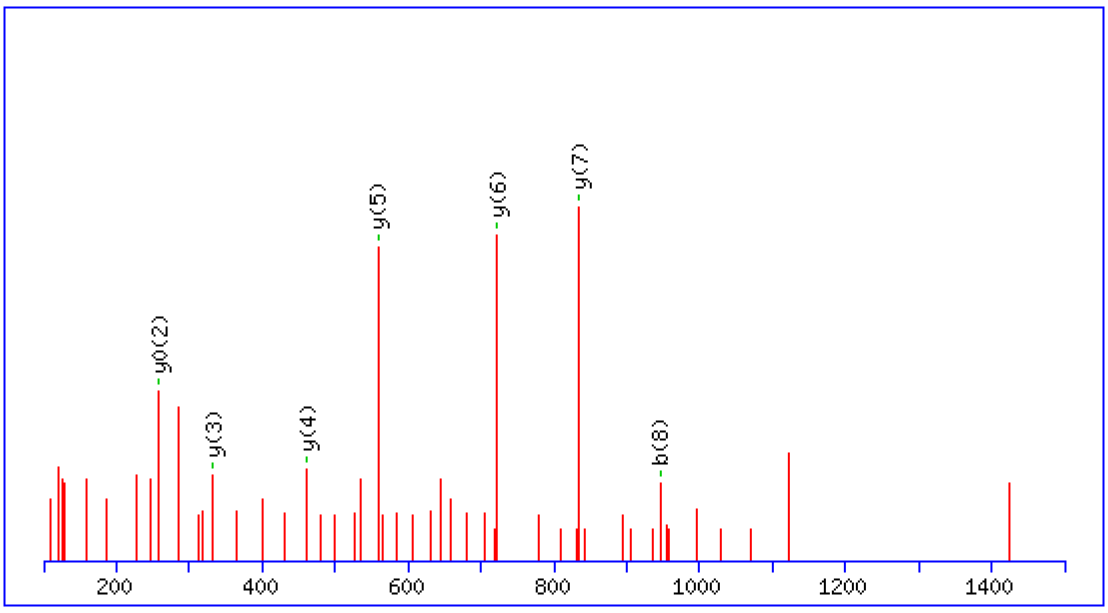
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VWIYPEGTR**
Found in **PLCB_HUMAN**, 1-acyl-sn-glycerol-3-phosphate acyltransferase beta OS=Homo sapiens GN=AGPAT2 PE=1 SV=1

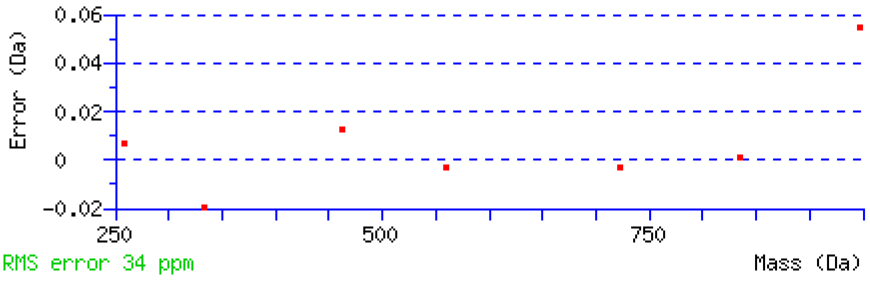
Match to Query 23267: 1119.579308 from(560.796930,2+) rtinseconds(2383) index(27751)
Title: Locus:1.1.1.2326.22
Data file 2011-11-13 - TFD - EP 7-5.mgf

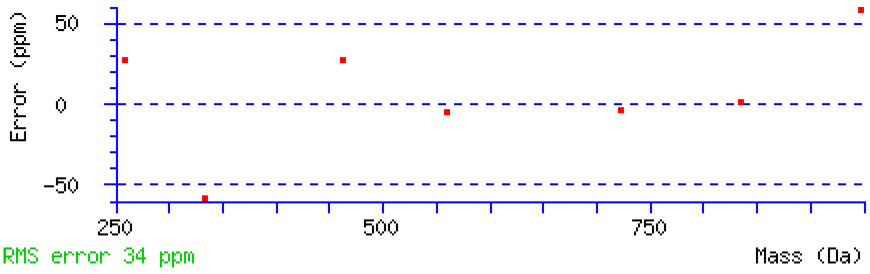
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1119.571289
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.0061
Matches : 7/68 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483			V							9
2	286.155003	143.581140			W	1021.510158	511.258717	1004.483609	502.745443	1003.499593	502.253435	8
3	399.239067	200.123172			I	*835.430845*	418.219061	818.404296	409.705786	817.420280	409.213778	7
4	562.302396	281.654836			Y	*722.346781*	361.677029	705.320232	353.163754	704.336216	352.671746	6
5	659.355160	330.181218			P	*559.283452*	280.145364	542.256903	271.632090	541.272887	271.140082	5
6	788.397753	394.702515	770.387188	385.697232	E	*462.230688*	231.618982	445.204139	223.105707	444.220123	222.613700	4
7	845.419217	423.213247	827.408652	414.207964	G	*333.188095*	167.097685	316.161546	158.584411	315.177530	158.092403	3
8	946.466896	473.737086	928.456331	464.731804	T	276.166631	138.586953	259.140082	130.073679	258.156066	129.581671	2
9					R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.7	1119.571289	0.008019	VWIYPEGTR

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

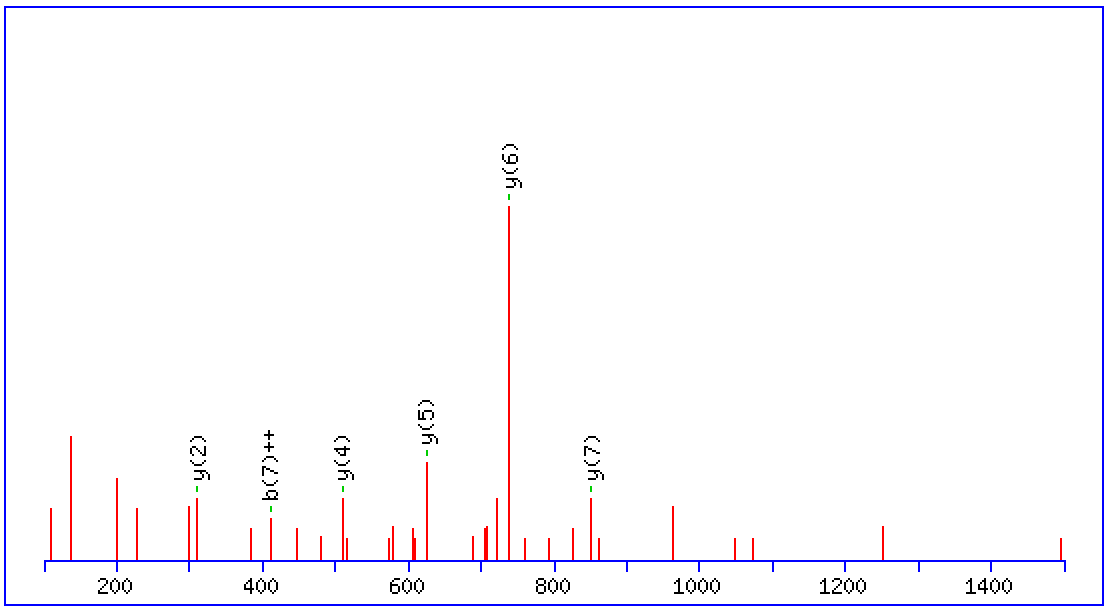
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILIDSIYK**
Found in **PLCH1_HUMAN**, 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase eta-1 OS=Homo sapiens GN=PLCH1 PE=1 SV=1

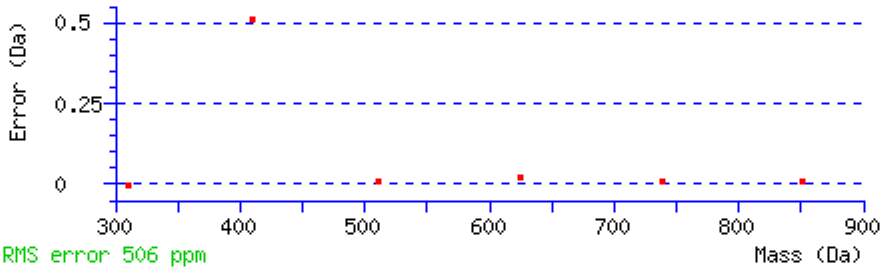
Match to Query 14098: 963.567548 from(482.791050,2+) rtinseconds(2498) index(31505)
Title: Locus:1.1.1.2378.10
Data file 2011-11-14 - TFD - EP 8-2.mgf

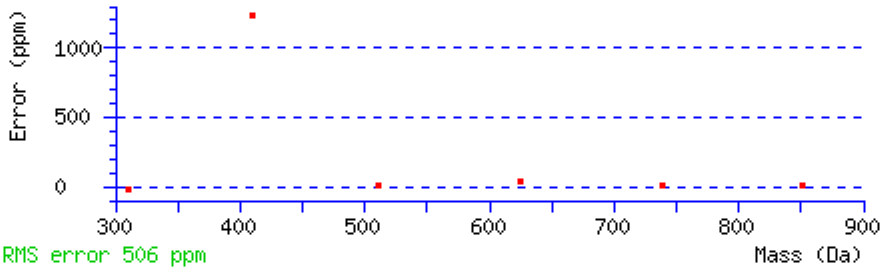
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 963.564056
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 37  Expect: 0.0005
Matches : 6/58 fragment ions using 8 most intense peaks  (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							8
2	227.175404	114.091340			L	*851.487296*	426.247286	834.460747	417.734012	833.476731	417.242004	7
3	340.259468	170.633372			I	*738.403232*	369.705254	721.376683	361.191980	720.392667	360.699972	6
4	455.286411	228.146843	437.275846	219.141561	D	*625.319168*	313.163222	608.292619	304.649948	607.308603	304.157940	5
5	542.318439	271.662858	524.307874	262.657575	S	*510.292225*	255.649751	493.265676	247.136476	492.281660	246.644468	4
6	655.402503	328.204890	637.391938	319.199607	I	423.260197	212.133737	406.233648	203.620462			3
7	818.465832	409.736554	800.455267	400.731272	Y	*310.176133*	155.591705	293.149584	147.078430			2
8					K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.5	963.564056	0.003492	ILIDSIYK
11.5	963.564056	0.003492	LLEIVSYK

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

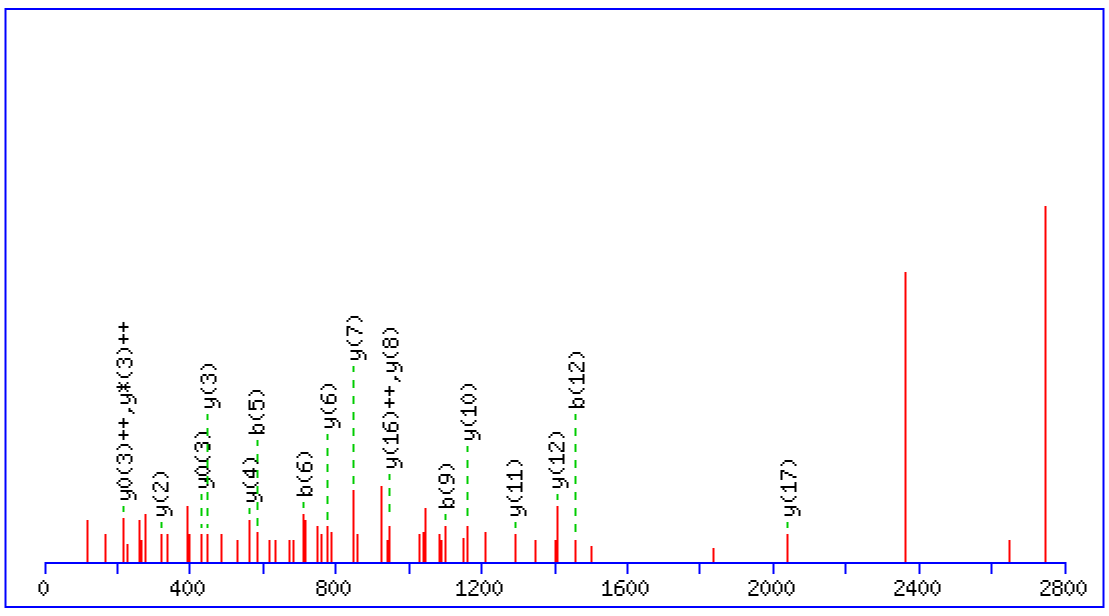
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DKPELQFPFLQDEDTVATLLECK**
Found in **CN37_HUMAN**, 2',3'-cyclic-nucleotide 3'-phosphodiesterase OS=Homo sapiens GN=CNP PE=1 SV=2

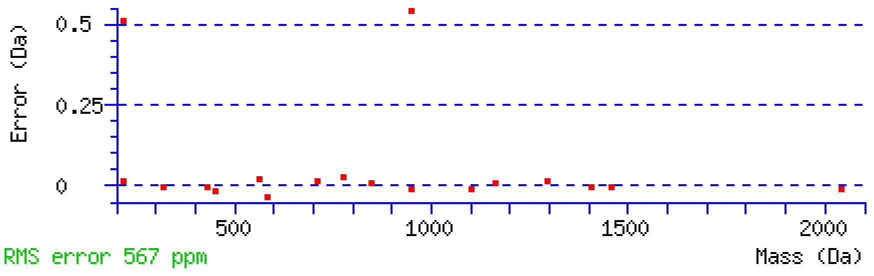
Match to Query 75013: 2749.350372 from(917.457400,3+) rtinseconds(4465) index(68571)
Title: Locus:1.1.1.2985.35
Data file 2011-11-12 - TFD - EP 6-4.mgf

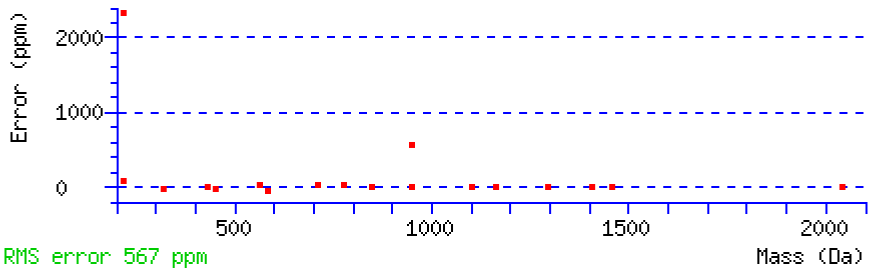
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2749.352036
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 48  Expect: 3.3e-005
Matches : 18/258 fragment ions using 32 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.034219	58.520748			98.023654	49.515465	D							23
2	244.129182	122.568229	227.102633	114.054955	226.118617	113.562947	K	2635.332385	1318.169830	2618.305836	1309.656556	2617.321820	1309.164548	22
3	341.181946	171.094611	324.155397	162.581336	323.171381	162.089328	P	2507.237422	1254.122349	2490.210873	1245.609074	2489.226857	1245.117066	21
4	470.224539	235.615907	453.197990	227.102633	452.213974	226.610625	E	2410.184658	1205.595967	2393.158109	1197.082692	2392.174093	1196.590684	20
5	**583.308603**	292.157940	566.282054	283.644665	565.298038	283.152657	L	2281.142065	1141.074670	2264.115516	1132.561396	2263.131500	1132.069388	19
6	**711.367181**	356.187229	694.340632	347.673954	693.356616	347.181946	Q	2168.058001	1084.532638	2151.031452	1076.019364	2150.047436	1075.527356	18
7	858.435595	429.721436	841.409046	421.208161	840.425030	420.716153	F	***2039.999423***	1020.503350	2022.972874	1011.990075	2021.988858	1011.498067	17
8	955.488359	478.247818	938.461810	469.734543	937.477794	469.242535	P	1892.931009	946.969143	1875.904460	938.455868	1874.920444	937.963860	16
9	**1102.556773**	551.782025	1085.530224	543.268750	1084.546208	542.776742	F	1795.878245	898.442761	1778.851696	889.929486	1777.867680	889.437478	15
10	1215.640837	608.324056	1198.614288	599.810782	1197.630272	599.318774	L	1648.809831	824.908554	1631.783282	816.395279	1630.799266	815.903271	14
11	1343.699415	672.353345	1326.672866	663.840071	1325.688850	663.348063	Q	1535.725767	768.366522	1518.699218	759.853247	1517.715202	759.361239	13
12	**1458.726358**	729.866817	1441.699809	721.353543	1440.715793	720.861534	D	***1407.667189***	704.337233	1390.640640	695.823958	1389.656624	695.331950	12
13	1587.768951	794.388113	1570.742402	785.874839	1569.758386	785.382831	E	***1292.640246***	646.823761	1275.613697	638.310487	1274.629681	637.818479	11
14	1702.795894	851.901585	1685.769345	843.388310	1684.785329	842.896302	D	***1163.597653***	582.302465	1146.571104	573.789190	1145.587088	573.297182	10
15	1803.843573	902.425424	1786.817024	893.912150	1785.833008	893.420142	T	1048.570710	524.788993	1031.544161	516.275719	1030.560145	515.783711	9
16	1902.911987	951.959632	1885.885438	943.446357	1884.901422	942.954349	V	***947.523031***	474.265154	930.496482	465.751879	929.512466	465.259871	8
17	1973.949101	987.478188	1956.922552	978.964914	1955.938536	978.472906	A	***848.454617***	424.730947	831.428068	416.217672	830.444052	415.725664	7
18	2074.996780	1038.002028	2057.970231	1029.488753	2056.986215	1028.996745	T	***777.417503***	389.212390	760.390954	380.699115	759.406938	380.207107	6
19	2188.080844	1094.544060	2171.054295	1086.030785	2170.070279	1085.538777	L	676.369824	338.688550	659.343275	330.175276	658.359259	329.683268	5
20	2301.164908	1151.086092	2284.138359	1142.572817	2283.154343	1142.080809	L	***563.285760***	282.146518	546.259211	273.633244	545.275195	273.141236	4
21	2430.207501	1215.607388	2413.180952	1207.094114	2412.196936	1206.602106	E	***450.201696***	225.604486	433.175147	217.091212	432.191131	216.599204	3
22	2604.253800	1302.630538	2587.227251	1294.117263	2586.243235	1293.625255	C	***321.159103***	161.083190	304.132554	152.569915			2
23							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.9	2749.352036	-0.001664	DKPELQFPFLQDEDTVATLLECK
0.0	2749.353195	-0.002823	AVFPPEPGAAKPGGAAAEGAGPGAARGAQR

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

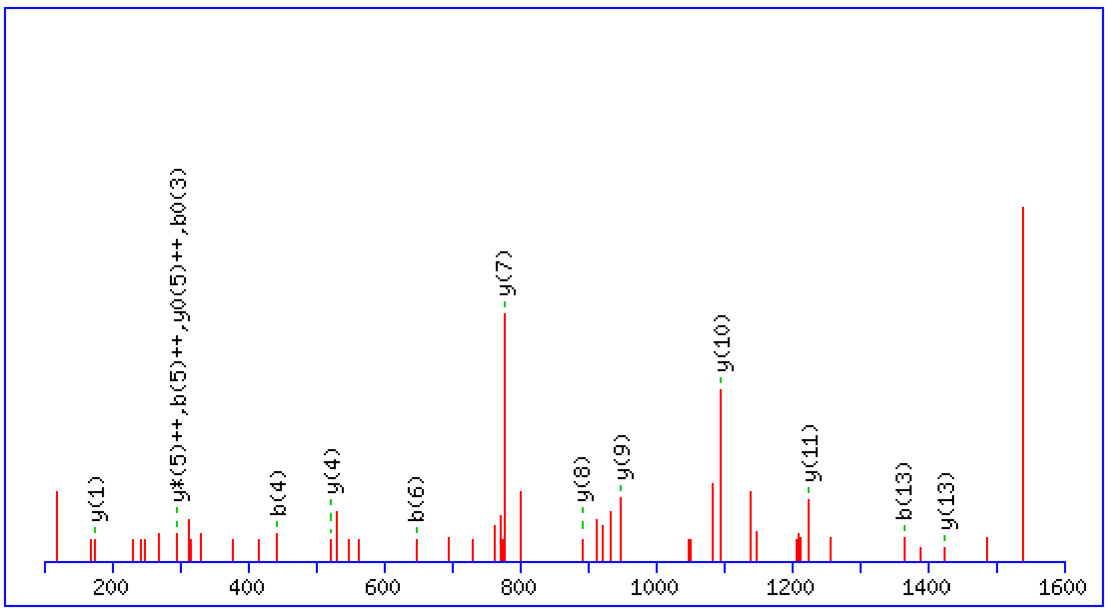
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSLEFGDPASSLFR**
Found in **PDE12_HUMAN**, 2',5'-phosphodiesterase 12 OS=Homo sapiens GN=PDE12 PE=1 SV=2

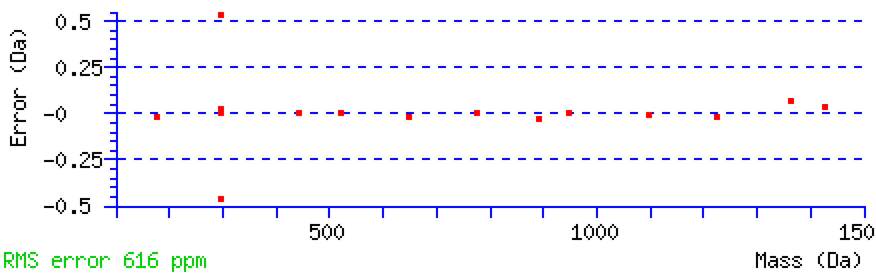
Match to Query 49757: 1537.786868 from(769.900710,2+) rtinseconds(3789) index(55486)
Title: Locus:1.1.1.2857.42
Data file 2011-11-14 - TFD - EP 8-2.mgf

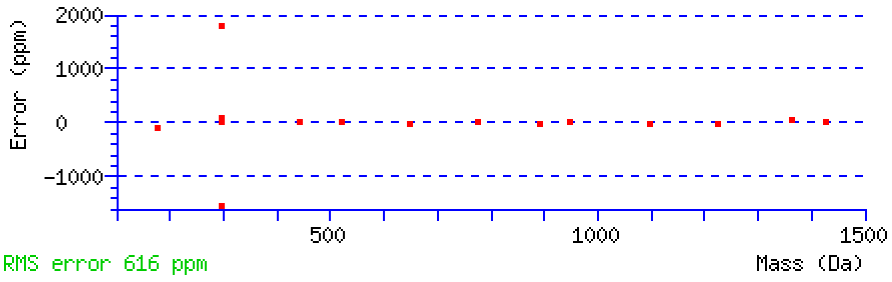
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1537.777649
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 43 **Expect:** 0.00044
Matches : 15/122 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							14
2	201.123368	101.065322	183.112803	92.060039	S	***1425.700870***	713.354073	1408.674321	704.840799	1407.690305	704.348791	13
3	314.207432	157.607354	296.196867	148.602071	L	1338.668842	669.838059	1321.642293	661.324785	1320.658277	660.832777	12
4	**443.250025**	222.128650	425.239460	213.123368	E	***1225.584778***	613.296027	1208.558229	604.782753	1207.574213	604.290745	11
5	590.318439	295.662858	572.307874	286.657575	F	***1096.542185***	548.774731	1079.515636	540.261456	1078.531620	539.769448	10
6	**647.339903**	324.173590	629.329338	315.168307	G	***949.473771***	475.240524	932.447222	466.727249	931.463206	466.235241	9
7	762.366846	381.687061	744.356281	372.681779	D	***892.452307***	446.729792	875.425758	438.216517	874.441742	437.724509	8
8	859.419610	430.213443	841.409045	421.208161	P	***777.425364***	389.216320	760.398815	380.703046	759.414799	380.211038	7
9	930.456724	465.732000	912.446159	456.726718	A	680.372600	340.689938	663.346051	332.176664	662.362035	331.684656	6
10	1017.488752	509.248014	999.478187	500.242731	S	609.335486	305.171381	592.308937	296.658107	591.324921	296.166099	5
11	1104.520780	552.764028	1086.510215	543.758746	S	***522.303458***	261.655367	505.276909	253.142093	504.292893	252.650085	4
12	1217.604844	609.306060	1199.594279	600.300777	L	435.271430	218.139353	418.244881	209.626078			3
13	**1364.673258**	682.840267	1346.662693	673.834985	F	322.187366	161.597321	305.160817	153.084047			2
14					R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.6	1537.777649	0.009219	LSLEFGDPASSLFR
6.5	1537.788895	-0.002027	IVVPPHLGYGEEGR
3.0	1537.788895	-0.002027	IVVPPHLGYGEEGR
2.0	1537.792908	-0.006040	LLSGPYFWSLPSR

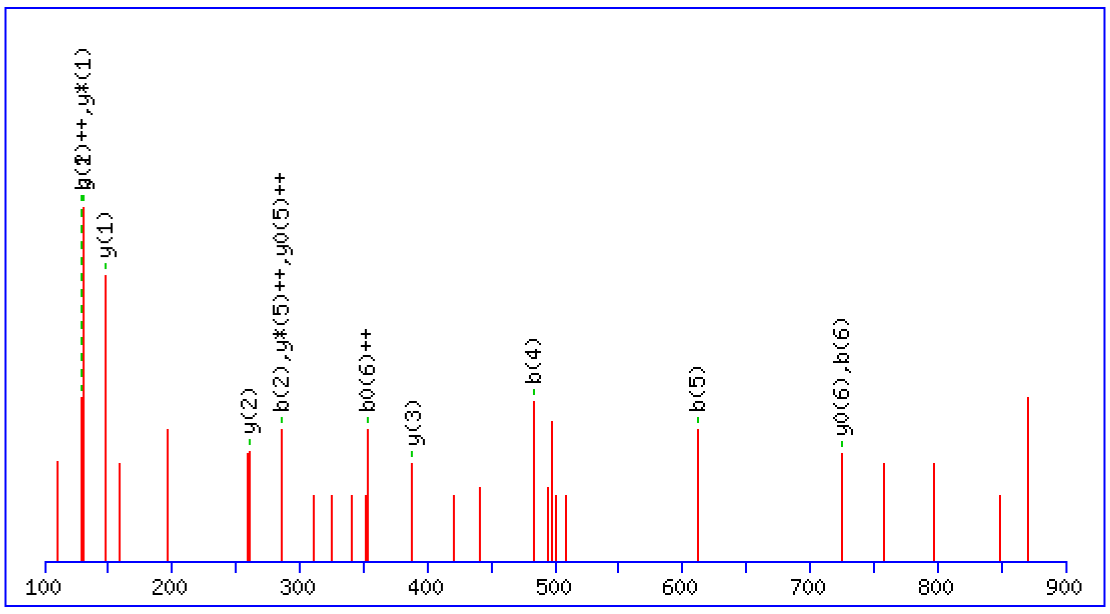
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QRPTKLK**
Found in **OAS1_HUMAN**, 2'-5'-oligoadenylate synthase 1 OS=Homo sapiens GN=OAS1 PE=1 SV=4

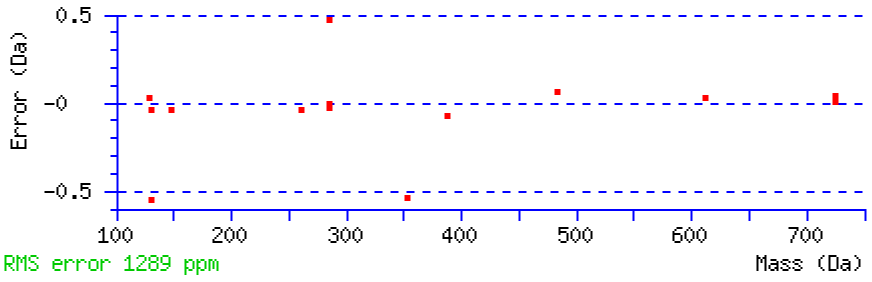
Match to Query 4554: 869.539008 from(435.776780,2+) rtinseconds(1614) index(4113)
Title: Locus:1.1.1.2271.5
Data file 2011-11-13 - TFD - EP 7-8.mgf

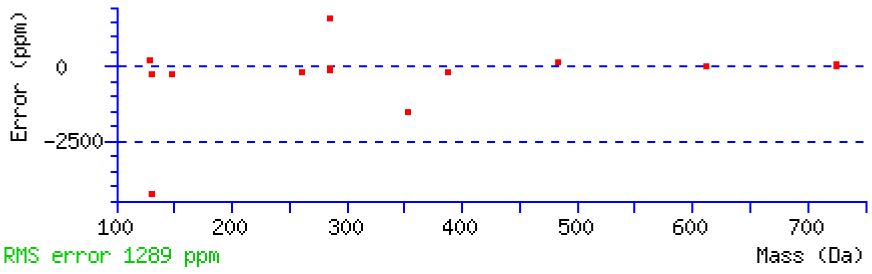
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [900] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 869.544662
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 34  Expect: 0.003
Matches : 14/60 fragment ions using 17 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	***129.065854***	65.036565	112.039305	56.523291			**Q**							7
2	***285.166965***	143.087121	268.140416	134.573846			**R**	742.493385	371.750331	725.466836	363.237056	724.482820	362.745048	6
3	382.219729	191.613502	365.193180	183.100228			**P**	586.392274	293.699775	569.365725	285.186501	568.381709	284.694493	5
4	***483.267408***	242.137342	466.240859	233.624068	465.256843	233.132060	**T**	489.339510	245.173393	472.312961	236.660119	471.328945	236.168111	4
5	***611.362371***	306.184824	594.335822	297.671549	593.351806	297.179541	**K**	**388.291831**	194.649554	371.265282	186.136279			3
6	***724.446435***	362.726856	707.419886	354.213581	706.435870	353.721573	**L**	**260.196868**	130.602072	243.170319	122.088798			2
7							**K**	**147.112804**	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.3	869.544662	-0.005654	QRPTKLK
29.9	869.533432	0.005576	LKQIGALQ
22.2	869.533432	0.005576	KAAVPQIK
22.2	869.533432	0.005576	KPKPKPK
22.2	869.533432	0.005576	QPQLKLK
22.1	869.533432	0.005576	KPLKQPK
20.2	869.533432	0.005576	QLQQLLK
20.2	869.533432	0.005576	QQLQLLK
18.5	869.544662	-0.005654	TRKPKPK
18.2	869.533432	0.005576	QKQIIPK

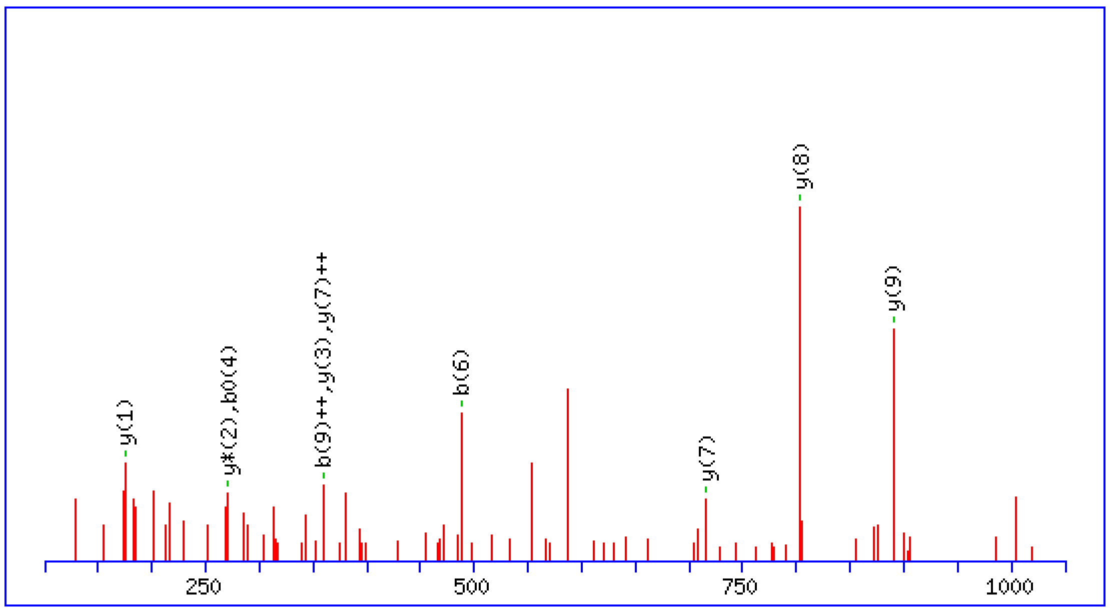
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GGSSAKGTALR**
Found in **OAS3_HUMAN**, 2'-5'-oligoadenylate synthase 3 OS=Homo sapiens GN=OAS3 PE=1 SV=3

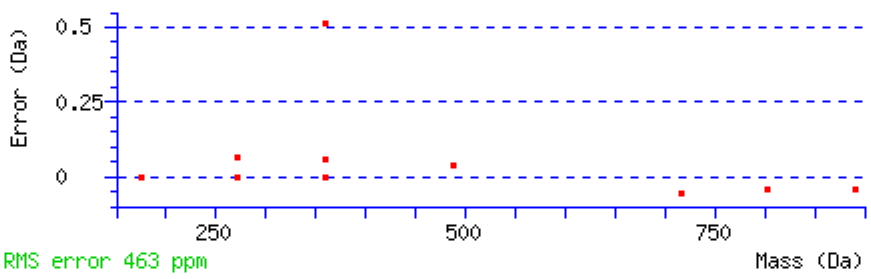
Match to Query 15905: 1003.533808 from(502.774180,2+) rtinseconds(1789) index(18447)
Title: Locus:1.1.1.2093.24
Data file 2011-11-14 - TFD - EP 8-1.mgf

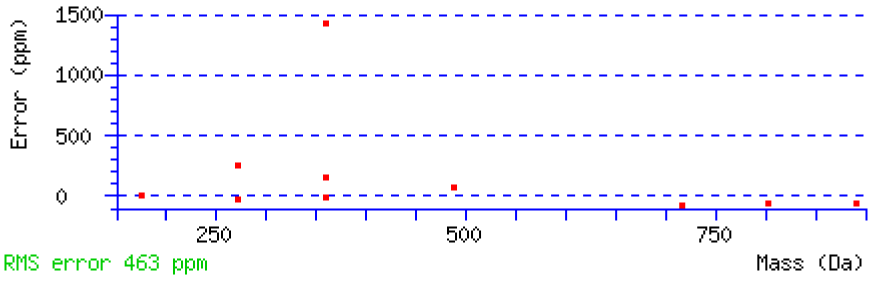
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1003.541046
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 35 **Expect:** 0.0019
Matches : 10/100 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	58.028740	29.518008					G							11
2	115.050204	58.028740					G	947.526870	474.267073	930.500321	465.753799	929.516305	465.261791	10
3	202.082232	101.544754			184.071667	92.539471	S	***890.505406***	445.756341	873.478857	437.243067	872.494841	436.751059	9
4	289.114260	145.060768			271.103695	136.055486	S	***803.473378***	402.240327	786.446829	393.727053	785.462813	393.235045	8
5	360.151374	180.579325			342.140809	171.574042	A	***716.441350***	358.724313	699.414801	350.211039	698.430785	349.719031	7
6	488.246337	244.626806	471.219788	236.113532	470.235772	235.621524	K	645.404236	323.205756	628.377687	314.692482	627.393671	314.200474	6
7	545.267801	273.137539	528.241252	264.624264	527.257236	264.132256	G	517.309273	259.158275	500.282724	250.645000	499.298708	250.152992	5
8	646.315480	323.661378	629.288931	315.148104	628.304915	314.656096	T	460.287809	230.647542	443.261260	222.134268	442.277244	221.642260	4
9	717.352594	359.179935	700.326045	350.666661	699.342029	350.174653	A	***359.240130***	180.123703	342.213581	171.610428			3
10	830.436658	415.721967	813.410109	407.208693	812.426093	406.716685	L	288.203016	144.605146	271.176467	136.091871			2
11							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of GGSSAKGTALR
(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	1003.541046	-0.007238	GGSSAKGTALR
5.6	1003.529800	0.004008	SLAASSPSIR
2.6	1003.529816	0.003992	TDKGDLSLR

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

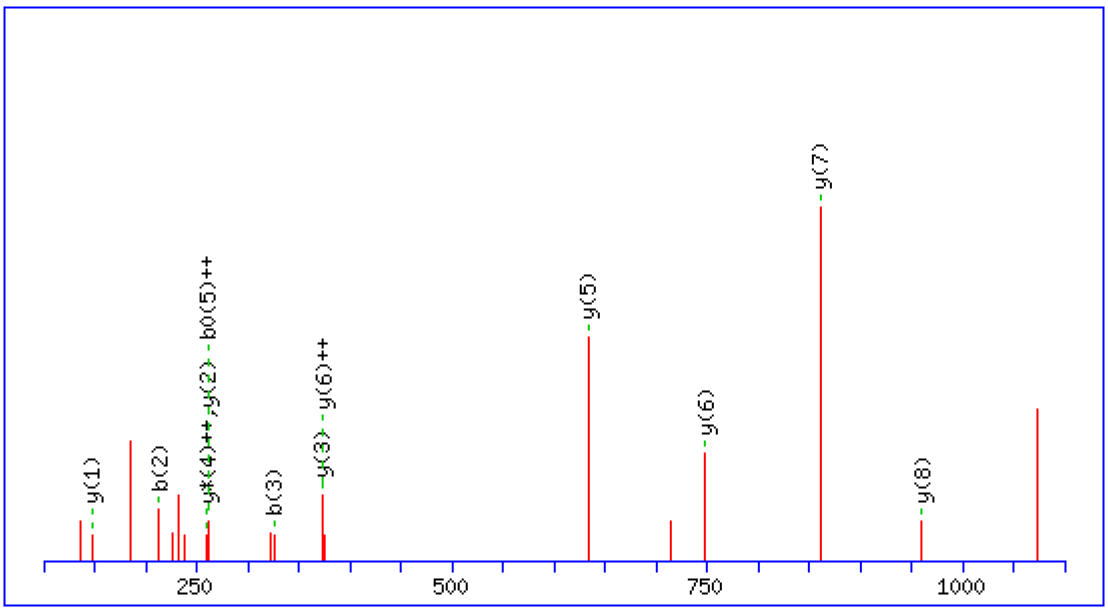
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LVLDPYLLK**
Found in **RT17_HUMAN**, 28S ribosomal protein S17, mitochondrial OS=Homo sapiens GN=MRPS17 PE=1 SV=1

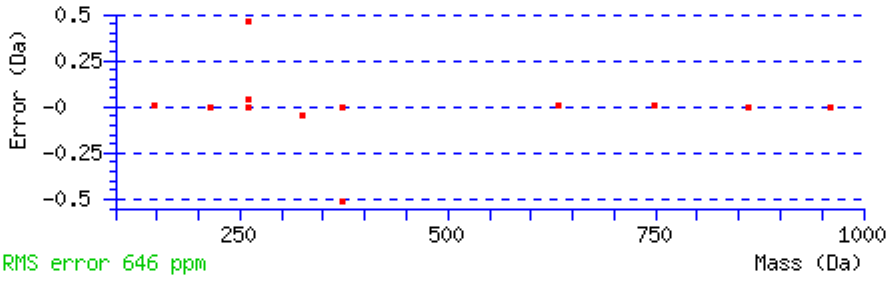
Match to Query 21007: 1072.652448 from(537.333500,2+) rtinseconds(3267) index(42987)
Title: Locus:1.1.1.2534.16
Data file 2011-11-13 - TFD - EP 7-6.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1100] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●

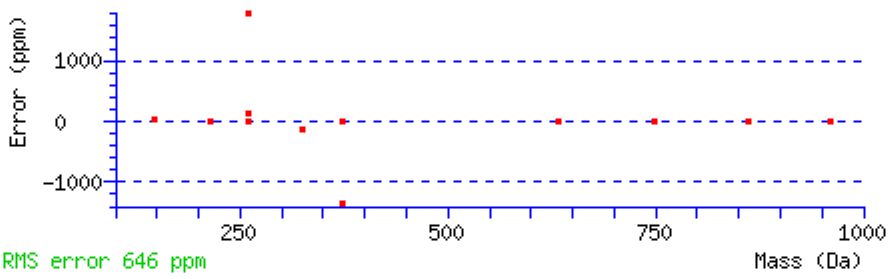


Monoisotopic mass of neutral peptide Mr(calc): 1072.653214
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 50 **Expect:** 9.4e-006
Matches : 12/64 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							9
2	**213.159754**	107.083515			V	***960.576446***	480.791861	943.549897	472.278587	942.565881	471.786579	8
3	**326.243818**	163.625547			L	***861.508032***	431.257654	844.481483	422.744380	843.497467	422.252372	7
4	441.270761	221.139018	423.260196	212.133736	D	***748.423968***	374.715622	731.397419	366.202348	730.413403	365.710340	6
5	538.323525	269.665401	520.312960	260.660118	P	***633.397025***	317.202151	616.370476	308.688876			5
6	701.386854	351.197065	683.376289	342.191783	Y	536.344261	268.675769	519.317712	260.162494			4
7	814.470918	407.739097	796.460353	398.733815	L	***373.280932***	187.144104	356.254383	178.630830			3
8	927.554982	464.281129	909.544417	455.275847	L	***260.196868***	130.602072	243.170319	122.088798			2
9					K	***147.112804***	74.060040	130.086255	65.546765			1



RMS error 646 ppm



RMS error 646 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
50.3	1072.653214	-0.000766	LVLDPYLLK
11.3	1072.649200	0.003248	VLSSLVTLNK

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

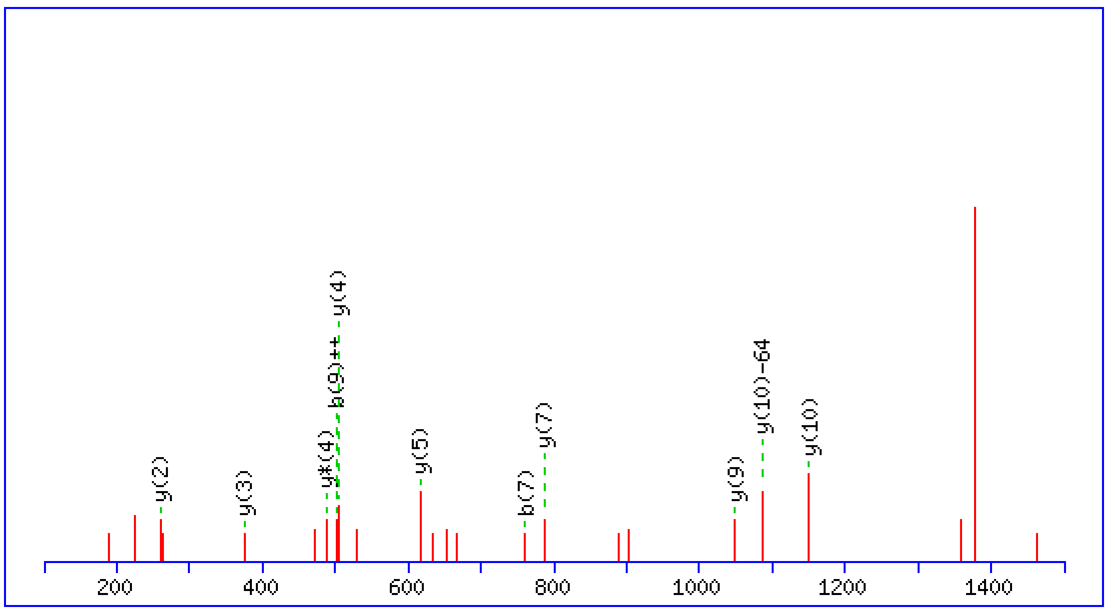
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILTMDGLIEDIK**
Found in **RT21_HUMAN**, 28S ribosomal protein S21, mitochondrial OS=Homo sapiens GN=MRPS21 PE=1 SV=2

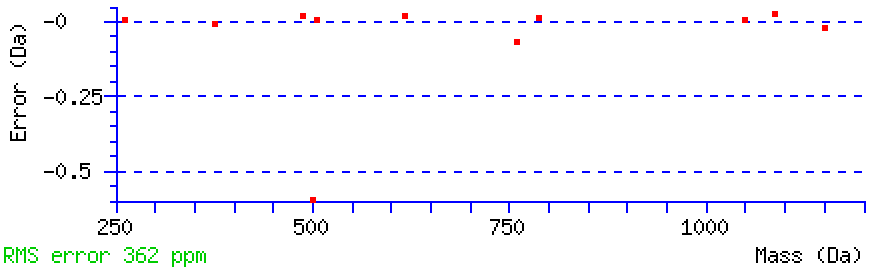
Match to Query 35353: 1375.726568 from(688.870560,2+) rtinseconds(2880) index(32335)
Title: Locus:1.1.1.2457.23
Data file 2011-11-14 - TFD - EP 8-7.mgf

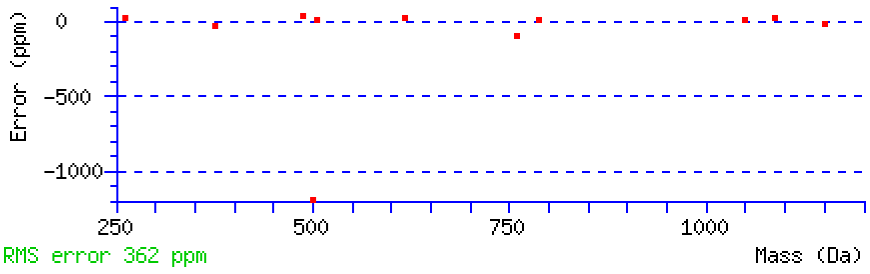
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1375.726852
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M4      : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 49  Expect: 0.00027
Matches : 11/152 fragment ions using 17 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							12
2	227.175404	114.091340			L	1263.650082	632.328679	1246.623533	623.815405	1245.639517	623.323397	11
3	328.223083	164.615179	310.212518	155.609897	T	***1150.566018***	575.786647	1133.539469	567.273373	1132.555453	566.781365	10
4	475.258483	238.132879	457.247918	229.127597	M	***1049.518339***	525.262808	1032.491790	516.749533	1031.507774	516.257525	9
5	590.285426	295.646351	572.274861	286.641069	D	902.482939	451.745108	885.456390	443.231833	884.472374	442.739825	8
6	647.306890	324.157083	629.296325	315.151801	G	***787.455996***	394.231636	770.429447	385.718362	769.445431	385.226354	7
7	760.390954	380.699115	742.380389	371.693833	L	730.434532	365.720904	713.407983	357.207630	712.423967	356.715622	6
8	873.475018	437.241147	855.464453	428.235865	I	***617.350468***	309.178872	600.323919	300.665597	599.339903	300.173589	5
9	1002.517611	501.762444	984.507046	492.757161	E	***504.266404***	252.636840	487.239855	244.123565	486.255839	243.631557	4
10	1117.544554	559.275915	1099.533989	550.270633	D	***375.223811***	188.115543	358.197262	179.602269	357.213246	179.110261	3
11	1230.628618	615.817947	1212.618053	606.812664	I	***260.196868***	130.602072	243.170319	122.088797			2
12					K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.5	1375.726852	-0.000284	ILTMDGLIEDIK
1.5	1375.720779	0.005789	FRLQQAEESIR
0.5	1375.719482	0.007086	SVSPSKTLSVPDK
0.2	1375.736053	-0.009485	AAPILRSFSWGR
0.0	1375.713593	0.012975	NWNTPIIFDLK
0.0	1375.720322	0.006246	IIKNPMDMGTIK

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

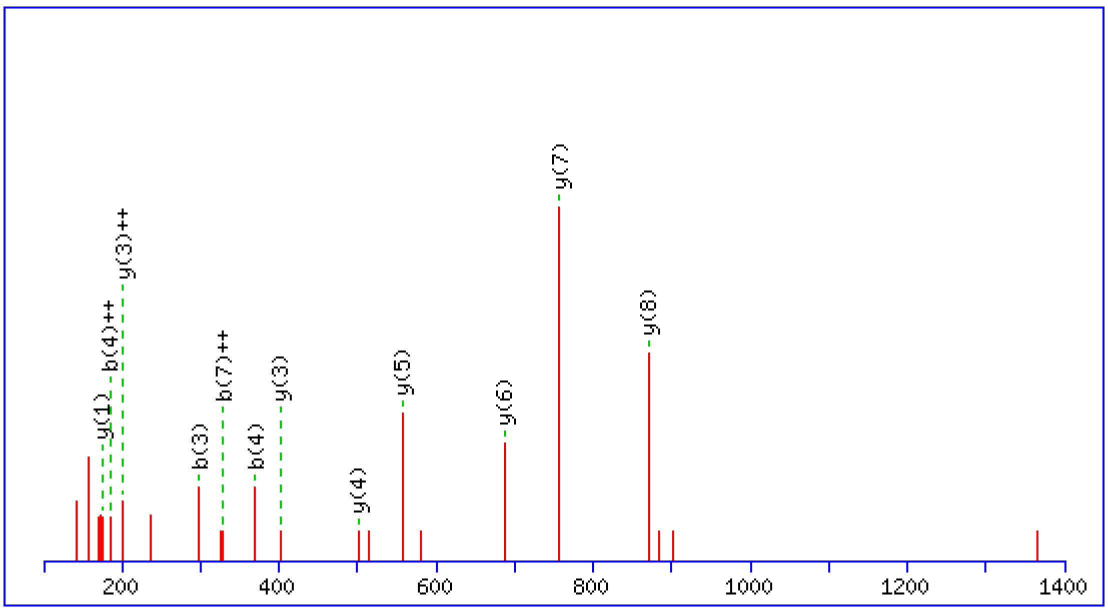
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALLAEGVILR**
Found in **RT23_HUMAN**, 28S ribosomal protein S23, mitochondrial OS=Homo sapiens GN=MRPS23 PE=1 SV=2

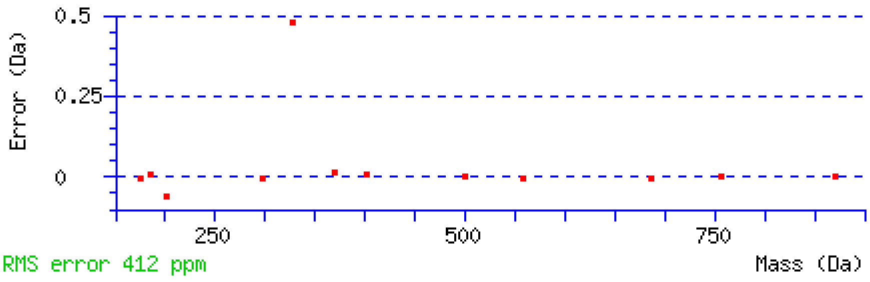
Match to Query 19692: 1053.651688 from(527.833120,2+) rtinseconds(2855) index(37514)
Title: Locus:1.1.1.2377.15
Data file 2011-11-12 - TFD - EP 6-5.mgf

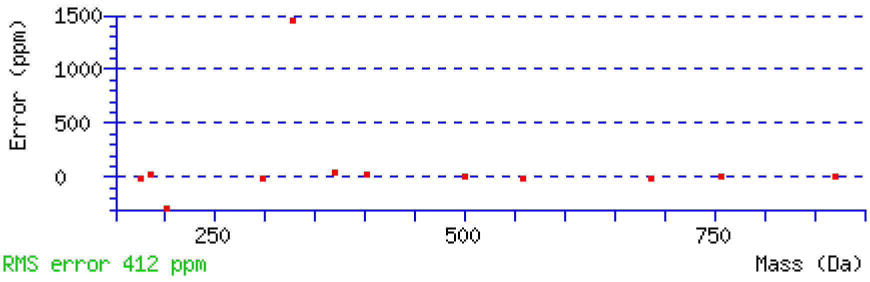
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1053.654602
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 48 **Expect:** 2.8e-005
Matches : 13/72 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			A							10
2	**185.128454**	93.067865			L	983.624793	492.316035	966.598244	483.802760	965.614228	483.310752	9
3	**298.212518**	149.609897			L	***870.540729***	435.774003	853.514180	427.260728	852.530164	426.768720	8
4	**369.249632**	**185.128454**			A	***757.456665***	379.231971	740.430116	370.718696	739.446100	370.226688	7
5	498.292225	249.649750	480.281660	240.644468	E	***686.419551***	343.713414	669.393002	335.200139	668.408986	334.708131	6
6	555.313689	278.160483	537.303124	269.155200	G	***557.376958***	279.192117	540.350409	270.678843			5
7	654.382103	**327.694690**	636.371538	318.689407	V	***500.355494***	250.681385	483.328945	242.168111			4
8	767.466167	384.236722	749.455602	375.231439	I	***401.287080***	201.147178	384.260531	192.633904			3
9	880.550231	440.778754	862.539666	431.773471	L	288.203016	144.605146	271.176467	136.091872			2
10					R	***175.118952***	88.063114	158.092403	79.549840			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.5	1053.654602	-0.002914	ALLAEGVILR
5.6	1053.655945	-0.004257	RFPRPLLR
0.4	1053.654602	-0.002914	LLALGLVAER

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

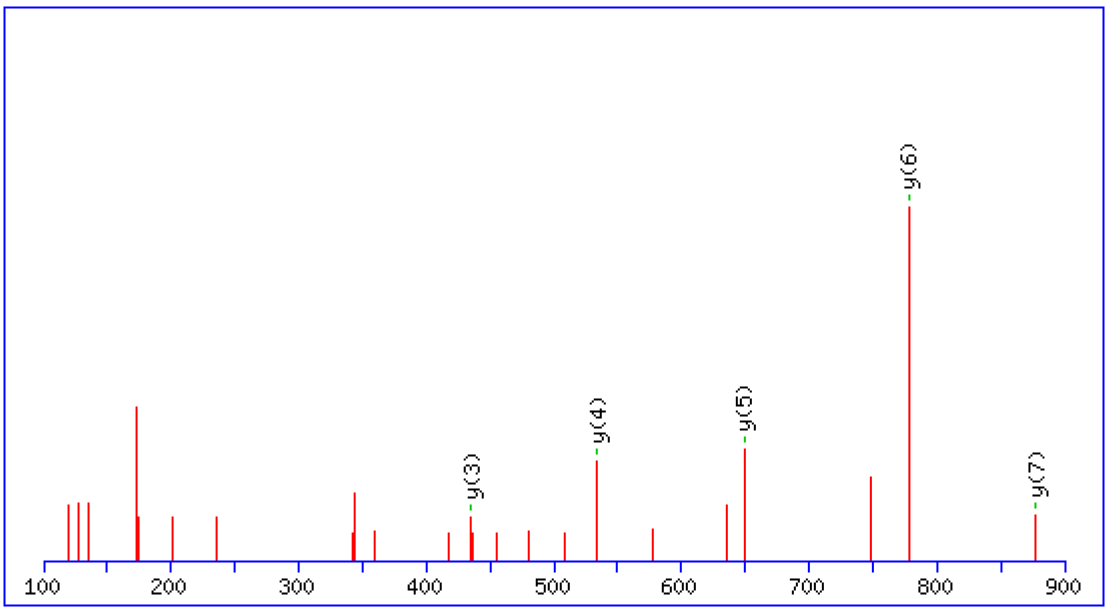
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TVEDVFLR**
Found in **RT24_HUMAN**, 28S ribosomal protein S24, mitochondrial OS=Homo sapiens GN=MRPS24 PE=1 SV=1

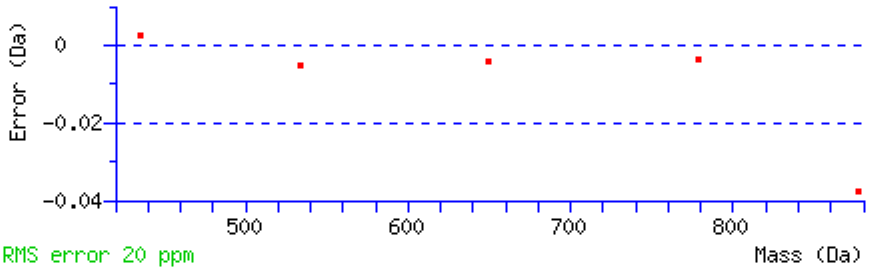
Match to Query 14249: 977.524548 from(489.769550,2+) rtinseconds(2570) index(27349)
Title: Locus:1.1.1.2311.12
Data file 2011-11-12 - TFD - EP 6-7.mgf

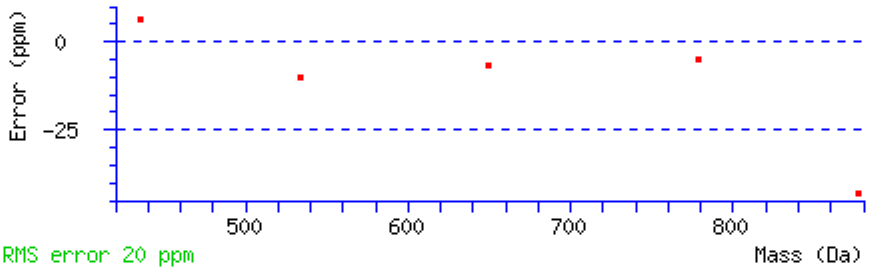
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 977.518204
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 38 **Expect:** 0.0022
Matches : 5/62 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116	84.044390	42.525833	T							8
2	201.123369	101.065322	183.112804	92.060040	V	*877.477794*	439.242535	860.451245	430.729261	859.467229	430.237253	7
3	330.165962	165.586619	312.155397	156.581336	E	*778.409380*	389.708328	761.382831	381.195054	760.398815	380.703046	6
4	445.192905	223.100090	427.182340	214.094808	D	*649.366787*	325.187032	632.340238	316.673757	631.356222	316.181749	5
5	544.261319	272.634298	526.250754	263.629015	V	*534.339844*	267.673560	517.313295	259.160286			4
6	691.329733	346.168505	673.319168	337.163222	F	*435.271430*	218.139353	418.244881	209.626079			3
7	804.413797	402.710537	786.403232	393.705254	L	288.203016	144.605146	271.176467	136.091872			2
8					R	175.118952	88.063114	158.092403	79.549840			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.5	977.518204	0.006344	TVEDVFLR
9.5	977.521576	0.002972	VMLTTAGGTK
5.1	977.533463	-0.008915	SLPVFPFR
1.1	977.529434	-0.004886	TVRSFPGSK
1.1	977.518158	0.006390	SLEPYNKK

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

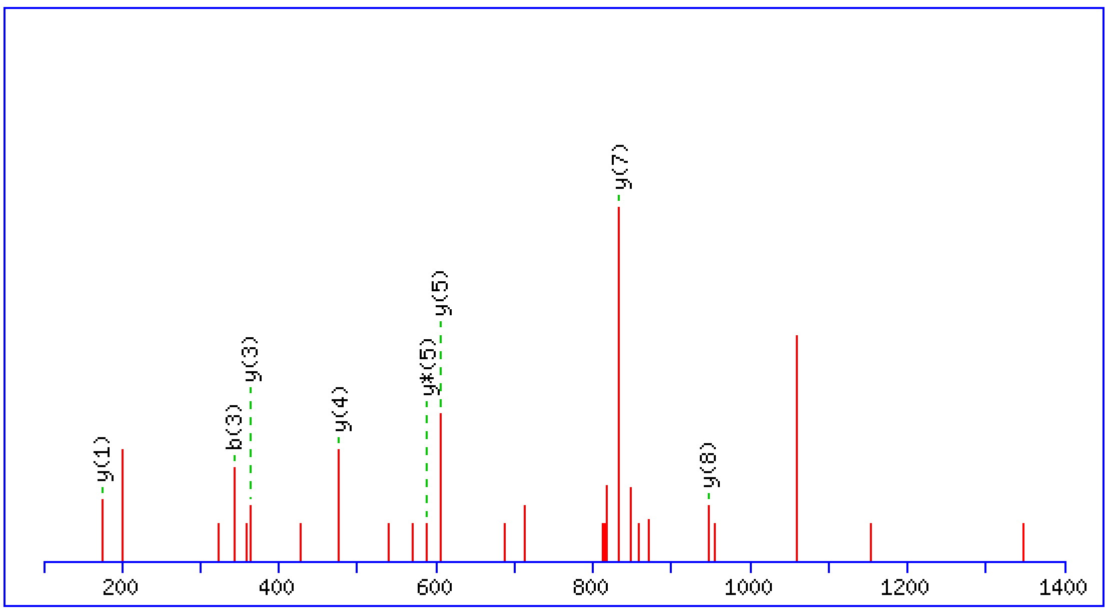
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLDLELTSR**
Found in **RT28_HUMAN**, 28S ribosomal protein S28, mitochondrial OS=Homo sapiens GN=MRPS28 PE=1 SV=1

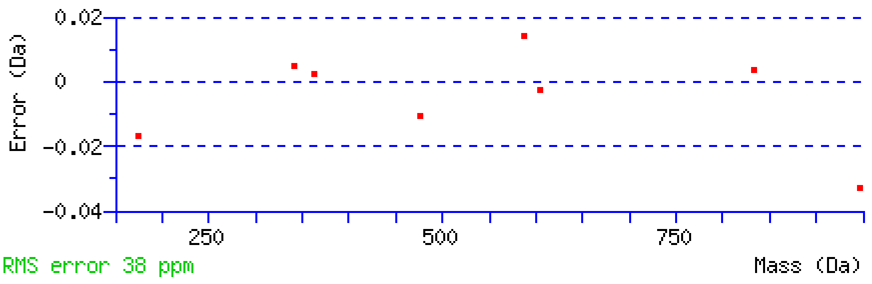
Match to Query 20975: 1058.603168 from(530.308860,2+) rtinseconds(2785) index(33934)
Title: Locus:1.1.1.2334.13
Data file 2011-11-14 - TFD - EP 8-6.mgf

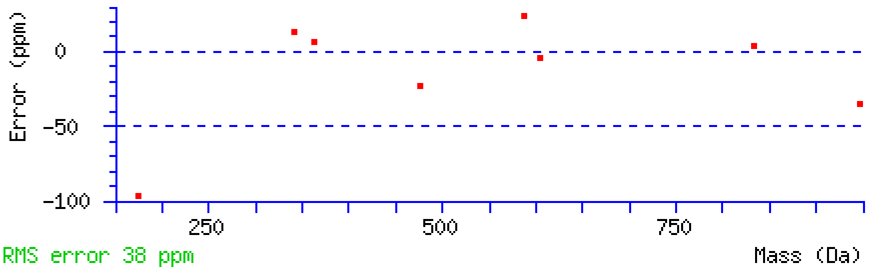
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1058.597153
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 38  Expect: 0.0013
Matches : 8/74 fragment ions using 15 most intense peaks   (help)
```

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308			L							9
2	227.175404	114.091340			L	***946.520387***	473.763832	929.493838	465.250557	928.509822	464.758549	8
3	342.202347	171.604811	324.191782	162.599529	D	***833.436323***	417.221800	816.409774	408.708525	815.425758	408.216517	7
4	455.286411	228.146843	437.275846	219.141561	L	718.409380	359.708328	701.382831	351.195054	700.398815	350.703046	6
5	584.329004	292.668140	566.318439	283.662858	E	***605.325316***	303.166296	588.298767	294.653022	587.314751	294.161014	5
6	697.413068	349.210172	679.402503	340.204890	L	***476.282723***	238.645000	459.256174	230.131725	458.272158	229.639717	4
7	798.460747	399.734012	780.450182	390.728729	T	***363.198659***	182.102968	346.172110	173.589693	345.188094	173.097685	3
8	885.492775	443.250026	867.482210	434.244743	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
9					R	***175.118952***	88.063114	158.092403	79.549840			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.7	1058.597153	0.006015	LLDLELTSR
10.3	1058.605881	-0.002713	ILKVNMWR
8.8	1058.608398	-0.005230	TAAQVLLSTR
5.1	1058.597137	0.006031	IEVLKSENK
2.6	1058.601852	0.001316	LRALLGCSR
2.1	1058.597137	0.006031	LLISLSEER
1.8	1058.609726	-0.006558	IIHDRHLR
1.7	1058.608383	-0.005215	LLASTRPASK
1.4	1058.608383	-0.005215	LLNIRTSDK
0.7	1058.608383	-0.005215	LIRDTNSIK

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

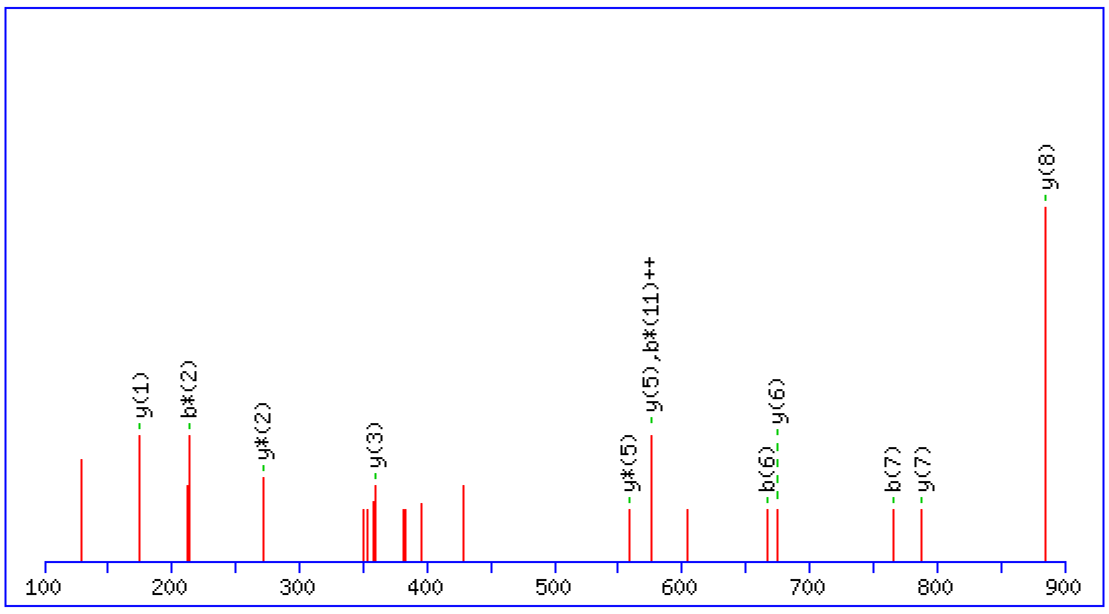
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DNPKPNVSEALR**
Found in **RT36_HUMAN**, 28S ribosomal protein S36, mitochondrial OS=Homo sapiens GN=MRPS36 PE=1 SV=2

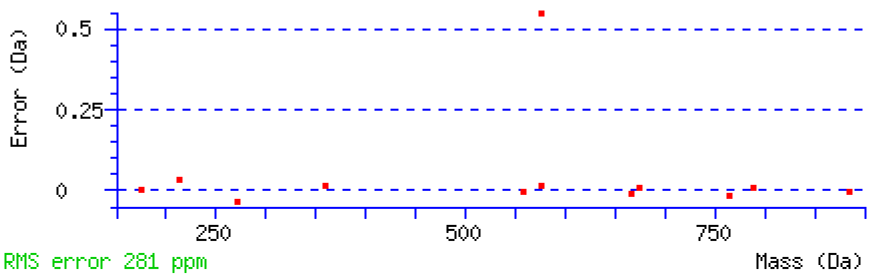
Match to Query 34473: 1338.689022 from(447.236950,3+) rtinseconds(1582) index(7661)
Title: Locus:1.1.1.2059.6
Data file 2011-11-10 - TFD - EP 4-7.mgf

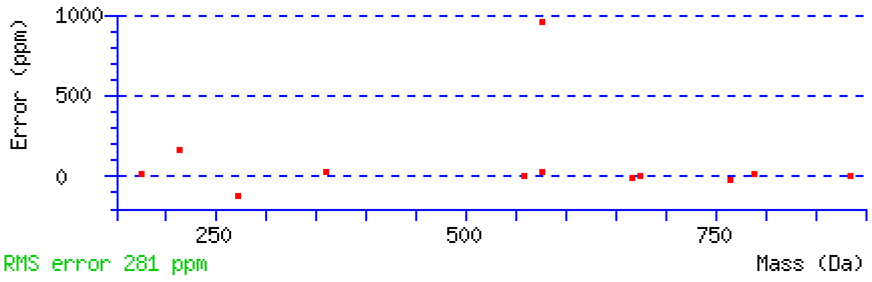
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1338.689148
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 51  Expect: 8.2e-005
Matches : 12/124 fragment ions using 13 most intense peaks   (help)
```

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	116.034219	58.520748			98.023654	49.515465	D							12
2	230.077146	115.542211	213.050597	107.028937	212.066581	106.536928	N	1224.669510	612.838393	1207.642961	604.325118	1206.658945	603.833110	11
3	327.129910	164.068593	310.103361	155.555319	309.119345	155.063311	P	1110.626583	555.816929	1093.600034	547.303655	1092.616018	546.811647	10
4	455.224873	228.116075	438.198324	219.602800	437.214308	219.110792	K	1013.573819	507.290547	996.547270	498.777273	995.563254	498.285265	9
5	552.277637	276.642457	535.251088	268.129182	534.267072	267.637174	P	***885.478856***	443.243066	868.452307	434.729791	867.468291	434.237783	8
6	**666.320564**	333.663920	649.294015	325.150646	648.309999	324.658638	N	***788.426092***	394.716684	771.399543	386.203409	770.415527	385.711401	7
7	**765.388978**	383.198127	748.362429	374.684852	747.378413	374.192844	V	***674.383165***	337.695220	657.356616	329.181946	656.372600	328.689938	6
8	852.421006	426.714141	835.394457	418.200866	834.410441	417.708858	S	***575.314751***	288.161013	558.288202	279.647739	557.304186	279.155731	5
9	981.463599	491.235437	964.437050	482.722163	963.453034	482.230155	E	488.282723	244.644999	471.256174	236.131725	470.272158	235.639717	4
10	1052.500713	526.753994	1035.474164	518.240720	1034.490148	517.748712	A	***359.240130***	180.123703	342.213581	171.610428			3
11	1165.584777	583.296026	1148.558228	574.782752	1147.574212	574.290744	L	288.203016	144.605146	271.176467	136.091871			2
12							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
50.9	1338.689148	-0.000126	DNPKPNVSEALR
8.1	1338.700394	-0.011372	AKNLPQPQSGQR
7.4	1338.700394	-0.011372	AKNLPQPQSGQR
2.0	1338.700409	-0.011387	VLPGSNGKPNGQR
0.4	1338.693176	-0.004154	LVPEYIHAPER
0.1	1338.700394	-0.011372	QDTIAHLERTR

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

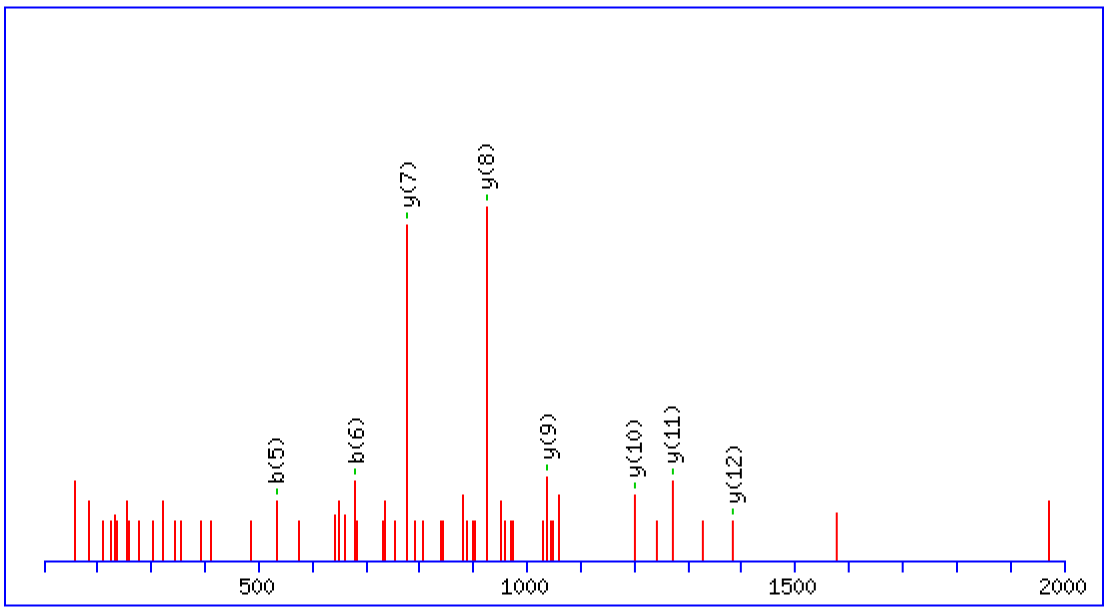
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AIAYLFPSGLFEK**
Found in **RT09_HUMAN**, 28S ribosomal protein S9, mitochondrial OS=Homo sapiens GN=MRPS9 PE=1 SV=2

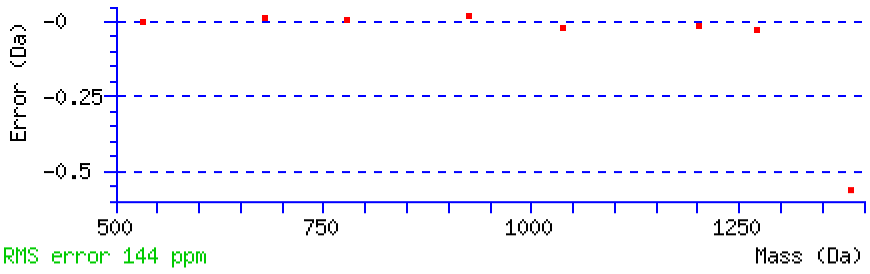
Match to Query 44783: 1454.773888 from(728.394220,2+) rtinseconds(3937) index(58511)
Title: Locus:1.1.1.2908.25
Data file 2011-11-12 - TFD - EP 5-4.mgf

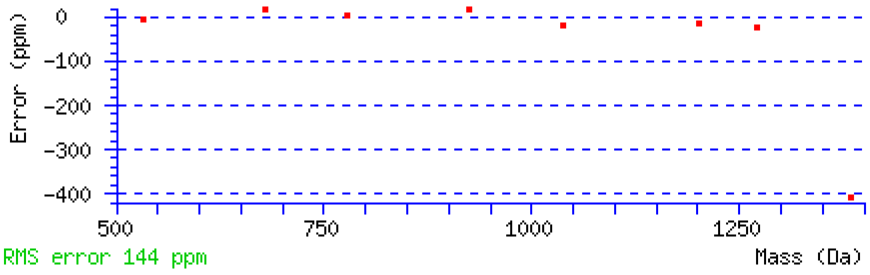
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1454.780930
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 38  Expect: 0.0018
Matches : 8/104 fragment ions using 13 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			A							13
2	185.128454	93.067865			I	***1384.751116***	692.879196	1367.724567	684.365922	1366.740551	683.873914	12
3	256.165568	128.586422			A	***1271.667052***	636.337164	1254.640503	627.823890	1253.656487	627.331882	11
4	419.228897	210.118087			Y	***1200.629938***	600.818607	1183.603389	592.305333	1182.619373	591.813325	10
5	**532.312961**	266.660119			L	***1037.566609***	519.286943	1020.540060	510.773668	1019.556044	510.281660	9
6	**679.381375**	340.194326			F	***924.482545***	462.744911	907.455996	454.231636	906.471980	453.739628	8
7	776.434139	388.720708			P	***777.414131***	389.210704	760.387582	380.697429	759.403566	380.205421	7
8	863.466167	432.236722	845.455602	423.231439	S	680.361367	340.684322	663.334818	332.171047	662.350802	331.679039	6
9	920.487631	460.747454	902.477066	451.742171	G	593.329339	297.168308	576.302790	288.655033	575.318774	288.163025	5
10	1033.571695	517.289486	1015.561130	508.284203	L	536.307875	268.657576	519.281326	260.144301	518.297310	259.652293	4
11	1180.640109	590.823693	1162.629544	581.818410	F	423.223811	212.115544	406.197262	203.602269	405.213246	203.110261	3
12	1309.682702	655.344989	1291.672137	646.339707	E	276.155397	138.581337	259.128848	130.068062	258.144832	129.576054	2
13					K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.0	1454.780930	-0.007042	AIAYLFPSGLFEK

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

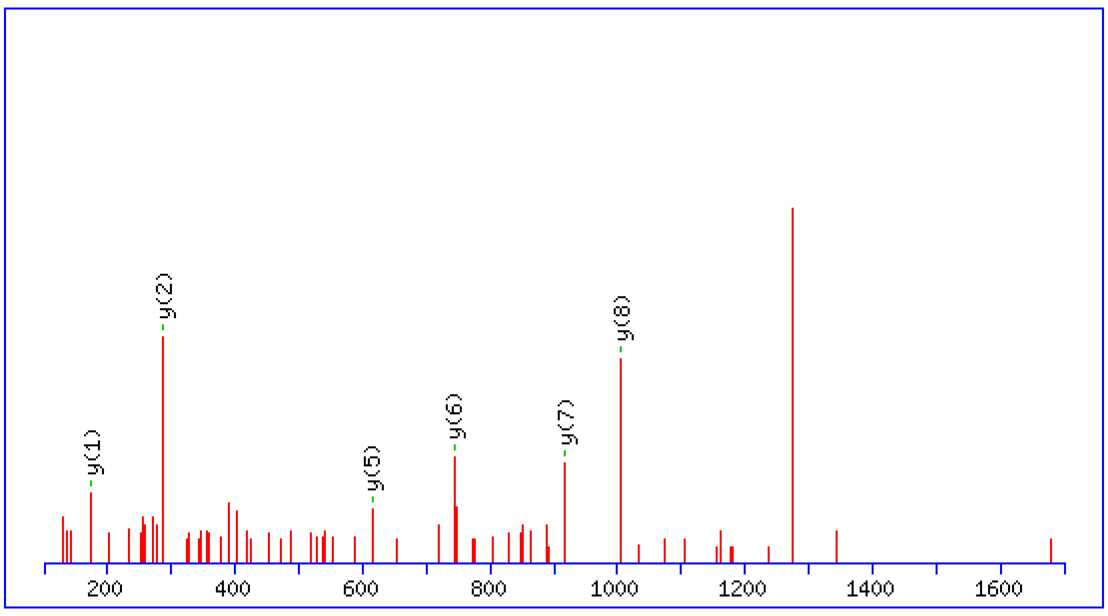
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGVSCEVIDLR**
Found in **ODBB_HUMAN**, 2-oxoisovalerate dehydrogenase subunit beta, mitochondrial OS=Homo sapiens GN=BCKDHB PE=1 SV=2

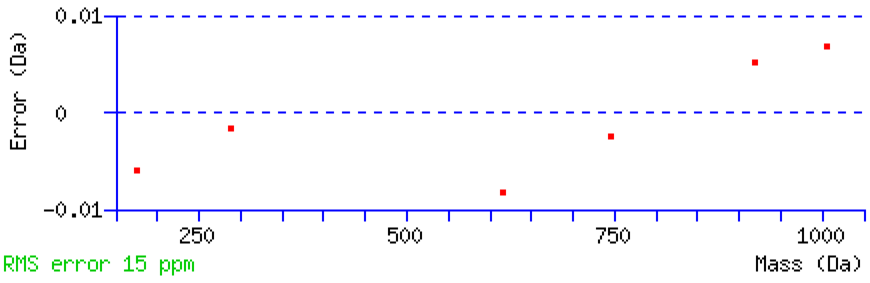
Match to Query 34868: 1273.672388 from(637.843470,2+) rtinseconds(2746) index(37073)
Title: Locus:1.1.1.2341.33
Data file 2011-11-12 - TFD - EP 6-4.mgf

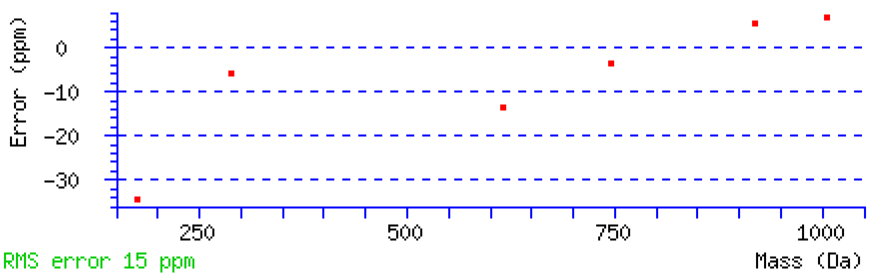
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1273.670013
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 36  Expect: 0.0035
Matches : 6/90 fragment ions using 12 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							11
2	171.112804	86.060040			G	1161.593235	581.300256	1144.566686	572.786981	1143.582670	572.294973	10
3	270.181218	135.594247			V	1104.571771	552.789523	1087.545222	544.276249	1086.561206	543.784241	9
4	357.213246	179.110261	339.202681	170.104978	S	***1005.503357***	503.255316	988.476808	494.742042	987.492792	494.250034	8
5	531.259545	266.133411	513.248980	257.128128	C	*918.471329*	459.739303	901.444780	451.226028	900.460764	450.734020	7
6	660.302138	330.654707	642.291573	321.649425	E	*744.425030*	372.716153	727.398481	364.202879	726.414465	363.710871	6
7	759.370552	380.188914	741.359987	371.183631	V	*615.382437*	308.194857	598.355888	299.681582	597.371872	299.189574	5
8	872.454616	436.730946	854.444051	427.725664	I	516.314023	258.660650	499.287474	250.147375	498.303458	249.655367	4
9	987.481559	494.244418	969.470994	485.239135	D	403.229959	202.118617	386.203410	193.605343	385.219394	193.113335	3
10	1100.565623	550.786450	1082.555058	541.781167	L	*288.203016*	144.605146	271.176467	136.091871			2
11					R	*175.118952*	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.0	1273.670013	0.002375	LGVSCEVIDLR
9.2	1273.662628	0.009760	VVEGTAAQSSGLR
5.9	1273.670013	0.002375	AASLSTMVPLPR
5.1	1273.681900	-0.009512	VNWEIFTPLR
2.6	1273.666641	0.005747	QLLPGDEFSLR
2.0	1273.681213	-0.008825	LRPESMEKLR
2.0	1273.681213	-0.008825	LRPESMEKLR
1.8	1273.681229	-0.008841	MSRGSIEIPLR
1.2	1273.677872	-0.005484	RLFNLDVPER
1.1	1273.670013	0.002375	AASLSTMVPLPR

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

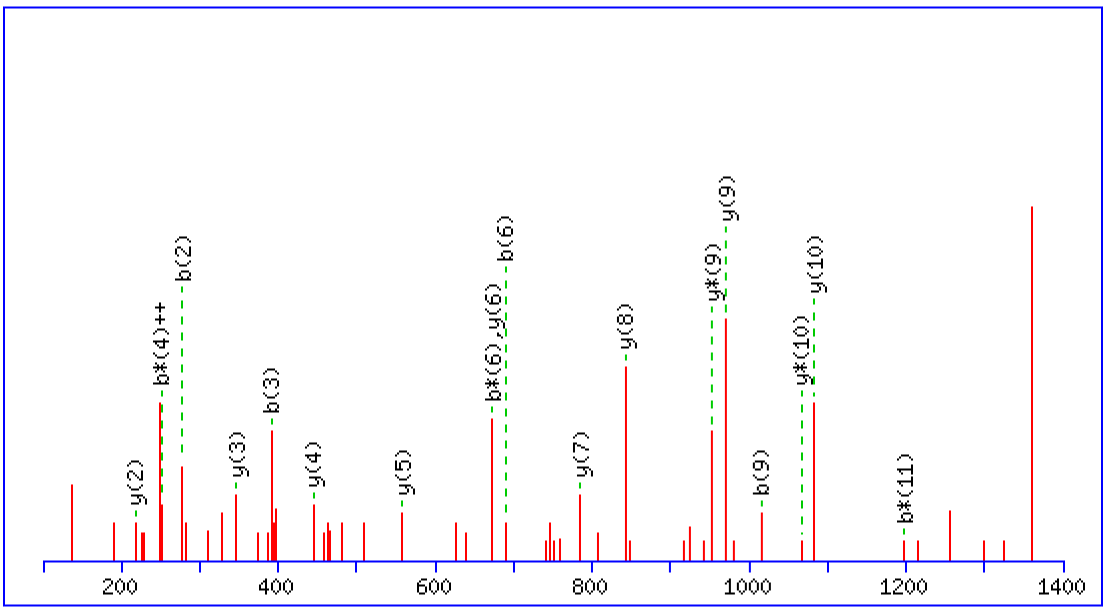
{MATRIX SCIENCE}
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NYIQGINLVQAK**
Found in **RM12_HUMAN**, 39S ribosomal protein L12, mitochondrial OS=Homo sapiens GN=MRPL12 PE=1 SV=2

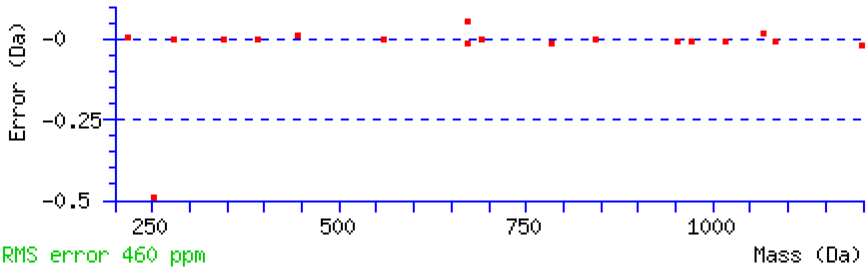
Match to Query 42397: 1359.747868 from(680.881210,2+) rtinseconds(2653) index(33038)
Title: Locus:1.1.1.2230.37
Data file 2011-11-12 - TFD - EP 5-6.mgf

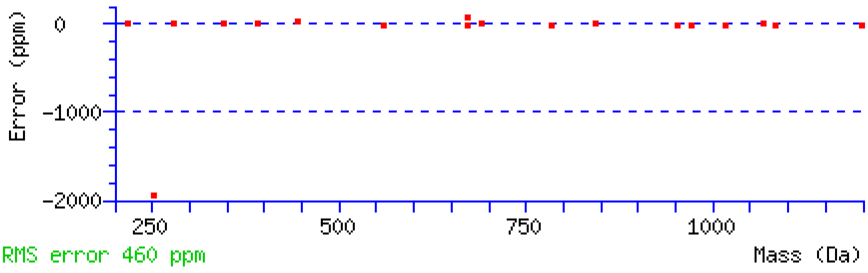
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1400] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1359.751022
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 57  Expect: 1.6e-005
Matches : 18/88 fragment ions using 33 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	115.050203	58.028740	98.023654	49.515465	N					12
2	**278.113532**	139.560404	261.086983	131.047130	Y	1246.715400	623.861338	1229.688851	615.348064	11
3	**391.197596**	196.102436	374.171047	187.589162	I	***1083.652071***	542.329674	1066.625522	533.816399	10
4	519.256174	260.131725	502.229625	251.618451	Q	***970.568007***	485.787642	953.541458	477.274367	9
5	576.277638	288.642457	559.251089	280.129183	G	***842.509429***	421.758353	825.482880	413.245078	8
6	**689.361702**	345.184489	672.335153	336.671215	I	***785.487965***	393.247620	768.461416	384.734346	7
7	803.404629	402.205953	786.378080	393.692678	N	***672.403901***	336.705588	655.377352	328.192314	6
8	916.488693	458.747985	899.462144	450.234710	L	***558.360974***	279.684125	541.334425	271.170850	5
9	**1015.557107**	508.282192	998.530558	499.768917	V	***445.276910***	223.142093	428.250361	214.628818	4
10	1143.615685	572.311481	1126.589136	563.798206	Q	***346.208496***	173.607886	329.181947	165.094611	3
11	1214.652799	607.830038	1197.626250	599.316763	A	***218.149918***	109.578597	201.123369	101.065322	2
12					K	147.112804	74.060040	130.086255	65.546765	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
57.5	1359.751022	-0.003154	NYIQGINLVQAK
10.8	1359.755066	-0.007198	FPGVAIYLVEPR

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

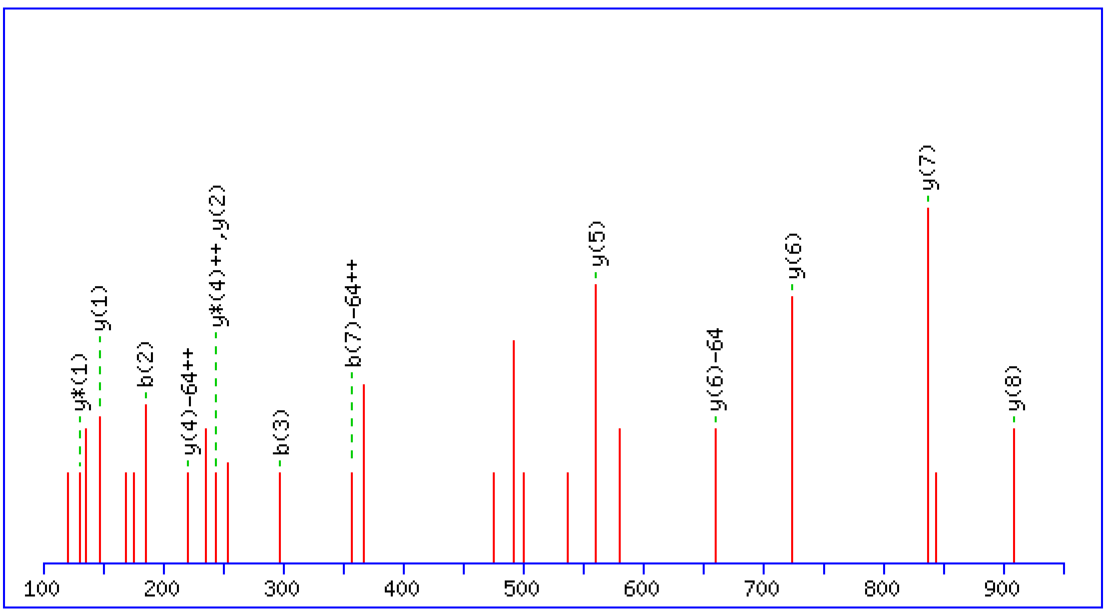
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LAIYGMLPK**
Found in **RM13_HUMAN**, 39S ribosomal protein L13, mitochondrial OS=Homo sapiens GN=MRPL13 PE=1 SV=1

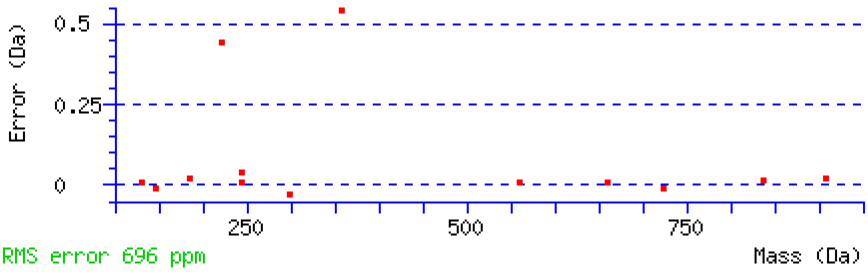
Match to Query 18268: 1020.562688 from(511.288620,2+) rtinseconds(2443) index(27880)
Title: Locus:1.1.1.2203.19
Data file 2011-11-14 - TFD - EP 8-6.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●

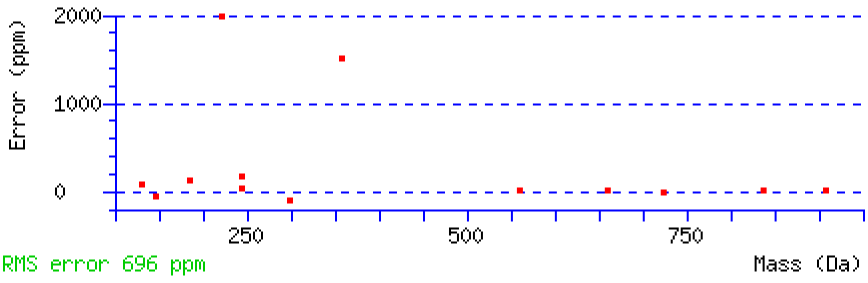


Monoisotopic mass of neutral peptide Mr(calc): 1020.567764
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M6 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 39 **Expect:** 0.0028
Matches : 13/74 fragment ions using 23 most intense peaks (help)

#	b	b++	Seq.	y	y++	y*	y*++	#
1	114.091340	57.549308	L					9
2	**185.128454**	93.067865	A	***908.491003***	454.749140	891.464454	446.235865	8
3	**298.212518**	149.609897	I	***837.453889***	419.230583	820.427340	410.717308	7
4	461.275847	231.141561	Y	***724.369825***	362.688551	707.343276	354.175276	6
5	518.297311	259.652294	G	***561.306496***	281.156886	544.279947	272.643612	5
6	665.332711	333.169994	M	504.285032	252.646154	487.258483	244.132880	4
7	778.416775	389.712026	L	357.249632	179.128454	340.223083	170.615180	3
8	875.469539	438.238408	P	***244.165568***	122.586422	227.139019	114.073148	2
9			K	***147.112804***	74.060040	130.086255	65.546765	1



RMS error 696 ppm



RMS error 696 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.8	1020.567764	-0.005076	LAIYGMLPK
24.1	1020.567764	-0.005076	LAIYGMLPK
16.0	1020.567780	-0.005092	LAPIMFGIK
6.0	1020.560379	0.002309	ALLTAETFR
4.4	1020.560394	0.002294	LSPPPLPPR
4.1	1020.560394	0.002294	LSPPPLPPR
3.5	1020.560394	0.002294	LSPPPLPPR
2.1	1020.557693	0.004995	RNVDHRPK
1.5	1020.571609	-0.008921	LAHPVASAQK
0.8	1020.560364	0.002324	LEFAKANTK

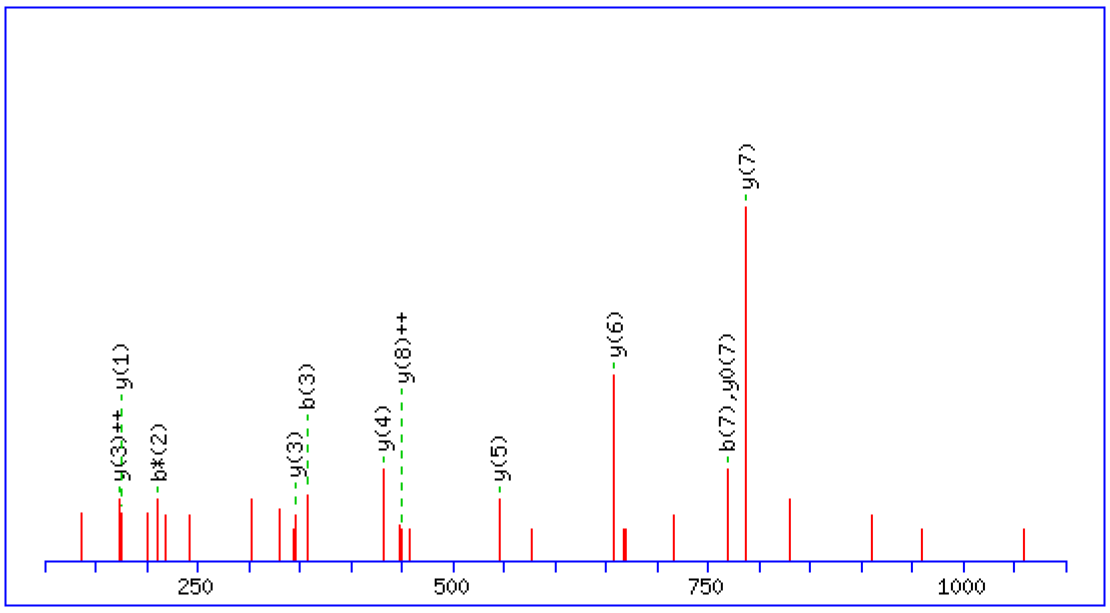
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NLELLSVAR**
Found in **RM18_HUMAN**, 39S ribosomal protein L18, mitochondrial OS=Homo sapiens GN=MRPL18 PE=1 SV=1

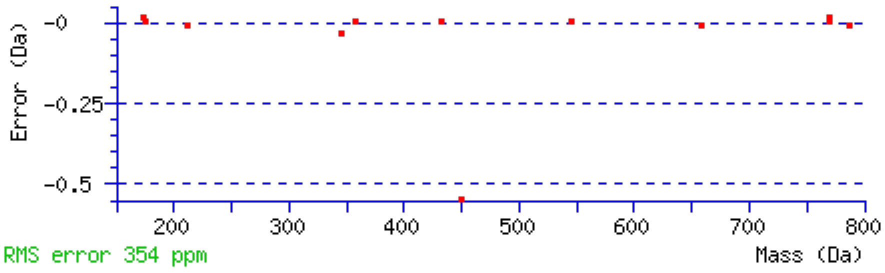
Match to Query 19698: 1013.584688 from(507.799620,2+) rtinseconds(2729) index(34463)
Title: Locus:1.1.1.2259.12
Data file 2011-11-12 - TFD - EP 5-6.mgf

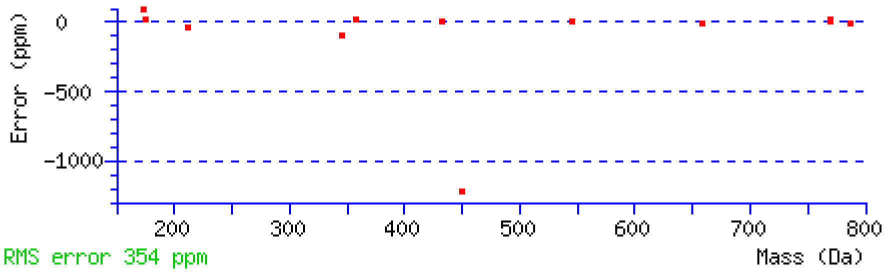
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1013.586914
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.003
Matches : 12/86 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			**N**							9
2	228.134267	114.570771	211.107718	106.057497			**L**	900.551293	450.779285	883.524744	442.266010	882.540728	441.774002	8
3	**357.176860**	179.092068	340.150311	170.578793	339.166295	170.086785	**E**	***787.467229***	394.237253	770.440680	385.723978	769.456664	385.231970	7
4	470.260924	235.634100	453.234375	227.120826	452.250359	226.628818	**L**	***658.424636***	329.715956	641.398087	321.202681	640.414071	320.710673	6
5	583.344988	292.176132	566.318439	283.662858	565.334423	283.170850	**L**	***545.340572***	273.173924	528.314023	264.660649	527.330007	264.168641	5
6	670.377016	335.692146	653.350467	327.178872	652.366451	326.686864	**S**	***432.256508***	216.631892	415.229959	208.118617	414.245943	207.626609	4
7	**769.445430**	385.226353	752.418881	376.713078	751.434865	376.221071	**V**	***345.224480***	173.115878	328.197931	164.602603			3
8	840.482544	420.744910	823.455995	412.231635	822.471979	411.739627	**A**	246.156066	123.581671	229.129517	115.068396			2
9							**R**	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.5	1013.586914	-0.002226	NLELLSVAR
20.6	1013.586914	-0.002226	QVEILREK
8.4	1013.586914	-0.002226	LDKLIEQR
1.8	1013.590973	-0.006285	GLGLGFPLPK
0.1	1013.586929	-0.002241	RLSSTPLPK

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

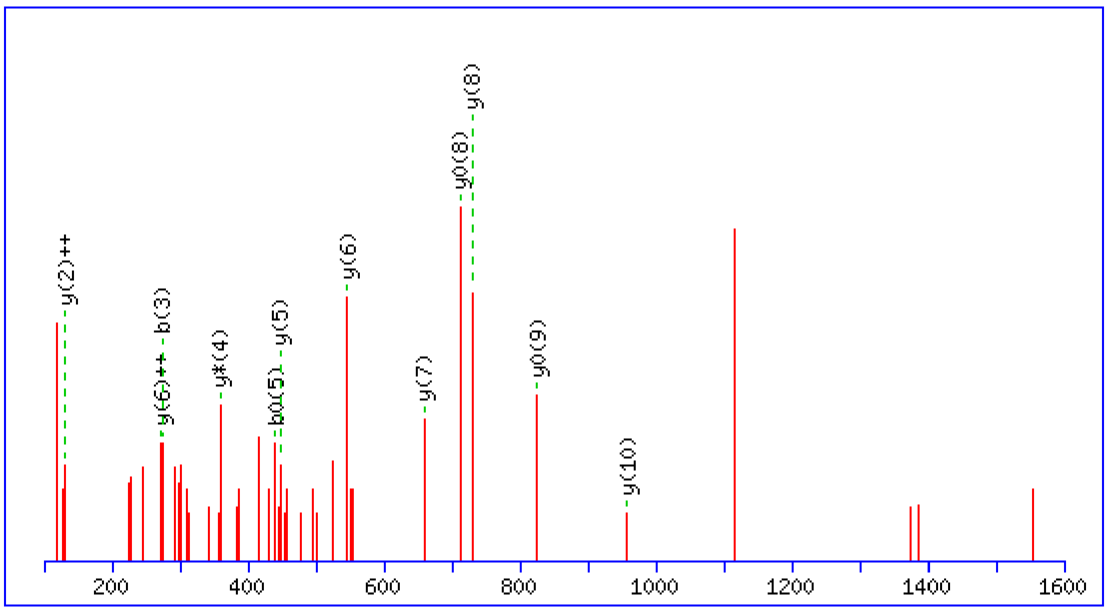
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SADIALVAGGSR**
Found in **RM02_HUMAN**, 39S ribosomal protein L2, mitochondrial OS=Homo sapiens GN=MRPL2 PE=1 SV=2

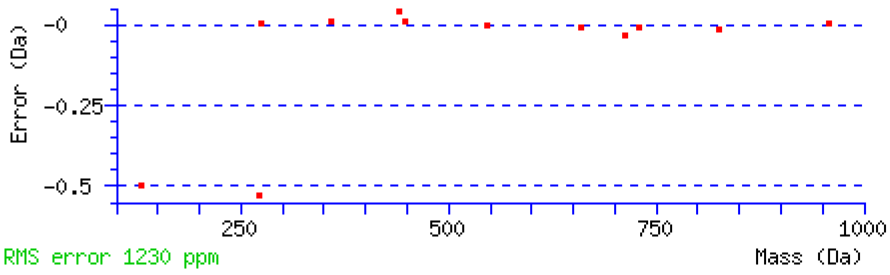
Match to Query 24670: 1115.593508 from(558.804030,2+) rtinseconds(1921) index(19795)
Title: Locus:1.1.1.2053.32
Data file 2011-11-14 - TFD - EP 8-5.mgf

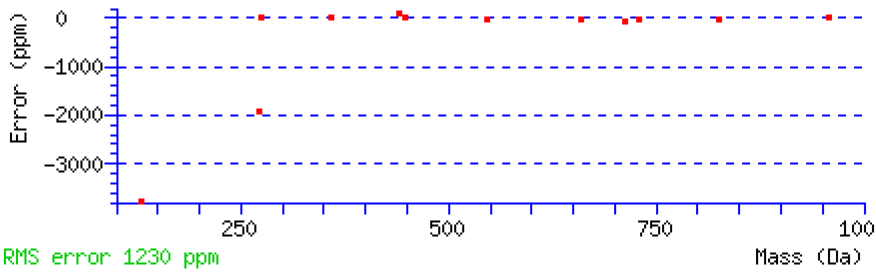
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1115.593475
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 35  Expect: 0.0012
Matches : 12/108 fragment ions using 15 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	S							12
2	159.076418	80.041847	141.065853	71.036564	A	1029.568735	515.288006	1012.542186	506.774731	1011.558170	506.282723	11
3	274.103361	137.555319	256.092796	128.550036	D	***958.531621***	479.769449	941.505072	471.256174	940.521056	470.764166	10
4	387.187425	194.097351	369.176860	185.092068	I	843.504678	422.255977	826.478129	413.742703	825.494113	413.250695	9
5	458.224539	229.615907	440.213974	220.610625	A	***730.420614***	365.713945	713.394065	357.200671	712.410049	356.708663	8
6	571.308603	286.157940	553.298038	277.152657	L	***659.383500***	330.195388	642.356951	321.682114	641.372935	321.190106	7
7	670.377017	335.692147	652.366452	326.686864	V	***546.299436***	273.653356	529.272887	265.140082	528.288871	264.648074	6
8	741.414131	371.210704	723.403566	362.205421	A	***447.231022***	224.119149	430.204473	215.605875	429.220457	215.113867	5
9	798.435595	399.721436	780.425030	390.716153	G	376.193908	188.600592	359.167359	180.087318	358.183343	179.595310	4
10	855.457059	428.232168	837.446494	419.226885	G	319.172444	160.089860	302.145895	151.576586	301.161879	151.084578	3
11	942.489087	471.748182	924.478522	462.742899	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
12					R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of SADIALVAGGSR
(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	1115.593475	0.000033	SADIALVAGGSR
3.4	1115.583588	0.009920	DWRSGKPVR

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

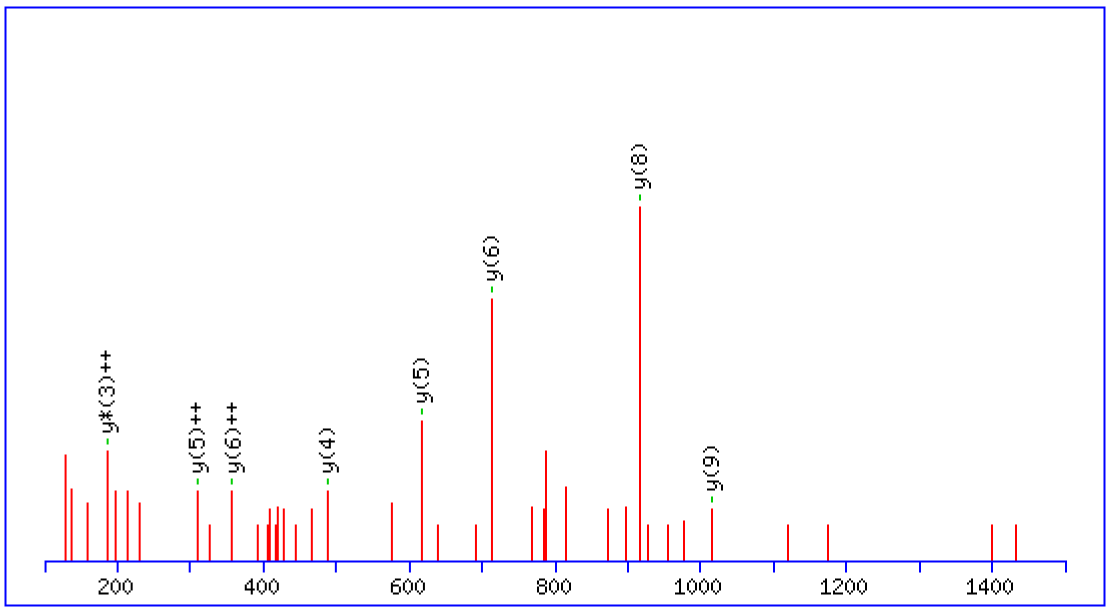
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IVTTPQTVLR**
Found in **RM21_HUMAN**, 39S ribosomal protein L21, mitochondrial OS=Homo sapiens GN=MRPL21 PE=1 SV=2

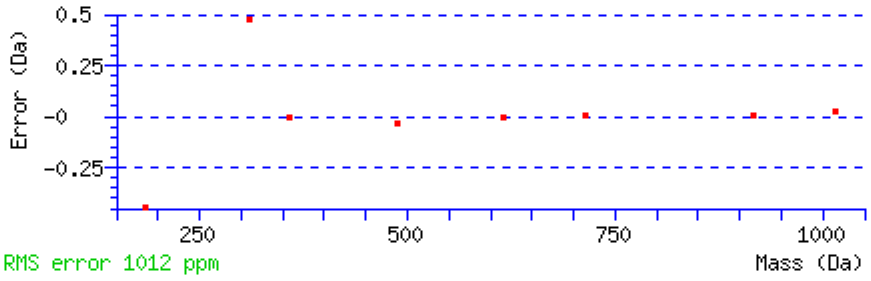
Match to Query 25951: 1126.675468 from(564.345010,2+) rtinseconds(1981) index(19097)
Title: Locus:1.1.1.2027.36
Data file 2011-11-14 - TFD - EP 8-6.mgf

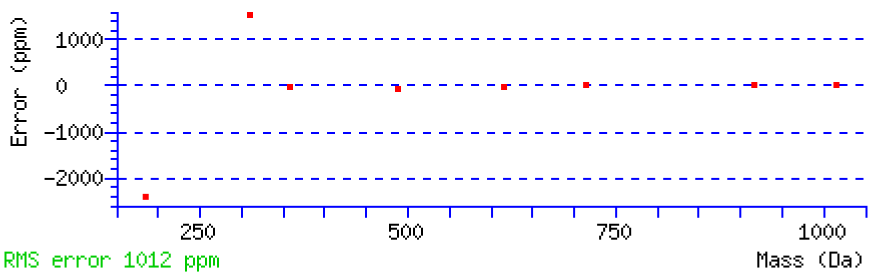
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1126.671021
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.00059
Matches : 8/88 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					I							10
2	213.159754	107.083515					V	***1014.594223***	507.800750	997.567674	499.287475	996.583658	498.795467	9
3	314.207433	157.607354			296.196868	148.602072	T	***915.525809***	458.266543	898.499260	449.753268	897.515244	449.261260	8
4	415.255112	208.131194			397.244547	199.125912	T	814.478130	407.742703	797.451581	399.229429	796.467565	398.737421	7
5	512.307876	256.657576			494.297311	247.652294	P	***713.430451***	357.218864	696.403902	348.705589	695.419886	348.213581	6
6	640.366454	320.686865	623.339905	312.173591	622.355889	311.681583	Q	***616.377687***	308.692482	599.351138	300.179207	598.367122	299.687199	5
7	741.414133	371.210705	724.387584	362.697430	723.403568	362.205422	T	***488.319109***	244.663193	471.292560	236.149918	470.308544	235.657910	4
8	840.482547	420.744912	823.455998	412.231637	822.471982	411.739629	V	387.271430	194.139353	370.244881	185.626079			3
9	953.566611	477.286944	936.540062	468.773669	935.556046	468.281661	L	288.203016	144.605146	271.176467	136.091872			2
10							R	175.118952	88.063114	158.092403	79.549840			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.3	1126.671021	0.004447	IVTTPQTVLR
8.0	1126.671021	0.004447	IVNTVPITVR
1.0	1126.670990	0.004478	LVALLNTLDR
0.3	1126.670975	0.004493	VLAEVEALKR

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

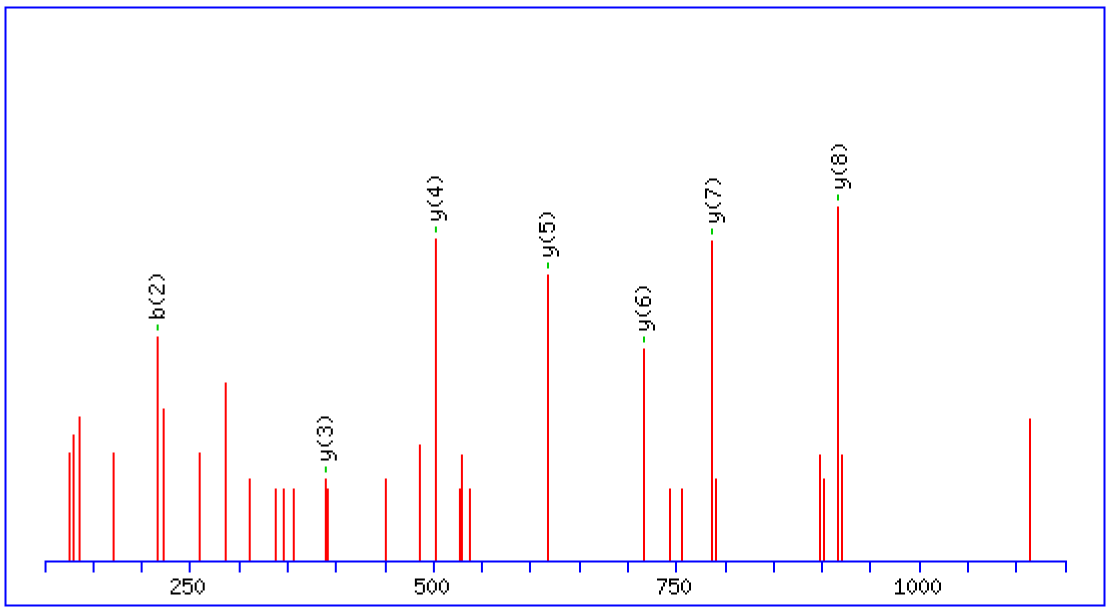
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NTEAVDLITR**
Found in **RM27_HUMAN**, 39S ribosomal protein L27, mitochondrial OS=Homo sapiens GN=MRPL27 PE=1 SV=1

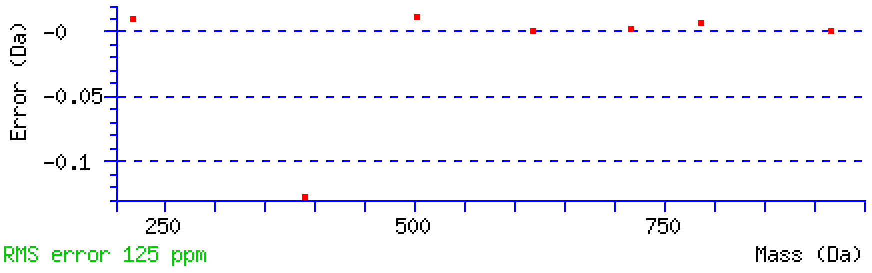
Match to Query 22774: 1130.599388 from(566.306970,2+) rtinseconds(2151) index(19857)
Title: Locus:1.1.1.2226.22
Data file 2011-11-10 - TFD - EP 3-7.mgf

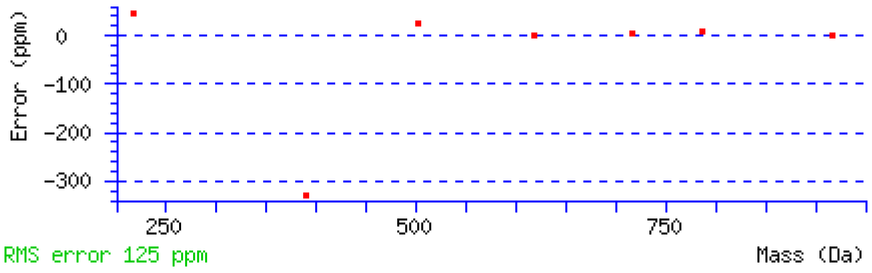
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1130.593140
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 51 **Expect:** 0.0001
Matches : 7/104 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			N							10
2	216.097882	108.552579	199.071333	100.039305	198.087317	99.547296	T	1017.557502	509.282389	1000.530953	500.769115	999.546937	500.277107	9
3	345.140475	173.073875	328.113926	164.560601	327.129910	164.068593	E	***916.509823***	458.758550	899.483274	450.245275	898.499258	449.753267	8
4	416.177589	208.592432	399.151040	200.079158	398.167024	199.587150	A	***787.467230***	394.237253	770.440681	385.723979	769.456665	385.231971	7
5	515.246003	258.126640	498.219454	249.613365	497.235438	249.121357	V	***716.430116***	358.718696	699.403567	350.205422	698.419551	349.713414	6
6	630.272946	315.640111	613.246397	307.126836	612.262381	306.634828	D	***617.361702***	309.184489	600.335153	300.671215	599.351137	300.179207	5
7	743.357010	372.182143	726.330461	363.668868	725.346445	363.176860	L	***502.334759***	251.671018	485.308210	243.157743	484.324194	242.665735	4
8	856.441074	428.724175	839.414525	420.210900	838.430509	419.718892	I	***389.250695***	195.128986	372.224146	186.615711	371.240130	186.123703	3
9	957.488753	479.248015	940.462204	470.734740	939.478188	470.242732	T	276.166631	138.586954	259.140082	130.073679	258.156066	129.581671	2
10							R	175.118952	88.063114	158.092403	79.549840			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.0	1130.593140	0.006248	NTEAVDLITR
8.2	1130.608383	-0.008995	EPGYIRAPTK
4.8	1130.593124	0.006264	SKELSPGSAQK

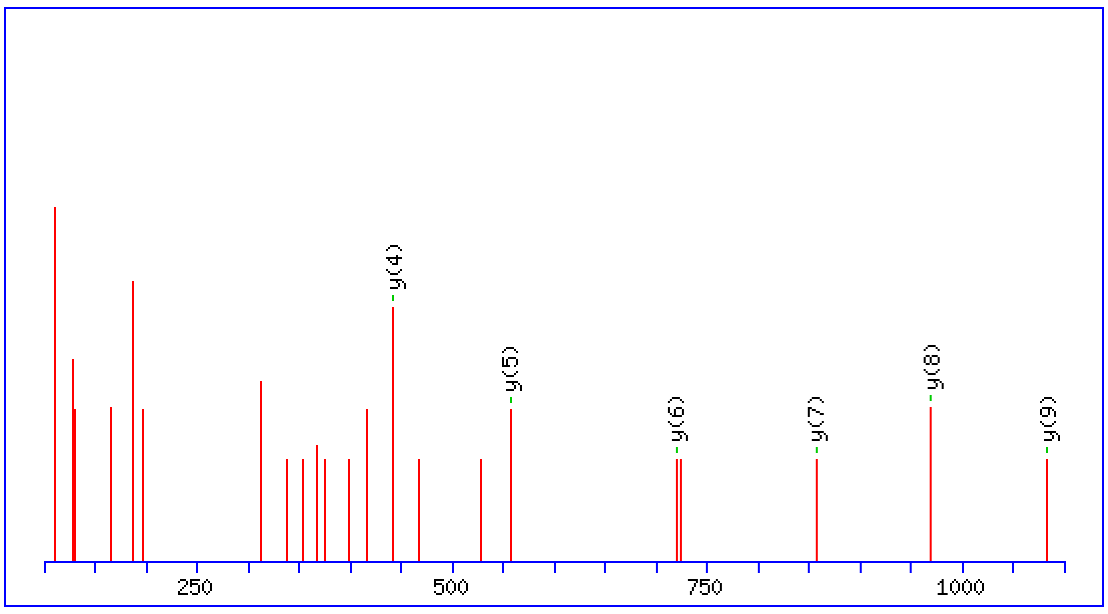
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **LTLLHYDPVVK**
Found in **RM33_HUMAN**, 39S ribosomal protein L33, mitochondrial OS=Homo sapiens GN=MRPL33 PE=1 SV=1

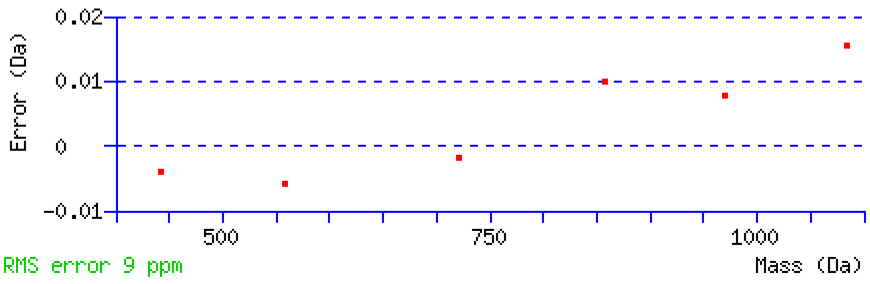
Match to Query 19749: 1296.747912 from(433.256580,3+) rtinseconds(2607) index(14501)
Title: Locus:1.1.1.2649.4
Data file 2011-11-13 - TFD - EP 7-8.mgf

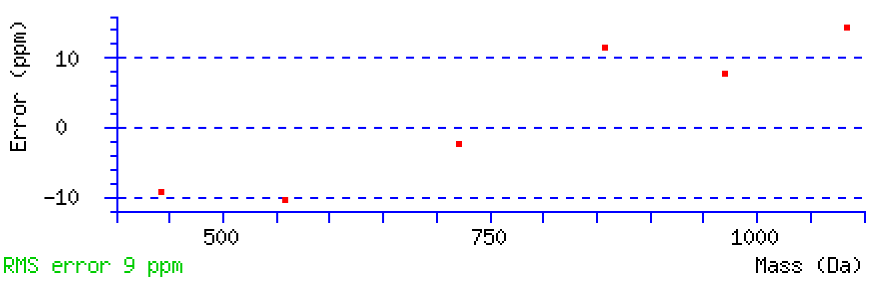
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1296.744171
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 47  Expect: 0.00011
Matches : 6/90 fragment ions using 8 most intense peaks   (help)
```

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308			L							11
2	215.139019	108.073147	197.128454	99.067865	T	1184.667387	592.837332	1167.640838	584.324057	1166.656822	583.832049	10
3	328.223083	164.615179	310.212518	155.609897	L	***1083.619708***	542.313492	1066.593159	533.800218	1065.609143	533.308210	9
4	441.307147	221.157211	423.296582	212.151929	L	***970.535644***	485.771460	953.509095	477.258186	952.525079	476.766178	8
5	578.366059	289.686668	560.355494	280.681385	H	***857.451580***	429.229428	840.425031	420.716154	839.441015	420.224146	7
6	741.429388	371.218332	723.418823	362.213050	Y	***720.392668***	360.699972	703.366119	352.186698	702.382103	351.694690	6
7	856.456331	428.731804	838.445766	419.726521	D	***557.329339***	279.168308	540.302790	270.655033	539.318774	270.163025	5
8	953.509095	477.258186	935.498530	468.252903	P	***442.302396***	221.654836	425.275847	213.141562			4
9	1052.577509	526.792393	1034.566944	517.787110	V	345.249632	173.128454	328.223083	164.615180			3
10	1151.645923	576.326600	1133.635358	567.321317	V	246.181218	123.594247	229.154669	115.080973			2
11					K	147.112804	74.060040	130.086255	65.546765			1



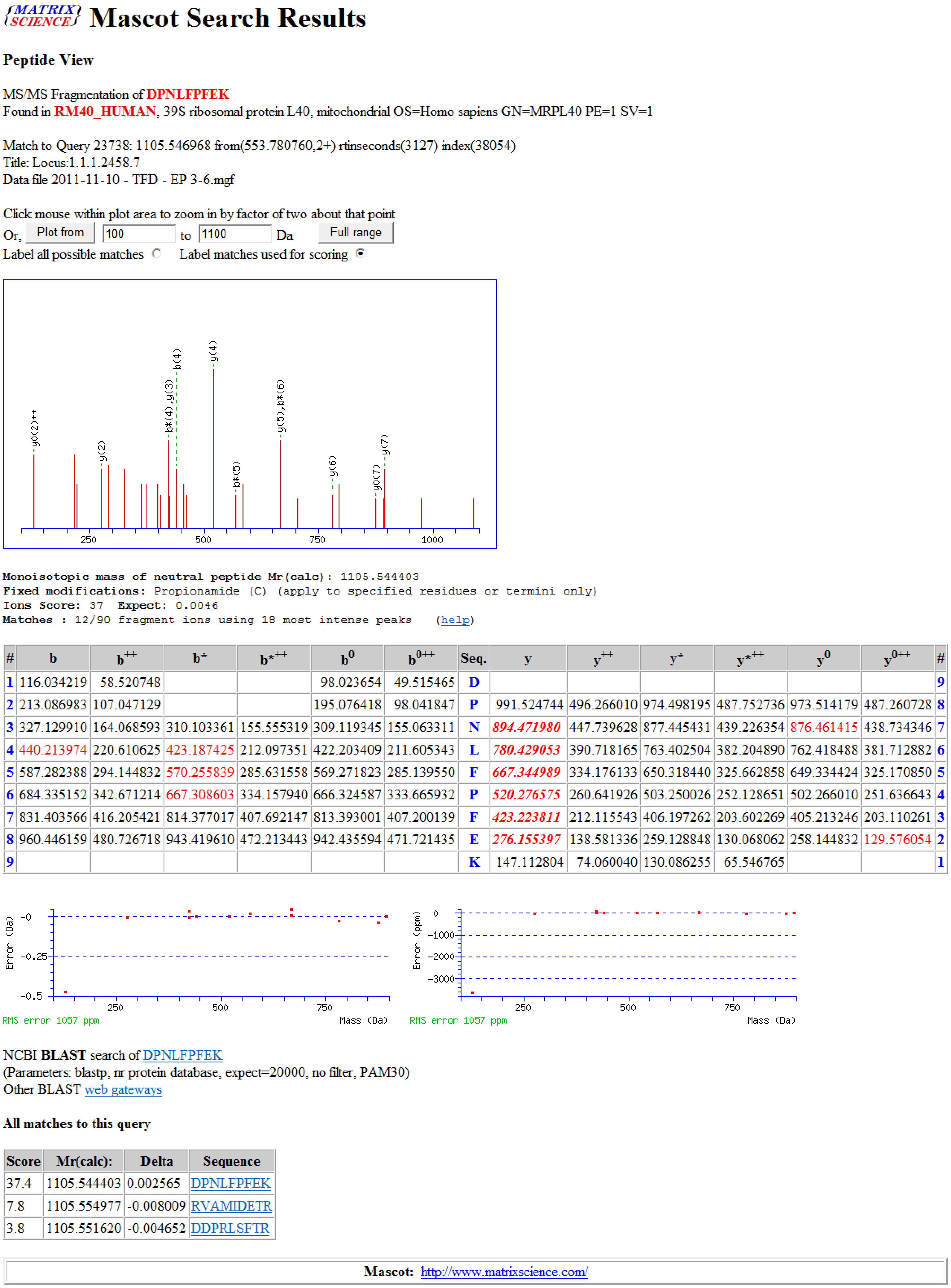


NCBI **BLAST** search of LTLLHYDPVVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.8	1296.744171	0.003741	LTLLHYDPVVK
6.1	1296.751358	-0.003446	IDVIGNEILRR
1.9	1296.751328	-0.003416	ALAAELNQLRAK
0.8	1296.747543	0.000369	AGIPCPTVVLLK
0.1	1296.747543	0.000369	AGIPCPTVVLLK

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



Mascot Search Results

Peptide View

MS/MS Fragmentation of **DPNLFPFEK**
Found in **RM40_HUMAN**, 39S ribosomal protein L40, mitochondrial OS=Homo sapiens GN=MRPL40 PE=1 SV=1

Match to Query 23738: 1105.546968 from(553.780760,2+) rtinseconds(3127) index(38054)
Title: Locus:1.1.1.2458.7
Data file 2011-11-10 - TFD - EP 3-6.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1105.544403
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 37 **Expect:** 0.0046
Matches : 12/90 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	116.034219	58.520748			98.023654	49.515465	**D**							9
2	213.086983	107.047129			195.076418	98.041847	**P**	991.524744	496.266010	974.498195	487.752736	973.514179	487.260728	8
3	327.129910	164.068593	310.103361	155.555319	309.119345	155.063311	**N**	***894.471980***	447.739628	877.445431	439.226354	876.461415	438.734346	7
4	440.213974	220.610625	423.187425	212.097351	422.203409	211.605343	**L**	***780.429053***	390.718165	763.402504	382.204890	762.418488	381.712882	6
5	587.282388	294.144832	570.255839	285.631558	569.271823	285.139550	**F**	***667.344989***	334.176133	650.318440	325.662858	649.334424	325.170850	5
6	684.335152	342.671214	667.308603	334.157940	666.324587	333.665932	**P**	***520.276575***	260.641926	503.250026	252.128651	502.266010	251.636643	4
7	831.403566	416.205421	814.377017	407.692147	813.393001	407.200139	**F**	***423.223811***	212.115543	406.197262	203.602269	405.213246	203.110261	3
8	960.446159	480.726718	943.419610	472.213443	942.435594	471.721435	**E**	***276.155397***	138.581336	259.128848	130.068062	258.144832	129.576054	2
9							**K**	147.112804	74.060040	130.086255	65.546765			1

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.4	1105.544403	0.002565	DPNLFPFEK
7.8	1105.554977	-0.008009	RVAMIDETR
3.8	1105.551620	-0.004652	DDPRLSFTR

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

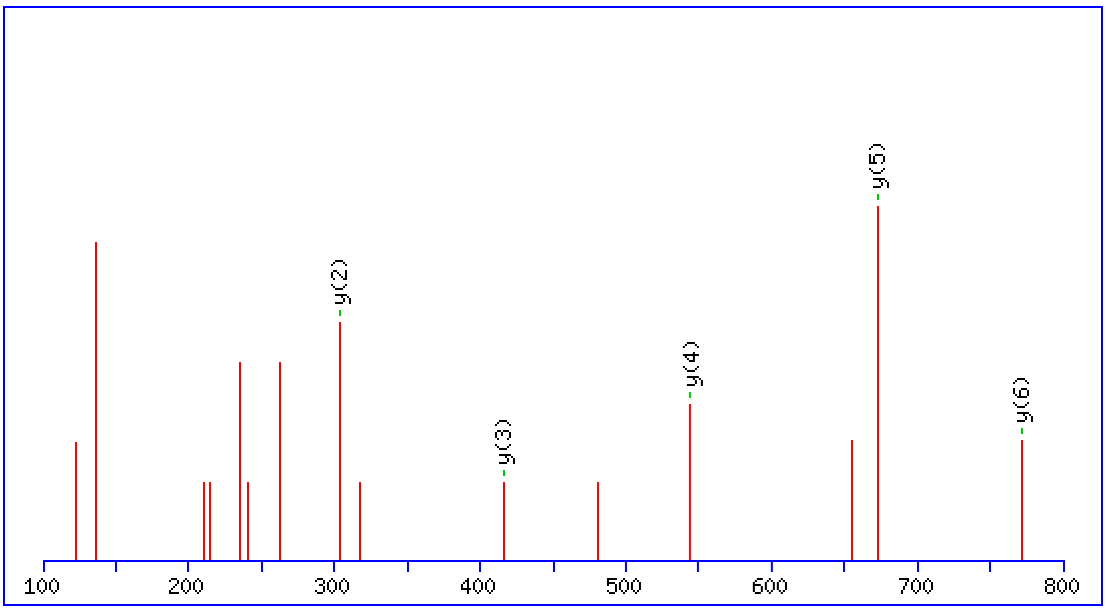
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YVQQLQR**
Found in **RM43_HUMAN**, 39S ribosomal protein L43, mitochondrial OS=Homo sapiens GN=MRPL43 PE=1 SV=1

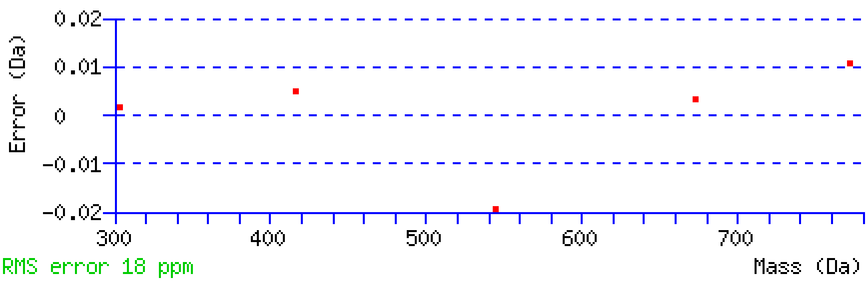
Match to Query 11172: 933.502308 from(467.758430,2+) rtinseconds(1163) index(4035)
Title: Locus:1.1.1.1710.20
Data file 2011-11-10 - TFD - EP 3-6.mgf

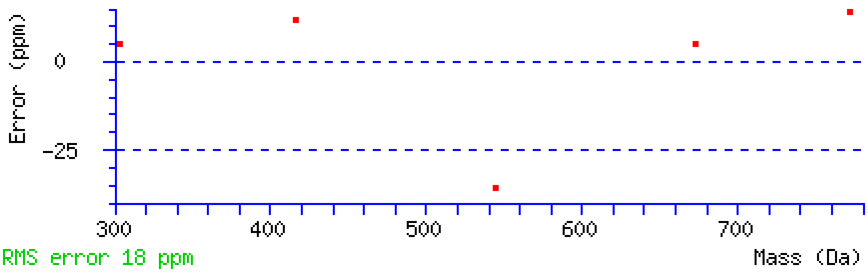
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 933.503204
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.00085
Matches : 5/44 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	164.070605	82.538940			Y					7
2	263.139019	132.073148			V	*771.447164*	386.227220	754.420615	377.713946	6
3	391.197597	196.102437	374.171048	187.589162	Q	*672.378750*	336.693013	655.352201	328.179739	5
4	519.256175	260.131726	502.229626	251.618451	Q	*544.320172*	272.663724	527.293623	264.150450	4
5	632.340239	316.673758	615.313690	308.160483	L	*416.261594*	208.634435	399.235045	200.121161	3
6	760.398817	380.703047	743.372268	372.189772	Q	*303.177530*	152.092403	286.150981	143.579129	2
7					R	175.118952	88.063114	158.092403	79.549840	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.8	933.503204	-0.000896	YVQQLQR

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

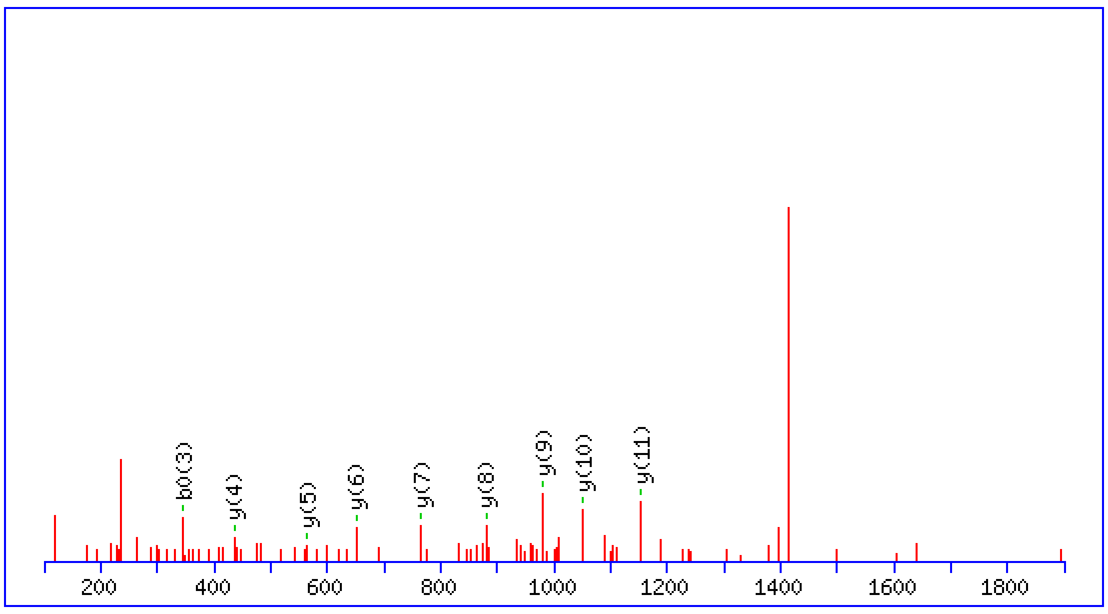
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DFTATDLSEFAAK**
Found in **THIM_HUMAN**, 3-ketoacyl-CoA thiolase, mitochondrial OS=Homo sapiens GN=ACAA2 PE=1 SV=2

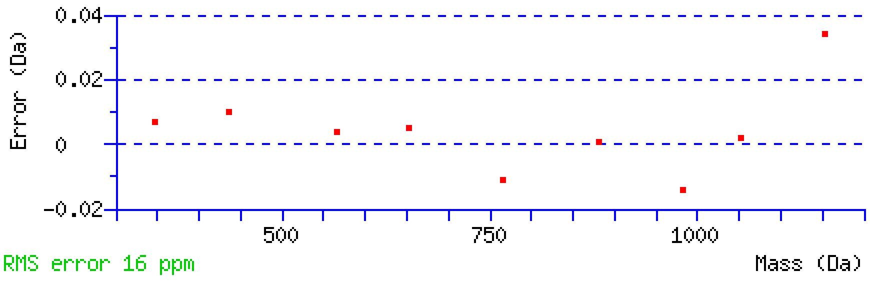
Match to Query 42531: 1414.674868 from(708.344710,2+) rtinseconds(3094) index(43253)
Title: Locus:1.1.1.2518.34
Data file 2011-11-10 - TFD - EP 3-4.mgf

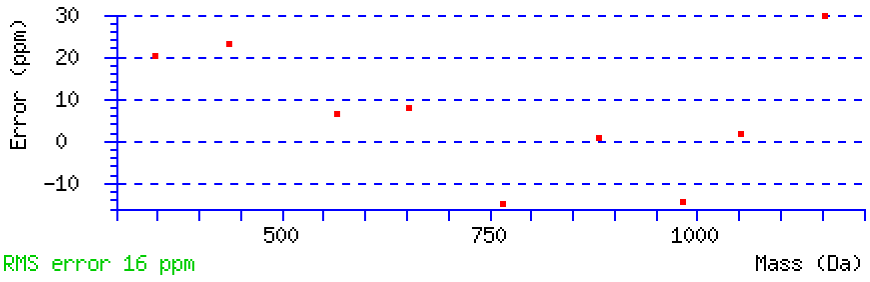
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1414.661621
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 63  Expect: 1.5e-006
Matches : 9/112 fragment ions using 13 most intense peaks   (help)
```

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	116.034219	58.520748	98.023654	49.515465	**D**							13
2	263.102633	132.054954	245.092068	123.049672	**F**	1300.641960	650.824618	1283.615411	642.311344	1282.631395	641.819335	12
3	364.150312	182.578794	346.139747	173.573512	**T**	***1153.573546***	577.290411	1136.546997	568.777137	1135.562981	568.285129	11
4	435.187426	218.097351	417.176861	209.092069	**A**	***1052.525867***	526.766572	1035.499318	518.253297	1034.515302	517.761289	10
5	536.235105	268.621191	518.224540	259.615908	**T**	***981.488753***	491.248015	964.462204	482.734740	963.478188	482.242732	9
6	651.262048	326.134662	633.251483	317.129380	**D**	***880.441074***	440.724175	863.414525	432.210900	862.430509	431.718892	8
7	764.346112	382.676694	746.335547	373.671412	**L**	***765.414131***	383.210704	748.387582	374.697429	747.403566	374.205421	7
8	851.378140	426.192708	833.367575	417.187426	**S**	***652.330067***	326.668672	635.303518	318.155397	634.319502	317.663389	6
9	980.420733	490.714005	962.410168	481.708722	**E**	***565.298039***	283.152658	548.271490	274.639383	547.287474	274.147375	5
10	1127.489147	564.248212	1109.478582	555.242929	**F**	***436.255446***	218.631361	419.228897	210.118086			4
11	1198.526261	599.766769	1180.515696	590.761486	**A**	289.187032	145.097154	272.160483	136.583879			3
12	1269.563375	635.285326	1251.552810	626.280043	**A**	218.149918	109.578597	201.123369	101.065322			2
13					**K**	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
63.2	1414.661621	0.013247	DFTATDLSEFAAK
1.0	1414.669662	0.005206	MCESYSRSLLR
0.4	1414.666321	0.008547	CRTLYPFSGER

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

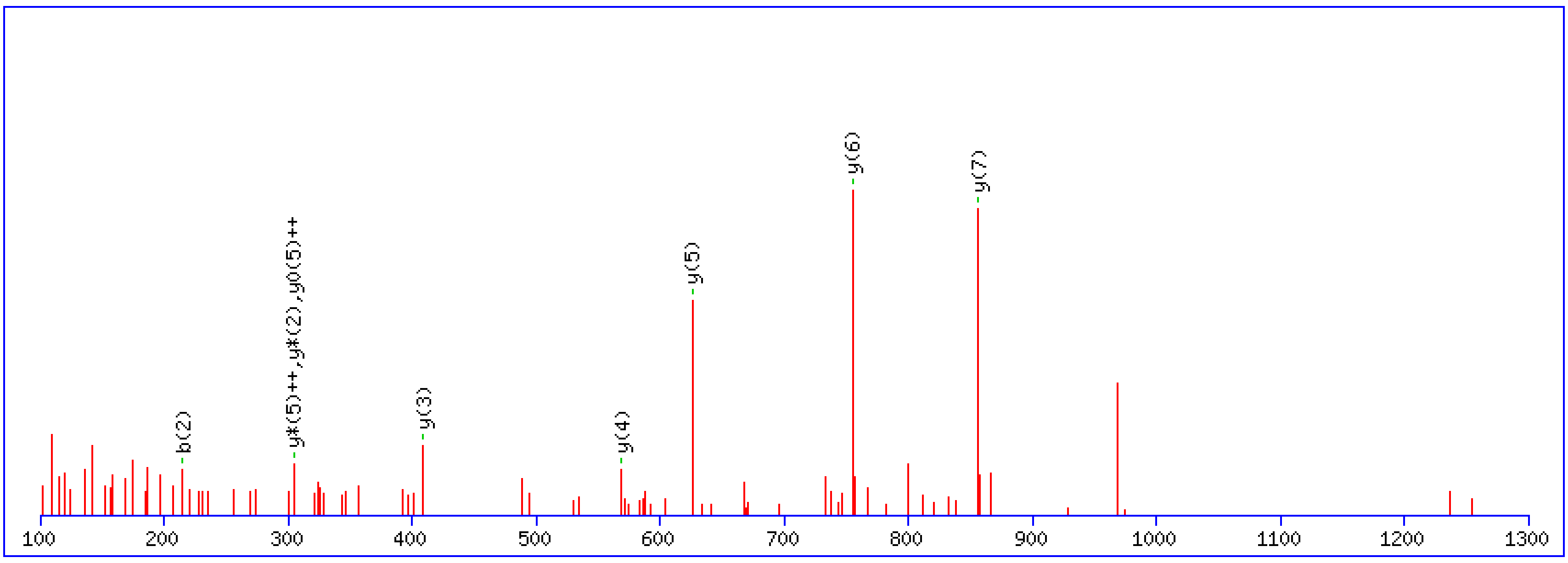
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LTEGCSFR**
Found in **RS27L_HUMAN**, 40S ribosomal protein S27-like OS=Homo sapiens GN=RPS27L PE=1 SV=3

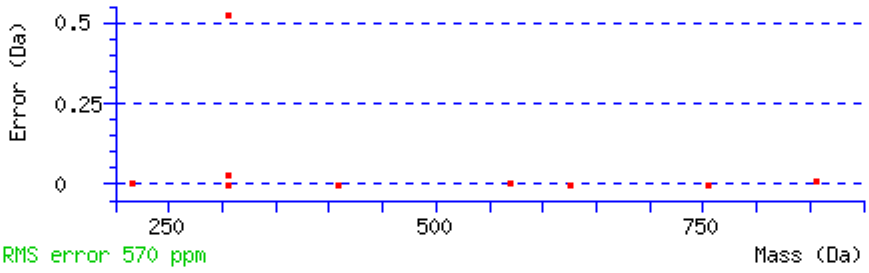
Match to Query 7887: 968.437688 from(485.226120,2+) rtinseconds(1145) index(6338)
Title: Locus:1.1.1.882.18
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 3.mgf

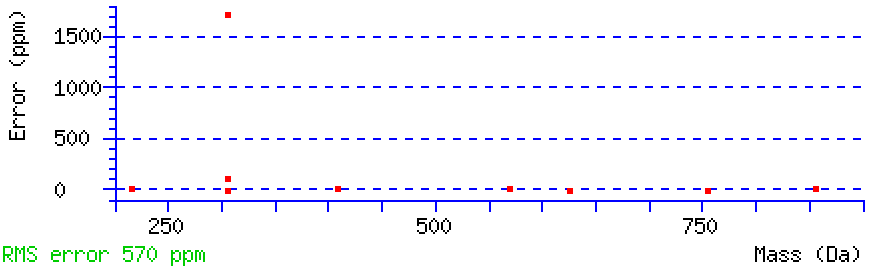
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 968.438568
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 38 **Expect:** 0.00085
Matches : 9/64 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308			L							8
2	215.139019	108.073147	197.128454	99.067865	T	***856.361779***	428.684528	839.335230	420.171253	838.351214	419.679245	7
3	344.181612	172.594444	326.171047	163.589162	E	***755.314100***	378.160688	738.287551	369.647413	737.303535	369.155405	6
4	401.203076	201.105176	383.192511	192.099894	G	***626.271507***	313.639391	609.244958	305.126117	608.260942	304.634109	5
5	561.233725	281.120501	543.223160	272.115218	C	***569.250043***	285.128660	552.223494	276.615385	551.239478	276.123377	4
6	648.265753	324.636515	630.255188	315.631232	S	***409.219394***	205.113335	392.192845	196.600060	391.208829	196.108052	3
7	795.334167	398.170722	777.323602	389.165439	F	322.187366	161.597321	305.160817	153.084046			2
8					R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.0	968.438568	-0.000880	LTEGCSFR
4.9	968.438568	-0.000880	PGYTCSIR
0.0	968.438568	-0.000880	PTPMPHNK
0.0	968.438568	-0.000880	PTPMPHNK
0.0	968.438568	-0.000880	PTPMPHNK

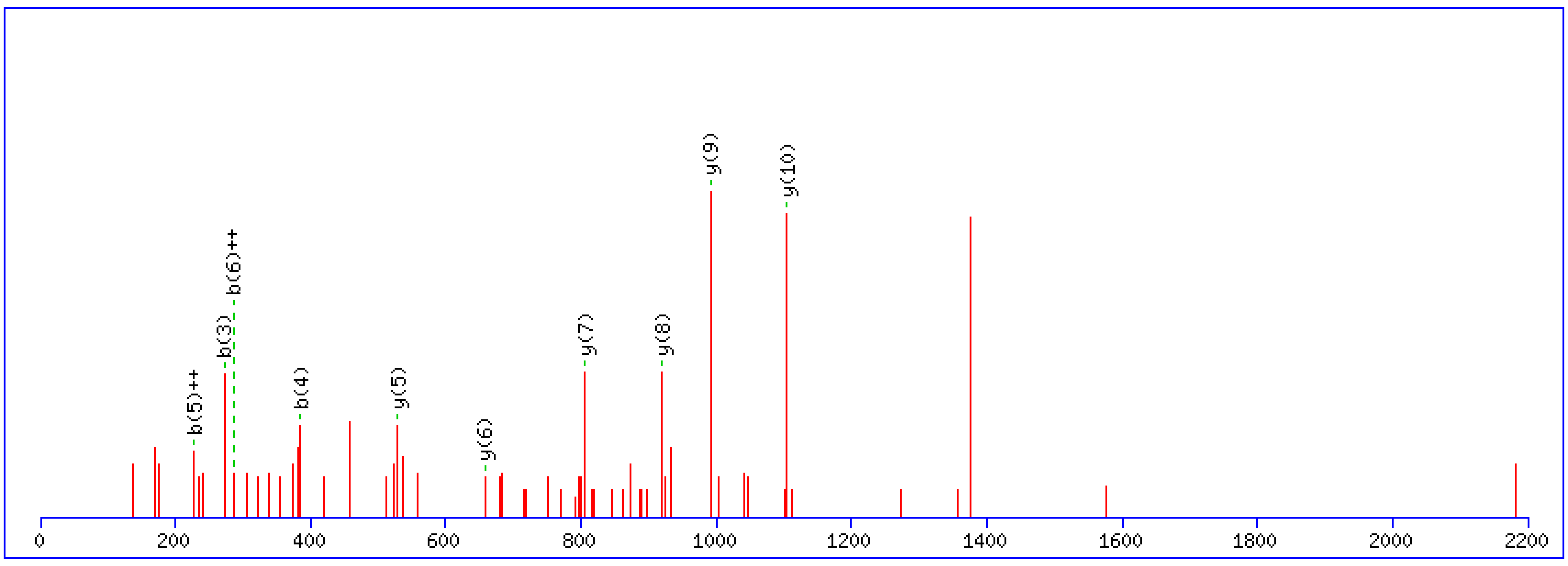
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DGVLADFEAGLLR**
Found in **NT5C_HUMAN**, 5'(3')-deoxyribonucleotidase, cytosolic type OS=Homo sapiens GN=NT5C PE=1 SV=2

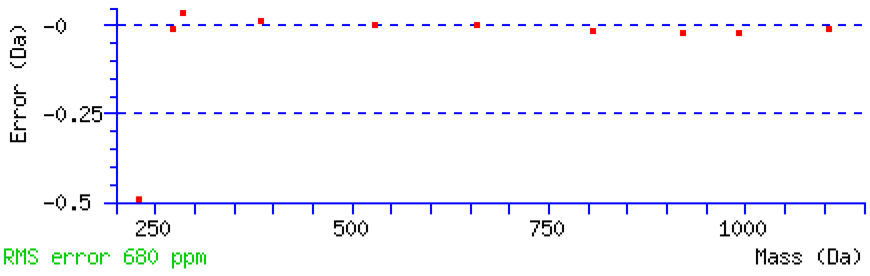
Match to Query 37011: 1374.704968 from(688.359760,2+) rtinseconds(3958) index(59390)
Title: Locus:1.1.1.1943.20
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 3.mgf

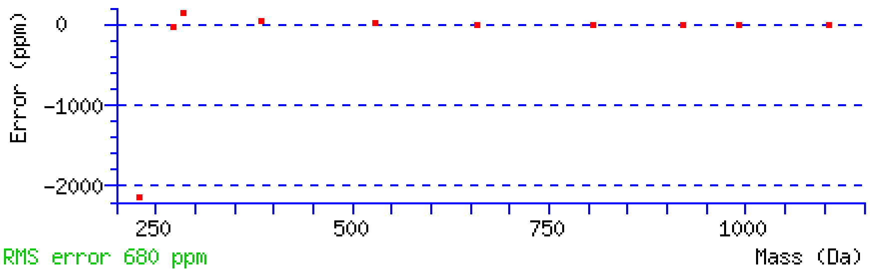
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [0] to [2200] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1374.714325
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.012
Matches : 10/110 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.034219	58.520748	98.023654	49.515465	D							13
2	173.055683	87.031479	155.045118	78.026197	G	1260.694664	630.850970	1243.668115	622.337696	1242.684099	621.845687	12
3	**272.124097**	136.565687	254.113532	127.560404	V	1203.673200	602.340238	1186.646651	593.826964	1185.662635	593.334955	11
4	**385.208161**	193.107719	367.197596	184.102436	L	***1104.604786***	552.806031	1087.578237	544.292757	1086.594221	543.800748	10
5	456.245275	**228.626276**	438.234710	219.620993	A	***991.520722***	496.263999	974.494173	487.750724	973.510157	487.258716	9
6	571.272218	**286.139747**	553.261653	277.134465	D	***920.483608***	460.745442	903.457059	452.232167	902.473043	451.740159	8
7	718.340632	359.673954	700.330067	350.668672	F	***805.456665***	403.231970	788.430116	394.718696	787.446100	394.226688	7
8	847.383225	424.195251	829.372660	415.189968	E	***658.388251***	329.697764	641.361702	321.184489	640.377686	320.692481	6
9	918.420339	459.713808	900.409774	450.708525	A	***529.345658***	265.176467	512.319109	256.663192			5
10	975.441803	488.224540	957.431238	479.219257	G	458.308544	229.657910	441.281995	221.144635			4
11	1088.525867	544.766572	1070.515302	535.761289	L	401.287080	201.147178	384.260531	192.633903			3
12	1201.609931	601.308604	1183.599366	592.303321	L	288.203016	144.605146	271.176467	136.091871			2
13					R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.2	1374.714325	-0.009357	DGVLADFEAGLLR
10.0	1374.693207	0.011761	FPAPPAPPAPPPR
5.7	1374.714325	-0.009357	LTGPSGLSSYHLK
5.1	1374.711624	-0.006656	LSREGSSHHLPR
3.6	1374.714325	-0.009357	LDAPPPPAAPLPR
3.4	1374.692520	0.012448	VTALQEECRAAK
3.3	1374.700424	0.004544	KGAGGGGPPQAPPPR
3.3	1374.700424	0.004544	KGAGGGGPPQAPPPR
3.3	1374.700424	0.004544	KGAGGGGPPQAPPPR
2.4	1374.714325	-0.009357	LDAPPPPAAPLPR

{MATRIX SCIENCE}

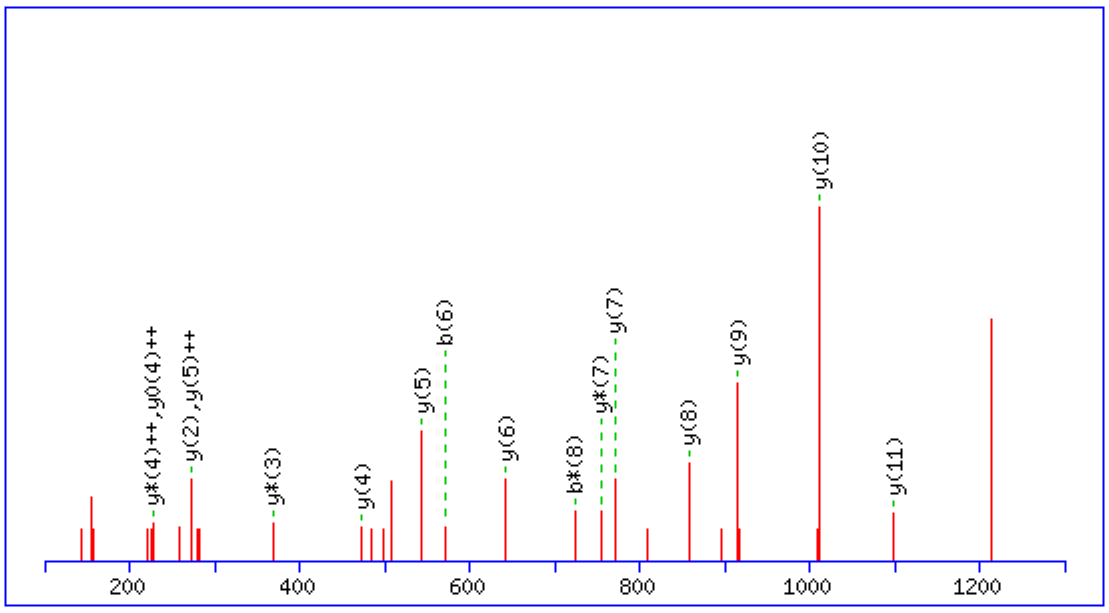
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NSPGSQVASNPR**
Found in **XRN2_HUMAN**, 5'-3' exoribonuclease 2 OS=Homo sapiens GN=XRN2 PE=1 SV=1

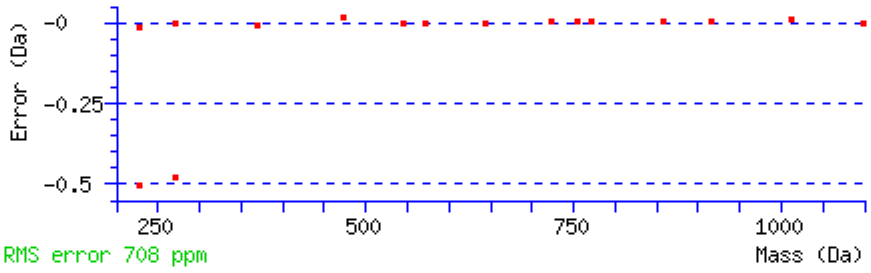
Match to Query 536245: 1212.583448 from(607.299000,2+) rtinseconds(884) index(241616)
Title: Locus:1.1.1.776.31
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

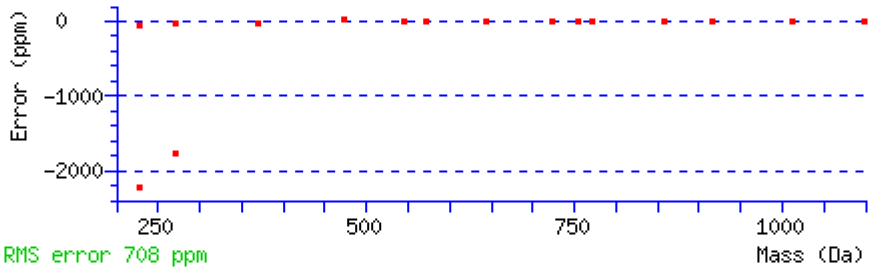
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



`Monoisotopic mass of neutral peptide Mr(calc):` 1212.584702
`Fixed modifications:` Carbamidomethyl (C) (apply to specified residues or termini only)
`Ions Score:` 78 `Expect:` 9.6e-008
`Matches :` 16/124 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			N							12
2	202.082231	101.544753	185.055682	93.031479	184.071666	92.539471	S	***1099.549061***	550.278168	1082.522512	541.764894	1081.538496	541.272886	11
3	299.134995	150.071135	282.108446	141.557861	281.124430	141.065853	P	***1012.517033***	506.762154	995.490484	498.248880	994.506468	497.756872	10
4	356.156459	178.581867	339.129910	170.068593	338.145894	169.576585	G	***915.464269***	458.235773	898.437720	449.722498	897.453704	449.230490	9
5	443.188487	222.097881	426.161938	213.584607	425.177922	213.092599	S	***858.442805***	429.725040	841.416256	421.211766	840.432240	420.719758	8
6	571.247065	286.127171	554.220516	277.613896	553.236500	277.121888	Q	***771.410777***	386.209026	754.384228	377.695752	753.400212	377.203744	7
7	670.315479	335.661378	653.288930	327.148103	652.304914	326.656095	V	***643.352199***	322.179737	626.325650	313.666463	625.341634	313.174455	6
8	741.352593	371.179935	724.326044	362.666660	723.342028	362.174652	A	***544.283785***	272.645531	527.257236	264.132256	526.273220	263.640248	5
9	828.384621	414.695948	811.358072	406.182674	810.374056	405.690666	S	***473.246671***	237.126973	456.220122	228.613699	455.236106	228.121691	4
10	942.427548	471.717412	925.400999	463.204137	924.416983	462.712129	N	386.214643	193.610959	369.188094	185.097685			3
11	1039.480312	520.243794	1022.453763	511.730519	1021.469747	511.238511	P	***272.171716***	136.589496	255.145167	128.076221			2
12							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
77.5	1212.584702	-0.001254	NSPGSQVASNPR
2.7	1212.580872	0.002576	HPGVAEVKTEM

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

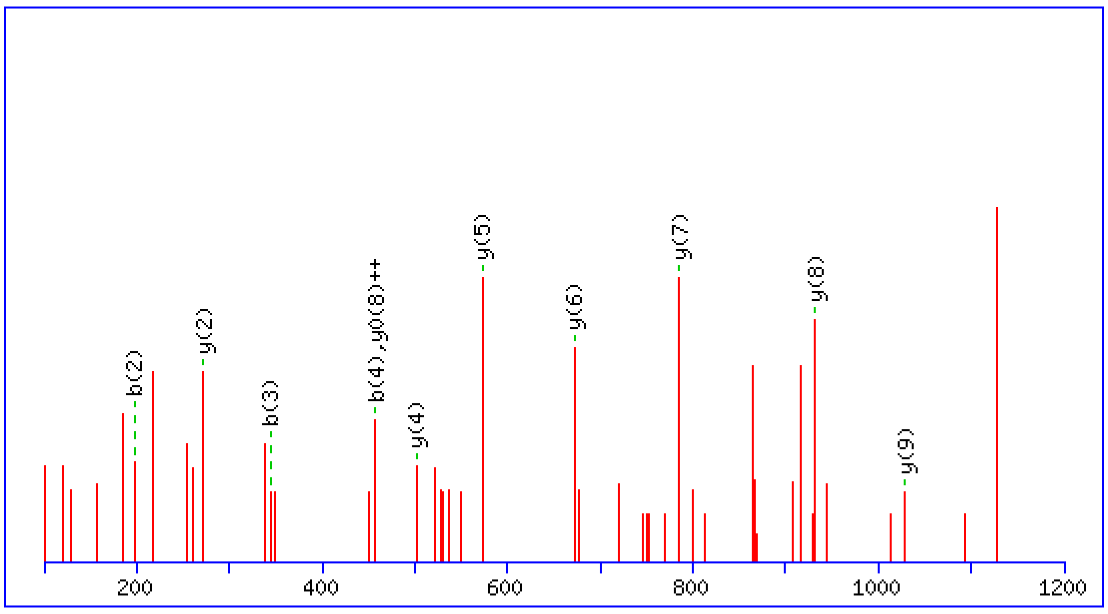
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VPFLVAETPR**
Found in **AAPK1_HUMAN**, 5'-AMP-activated protein kinase catalytic subunit alpha-1 OS=Homo sapiens GN=PRKAA1 PE=1 SV=4

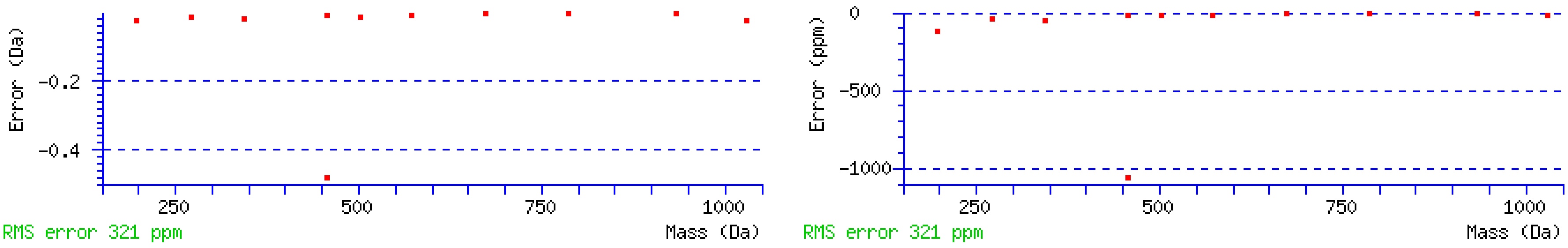
Match to Query 22785: 1127.636288 from(564.825420,2+) rtinseconds(2614) index(34377)
Title: Locus:1.1.1.2418.23
Data file 2011-11-14 - TFD - EP 8-3.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1127.633896
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 46 **Expect:** 0.00022
Matches : 11/74 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483			V							10
2	**197.128454**	99.067865			P	***1029.572758***	515.290017	1012.546209	506.776743	1011.562193	506.284735	9
3	**344.196868**	172.602072			F	***932.519994***	466.763635	915.493445	458.250361	914.509429	457.758353	8
4	**457.280932**	229.144104			L	***785.451580***	393.229428	768.425031	384.716154	767.441015	384.224146	7
5	556.349346	278.678311			V	***672.367516***	336.687396	655.340967	328.174122	654.356951	327.682114	6
6	627.386460	314.196868			A	***573.299102***	287.153189	556.272553	278.639915	555.288537	278.147907	5
7	756.429053	378.718165	738.418488	369.712882	E	***502.261988***	251.634632	485.235439	243.121358	484.251423	242.629350	4
8	857.476732	429.242004	839.466167	420.236721	T	373.219395	187.113336	356.192846	178.600061	355.208830	178.108053	3
9	954.529496	477.768386	936.518931	468.763104	P	***272.171716***	136.589496	255.145167	128.076222			2
10					R	175.118952	88.063114	158.092403	79.549840			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.1	1127.633896	0.002392	VPFLVAETPR

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

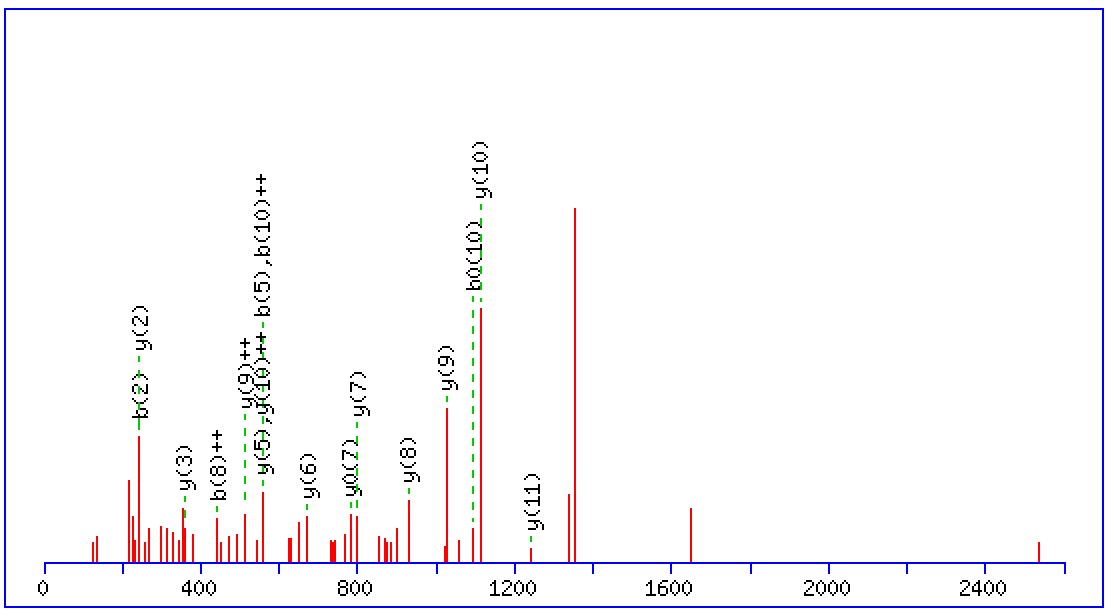
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IESPEEISLLPK**
Found in **MTHFS_HUMAN**, 5-formyltetrahydrofolate cyclo-ligase OS=Homo sapiens GN=MTHFS PE=1 SV=2

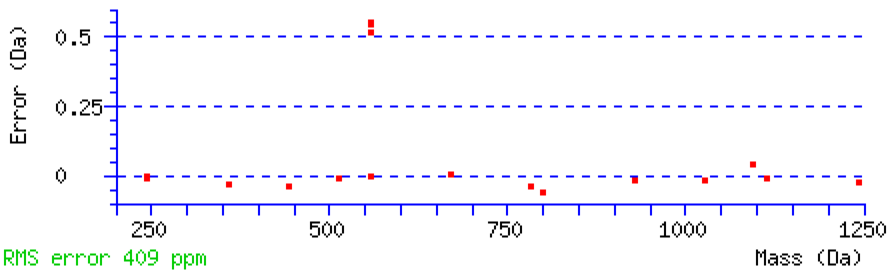
Match to Query 37583: 1353.735908 from(677.875230,2+) rtinseconds(2870) index(34924)
Title: Locus:1.1.1.2677.36
Data file 2011-11-12 - TFD - EP 5-5.mgf

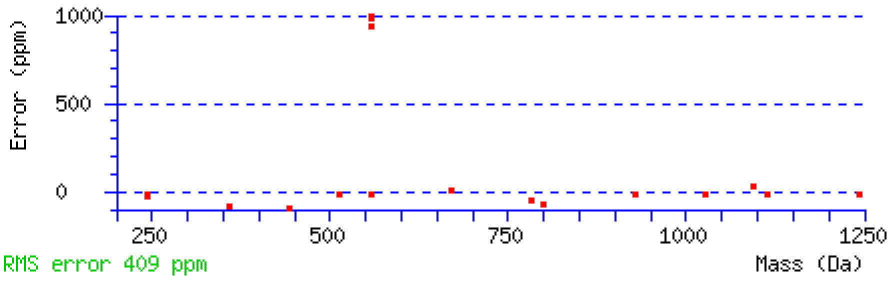
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1353.739105
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 73  Expect: 4.2e-007
Matches : 17/100 fragment ions using 23 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							12
2	**243.133933**	122.070605	225.123368	113.065322	E	***1241.662359***	621.334818	1224.635810	612.821543	1223.651794	612.329535	11
3	330.165961	165.586618	312.155396	156.581336	S	***1112.619766***	556.813521	1095.593217	548.300247	1094.609201	547.808239	10
4	427.218725	214.113001	409.208160	205.107718	P	***1025.587738***	513.297507	1008.561189	504.784233	1007.577173	504.292225	9
5	**556.261318**	278.634297	538.250753	269.629015	E	***928.534974***	464.771125	911.508425	456.257851	910.524409	455.765843	8
6	685.303911	343.155594	667.293346	334.150311	E	***799.492381***	400.249829	782.465832	391.736554	781.481816	391.244546	7
7	798.387975	399.697626	780.377410	390.692343	I	***670.449788***	335.728532	653.423239	327.215258	652.439223	326.723250	6
8	885.420003	**443.213640**	867.409438	434.208357	S	***557.365724***	279.186500	540.339175	270.673226	539.355159	270.181218	5
9	998.504067	499.755672	980.493502	490.750389	L	470.333696	235.670486	453.307147	227.157211			4
10	1111.588131	**556.297704**	1093.577566	547.292421	L	***357.249632***	179.128454	340.223083	170.615179			3
11	1208.640895	604.824086	1190.630330	595.818803	P	***244.165568***	122.586422	227.139019	114.073148			2
12					K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
73.3	1353.739105	-0.003197	IESPEEISLLPK
10.2	1353.736435	-0.000527	LEQVRPQELSR
7.0	1353.743820	-0.007912	LQMILNEIQPR
6.6	1353.725220	0.010688	NELQLVDLPTGR
3.6	1353.725220	0.010688	TTQEPLARDPVK
3.3	1353.736435	-0.000527	SRPKEPSPSLTR
3.3	1353.736450	-0.000542	LQEAGVSIPPRR
2.6	1353.747665	-0.011757	IEPQRPARSLR
2.3	1353.732590	0.003318	LLKMNGPEDLPK
0.6	1353.740479	-0.004571	LPTTGYLVYRR

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

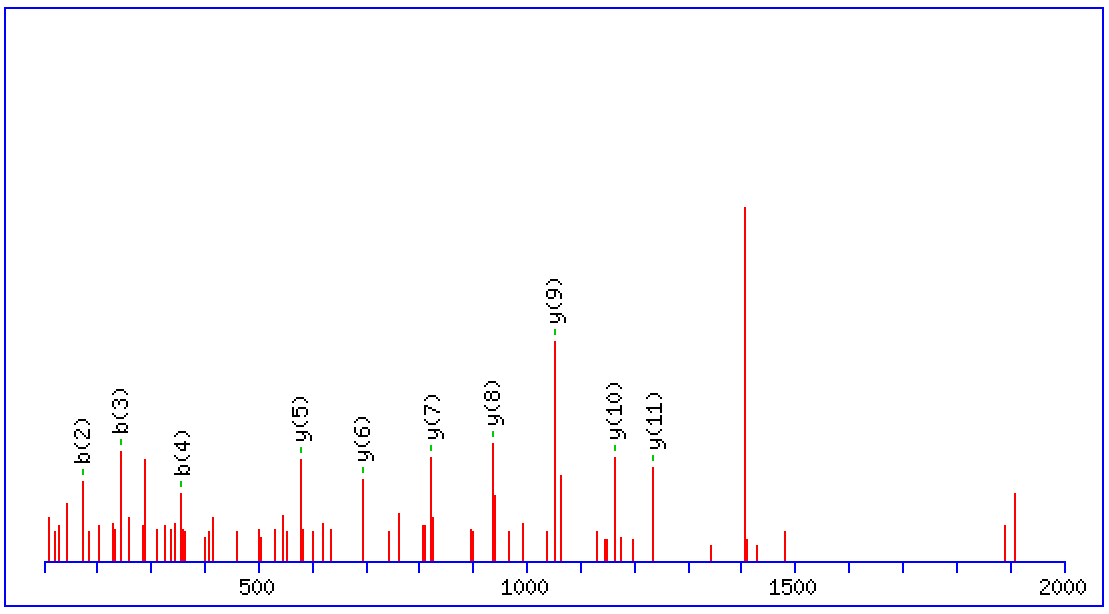
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLALDLEDGNFLK**
Found in **NT5D1_HUMAN**, 5'-nucleotidase domain-containing protein 1 OS=Homo sapiens GN=NT5DC1 PE=1 SV=1

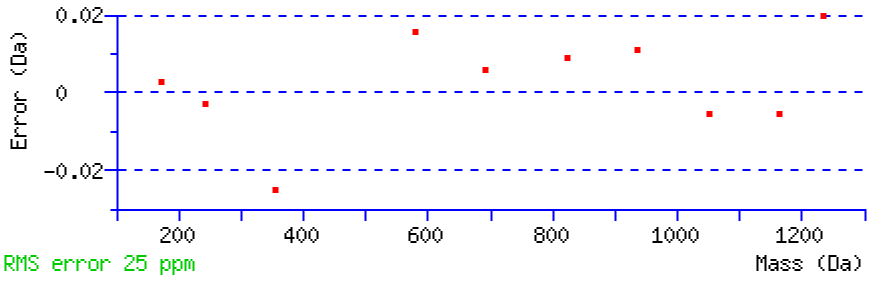
Match to Query 35315: 1403.735768 from(702.875160,2+) rtinseconds(3457) index(50483)
Title: Locus:1.1.1.2804.17
Data file 2011-11-10 - TFD - EP 4-3.mgf

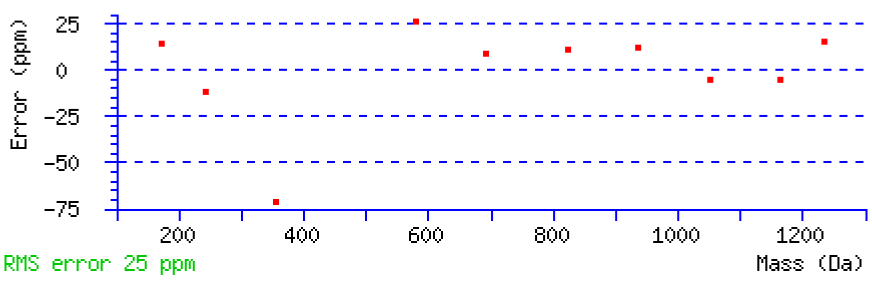
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1403.729630
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 57 **Expect:** 2.6e-005
Matches : 10/108 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	58.028740	29.518008					G							13
2	**171.112804**	86.060040					L	1347.715458	674.361367	1330.688909	665.848093	1329.704893	665.356085	12
3	**242.149918**	121.578597					A	***1234.631394***	617.819335	1217.604845	609.306061	1216.620829	608.814053	11
4	**355.233982**	178.120629					L	***1163.594280***	582.300778	1146.567731	573.787504	1145.583715	573.295496	10
5	470.260925	235.634100			452.250360	226.628818	D	***1050.510216***	525.758746	1033.483667	517.245472	1032.499651	516.753464	9
6	583.344989	292.176133			565.334424	283.170850	L	***935.483273***	468.245275	918.456724	459.732000	917.472708	459.239992	8
7	712.387582	356.697429			694.377017	347.692147	E	***822.399209***	411.703243	805.372660	403.189968	804.388644	402.697960	7
8	827.414525	414.210901			809.403960	405.205618	D	***693.356616***	347.181946	676.330067	338.668672	675.346051	338.176664	6
9	884.435989	442.721633			866.425424	433.716350	G	***578.329673***	289.668475	561.303124	281.155200			5
10	998.478916	499.743096	981.452367	491.229822	980.468351	490.737814	N	521.308209	261.157743	504.281660	252.644468			4
11	1145.547330	573.277303	1128.520781	564.764029	1127.536765	564.272021	F	407.265282	204.136279	390.238733	195.623004			3
12	1258.631394	629.819335	1241.604845	621.306061	1240.620829	620.814053	L	260.196868	130.602072	243.170319	122.088797			2
13							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.8	1403.729630	0.006138	GLALDLEDGNFLK
13.3	1403.723114	0.012654	VAAINGCGIGPFSK
8.3	1403.729645	0.006123	IQIDEDGKVFPK
1.3	1403.734329	0.001439	IQLRSQCATWK
0.5	1403.740875	-0.005107	QPIRGSDEVLFK

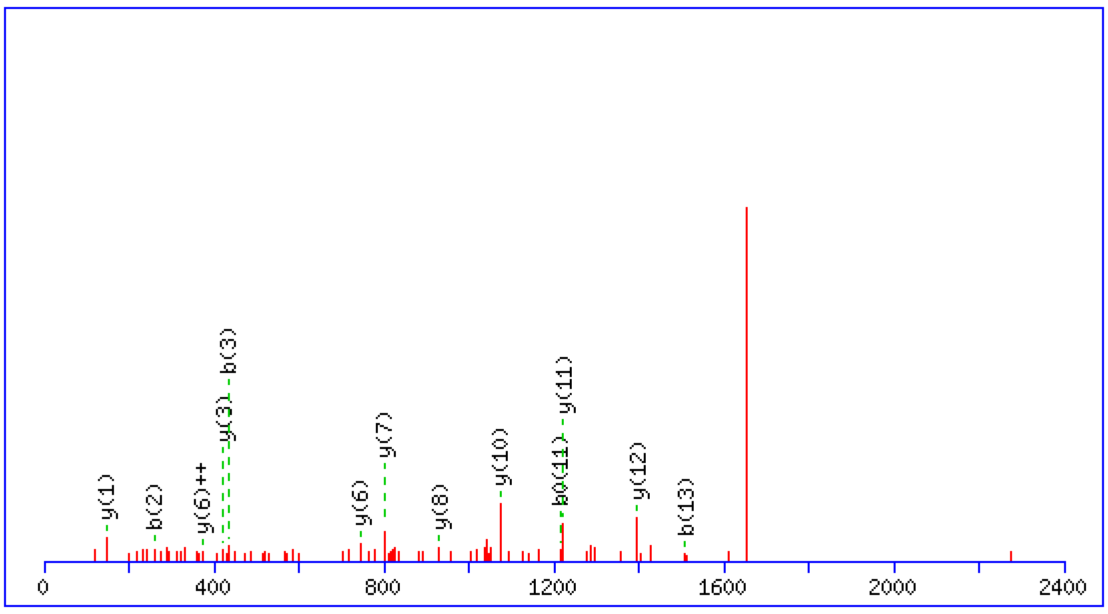
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FLCFGSEGGTYYIK**
Found in **RO60_HUMAN**, 60 kDa SS-A/Ro ribonucleoprotein OS=Homo sapiens GN=TROVE2 PE=1 SV=2

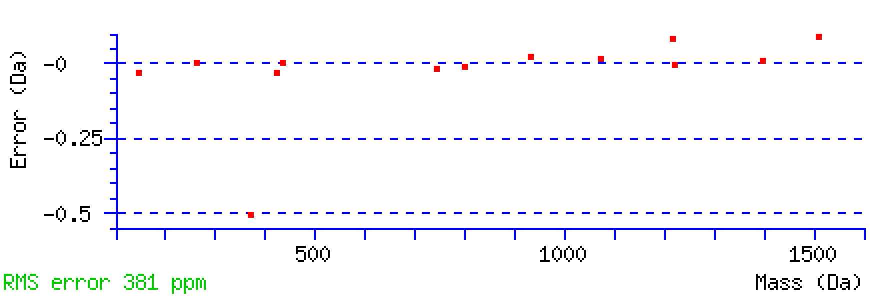
Match to Query 52354: 1654.780488 from(828.397520,2+) rtinseconds(3217) index(46091)
Title: Locus:1.1.1.2595.41
Data file 2011-11-12 - TFD - EP 6-3.mgf

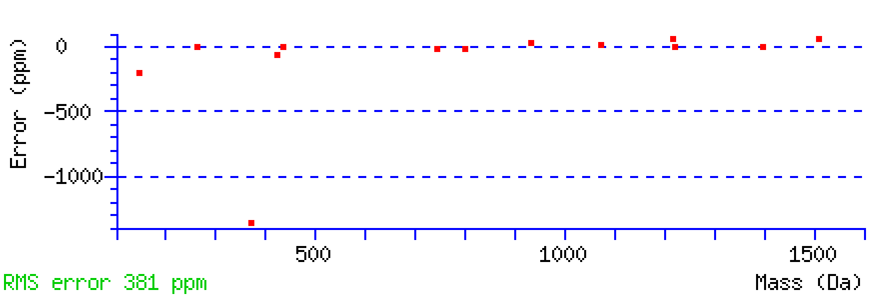
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1654.770126
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 38  Expect: 0.0014
Matches : 13/112 fragment ions using 29 most intense peaks   (help)
```

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	148.075690	74.541483			F							14
2	**261.159754**	131.083515			L	1508.708995	754.858136	1491.682446	746.344861	1490.698430	745.852853	13
3	**435.206053**	218.106664			C	***1395.624931***	698.316104	1378.598382	689.802829	1377.614366	689.310821	12
4	582.274467	291.640872			F	***1221.578632***	611.292954	1204.552083	602.779680	1203.568067	602.287671	11
5	639.295931	320.151604			G	***1074.510218***	537.758747	1057.483669	529.245473	1056.499653	528.753465	10
6	726.327959	363.667618	708.317394	354.662335	S	1017.488754	509.248015	1000.462205	500.734741	999.478189	500.242733	9
7	855.370552	428.188914	837.359987	419.183631	E	***930.456726***	465.732001	913.430177	457.218727	912.446161	456.726719	8
8	912.392016	456.699646	894.381451	447.694364	G	***801.414133***	401.210705	784.387584	392.697430	783.403568	392.205422	7
9	969.413480	485.210378	951.402915	476.205096	G	***744.392669***	372.699973	727.366120	364.186698	726.382104	363.694690	6
10	1070.461159	535.734218	1052.450594	526.728935	T	687.371205	344.189241	670.344656	335.675966	669.360640	335.183958	5
11	1233.524488	617.265882	1215.513923	608.260600	Y	586.323526	293.665401	569.296977	285.152127			4
12	1396.587817	698.797547	1378.577252	689.792264	Y	***423.260197***	212.133736	406.233648	203.620462			3
13	**1509.671881**	755.339579	1491.661316	746.334296	I	260.196868	130.602072	243.170319	122.088797			2
14					K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.1	1654.770126	0.010362	FLCFGSEGGTYYIK

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

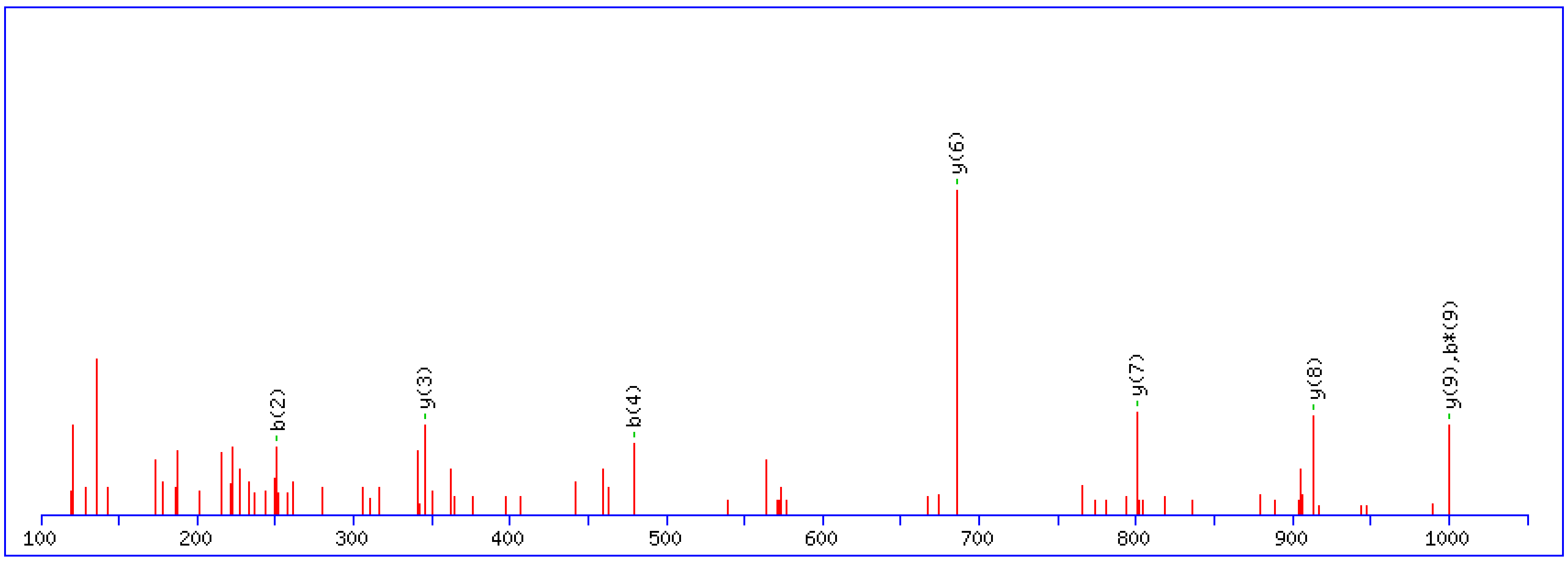
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YSLDPENPTK**
Found in **RL17_HUMAN**, 60S ribosomal protein L17 OS=Homo sapiens GN=RPL17 PE=1 SV=3

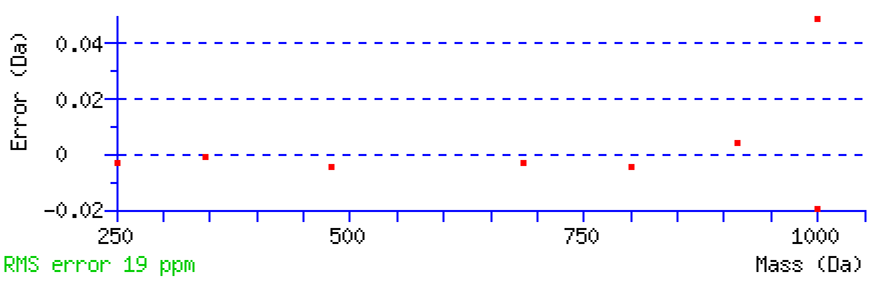
Match to Query 19247: 1162.554428 from(582.284490,2+) rtinseconds(1761) index(18188)
Title: Locus:1.1.1.1053.29
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 2.mgf

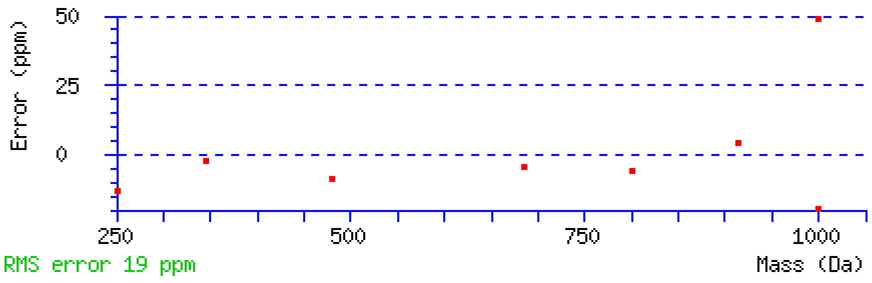
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1050] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1162.550598
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 42  Expect: 0.00066
Matches : 8/92 fragment ions using 9 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.070605	82.538940					Y							10
2	**251.102633**	126.054954			233.092068	117.049672	S	***1000.494566***	500.750921	983.468017	492.237647	982.484001	491.745639	9
3	364.186697	182.596986			346.176132	173.591704	L	***913.462538***	457.234907	896.435989	448.721633	895.451973	448.229625	8
4	**479.213640**	240.110458			461.203075	231.105176	D	***800.378474***	400.692875	783.351925	392.179601	782.367909	391.687593	7
5	576.266404	288.636840			558.255839	279.631558	P	***685.351531***	343.179404	668.324982	334.666129	667.340966	334.174121	6
6	705.308997	353.158137			687.298432	344.152854	E	588.298767	294.653022	571.272218	286.139747	570.288202	285.647739	5
7	819.351924	410.179600	802.325375	401.666326	801.341359	401.174318	N	459.256174	230.131725	442.229625	221.618450	441.245609	221.126443	4
8	916.404688	458.705982	899.378139	450.192708	898.394123	449.700700	P	***345.213247***	173.110262	328.186698	164.596987	327.202682	164.104979	3
9	1017.452367	509.229822	1000.425818	500.716547	999.441802	500.224539	T	248.160483	124.583879	231.133934	116.070605	230.149918	115.578597	2
10							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.4	1162.550598	0.003830	YSLDPENPTK
8.1	1162.544083	0.010345	WIRDNEVTM
1.9	1162.565872	-0.011444	YPPPSFPTNK
1.9	1162.565872	-0.011444	YPPPSFPTNK
1.3	1162.565872	-0.011444	YPPPSFPTNK

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

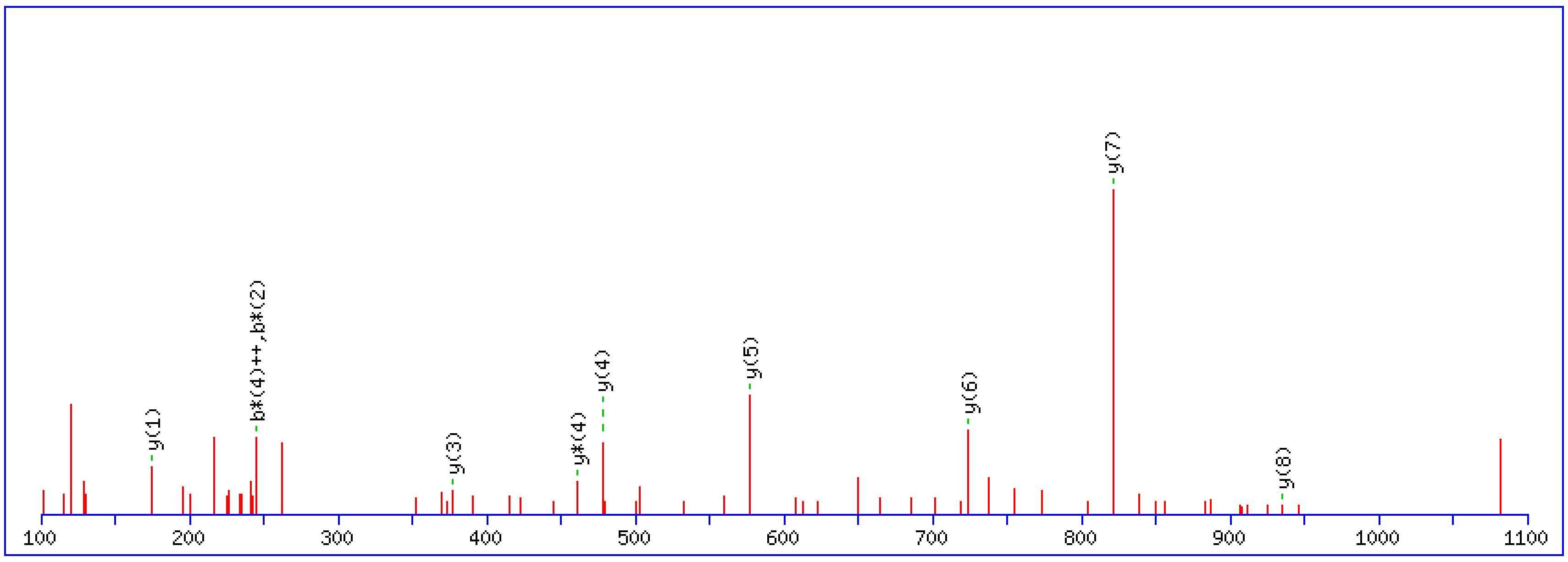
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FNPFVTSDR**
Found in **RL26L_HUMAN**, 60S ribosomal protein L26-like 1 OS=Homo sapiens GN=RPL26L1 PE=1 SV=1

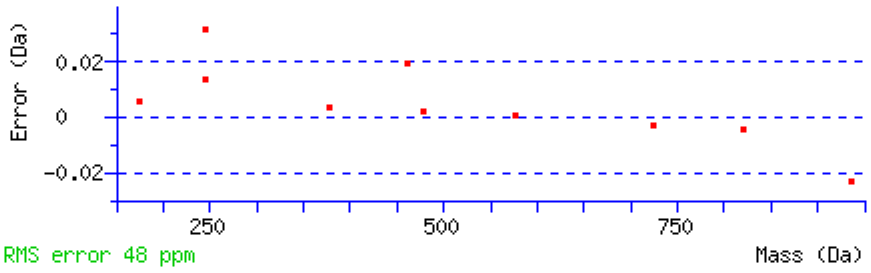
Match to Query 15052: 1081.517788 from(541.766170,2+) rtinseconds(2217) index(26688)
Title: Locus:1.1.1.1289.18
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 3.mgf

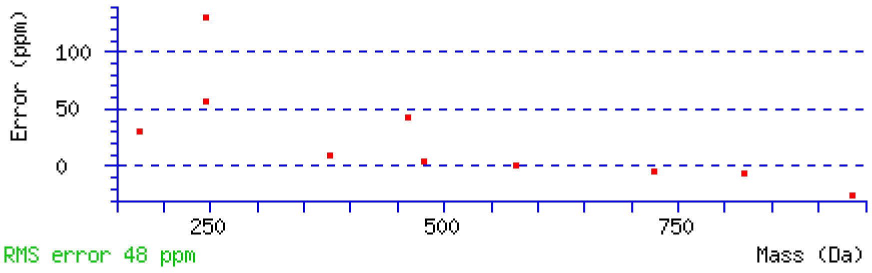
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1081.519272
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 44 **Expect:** 0.00028
Matches : 10/82 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.075690	74.541483					**F**							9
2	262.118617	131.562946	245.092068	123.049672			**N**	***935.458121***	468.232699	918.431572	459.719424	917.447556	459.227416	8
3	359.171381	180.089328	342.144832	171.576054			**P**	***821.415194***	411.211235	804.388645	402.697960	803.404629	402.205952	7
4	506.239795	253.623535	489.213246	245.110261			**F**	***724.362430***	362.684853	707.335881	354.171579	706.351865	353.679571	6
5	605.308209	303.157742	588.281660	294.644468			**V**	***577.294016***	289.150646	560.267467	280.637372	559.283451	280.145364	5
6	706.355888	353.681582	689.329339	345.168307	688.345323	344.676299	**T**	***478.225602***	239.616439	461.199053	231.103164	460.215037	230.611156	4
7	793.387916	397.197596	776.361367	388.684321	775.377351	388.192313	**S**	***377.177923***	189.092599	360.151374	180.579325	359.167358	180.087317	3
8	908.414859	454.711067	891.388310	446.197793	890.404294	445.705785	**D**	290.145895	145.576585	273.119346	137.063311	272.135330	136.571303	2
9							**R**	***175.118952***	88.063114	158.092403	79.549840			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.0	1081.519272	-0.001484	FNPFVTSDR
6.0	1081.522629	-0.004841	KPSMFDVSR
4.3	1081.519241	-0.001453	AAWYTIDSR
3.5	1081.522614	-0.004826	NMALEVFSR

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

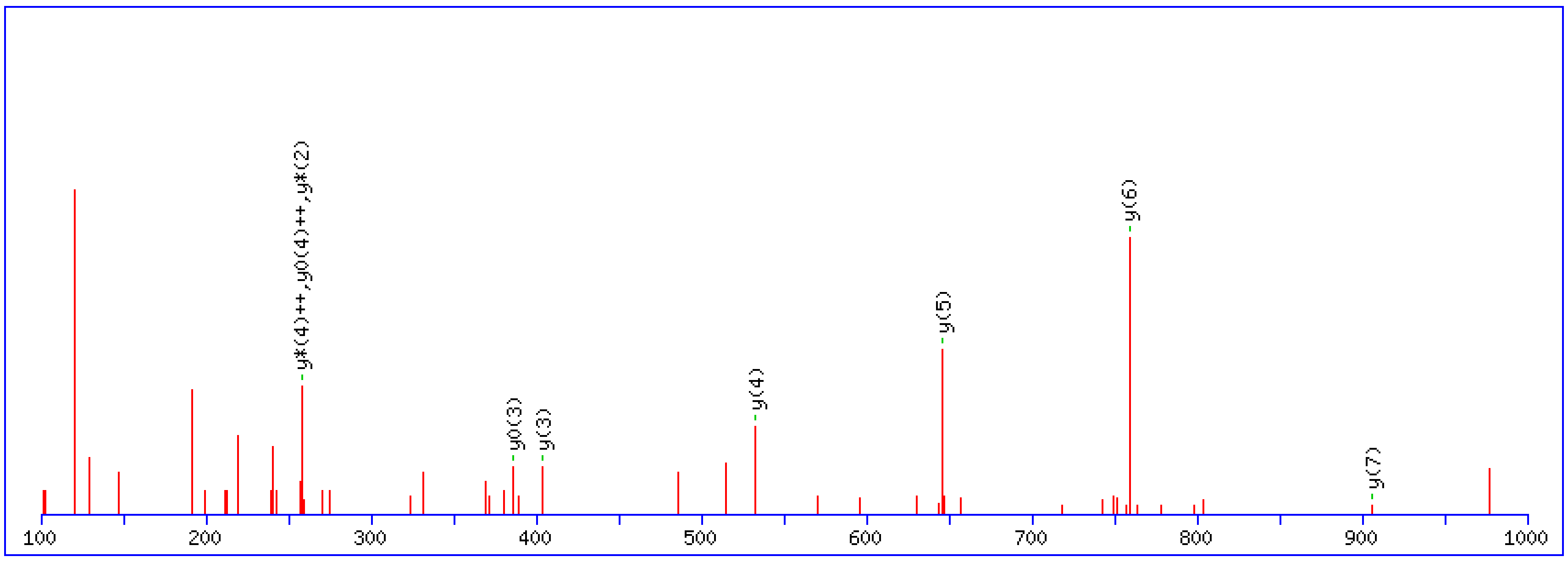
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AFLIEEQK**
Found in **RL34_HUMAN**, 60S ribosomal protein L34 OS=Homo sapiens GN=RPL34 PE=1 SV=3

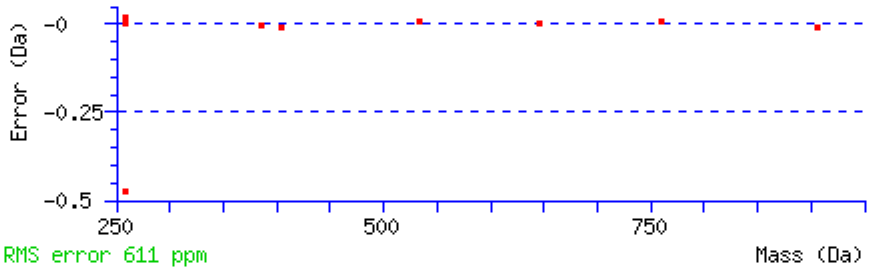
Match to Query 12053: 976.521788 from(489.268170,2+) rtinseconds(2014) index(23452)
Title: Locus:1.1.1.1156.15
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 1.mgf

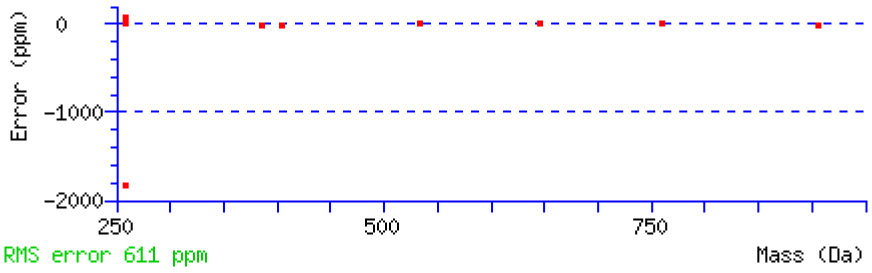
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 976.522919
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.00048
Matches : 9/60 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							8
2	219.112804	110.060040					F	***906.493110***	453.750193	889.466561	445.236919	888.482545	444.744911	7
3	332.196868	166.602072					L	***759.424696***	380.215986	742.398147	371.702712	741.414131	371.210704	6
4	445.280932	223.144104					I	***646.340632***	323.673954	629.314083	315.160680	628.330067	314.668672	5
5	574.323525	287.665401			556.312960	278.660118	E	***533.256568***	267.131922	516.230019	258.618648	515.246003	258.126640	4
6	703.366118	352.186697			685.355553	343.181415	E	***404.213975***	202.610626	387.187426	194.097351	386.203410	193.605343	3
7	831.424696	416.215986	814.398147	407.702712	813.414131	407.210704	Q	275.171382	138.089329	258.144833	129.576055			2
8							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of AFLIEEQK
(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	976.522919	-0.001131	AFLIEEQK
5.4	976.526276	-0.004488	MAEKILEK
2.1	976.520233	0.001555	AFSRNNLR
0.9	976.522934	-0.001146	SSFVAPLEK

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

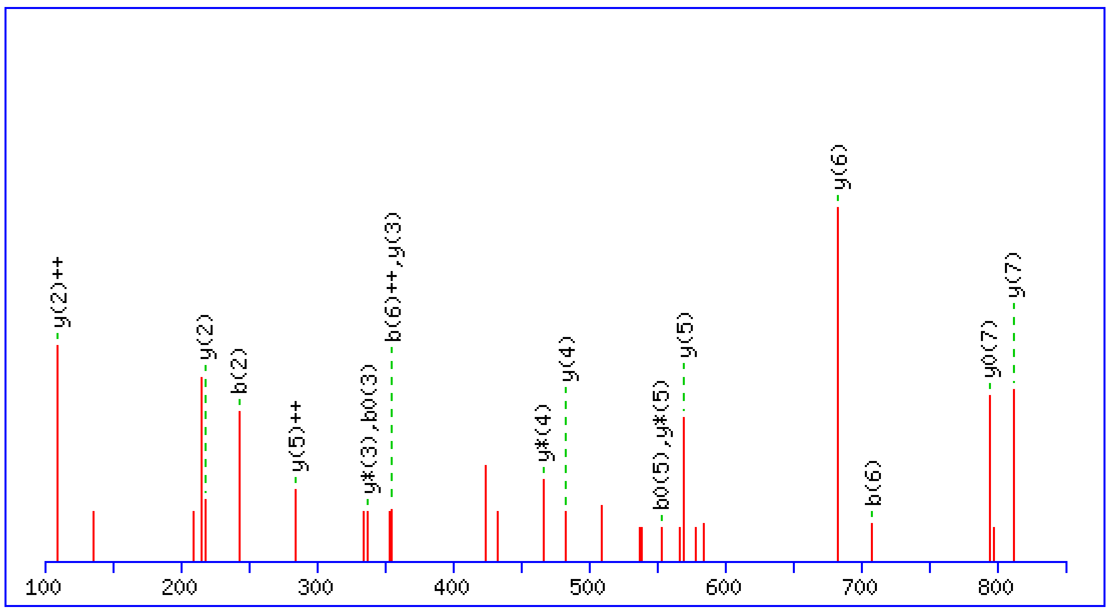
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IEISQHAK**
Found in **RL37A_HUMAN**, 60S ribosomal protein L37a OS=Homo sapiens GN=RPL37A PE=1 SV=2

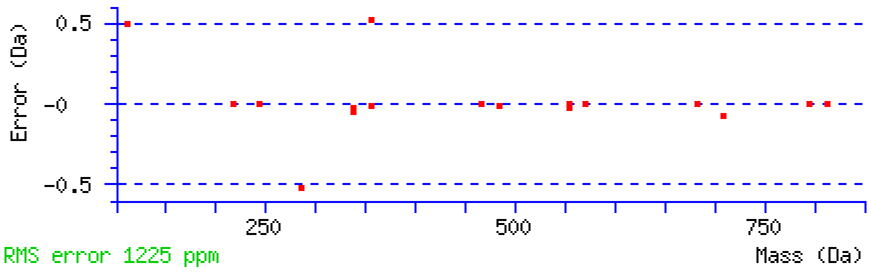
Match to Query 9779: 924.503308 from(463.258930,2+) rtinseconds(882) index(334)
Title: Locus:1.1.1.1786.3
Data file 2011-11-13 - TFD - EP 7-7.mgf

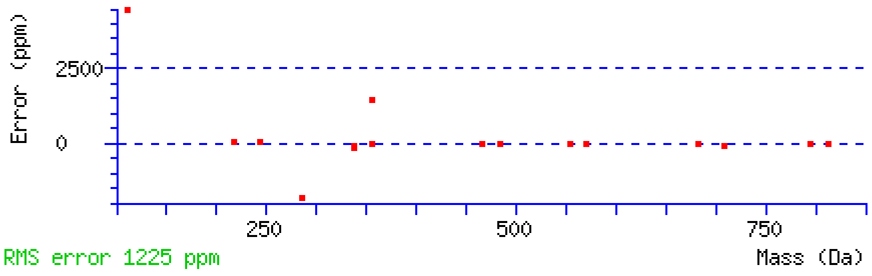
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 924.502853
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.00082
Matches : 17/66 fragment ions using 26 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					I							8
2	**243.133933**	122.070605			225.123368	113.065322	E	***812.426093***	406.716685	795.399544	398.203410	794.415528	397.711402	7
3	356.217997	178.612637			338.207432	169.607354	I	***683.383500***	342.195388	666.356951	333.682114	665.372935	333.190106	6
4	443.250025	222.128650			425.239460	213.123368	S	***570.299436***	285.653356	553.272887	277.140082	552.288871	276.648074	5
5	571.308603	286.157940	554.282054	277.644665	553.298038	277.152657	Q	***483.267408***	242.137342	466.240859	233.624067			4
6	**708.367515**	354.687396	691.340966	346.174121	690.356950	345.682113	H	***355.208830***	178.108053	338.182281	169.594778			3
7	779.404629	390.205953	762.378080	381.692678	761.394064	381.200670	A	***218.149918***	109.578597	201.123369	101.065322			2
8							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.7	924.502853	0.000455	IEISQHAK
7.3	924.502853	0.000455	LEVKASAAH
1.4	924.502869	0.000439	LEGVAAPPR
1.4	924.502869	0.000439	LEGVAAPPR
1.4	924.502853	0.000455	LERADPPK
1.3	924.502869	0.000439	AKGPSPPGAK
0.6	924.502869	0.000439	AKGPSPPGAK

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

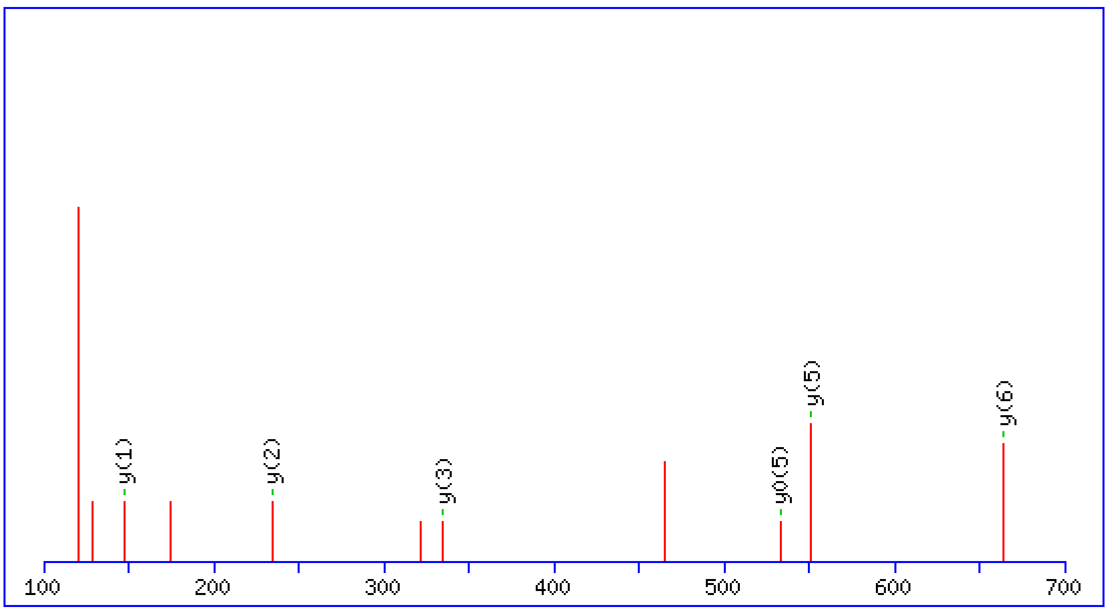
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FIDTTSK**
Found in **RL3L_HUMAN**, 60S ribosomal protein L3-like OS=Homo sapiens GN=RPL3L PE=1 SV=3

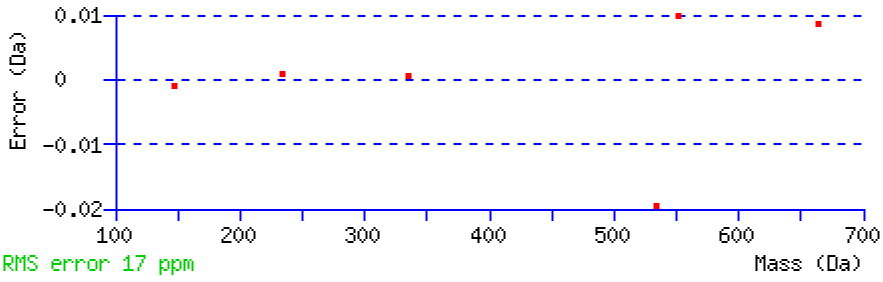
Match to Query 944: 810.413488 from(406.214020,2+) rtinseconds(994) index(3062)
Title: Locus:1.1.1.1813.3
Data file 2011-11-10 - TFD - EP 3-1.mgf

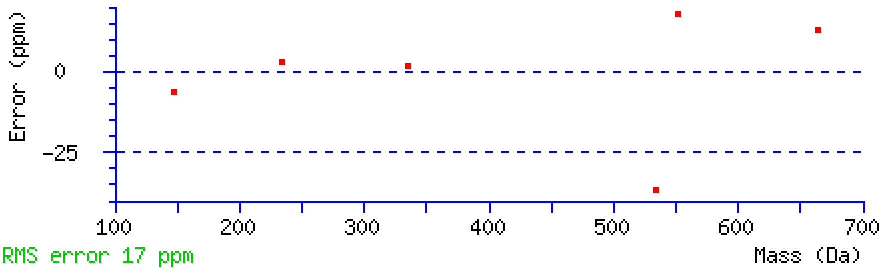
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 810.412338
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 40 **Expect:** 0.00075
Matches : 6/54 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	148.075690	74.541483			F							7
2	261.159754	131.083515			I	***664.351197***	332.679237	647.324648	324.165962	646.340632	323.673954	6
3	376.186697	188.596986	358.176132	179.591704	D	***551.267133***	276.137205	534.240584	267.623930	533.256568	267.131922	5
4	477.234376	239.120826	459.223811	230.115544	T	436.240190	218.623733	419.213641	210.110458	418.229625	209.618450	4
5	578.282055	289.644666	560.271490	280.639383	T	***335.192511***	168.099893	318.165962	159.586619	317.181946	159.094611	3
6	665.314083	333.160680	647.303518	324.155397	S	***234.144832***	117.576054	217.118283	109.062779	216.134267	108.570771	2
7					K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of FIDTTSK
(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	810.412338	0.001150	FIDTTSK
24.4	810.405807	0.007681	FLQTMR
9.6	810.405807	0.007681	FQLTMR
9.6	810.409164	0.004324	MKTLMR
9.3	810.417023	-0.003535	MLRGYR
8.8	810.405792	0.007696	FMETRK
8.8	810.412323	0.001165	FSELSTK
7.7	810.405807	0.007681	MGALTFR
7.4	810.412323	0.001165	LYSPTSK
5.7	810.405807	0.007681	LTGMAFR

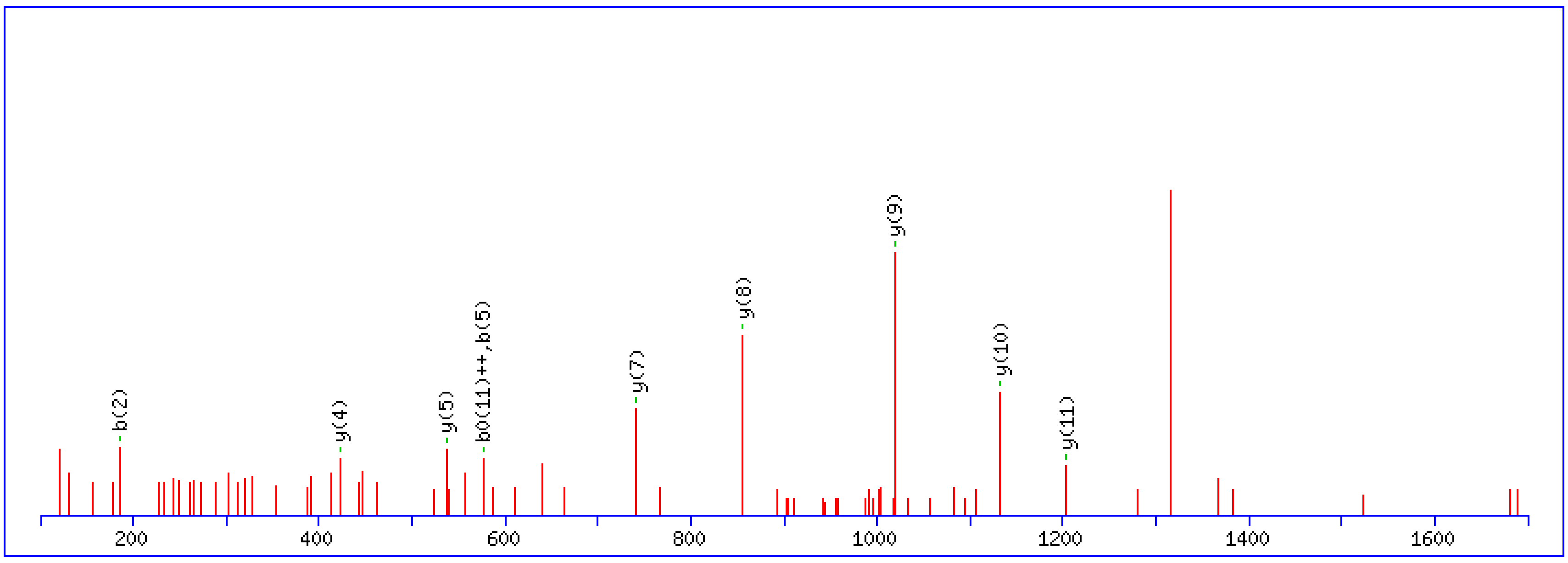
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LAIYDGFDGFAK**
Found in **K6PP_HUMAN**, 6-phosphofructokinase type C OS=Homo sapiens GN=PFKP PE=1 SV=2

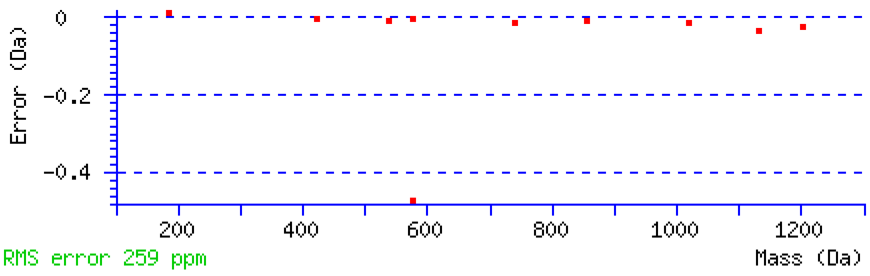
Match to Query 32523: 1315.632328 from(658.823440,2+) rtinseconds(3190) index(44985)
Title: Locus:1.1.1.1655.15
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 3.mgf

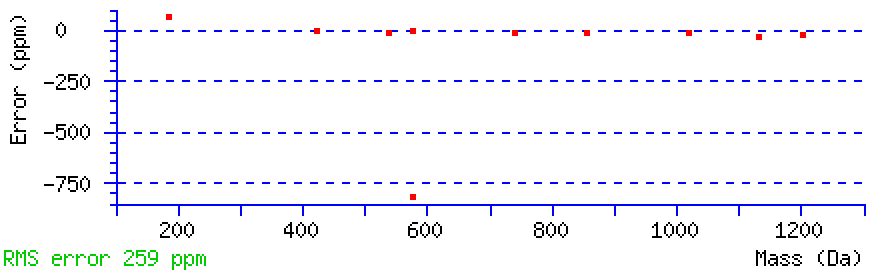
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1315.644852
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 38  Expect: 0.00035
Matches : 10/94 fragment ions using 23 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							12
2	**185.128454**	93.067865			A	***1203.568067***	602.287672	1186.541518	593.774397	1185.557502	593.282389	11
3	298.212518	149.609897			I	***1132.530953***	566.769115	1115.504404	558.255840	1114.520388	557.763832	10
4	461.275847	231.141561			Y	***1019.446889***	510.227083	1002.420340	501.713808	1001.436324	501.221800	9
5	**576.302790**	288.655033	558.292225	279.649751	D	***856.383560***	428.695418	839.357011	420.182144	838.372995	419.690136	8
6	633.324254	317.165765	615.313689	308.160483	G	***741.356617***	371.181947	724.330068	362.668672	723.346052	362.176664	7
7	780.392668	390.699972	762.382103	381.694690	F	684.335153	342.671215	667.308604	334.157940	666.324588	333.665932	6
8	895.419611	448.213444	877.409046	439.208161	D	***537.266739***	269.137008	520.240190	260.623733	519.256174	260.131725	5
9	952.441075	476.724176	934.430510	467.718893	G	***422.239796***	211.623536	405.213247	203.110261			4
10	1099.509489	550.258383	1081.498924	541.253100	F	365.218332	183.112804	348.191783	174.599529			3
11	1170.546603	585.776940	1152.536038	576.771657	A	218.149918	109.578597	201.123369	101.065322			2
12					K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.5	1315.644852	-0.012524	LAIYDGFDGFAK
0.7	1315.644180	-0.011852	LAEMPPSLDTSR

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

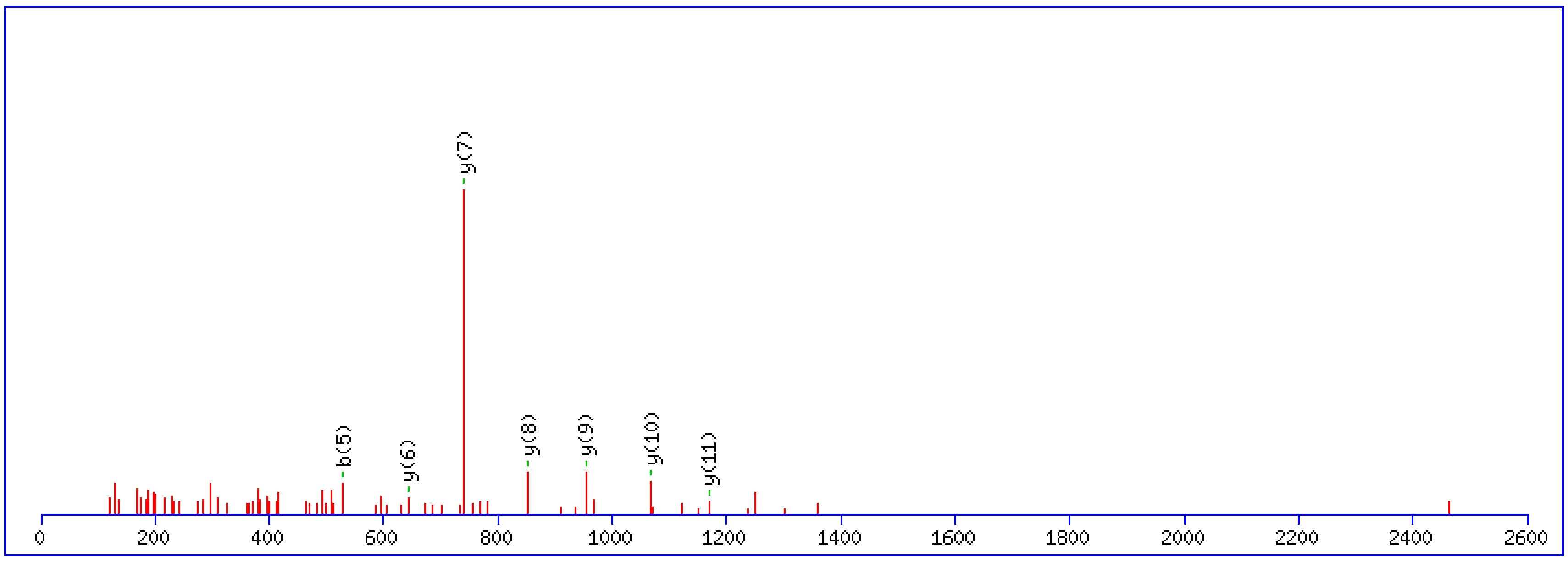
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VTLTLPVLNAAR**
Found in **6PGL_HUMAN**, 6-phosphogluconolactonase OS=Homo sapiens GN=PGLS PE=1 SV=2

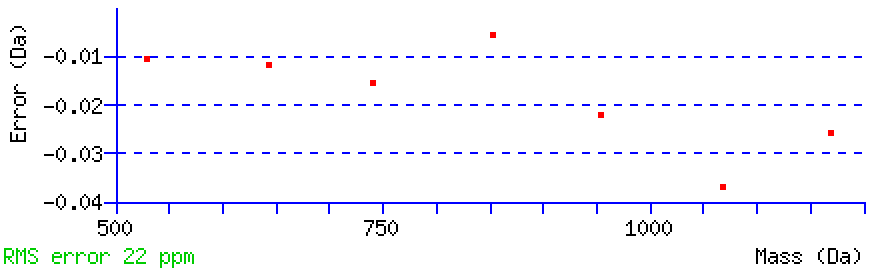
Match to Query 28985: 1266.759228 from(634.386890,2+) rtinseconds(3148) index(44191)
Title: Locus:1.1.1.1639.21
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 3.mgf

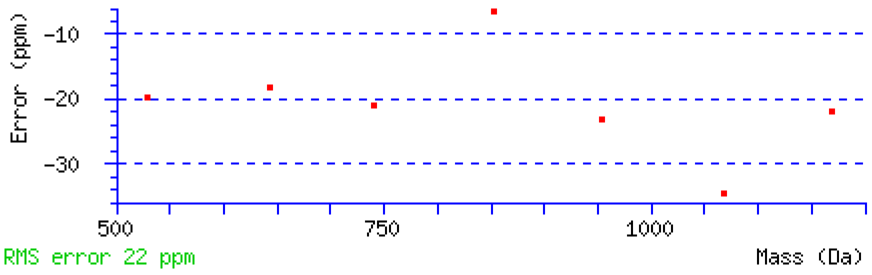
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1266.765961
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 40  Expect: 0.00018
Matches : 7/98 fragment ions using 12 most intense peaks   (help)
```

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	100.075690	50.541483					**V**							12
2	201.123369	101.065322			183.112804	92.060040	**T**	***1168.704835***	584.856056	1151.678286	576.342781	1150.694270	575.850773	11
3	314.207433	157.607354			296.196868	148.602072	**L**	***1067.657156***	534.332216	1050.630607	525.818942	1049.646591	525.326934	10
4	415.255112	208.131194			397.244547	199.125912	**T**	***954.573092***	477.790184	937.546543	469.276910	936.562527	468.784902	9
5	528.339176	264.673226			510.328611	255.667944	**L**	***853.525413***	427.266345	836.498864	418.753070			8
6	625.391940	313.199608			607.381375	304.194326	**P**	***740.441349***	370.724313	723.414800	362.211038			7
7	724.460354	362.733815			706.449789	353.728533	**V**	***643.388585***	322.197931	626.362036	313.684656			6
8	837.544418	419.275847			819.533853	410.270565	**L**	544.320171	272.663724	527.293622	264.150449			5
9	951.587345	476.297311	934.560796	467.784036	933.576780	467.292028	**N**	431.236107	216.121691	414.209558	207.608417			4
10	1022.624459	511.815868	1005.597910	503.302593	1004.613894	502.810585	**A**	317.193180	159.100228	300.166631	150.586953			3
11	1093.661573	547.334425	1076.635024	538.821150	1075.651008	538.329142	**A**	246.156066	123.581671	229.129517	115.068397			2
12							**R**	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.1	1266.765961	-0.006733	VTLTLPVLNAAR

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

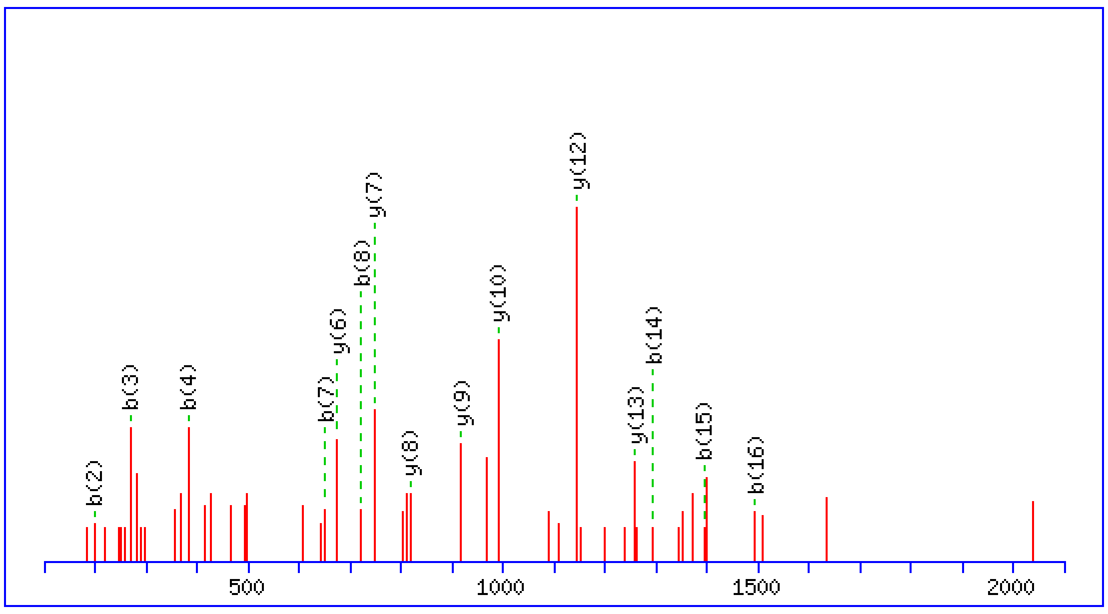
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVALIGVATAADTLVTK**
Found in **ABHDA_HUMAN**, Abhydrolase domain-containing protein 10, mitochondrial OS=Homo sapiens GN=ABHD10 PE=1 SV=1

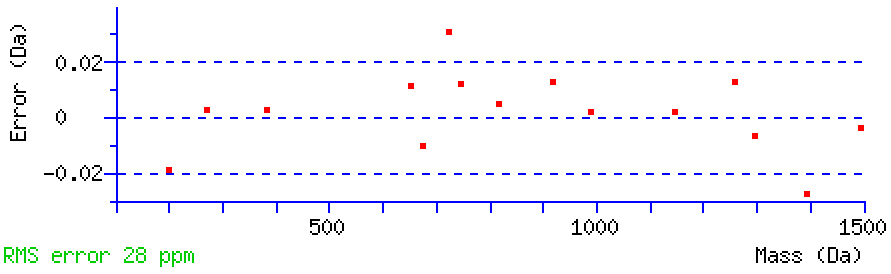
Match to Query 47988: 1640.975368 from(821.494960,2+) rtinseconds(3680) index(49831)
Title: Locus:1.1.1.2985.34
Data file 2011-11-12 - TFD - EP 5-5.mgf

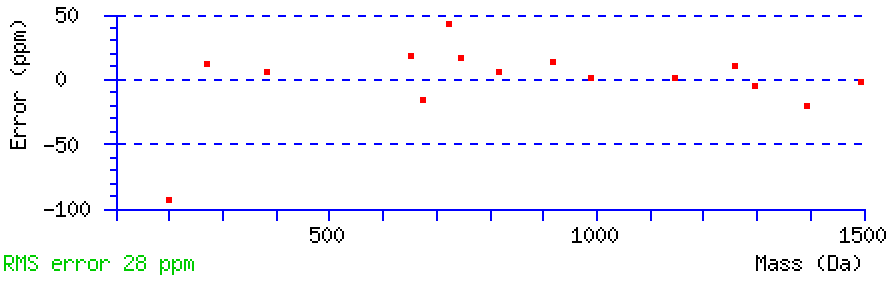
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1640.971283
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 50  Expect: 1.1e-005
Matches : 15/142 fragment ions using 37 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483			V							17
2	***199.144104***	100.075690			V	1542.910138	771.958707	1525.883589	763.445433	1524.899573	762.953424	16
3	***270.181218***	135.594247			A	1443.841724	722.424500	1426.815175	713.911226	1425.831159	713.419218	15
4	***383.265282***	192.136279			L	1372.804610	686.905943	1355.778061	678.392669	1354.794045	677.900660	14
5	496.349346	248.678311			I	***1259.720546***	630.363911	1242.693997	621.850637	1241.709981	621.358629	13
6	553.370810	277.189043			G	***1146.636482***	573.821879	1129.609933	565.308605	1128.625917	564.816597	12
7	***652.439224***	326.723250			V	1089.615018	545.311147	1072.588469	536.797873	1071.604453	536.305864	11
8	***723.476338***	362.241807			A	***990.546604***	495.776940	973.520055	487.263666	972.536039	486.771658	10
9	824.524017	412.765647	806.513452	403.760364	T	***919.509490***	460.258383	902.482941	451.745109	901.498925	451.253101	9
10	895.561131	448.284204	877.550566	439.278921	A	***818.461811***	409.734544	801.435262	401.221269	800.451246	400.729261	8
11	966.598245	483.802761	948.587680	474.797478	A	***747.424697***	374.215987	730.398148	365.702712	729.414132	365.210704	7
12	1081.625188	541.316232	1063.614623	532.310949	D	***676.387583***	338.697430	659.361034	330.184155	658.377018	329.692147	6
13	1182.672867	591.840072	1164.662302	582.834789	T	561.360640	281.183958	544.334091	272.670684	543.350075	272.178676	5
14	***1295.756931***	648.382103	1277.746366	639.376821	L	460.312961	230.660118	443.286412	222.146844	442.302396	221.654836	4
15	***1394.825345***	697.916311	1376.814780	688.911028	V	347.228897	174.118087	330.202348	165.604812	329.218332	165.112804	3
16	***1495.873024***	748.440150	1477.862459	739.434868	T	248.160483	124.583879	231.133934	116.070605	230.149918	115.578597	2
17					K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.7	1640.971283	0.004085	VVALIGVATAADTLVTK

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

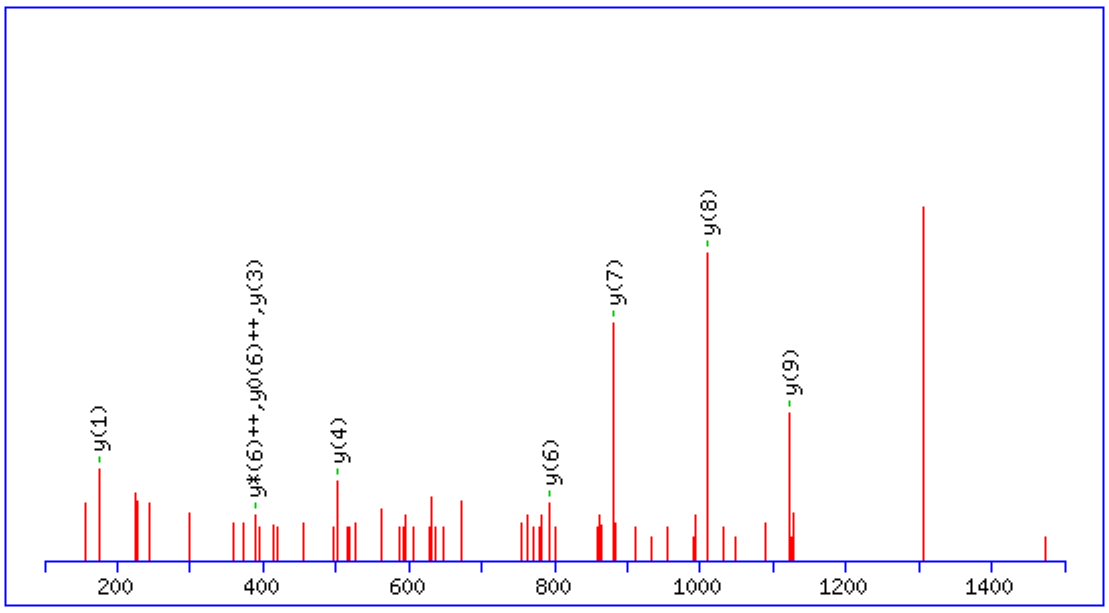
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALIESYQNLTR**
Found in **ABI1_HUMAN**, Abl interactor 1 OS=Homo sapiens GN=ABI1 PE=1 SV=4

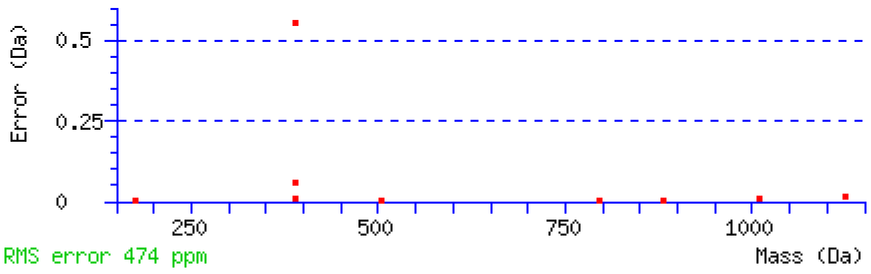
Match to Query 36725: 1306.697728 from(654.356140,2+) rtinseconds(2458) index(29767)
Title: Locus:1.1.1.2087.39
Data file 2011-11-12 - TFD - EP 6-6.mgf

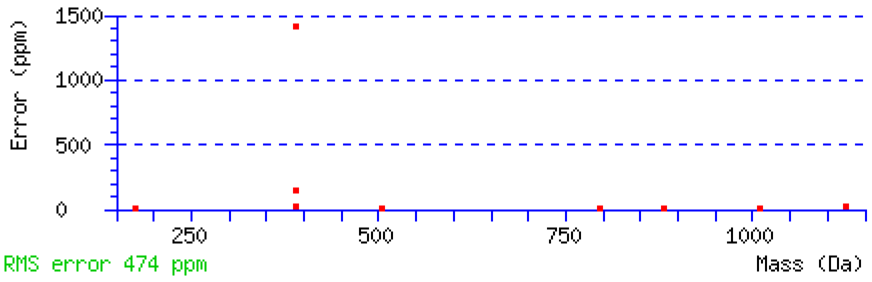
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1500] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1306.688080
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 57 **Expect:** 2e-005
Matches : 9/100 fragment ions using 10 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	72.044390	36.525833					A							11
2	185.128454	93.067865					L	1236.658278	618.832777	1219.631729	610.319503	1218.647713	609.827495	10
3	298.212518	149.609897					I	***1123.574214***	562.290745	1106.547665	553.777471	1105.563649	553.285462	9
4	427.255111	214.131193			409.244546	205.125911	E	***1010.490150***	505.748713	993.463601	497.235439	992.479585	496.743431	8
5	514.287139	257.647208			496.276574	248.641925	S	***881.447557***	441.227417	864.421008	432.714142	863.436992	432.222134	7
6	677.350468	339.178872			659.339903	330.173590	Y	***794.415529***	397.711403	777.388980	389.198128	776.404964	388.706120	6
7	805.409046	403.208161	788.382497	394.694887	787.398481	394.202879	Q	631.352200	316.179738	614.325651	307.666464	613.341635	307.174456	5
8	919.451973	460.229625	902.425424	451.716350	901.441408	451.224342	N	***503.293622***	252.150449	486.267073	243.637174	485.283057	243.145166	4
9	1032.536037	516.771657	1015.509488	508.258382	1014.525472	507.766374	L	***389.250695***	195.128985	372.224146	186.615711	371.240130	186.123703	3
10	1133.583716	567.295496	1116.557167	558.782222	1115.573151	558.290214	T	276.166631	138.586953	259.140082	130.073679	258.156066	129.581671	2
11							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.5	1306.688080	0.009648	ALIESYQNLTR
30.8	1306.699326	-0.001598	ALPESLGQHALR

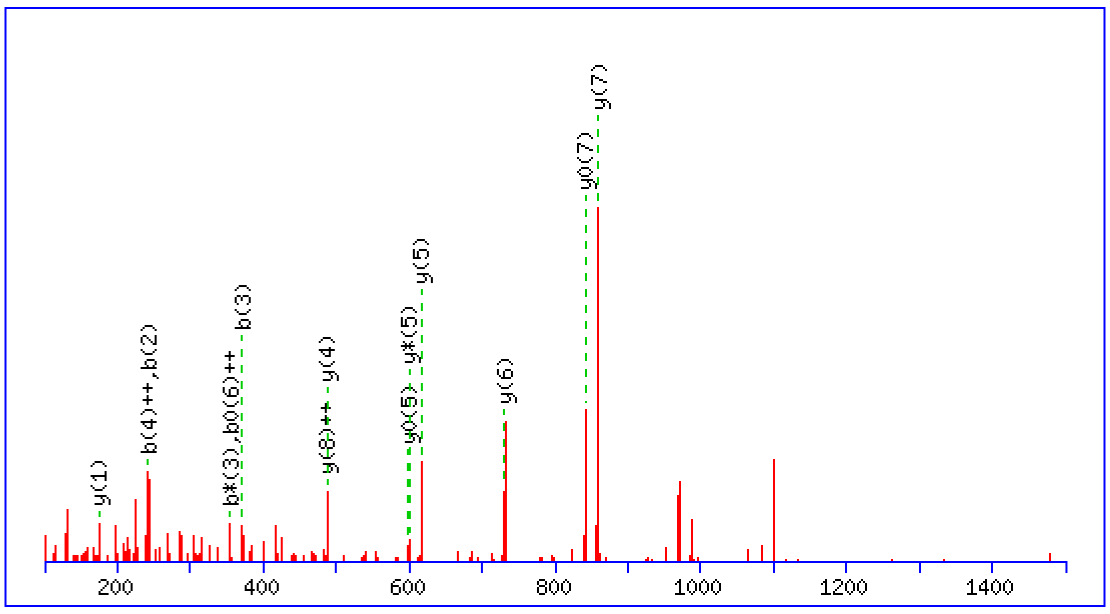
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **KLEIEIEAR**
Found in **ASPM_HUMAN**, Abnormal spindle-like microcephaly-associated protein OS=Homo sapiens GN=ASPM PE=1 SV=2

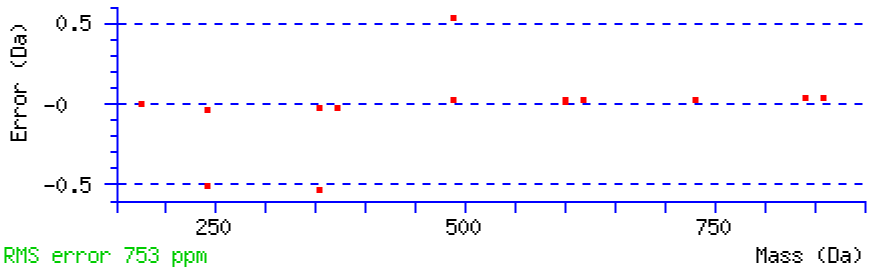
Match to Query 19510: 1099.628008 from(550.821280,2+) rtinseconds(1875) index(20826)
Title: Locus:1.1.1.2131.31
Data file 2011-11-10 - TFD - EP 3-3.mgf

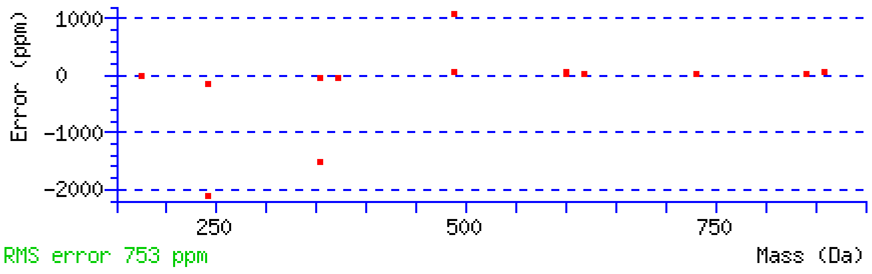
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1099.623672
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.0089
Matches : 14/88 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	129.102239	65.054757	112.075690	56.541483			K							9
2	**242.186303**	121.596790	225.159754	113.083515			L	972.536037	486.771657	955.509488	478.258382	954.525472	477.766374	8
3	**371.228896**	186.118086	354.202347	177.604812	353.218331	177.112804	E	***859.451973***	430.229625	842.425424	421.716350	841.441408	421.224342	7
4	484.312960	242.660118	467.286411	234.146844	466.302395	233.654836	I	***730.409380***	365.708328	713.382831	357.195054	712.398815	356.703046	6
5	613.355553	307.181415	596.329004	298.668140	595.344988	298.176132	E	***617.325316***	309.166296	600.298767	300.653022	599.314751	300.161014	5
6	726.439617	363.723447	709.413068	355.210172	708.429052	354.718164	I	***488.282723***	244.644999	471.256174	236.131725	470.272158	235.639717	4
7	855.482210	428.244743	838.455661	419.731469	837.471645	419.239461	E	375.198659	188.102967	358.172110	179.589693	357.188094	179.097685	3
8	926.519324	463.763300	909.492775	455.250026	908.508759	454.758018	A	246.156066	123.581671	229.129517	115.068396			2
9							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.9	1099.623672	0.004336	KLEIEIEAR
16.5	1099.634918	-0.006910	LKQENLSLR
15.1	1099.631073	-0.003065	LEELMKPLK
14.9	1099.634933	-0.006925	IQPLAKATSR
14.6	1099.634918	-0.006910	LGKALENLSR
13.6	1099.623703	0.004305	KPQLLEQTK
12.0	1099.634933	-0.006925	IQERVSKPK
11.4	1099.623703	0.004305	ELQKVQDIK
9.3	1099.638962	-0.010954	KLQIYGPGPK
9.0	1099.623688	0.004320	QLKNLVEEK

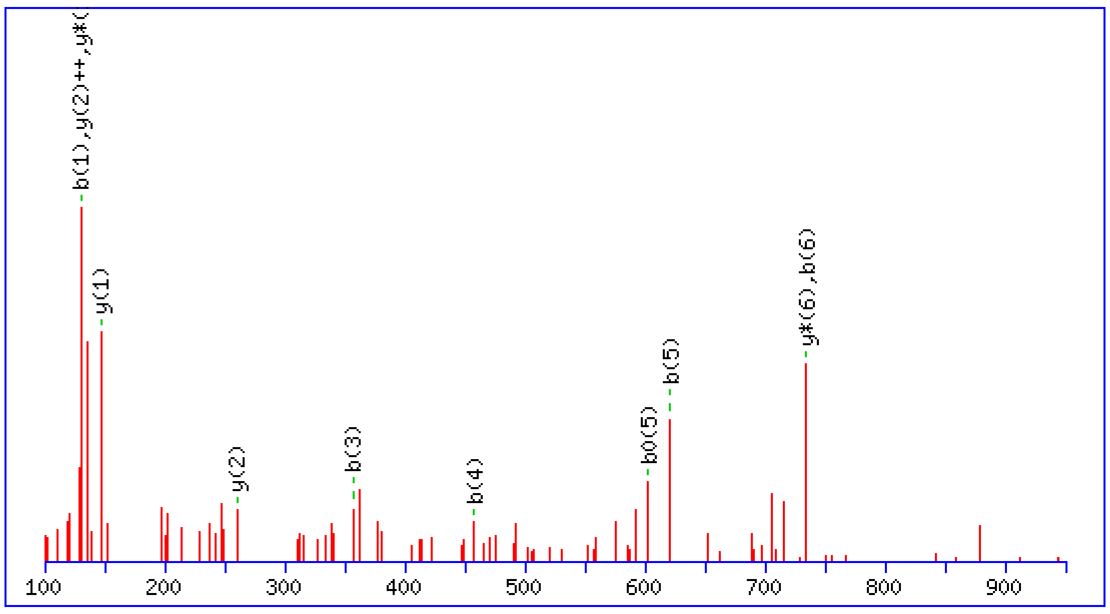
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ENITYLK**
Found in **ACACB_HUMAN**, Acetyl-CoA carboxylase 2 OS=Homo sapiens GN=ACACB PE=1 SV=3

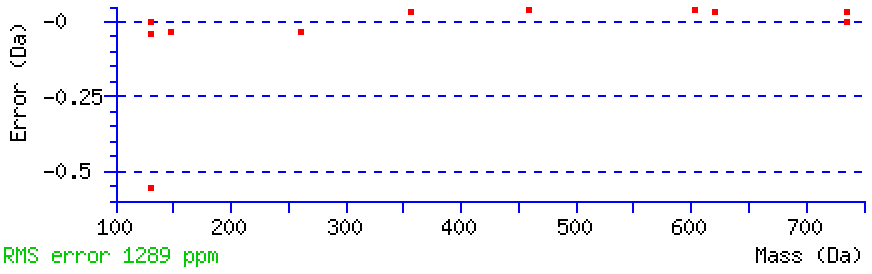
Match to Query 5970: 879.471648 from(440.743100,2+) rtinseconds(1790) index(19037)
Title: Locus:1.1.1.2010.8
Data file 2011-11-10 - TFD - EP 4-4.mgf

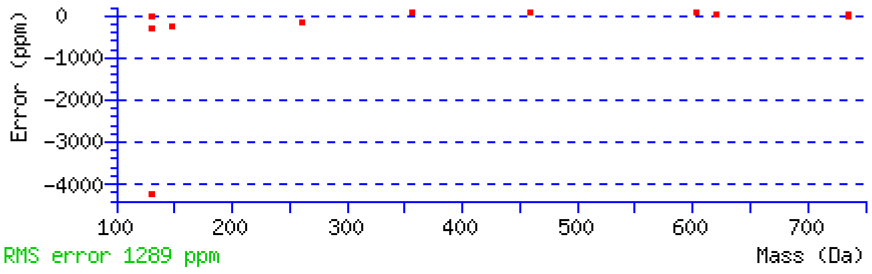
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 879.470154
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 30  Expect: 0.0068
Matches : 11/64 fragment ions using 16 most intense peaks   (help)
```

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	***130.049869***	65.528572			112.039304	56.523290	**E**							7
2	244.092796	122.550036	227.066247	114.036762	226.082231	113.544754	**N**	751.434867	376.221072	734.408318	367.707797	733.424302	367.215789	6
3	***357.176860***	179.092068	340.150311	170.578794	339.166295	170.086786	**I**	637.391940	319.199608	620.365391	310.686334	619.381375	310.194326	5
4	***458.224539***	229.615908	441.197990	221.102633	440.213974	220.610625	**T**	524.307876	262.657576	507.281327	254.144302	506.297311	253.652294	4
5	***621.287868***	311.147572	604.261319	302.634298	603.277303	302.142290	**Y**	423.260197	212.133737	406.233648	203.620462			3
6	***734.371932***	367.689604	717.345383	359.176330	716.361367	358.684322	**L**	**260.196868**	130.602072	243.170319	122.088798			2
7							**K**	**147.112804**	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.2	879.470154	0.001494	ENITYLK
22.8	879.470169	0.001479	KLDTYLQ
22.8	879.470154	0.001494	EQLSYLK
22.5	879.470154	0.001494	ENTIYLK
12.8	879.470154	0.001494	KSPEYLK
12.8	879.470154	0.001494	QLSEYLK
12.6	879.470169	0.001479	APEPLPPK
11.5	879.470169	0.001479	APEPLPPK
11.1	879.470184	0.001464	VDFASTLK
11.0	879.470184	0.001464	SSSFVLPK

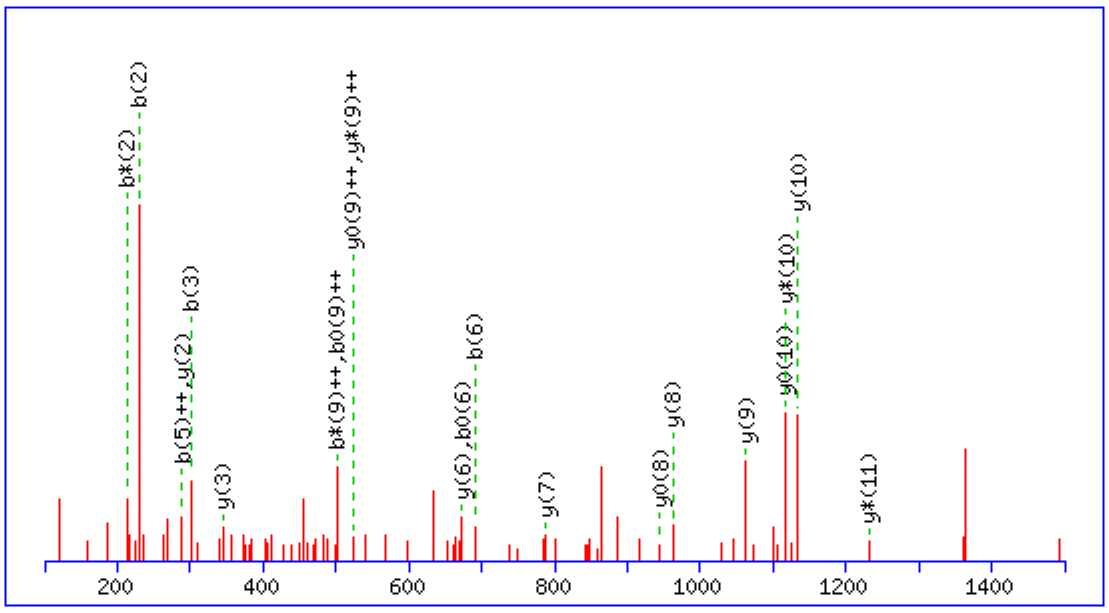
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DNATCDGPCGLR**
Found in **ACRO_HUMAN**, Acrosin OS=Homo sapiens GN=ACR PE=2 SV=4

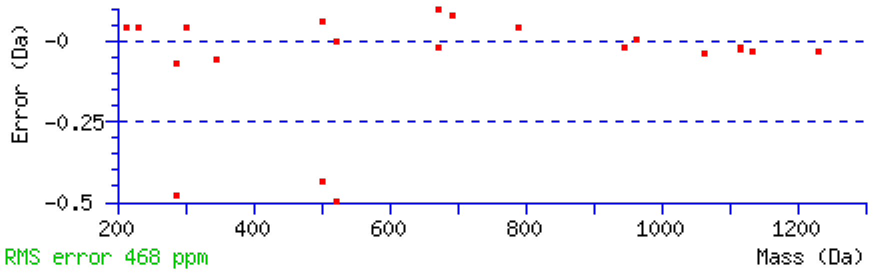
Match to Query 33080: 1362.570968 from(682.292760,2+) rtinseconds(2030) index(23357)
Title: Locus:1.1.1.2261.41
Data file 2011-11-10 - TFD - EP 4-3.mgf

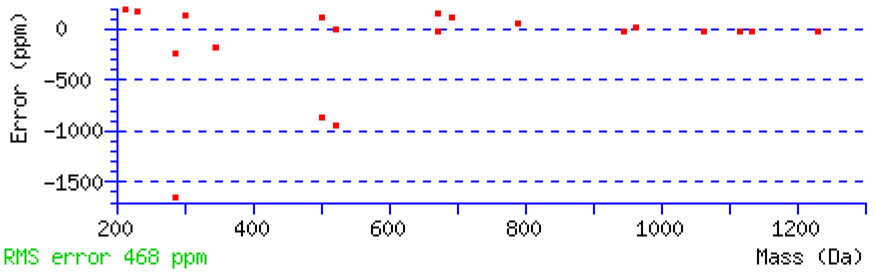
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1362.565628
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 37 **Expect:** 0.00056
Matches : 21/118 fragment ions using 33 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	116.034219	58.520748			98.023654	49.515465	D							12
2	**230.077146**	115.542211	213.050597	107.028937	212.066581	106.536928	N	1248.545969	624.776622	1231.519420	616.263348	1230.535404	615.771340	11
3	**301.114260**	151.060768	284.087711	142.547494	283.103695	142.055486	A	***1134.503042***	567.755159	1117.476493	559.241884	1116.492477	558.749876	10
4	402.161939	201.584608	385.135390	193.071333	384.151374	192.579325	T	***1063.465928***	532.236602	1046.439379	523.723327	1045.455363	523.231319	9
5	576.208238	288.607757	559.181689	280.094483	558.197673	279.602475	C	***962.418249***	481.712762	945.391700	473.199488	944.407684	472.707480	8
6	**691.235181**	346.121229	674.208632	337.607954	673.224616	337.115946	D	***788.371950***	394.689613	771.345401	386.176338	770.361385	385.684330	7
7	748.256645	374.631961	731.230096	366.118686	730.246080	365.626678	G	***673.345007***	337.176141	656.318458	328.662867			6
8	845.309409	423.158343	828.282860	414.645068	827.298844	414.153060	P	616.323543	308.665409	599.296994	300.152135			5
9	1019.355708	510.181492	1002.329159	501.668218	1001.345143	501.176210	C	519.270779	260.139027	502.244230	251.625753			4
10	1076.377172	538.692224	1059.350623	530.178950	1058.366607	529.686941	G	***345.224480***	173.115878	328.197931	164.602603			3
11	1189.461236	595.234256	1172.434687	586.720981	1171.450671	586.228973	L	***288.203016***	144.605146	271.176467	136.091871			2
12							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.2	1362.565628	0.005340	DNATCDGPCGLR

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

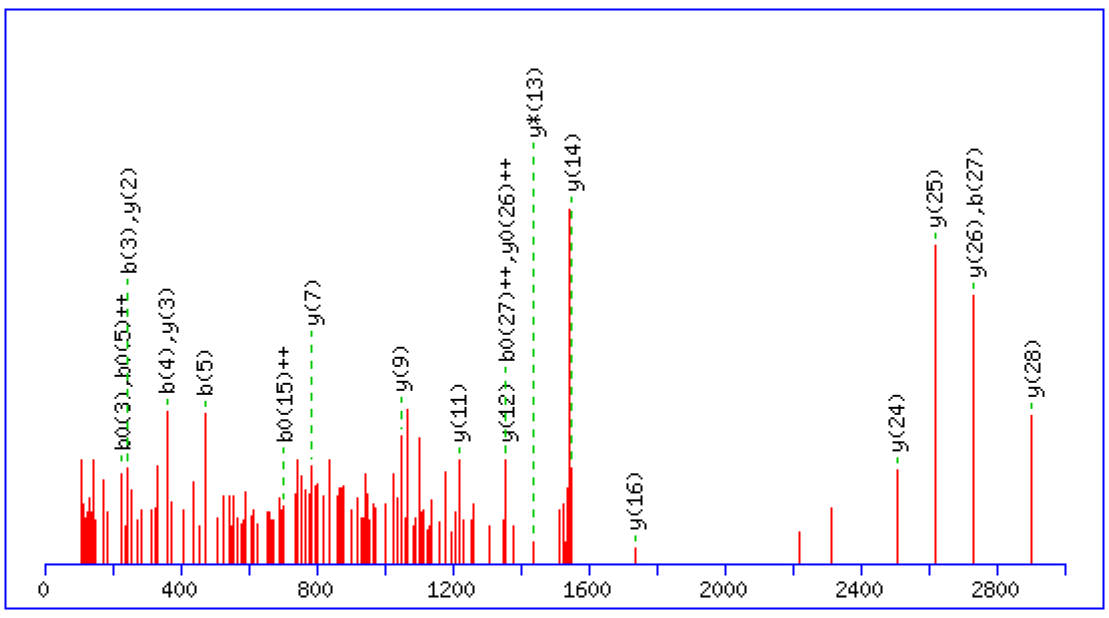
Mascot Search Results

Peptide View

MS/MS Fragmentation of **STGLILDSGATHTTAIPVHDGYVLQQGIVK**
Found in **ACL6A_HUMAN**, Actin-like protein 6A OS=Homo sapiens GN=ACTL6A PE=1 SV=1

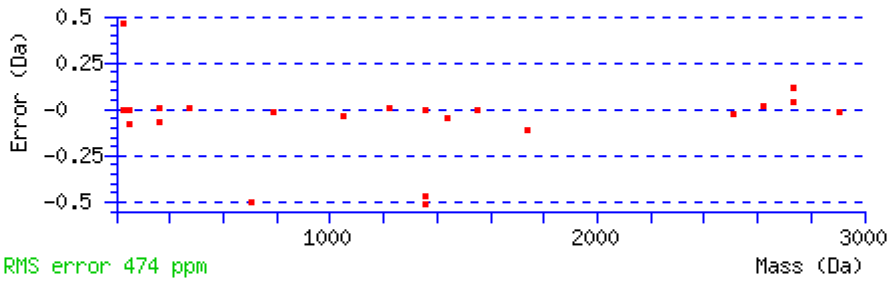
Match to Query 80891: 3090.635376 from(773.666120,4+) rtinseconds(2899) index(39274)
Title: Locus:1.1.1.2618.37
Data file 2011-11-12 - TFD - EP 5-3.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●

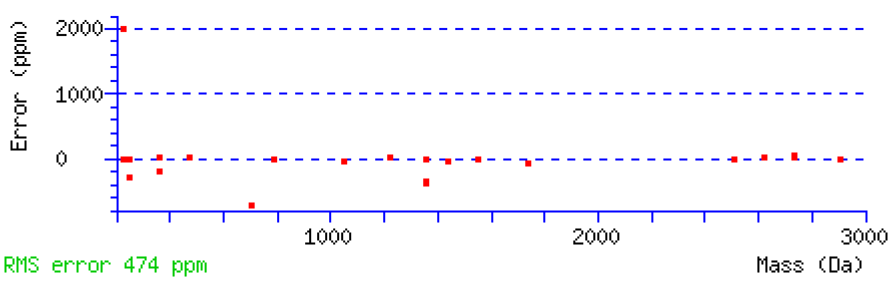


```
Monoisotopic mass of neutral peptide Mr(calc): 3090.634995
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 56  Expect: 5.9e-006
Matches : 22/280 fragment ions using 36 most intense peaks   (help)
```

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							30
2	189.086983	95.047129			171.076418	86.041847	T	3004.610217	1502.808746	2987.583668	1494.295472	2986.599652	1493.803464	29
3	**246.108447**	123.557861			228.097882	114.552579	G	***2903.562538***	1452.284907	2886.535989	1443.771632	2885.551973	1443.279624	28
4	**359.192511**	180.099893			341.181946	171.094611	L	2846.541074	1423.774175	2829.514525	1415.260900	2828.530509	1414.768892	27
5	**472.276575**	236.641925			454.266010	227.636643	I	***2733.457010***	1367.232143	2716.430461	1358.718868	2715.446445	1358.226860	26
6	585.360639	293.183958			567.350074	284.178675	L	***2620.372946***	1310.690111	2603.346397	1302.176836	2602.362381	1301.684828	25
7	700.387582	350.697429			682.377017	341.692146	D	***2507.288882***	1254.148079	2490.262333	1245.634804	2489.278317	1245.142796	24
8	787.419610	394.213443			769.409045	385.208160	S	2392.261939	1196.634607	2375.235390	1188.121333	2374.251374	1187.629325	23
9	844.441074	422.724175			826.430509	413.718892	G	2305.229911	1153.118593	2288.203362	1144.605319	2287.219346	1144.113311	22
10	915.478188	458.242732			897.467623	449.237449	A	2248.208447	1124.607861	2231.181898	1116.094587	2230.197882	1115.602579	21
11	1016.525867	508.766572			998.515302	499.761289	T	2177.171333	1089.089304	2160.144784	1080.576030	2159.160768	1080.084022	20
12	1153.584779	577.296028			1135.574214	568.290745	H	2076.123654	1038.565465	2059.097105	1030.052190	2058.113089	1029.560182	19
13	1254.632458	627.819867			1236.621893	618.814585	T	1939.064742	970.036009	1922.038193	961.522735	1921.054177	961.030727	18
14	1355.680137	678.343707			1337.669572	669.338424	T	1838.017063	919.512170	1820.990514	910.998895	1820.006498	910.506887	17
15	1426.717251	713.862264			1408.706686	704.856981	A	***1736.969384***	868.988330	1719.942835	860.475056	1718.958819	859.983048	16
16	1539.801315	770.404295			1521.790750	761.399013	I	1665.932270	833.469773	1648.905721	824.956499	1647.921705	824.464491	15
17	1636.854079	818.930678			1618.843514	809.925395	P	***1552.848206***	776.927741	1535.821657	768.414467	1534.837641	767.922459	14
18	1735.922493	868.464885			1717.911928	859.459602	V	1455.795442	728.401359	1438.768893	719.888085	1437.784877	719.396077	13
19	1872.981405	936.994341			1854.970840	927.989058	H	***1356.727028***	678.867152	1339.700479	670.353878	1338.716463	669.861870	12
20	1988.008348	994.507812			1969.997783	985.502530	D	***1219.668116***	610.337696	1202.641567	601.824422	1201.657551	601.332414	11
21	2045.029812	1023.018544			2027.019247	1014.013262	G	1104.641173	552.824225	1087.614624	544.310950			10
22	2208.093141	1104.550208			2190.082576	1095.544926	Y	***1047.619709***	524.313493	1030.593160	515.800218			9
23	2307.161555	1154.084415			2289.150990	1145.079133	V	884.556380	442.781828	867.529831	434.268554			8
24	2420.245619	1210.626447			2402.235054	1201.621165	L	***785.487966***	393.247621	768.461417	384.734347			7
25	2548.304197	1274.655736	2531.277648	1266.142462	2530.293632	1265.650454	Q	672.403902	336.705589	655.377353	328.192315			6
26	2676.362775	1338.685025	2659.336226	1330.171751	2658.352210	1329.679743	Q	544.345324	272.676300	527.318775	264.163026			5
27	**2733.384239**	1367.195757	2716.357690	1358.682483	2715.373674	1358.190475	G	416.286746	208.647011	399.260197	200.133736			4
28	2846.468303	1423.737790	2829.441754	1415.224515	2828.457738	1414.732507	I	***359.265282***	180.136279	342.238733	171.623004			3
29	2945.536717	1473.271996	2928.510168	1464.758722	2927.526152	1464.266714	V	***246.181218***	123.594247	229.154669	115.080972			2
30							K	147.112804	74.060040	130.086255	65.546765			1



RMS error 474 ppm



RMS error 474 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.9	3090.634995	0.000381	STGLILDSGATHTTAIPVHDGYVLQQGIVK
0.1	3090.621216	0.014160	EGVWILVSMDRPWEASPSVHILTEVLK

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

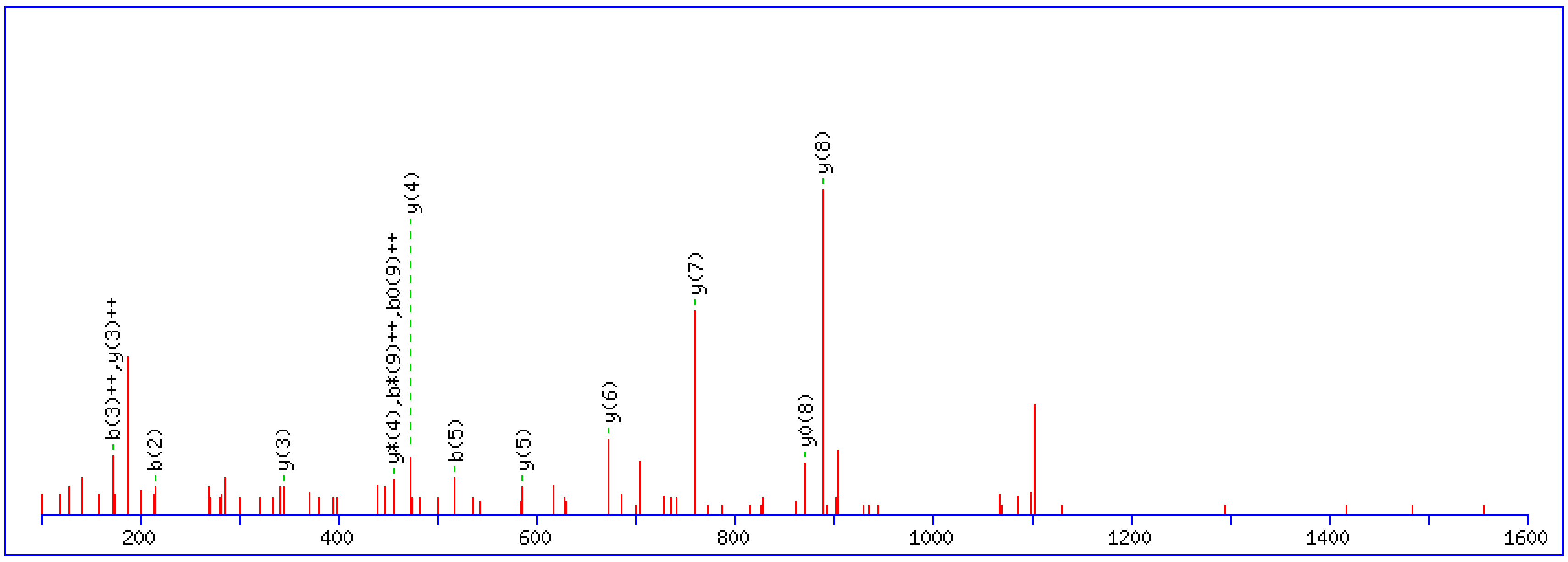
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLESSIQGLR**
Found in **ARC1A_HUMAN**, Actin-related protein 2/3 complex subunit 1A OS=Homo sapiens GN=ARPC1A PE=1 SV=2

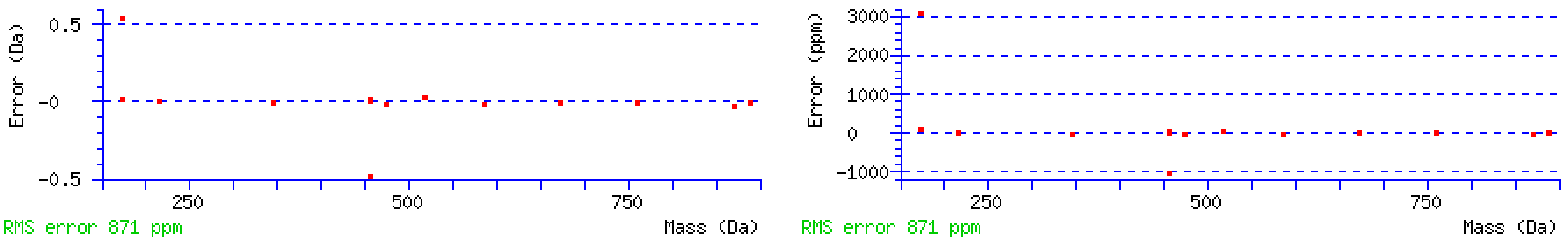
Match to Query 15219: 1102.595748 from(552.305150,2+) rtinseconds(2239) index(27224)
Title: Locus:1.1.1.1234.15
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 2.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1102.598221
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 38 **Expect:** 0.0018
Matches : 14/86 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							10
2	**215.139019**	108.073147			197.128454	99.067865	L	1002.557835	501.782556	985.531286	493.269281	984.547270	492.777273	9
3	344.181612	172.594444			326.171047	163.589162	E	***889.473771***	445.240524	872.447222	436.727249	871.463206	436.235241	8
4	431.213640	216.110458			413.203075	207.105176	S	***760.431178***	380.719227	743.404629	372.205953	742.420613	371.713945	7
5	**518.245668**	259.626472			500.235103	250.621190	S	***673.399150***	337.203213	656.372601	328.689939	655.388585	328.197931	6
6	631.329732	316.168504			613.319167	307.163222	I	***586.367122***	293.687199	569.340573	285.173925			5
7	759.388310	380.197793	742.361761	371.684519	741.377745	371.192511	Q	***473.283058***	237.145167	456.256509	228.631892			4
8	816.409774	408.708525	799.383225	400.195251	798.399209	399.703243	G	***345.224480***	173.115878	328.197931	164.602603			3
9	929.493838	465.250557	912.467289	456.737283	911.483273	456.245275	L	288.203016	144.605146	271.176467	136.091871			2
10							R	175.118952	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.9	1102.598221	-0.002473	TLESSIQGLR
8.3	1102.598221	-0.002473	TLESQLASVR
1.3	1102.598206	-0.002458	SISIETANLR

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

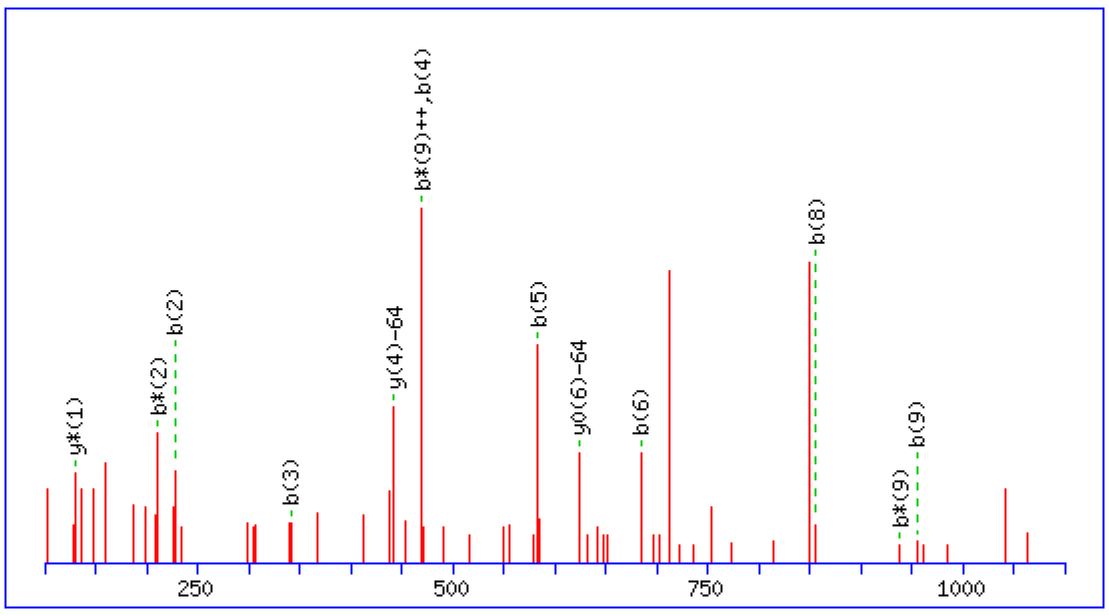
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **KVIELTGDVTPDMK**
Found in **HELC1_HUMAN**, Activating signal cointegrator 1 complex subunit 3 OS=Homo sapiens GN=ASCC3 PE=1 SV=3

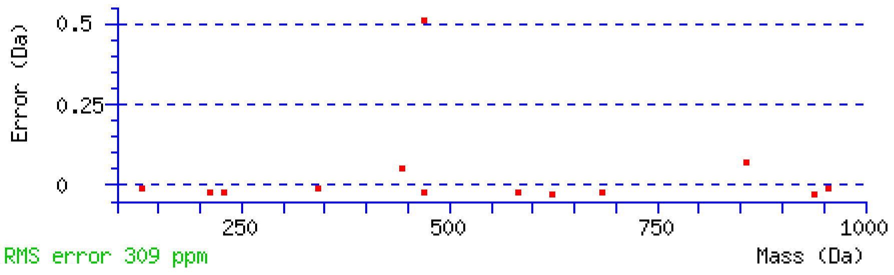
Match to Query 47812: 1560.795702 from(521.272510,3+) rtinseconds(2663) index(33849)
Title: Locus:1.1.1.2335.10
Data file 2011-11-14 - TFD - EP 8-5.mgf

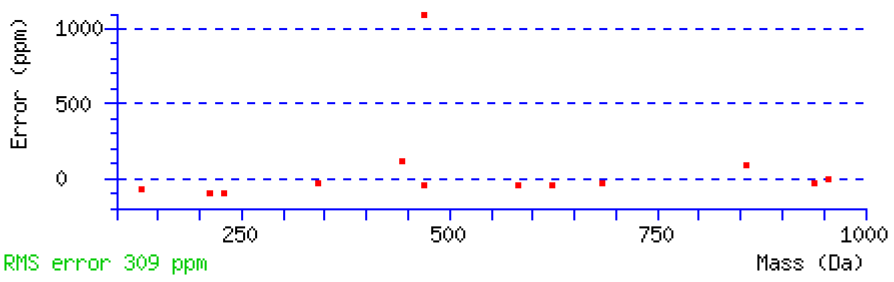
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1560.806915
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M13 : Oxidation (M), with neutral losses 63.998285(shown in table), 0.000000
Ions Score: 36 **Expect:** 0.00089
Matches : 13/222 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	129.102239	65.054757	112.075690	56.541483			**K**							**14**
2	***228.170653***	114.588965	211.144104	106.075690			**V**	1369.720940	685.364108	1352.694391	676.850834	1351.710375	676.358826	**13**
3	***341.254717***	171.130997	324.228168	162.617722			**I**	1270.652526	635.829901	1253.625977	627.316627	1252.641961	626.824619	**12**
4	***470.297310***	235.652293	453.270761	227.139019	452.286745	226.647011	**E**	1157.568462	579.287869	1140.541913	570.774595	1139.557897	570.282587	**11**
5	***583.381374***	292.194325	566.354825	283.681051	565.370809	283.189043	**L**	1028.525869	514.766573	1011.499320	506.253298	1010.515304	505.761290	**10**
6	***684.429053***	342.718165	667.402504	334.204890	666.418488	333.712882	**T**	915.441805	458.224541	898.415256	449.711266	897.431240	449.219258	**9**
7	741.450517	371.228897	724.423968	362.715622	723.439952	362.223614	**G**	814.394126	407.700701	797.367577	399.187427	796.383561	398.695419	**8**
8	***856.477460***	428.742368	839.450911	420.229094	838.466895	419.737086	**D**	757.372662	379.189969	740.346113	370.676695	739.362097	370.184687	**7**
9	***955.545874***	478.276575	938.519325	469.763301	937.535309	469.271293	**V**	642.345719	321.676498	625.319170	313.163223	624.335154	312.671215	**6**
10	1056.593553	528.800414	1039.567004	520.287140	1038.582988	519.795132	**T**	543.277305	272.142291	526.250756	263.629016	525.266740	263.137008	**5**
11	1153.646317	577.326797	1136.619768	568.813522	1135.635752	568.321514	**P**	442.229626	221.618451	425.203077	213.105177	424.219061	212.613169	**4**
12	1268.673260	634.840268	1251.646711	626.326994	1250.662695	625.834986	**D**	345.176862	173.092069	328.150313	164.578795	327.166297	164.086787	**3**
13	1351.710375	676.358826	1334.683826	667.845551	1333.699810	667.353543	**M**	230.149919	115.578597	213.123370	107.065323			**2**
14							**K**	147.112804	74.060040	130.086255	65.546765			**1**





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.8	1560.806915	-0.011213	KVIELTGDVTPDMK
34.5	1560.806915	-0.011213	KVIELTGDVTPDMK
34.4	1560.793594	0.002108	ARLEIEPEWAYGK
3.1	1560.804199	-0.008497	INLNESMQVVSRR
0.4	1560.783081	0.012621	KPRCGVPDVANYR

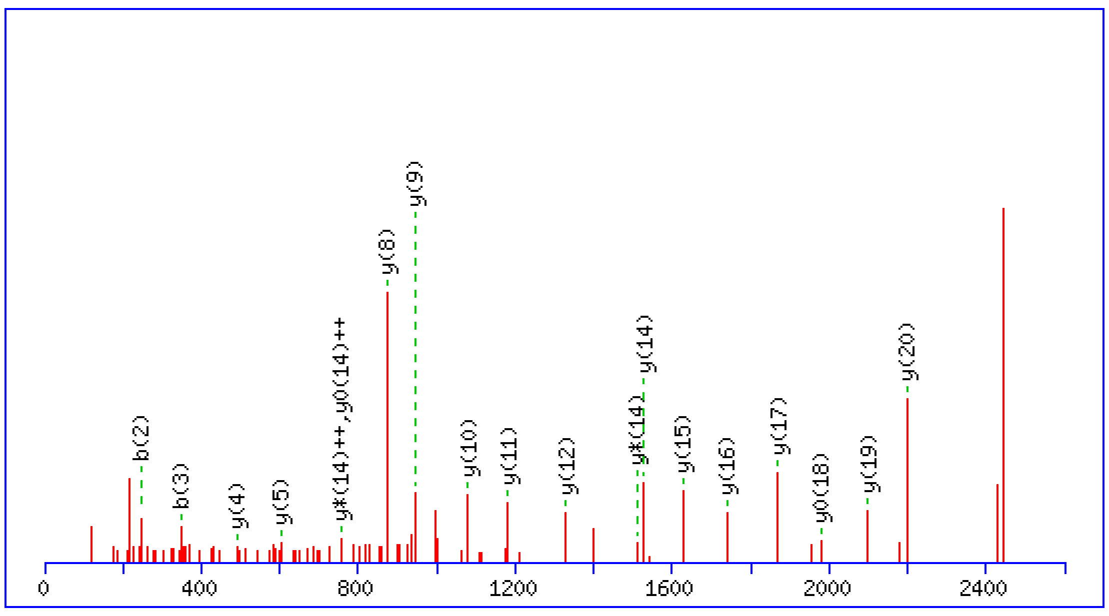
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VFTTQELVQAFTHAPATLEADR**
Found in **AHSA1_HUMAN**, Activator of 90 kDa heat shock protein ATPase homolog 1 OS=Homo sapiens GN=AHSA1 PE=1 SV=1

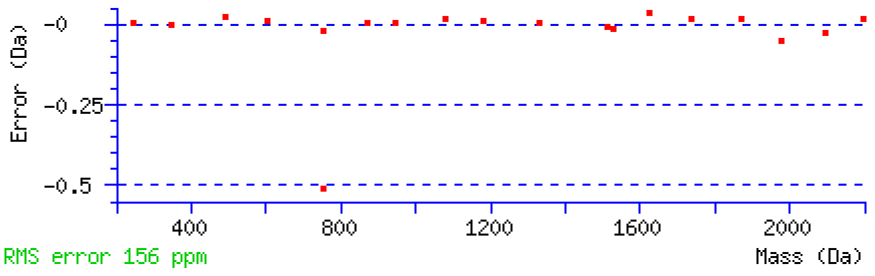
Match to Query 72188: 2444.241222 from(815.754350,3+) rtinseconds(4107) index(62376)
Title: Locus:1.1.1.2852.29
Data file 2011-11-12 - TFD - EP 6-4.mgf

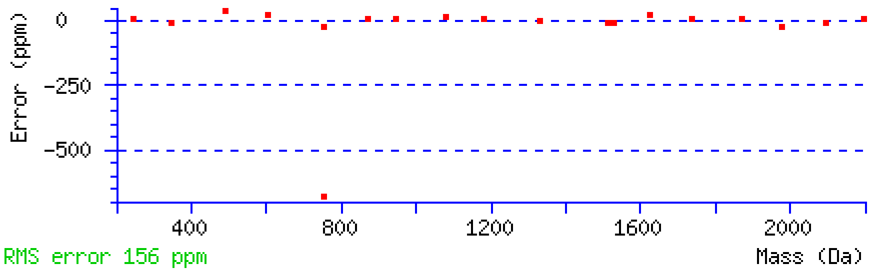
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [0] to [2600] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2444.233597
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 124 **Expect:** 4.6e-012
Matches : 19/238 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							22
2	**247.144104**	124.075690					F	2346.172455	1173.589865	2329.145906	1165.076591	2328.161890	1164.584583	21
3	**348.191783**	174.599529			330.181218	165.594247	T	***2199.104041***	1100.055658	2182.077492	1091.542384	2181.093476	1091.050376	20
4	449.239462	225.123369			431.228897	216.118087	T	***2098.056362***	1049.531819	2081.029813	1041.018544	2080.045797	1040.526536	19
5	577.298040	289.152658	560.271491	280.639384	559.287475	280.147376	Q	1997.008683	999.007980	1979.982134	990.494705	1978.998118	990.002697	18
6	706.340633	353.673955	689.314084	345.160680	688.330068	344.668672	E	***1868.950105***	934.978690	1851.923556	926.465416	1850.939540	925.973408	17
7	819.424697	410.215987	802.398148	401.702712	801.414132	401.210704	L	***1739.907512***	870.457394	1722.880963	861.944120	1721.896947	861.452112	16
8	918.493111	459.750194	901.466562	451.236919	900.482546	450.744911	V	***1626.823448***	813.915362	1609.796899	805.402087	1608.812883	804.910079	15
9	1046.551689	523.779483	1029.525140	515.266208	1028.541124	514.774200	Q	***1527.755034***	764.381155	1510.728485	755.867881	1509.744469	755.375873	14
10	1117.588803	559.298040	1100.562254	550.784765	1099.578238	550.292757	A	1399.696456	700.351866	1382.669907	691.838592	1381.685891	691.346583	13
11	1264.657217	632.832247	1247.630668	624.318972	1246.646652	623.826964	F	***1328.659342***	664.833309	1311.632793	656.320035	1310.648777	655.828026	12
12	1365.704896	683.356086	1348.678347	674.842812	1347.694331	674.350804	T	***1181.590928***	591.299102	1164.564379	582.785827	1163.580363	582.293819	11
13	1502.763808	751.885542	1485.737259	743.372268	1484.753243	742.880260	H	***1080.543249***	540.775262	1063.516700	532.261988	1062.532684	531.769980	10
14	1573.800922	787.404099	1556.774373	778.890825	1555.790357	778.398817	A	***943.484337***	472.245806	926.457788	463.732532	925.473772	463.240524	9
15	1670.853686	835.930481	1653.827137	827.417207	1652.843121	826.925199	P	***872.447223***	436.727249	855.420674	428.213975	854.436658	427.721967	8
16	1741.890800	871.449038	1724.864251	862.935764	1723.880235	862.443756	A	775.394459	388.200867	758.367910	379.687593	757.383894	379.195585	7
17	1842.938479	921.972878	1825.911930	913.459603	1824.927914	912.967595	T	704.357345	352.682310	687.330796	344.169036	686.346780	343.677028	6
18	1956.022543	978.514910	1938.995994	970.001635	1938.011978	969.509627	L	***603.309666***	302.158471	586.283117	293.645196	585.299101	293.153188	5
19	2085.065136	1043.036206	2068.038587	1034.522931	2067.054571	1034.030923	E	***490.225602***	245.616439	473.199053	237.103164	472.215037	236.611156	4
20	2156.102250	1078.554763	2139.075701	1070.041488	2138.091685	1069.549480	A	361.183009	181.095142	344.156460	172.581868	343.172444	172.089860	3
21	2271.129193	1136.068234	2254.102644	1127.554960	2253.118628	1127.062952	D	290.145895	145.576585	273.119346	137.063311	272.135330	136.571303	2
22							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
123.5	2444.233597	0.007625	VFTTQELVQAFTHAPATLEADR
2.4	2444.263443	-0.022221	VFAKPFLASLDGHRDGVNCLAK
0.0	2444.236954	0.004268	MVRGELVDESGGSPLEWIGLIR

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

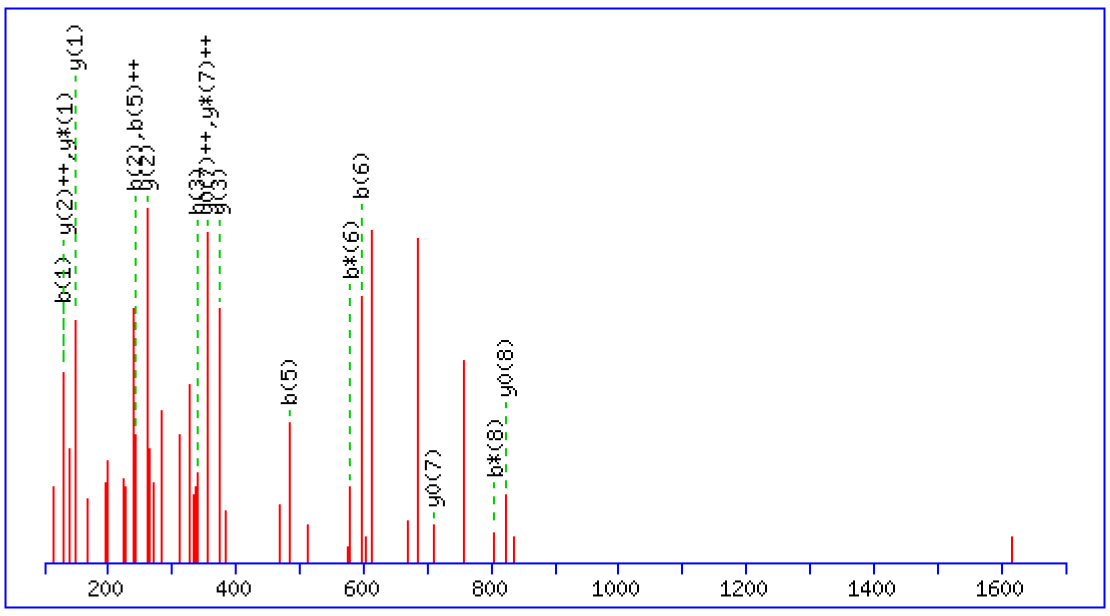
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KPPGSLLPK**
Found in **ACD11_HUMAN**, Acyl-CoA dehydrogenase family member 11 OS=Homo sapiens GN=ACAD11 PE=1 SV=2

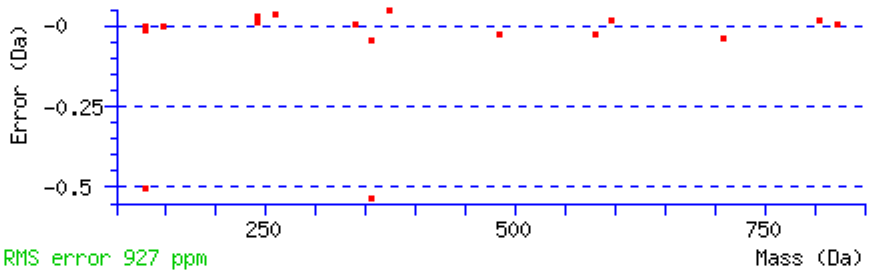
Match to Query 13611: 967.572168 from(484.793360,2+) rtinseconds(2914) index(40243)
Title: Locus:1.1.1.2405.3
Data file 2011-11-12 - TFD - EP 6-4.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●

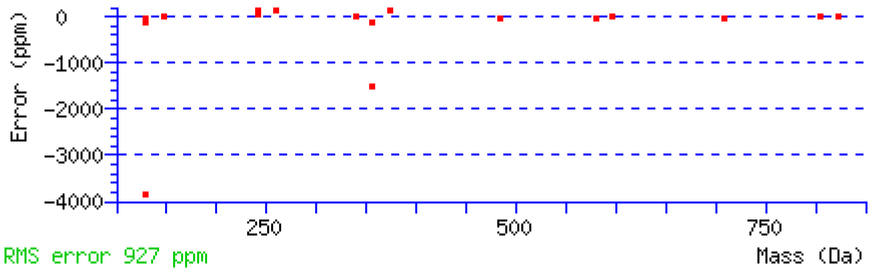


```
Monoisotopic mass of neutral peptide Mr(calc): 967.570221
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P2      : Oxidation (P)
P8      : Oxidation (P)
Ions Score: 48  Expect: 7.7e-005
Matches : 20/80 fragment ions using 26 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	***129.102239***	65.054757	112.075690	56.541483			K							9
2	***242.149918***	121.578597	225.123369	113.065322			P	840.482546	420.744911	823.455997	412.231637	822.471981	411.739629	8
3	***339.202682***	170.104979	322.176133	161.591704			P	727.434867	364.221072	710.408318	355.707797	709.424302	355.215789	7
4	396.224146	198.615711	379.197597	190.102436			G	630.382103	315.694690	613.355554	307.181415	612.371538	306.689407	6
5	***483.256174***	**242.131725**	466.229625	233.618450	465.245609	233.126442	S	573.360639	287.183958	556.334090	278.670683	555.350074	278.178675	5
6	***596.340238***	298.673757	579.313689	290.160483	578.329673	289.668475	L	486.328611	243.667944	469.302062	235.154669			4
7	***709.424302***	**355.215789**	692.397753	346.702515	691.413737	346.210507	L	**373.244547**	187.125912	356.217998	178.612637			3
8	***822.471981***	411.739629	805.445432	403.226354	804.461416	402.734346	P	**260.160483**	130.583879	243.133934	122.070605			2
9							K	**147.112804**	74.060040	130.086255	65.546765			1



RMS error 927 ppm



RMS error 927 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.8	967.570221	0.001947	KPPGSLLPK
36.7	967.570221	0.001947	KPPGSLLPK
34.9	967.570221	0.001947	KLKPPPPK
33.1	967.570221	0.001947	KIPPPKPK
27.6	967.570236	0.001932	KTPGPVLPK
23.8	967.570221	0.001947	APGKLPLPK
22.3	967.570221	0.001947	GPSLIPQIK
20.0	967.570221	0.001947	AVLNPTPIK
18.4	967.581436	-0.009268	ARSAPPLLK
18.4	967.570221	0.001947	VSPKLAPPK

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

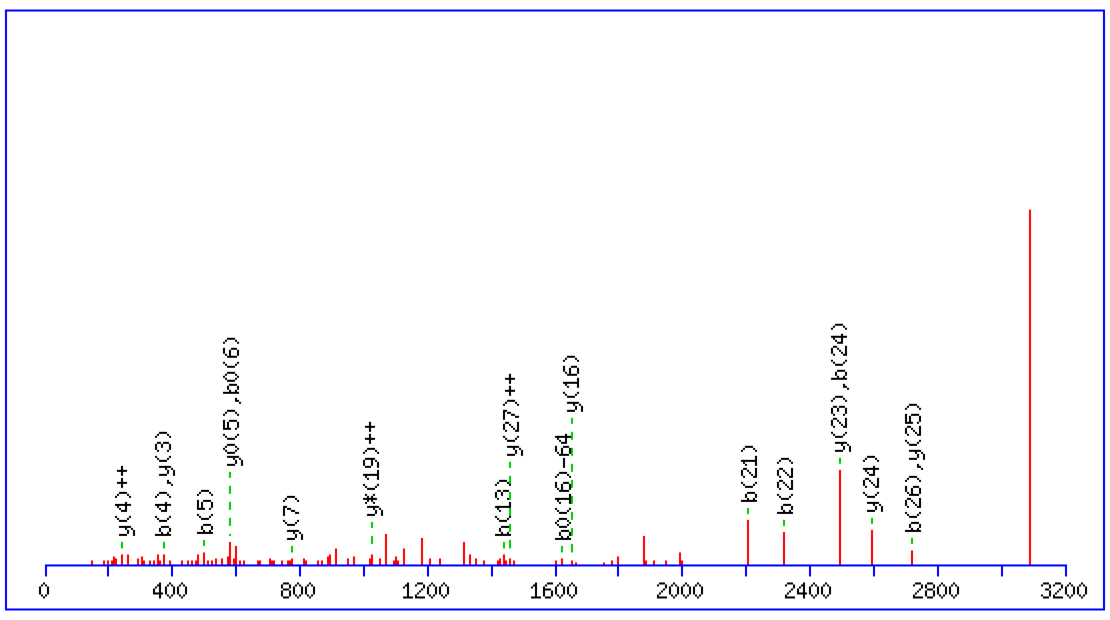
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IGPSEVENALMEHPAVVETAVISSPDPVR**
Found in **ACS2A_HUMAN**, Acyl-coenzyme A synthetase ACSM2A, mitochondrial OS=Homo sapiens GN=ACSM2A PE=1 SV=2

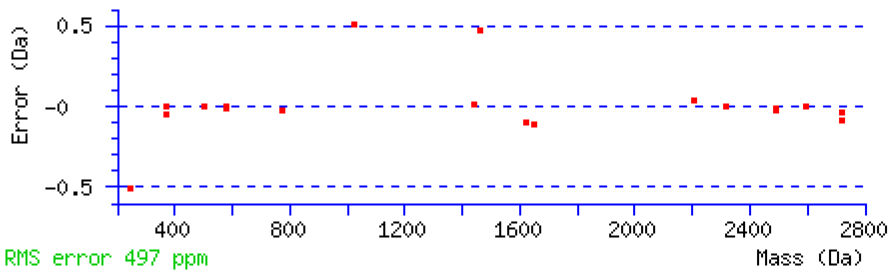
Match to Query 71705: 3090.492132 from(1031.171320,3+) rtinseconds(3605) index(52093)
Title: Locus:1.1.1.2789.49
Data file 2011-11-14 - TFD - EP 8-2.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3200 Da Full range
Label all possible matches ○ Label matches used for scoring ●

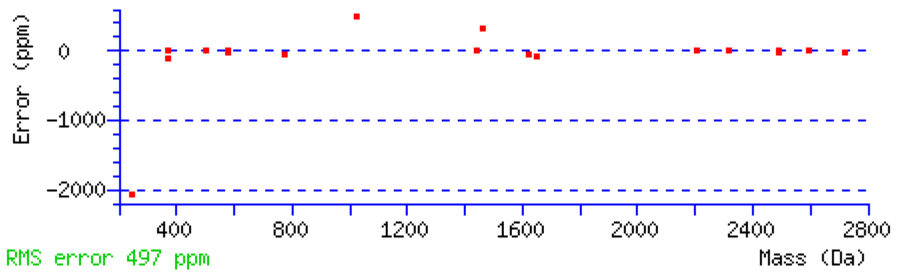


```
Monoisotopic mass of neutral peptide Mr(calc): 3090.517944
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P3      : Oxidation (P)
M11     : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
P25     : Oxidation (P)
Ions Score: 33  Expect: 0.0015
Matches : 19/478 fragment ions using 24 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					I							29
2	171.112804	86.060040					G	2978.441159	1489.724217	2961.414610	1481.210943	2960.430594	1480.718935	28
3	284.160483	142.583879					P	2921.419695	1461.213485	2904.393146	1452.700211	2903.409130	1452.208203	27
4	***371.192511***	186.099893			353.181946	177.094611	S	2808.372016	1404.689646	2791.345467	1396.176371	2790.361451	1395.684363	26
5	***500.235104***	250.621190			482.224539	241.615907	E	***2721.339988***	1361.173632	2704.313439	1352.660357	2703.329423	1352.168349	25
6	599.303518	300.155397			581.292953	291.150114	V	***2592.297395***	1296.652335	2575.270846	1288.139061	2574.286830	1287.647053	24
7	728.346111	364.676694			710.335546	355.671411	E	***2493.228981***	1247.118128	2476.202432	1238.604854	2475.218416	1238.112846	23
8	842.389038	421.698157	825.362489	413.184882	824.378473	412.692874	N	2364.186388	1182.596832	2347.159839	1174.083557	2346.175823	1173.591549	22
9	913.426152	457.216714	896.399603	448.703439	895.415587	448.211431	A	2250.143461	1125.575368	2233.116912	1117.062094	2232.132896	1116.570086	21
10	1026.510216	513.758746	1009.483667	505.245471	1008.499651	504.753463	L	2179.106347	1090.056811	2162.079798	1081.543537	2161.095782	1081.051529	20
11	1173.545616	587.276446	1156.519067	578.763172	1155.535051	578.271163	M	2066.022283	1033.514779	2048.995734	1025.001505	2048.011718	1024.509497	19
12	1302.588209	651.797742	1285.561660	643.284468	1284.577644	642.792460	E	1918.986883	959.997080	1901.960334	951.483805	1900.976318	950.991797	18
13	***1439.647121***	720.327198	1422.620572	711.813924	1421.636556	711.321916	H	1789.944290	895.475783	1772.917741	886.962509	1771.933725	886.470501	17
14	1536.699885	768.853580	1519.673336	760.340306	1518.689320	759.848298	P	***1652.885378***	826.946327	1635.858829	818.433053	1634.874813	817.941045	16
15	1607.736999	804.372137	1590.710450	795.858863	1589.726434	795.366855	A	1555.832614	778.419945	1538.806065	769.906671	1537.822049	769.414663	15
16	1706.805413	853.906344	1689.778864	845.393070	1688.794848	844.901062	V	1484.795500	742.901388	1467.768951	734.388114	1466.784935	733.896106	14
17	1805.873827	903.440551	1788.847278	894.927277	1787.863262	894.435269	V	1385.727086	693.367181	1368.700537	684.853907	1367.716521	684.361899	13
18	1934.916420	967.961848	1917.889871	959.448573	1916.905855	958.956565	E	1286.658672	643.832974	1269.632123	635.319700	1268.648107	634.827692	12
19	2035.964099	1018.485687	2018.937550	1009.972413	2017.953534	1009.480405	T	1157.616079	579.311678	1140.589530	570.798403	1139.605514	570.306395	11
20	2107.001213	1054.004244	2089.974664	1045.490970	2088.990648	1044.998962	A	1056.568400	528.787838	1039.541851	520.274564	1038.557835	519.782556	10
21	***2206.069627***	1103.538451	2189.043078	1095.025177	2188.059062	1094.533169	V	985.531286	493.269281	968.504737	484.756007	967.520721	484.263999	9
22	***2319.153691***	1160.080483	2302.127142	1151.567209	2301.143126	1151.075201	I	886.462872	443.735074	869.436323	435.221800	868.452307	434.729792	8
23	2406.185719	1203.596497	2389.159170	1195.083223	2388.175154	1194.591215	S	***773.378808***	387.193042	756.352259	378.679768	755.368243	378.187760	7
24	***2493.217747***	1247.112511	2476.191198	1238.599237	2475.207182	1238.107229	S	686.346780	343.677028	669.320231	335.163754	668.336215	334.671746	6
25	2606.265426	1303.636351	2589.238877	1295.123076	2588.254861	1294.631068	P	599.314752	300.161014	582.288203	291.647740	581.304187	291.155732	5
26	***2721.292369***	1361.149822	2704.265820	1352.636548	2703.281804	1352.144540	D	486.267073	243.637174	469.240524	235.123900	468.256508	234.631892	4
27	2818.345133	1409.676204	2801.318584	1401.162930	2800.334568	1400.670922	P	***371.240130***	186.123703	354.213581	177.610428			3
28	2917.413547	1459.210411	2900.386998	1450.697137	2899.402982	1450.205129	V	274.187366	137.597321	257.160817	129.084046			2
29							R	175.118952	88.063114	158.092403	79.549839			1



RMS error 497 ppm



RMS error 497 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.7	3090.517944	-0.025812	IGPSEVENALMEHPAVVETAVISSPDPVR
23.7	3090.517944	-0.025812	IGPSEVENALMEHPAVVETAVISSPDPVR
23.6	3090.517944	-0.025812	IGPSEVENALMEHPAVVETAVISSPDPVR
15.9	3090.517944	-0.025812	IGPSEVENALMEHPAVVETAVISSPDPVR
13.6	3090.517944	-0.025812	IGPSEVENALMEHPAVVETAVISSPDPVR
6.9	3090.517944	-0.025812	IGPSEVENALMEHPAVVETAVISSPDPVR
2.5	3090.469009	0.023123	MAAAAAALSGAGTPPAGGGAGGGGAGGGGSPPGGWAVAR
1.5	3090.469009	0.023123	MAAAAAALSGAGTPPAGGGAGGGGAGGGGSPPGGWAVAR
1.4	3090.497635	-0.005503	ILEKTANPQWNQNILPAMFPSMCEK
1.2	3090.469009	0.023123	MAAAAAALSGAGTPPAGGGAGGGGAGGGGSPPGGWAVAR

{MATRIX SCIENCE}

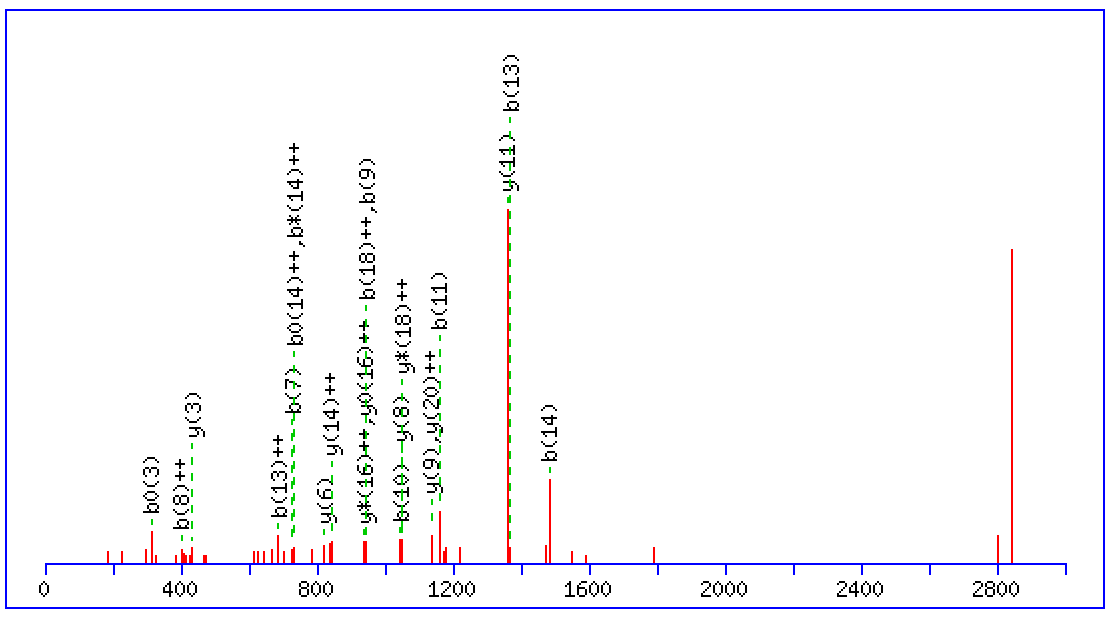
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DSENKGPAFVNPLIPESPEEEELFR**
Found in **ACOT9_HUMAN**, Acyl-coenzyme A thioesterase 9, mitochondrial OS=Homo sapiens GN=ACOT9 PE=1 SV=2

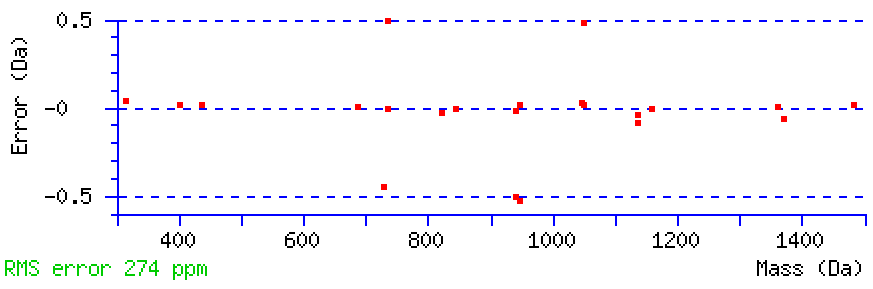
Match to Query 71058: 2842.368612 from(948.463480,3+) rtinseconds(3759) index(55712)
Title: Locus:1.1.1.2767.44
Data file 2011-11-10 - TFD - EP 3-4.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●

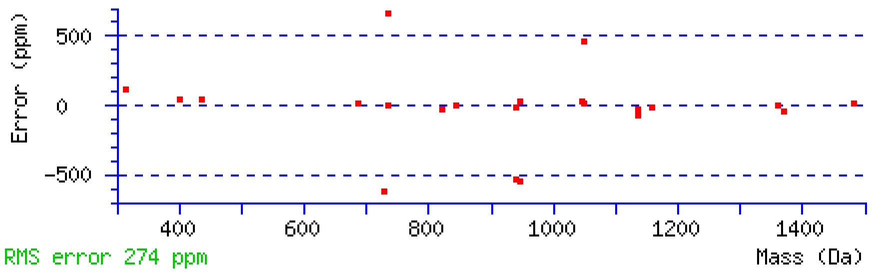


```
Monoisotopic mass of neutral peptide Mr(calc): 2842.366074
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 31  Expect: 0.0019
Matches : 22/276 fragment ions using 34 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	116.034219	58.520748			98.023654	49.515465	D							25
2	203.066247	102.036761			185.055682	93.031479	S	2728.346451	1364.676863	2711.319902	1356.163589	2710.335886	1355.671581	24
3	332.108840	166.558058			314.098275	157.552776	E	2641.314423	1321.160849	2624.287874	1312.647575	2623.303858	1312.155567	23
4	446.151767	223.579522	429.125218	215.066247	428.141202	214.574239	N	2512.271830	1256.639553	2495.245281	1248.126278	2494.261265	1247.634270	22
5	574.246730	287.627003	557.220181	279.113729	556.236165	278.621721	K	2398.228903	1199.618089	2381.202354	1191.104815	2380.218338	1190.612807	21
6	631.268194	316.137735	614.241645	307.624461	613.257629	307.132453	G	2270.133940	1135.570608	2253.107391	1127.057333	2252.123375	1126.565325	20
7	***728.320958***	364.664117	711.294409	356.150843	710.310393	355.658835	P	2213.112476	1107.059876	2196.085927	1098.546601	2195.101911	1098.054593	19
8	799.358072	**400.182674**	782.331523	391.669400	781.347507	391.177392	A	2116.059712	1058.533494	2099.033163	1050.020219	2098.049147	1049.528211	18
9	***946.426486***	473.716881	929.399937	465.203607	928.415921	464.711599	F	2045.022598	1023.014937	2027.996049	1014.501663	2027.012033	1014.009655	17
10	***1045.494900***	523.251088	1028.468351	514.737814	1027.484335	514.245806	V	1897.954184	949.480730	1880.927635	940.967456	1879.943619	940.475448	16
11	***1159.537827***	580.272552	1142.511278	571.759277	1141.527262	571.267269	N	1798.885770	899.946523	1781.859221	891.433249	1780.875205	890.941241	15
12	1256.590591	628.798934	1239.564042	620.285659	1238.580026	619.793651	P	1684.842843	842.925060	1667.816294	834.411785	1666.832278	833.919777	14
13	***1369.674655***	**685.340966**	1352.648106	676.827691	1351.664090	676.335683	L	1587.790079	794.398678	1570.763530	785.885403	1569.779514	785.393395	13
14	***1482.758719***	741.882997	1465.732170	733.369723	1464.748154	732.877715	I	1474.706015	737.856646	1457.679466	729.343371	1456.695450	728.851363	12
15	1579.811483	790.409380	1562.784934	781.896105	1561.800918	781.404097	P	***1361.621951***	681.314614	1344.595402	672.801339	1343.611386	672.309331	11
16	1708.854076	854.930676	1691.827527	846.417401	1690.843511	845.925393	E	1264.569187	632.788232	1247.542638	624.274957	1246.558622	623.782949	10
17	1795.886104	898.446690	1778.859555	889.933416	1777.875539	889.441407	S	***1135.526594***	568.266935	1118.500045	559.753661	1117.516029	559.261653	9
18	1892.938868	**946.973072**	1875.912319	938.459798	1874.928303	937.967789	P	***1048.494566***	524.750921	1031.468017	516.237647	1030.484001	515.745639	8
19	2021.981461	1011.494369	2004.954912	1002.981094	2003.970896	1002.489086	E	951.441802	476.224539	934.415253	467.711265	933.431237	467.219257	7
20	2151.024054	1076.015665	2133.997505	1067.502390	2133.013489	1067.010382	E	***822.399209***	411.703243	805.372660	403.189968	804.388644	402.697960	6
21	2280.066647	1140.536962	2263.040098	1132.023687	2262.056082	1131.531679	E	693.356616	347.181946	676.330067	338.668672	675.346051	338.176664	5
22	2409.109240	1205.058258	2392.082691	1196.544983	2391.098675	1196.052976	E	564.314023	282.660650	547.287474	274.147375	546.303458	273.655367	4
23	2522.193304	1261.600290	2505.166755	1253.087016	2504.182739	1252.595008	L	***435.271430***	218.139353	418.244881	209.626078			3
24	2669.261718	1335.134497	2652.235169	1326.621222	2651.251153	1326.129215	F	322.187366	161.597321	305.160817	153.084046			2
25							R	175.118952	88.063114	158.092403	79.549839			1



RMS error 274 ppm



RMS error 274 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.3	2842.366074	0.002538	DSENKGPAFVNPLIPESPEEEELFR
2.2	2842.354218	0.014394	ENLTGINSTVEEPVSPMLPPSAVEER
2.2	2842.354218	0.014394	ENLTGINSTVEEPVSPMLPPSAVEER
2.1	2842.354218	0.014394	ENLTGINSTVEEPVSPMLPPSAVEER
2.1	2842.354218	0.014394	ENLTGINSTVEEPVSPMLPPSAVEER
0.6	2842.394608	-0.025996	LLNYATTPDLENFIEAVSISLMDNK
0.3	2842.354233	0.014379	KLMSSSGTSDASPSGSPVLASYKPAPPK

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

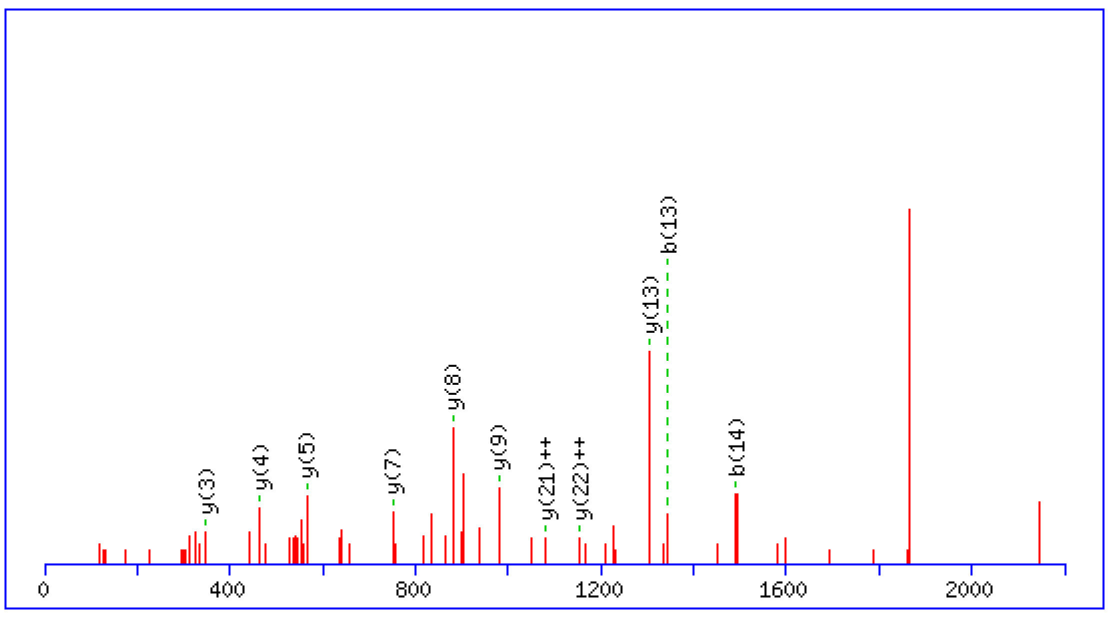
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TSGELFAQAPVDQFPGTAVESVTDSSR**
Found in **NECP2_HUMAN**, Adaptin ear-binding coat-associated protein 2 OS=Homo sapiens GN=NECAP2 PE=1 SV=1

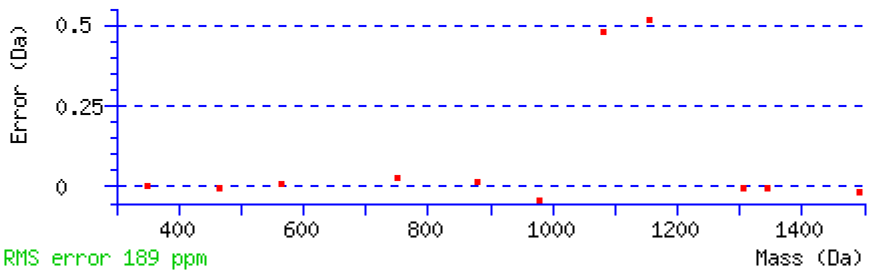
Match to Query 73345: 2795.327322 from(932.783050,3+) rtinseconds(3479) index(50927)
Title: Locus:1.1.1.2647.48
Data file 2011-11-10 - TFD - EP 4-4.mgf

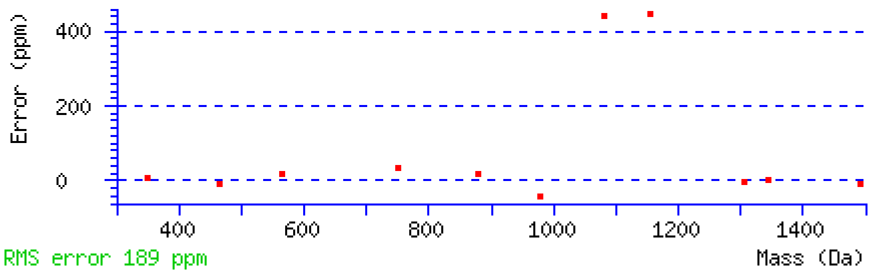
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [0] to [2200] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2795.325012
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 33  Expect: 0.0011
Matches : 11/296 fragment ions using 19 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	102.054955	51.531116			84.044390	42.525833	T							27
2	189.086983	95.047129			171.076418	86.041847	S	2695.284582	1348.145929	2678.258033	1339.632654	2677.274017	1339.140646	26
3	246.108447	123.557861			228.097882	114.552579	G	2608.252554	1304.629915	2591.226005	1296.116640	2590.241989	1295.624632	25
4	375.151040	188.079158			357.140475	179.073876	E	2551.231090	1276.119183	2534.204541	1267.605908	2533.220525	1267.113900	24
5	488.235104	244.621190			470.224539	235.615908	L	2422.188497	1211.597886	2405.161948	1203.084612	2404.177932	1202.592604	23
6	635.303518	318.155397			617.292953	309.150115	F	2309.104433	1155.055854	2292.077884	1146.542580	2291.093868	1146.050572	22
7	706.340632	353.673954			688.330067	344.668672	A	2162.036019	1081.521647	2145.009470	1073.008373	2144.025454	1072.516365	21
8	834.399210	417.703243	817.372661	409.189969	816.388645	408.697961	Q	2090.998905	1046.003090	2073.972356	1037.489816	2072.988340	1036.997808	20
9	905.436324	453.221800	888.409775	444.708526	887.425759	444.216518	A	1962.940327	981.973802	1945.913778	973.460527	1944.929762	972.968519	19
10	1002.489088	501.748182	985.462539	493.234908	984.478523	492.742900	P	1891.903213	946.455245	1874.876664	937.941970	1873.892648	937.449962	18
11	1101.557502	551.282389	1084.530953	542.769115	1083.546937	542.277107	V	1794.850449	897.928863	1777.823900	889.415588	1776.839884	888.923580	17
12	1216.584445	608.795861	1199.557896	600.282586	1198.573880	599.790578	D	1695.782035	848.394656	1678.755486	839.881381	1677.771470	839.389373	16
13	**1344.643023**	672.825150	1327.616474	664.311875	1326.632458	663.819867	Q	1580.755092	790.881184	1563.728543	782.367910	1562.744527	781.875902	15
14	**1491.711437**	746.359357	1474.684888	737.846082	1473.700872	737.354074	F	1452.696514	726.851895	1435.669965	718.338621	1434.685949	717.846612	14
15	1588.764201	794.885739	1571.737652	786.372464	1570.753636	785.880456	P	***1305.628100***	653.317688	1288.601551	644.804414	1287.617535	644.312405	13
16	1645.785665	823.396471	1628.759116	814.883196	1627.775100	814.391188	G	1208.575336	604.791306	1191.548787	596.278032	1190.564771	595.786023	12
17	1746.833344	873.920310	1729.806795	865.407036	1728.822779	864.915028	T	1151.553872	576.280574	1134.527323	567.767300	1133.543307	567.275291	11
18	1817.870458	909.438867	1800.843909	900.925593	1799.859893	900.433585	A	1050.506193	525.756734	1033.479644	517.243460	1032.495628	516.751452	10
19	1916.938872	958.973074	1899.912323	950.459800	1898.928307	949.967792	V	***979.469079***	490.238178	962.442530	481.724903	961.458514	481.232895	9
20	2045.981465	1023.494371	2028.954916	1014.981096	2027.970900	1014.489088	E	***880.400665***	440.703970	863.374116	432.190696	862.390100	431.698688	8
21	2133.013493	1067.010385	2115.986944	1058.497110	2115.002928	1058.005102	S	***751.358072***	376.182674	734.331523	367.669399	733.347507	367.177391	7
22	2232.081907	1116.544592	2215.055358	1108.031317	2214.071342	1107.539309	V	664.326044	332.666660	647.299495	324.153385	646.315479	323.661377	6
23	2333.129586	1167.068431	2316.103037	1158.555156	2315.119021	1158.063148	T	***565.257630***	283.132453	548.231081	274.619178	547.247065	274.127170	5
24	2448.156529	1224.581902	2431.129980	1216.068628	2430.145964	1215.576620	D	***464.209951***	232.608613	447.183402	224.095339	446.199386	223.603331	4
25	2535.188557	1268.097916	2518.162008	1259.584642	2517.177992	1259.092634	S	***349.183008***	175.095142	332.156459	166.581868	331.172443	166.089860	3
26	2622.220585	1311.613930	2605.194036	1303.100656	2604.210020	1302.608648	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
27							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of TSGELFAQAPVDQFPGTAVESVTDSSR
(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	2795.325012	0.002310	TSGELFAQAPVDQFPGTAVESVTDSSR
1.7	2795.309738	0.017584	VDQDDDQDSSSLKLSQNIAVQTDFK
0.7	2795.327881	-0.000559	VLMLTLQNDPPTLETGVEDKEMMK
0.6	2795.327881	-0.000559	VLMLTLQNDPPTLETGVEDKEMMK

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

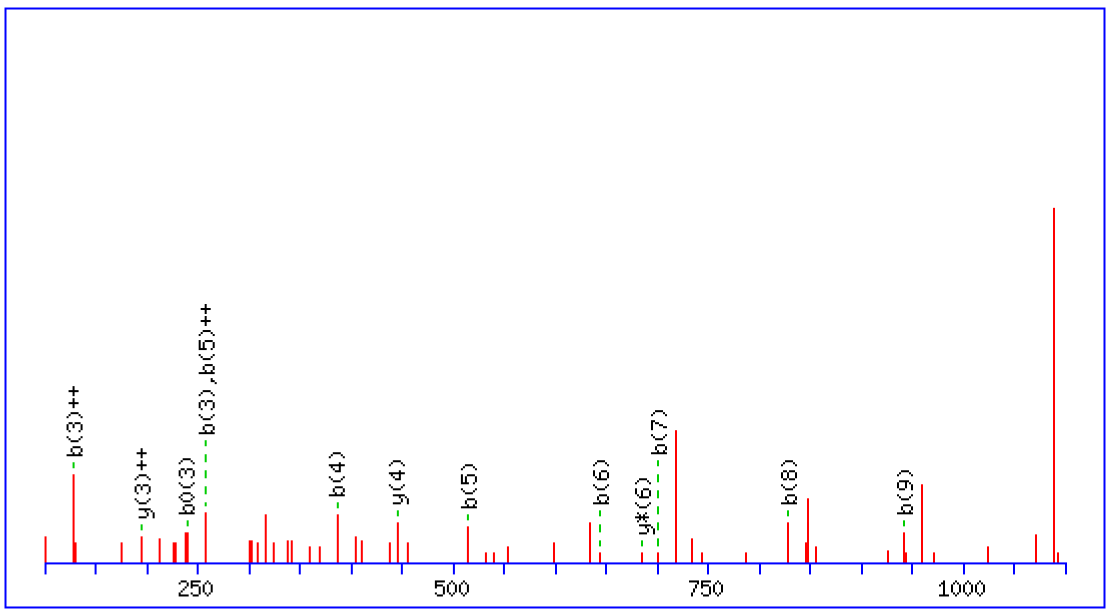
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GISEQEGKIK**
Found in **ADCY8_HUMAN**, Adenylate cyclase type 8 OS=Homo sapiens GN=ADCY8 PE=1 SV=1

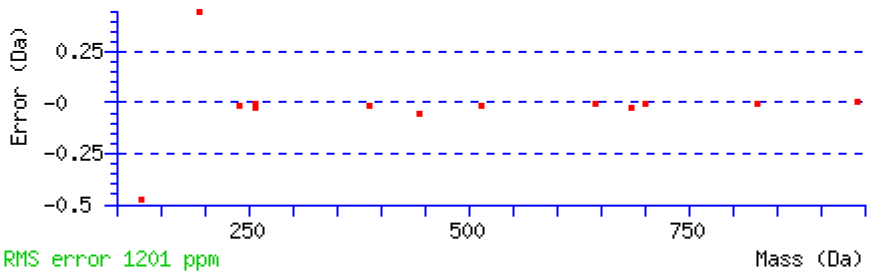
Match to Query 21377: 1087.587408 from(544.800980,2+) rtinseconds(785) index(607)
Title: Locus:1.1.1.1627.23
Data file 2011-11-10 - TFD - EP 4-4.mgf

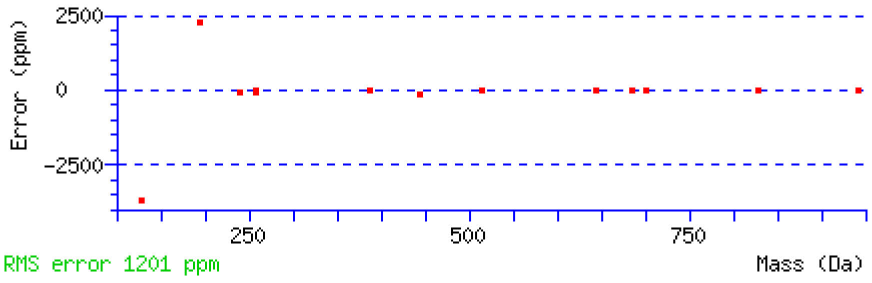
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1087.587311
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.011
Matches : 13/88 fragment ions using 29 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							10
2	171.112804	86.060040					I	1031.573151	516.290214	1014.546602	507.776939	1013.562586	507.284931	9
3	*258.144832*	**129.576054**			240.134267	120.570772	S	918.489087	459.748182	901.462538	451.234907	900.478522	450.742899	8
4	*387.187425*	194.097351			369.176860	185.092068	E	831.457059	416.232168	814.430510	407.718893	813.446494	407.226885	7
5	*515.246003*	**258.126640**	498.219454	249.613365	497.235438	249.121357	Q	702.414466	351.710871	685.387917	343.197597	684.403901	342.705589	6
6	*644.288596*	322.647936	627.262047	314.134662	626.278031	313.642654	E	574.355888	287.681582	557.329339	279.168308	556.345323	278.676300	5
7	*701.310060*	351.158668	684.283511	342.645394	683.299495	342.153386	G	445.313295	223.160286	428.286746	214.647011			4
8	*829.405023*	415.206150	812.378474	406.692875	811.394458	406.200867	K	388.291831	194.649554	371.265282	186.136279			3
9	*942.489087*	471.748182	925.462538	463.234907	924.478522	462.742899	I	260.196868	130.602072	243.170319	122.088798			2
10							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.5	1087.587311	0.000097	GISEQEGKIK
29.6	1087.587311	0.000097	KLNVTEQEK
16.9	1087.587296	0.000112	QEESLKNIK
10.0	1087.591354	-0.003946	KPEPLDFVK
10.0	1087.580780	0.006628	QLEMLKNGR
9.3	1087.587311	0.000097	QLTDNLKEK
7.5	1087.587311	0.000097	KELLDISDR
6.5	1087.587311	0.000097	QEETISIIR
6.4	1087.580780	0.006628	QLNIARDMK
5.1	1087.577438	0.009970	QISHPLHPK

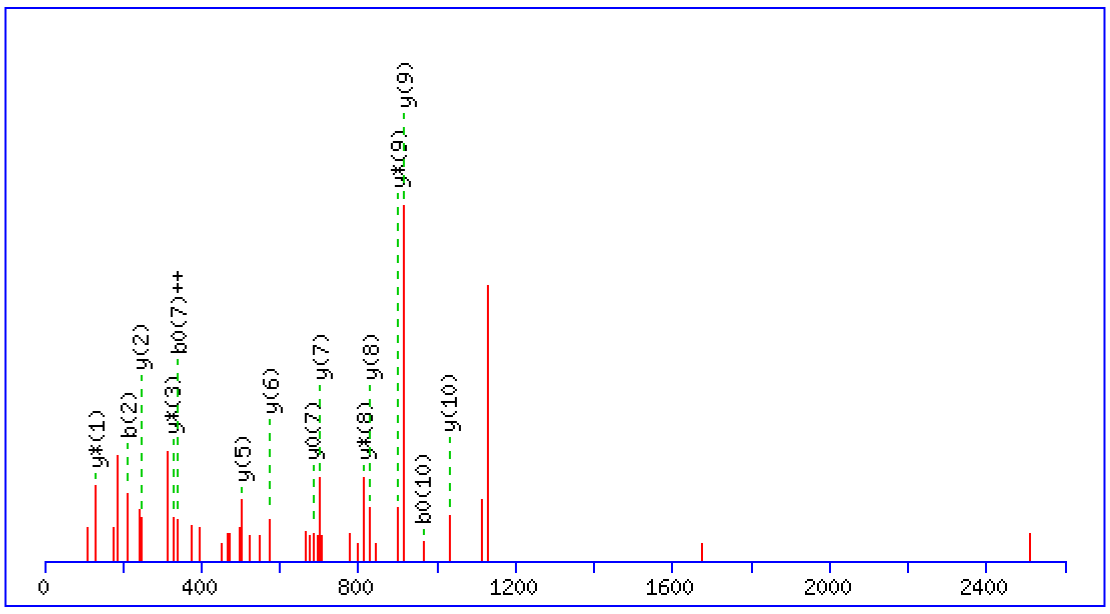
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLSQQAASVVK**
Found in **PUR8_HUMAN**, Adenylosuccinate lyase OS=Homo sapiens GN=ADSL PE=1 SV=2

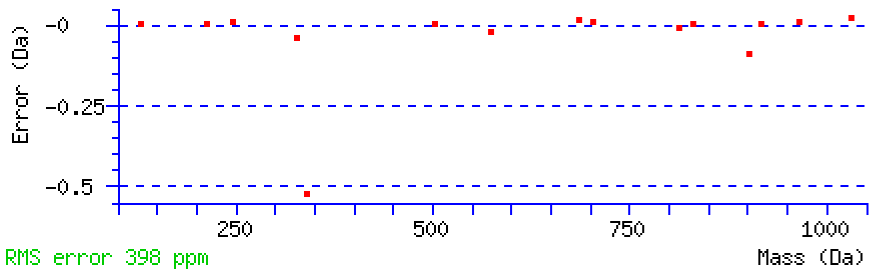
Match to Query 18316: 1128.655248 from(565.334900,2+) rtinseconds(1438) index(11999)
Title: Locus:1.1.1.2034.33
Data file 2011-11-10 - TFD - EP 4-3.mgf

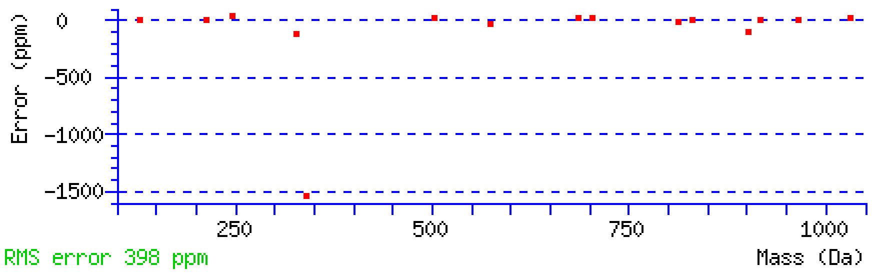
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1128.650269
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 35 **Expect:** 0.0017
Matches : 15/104 fragment ions using 32 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							11
2	213.159754	107.083515					L	***1030.589136***	515.798206	1013.562587	507.284932	1012.578571	506.792924	10
3	300.191782	150.599529			282.181217	141.594247	S	***917.505072***	459.256174	900.478523	450.742900	899.494507	450.250892	9
4	428.250360	214.628818	411.223811	206.115544	410.239795	205.623536	Q	***830.473044***	415.740160	813.446495	407.226886	812.462479	406.734878	8
5	556.308938	278.658107	539.282389	270.144833	538.298373	269.652825	Q	***702.414466***	351.710871	685.387917	343.197597	684.403901	342.705589	7
6	627.346052	314.176664	610.319503	305.663390	609.335487	305.171382	A	***574.355888***	287.681582	557.329339	279.168308	556.345323	278.676300	6
7	698.383166	349.695221	681.356617	341.181947	680.372601	340.689939	A	***503.318774***	252.163025	486.292225	243.649750	485.308209	243.157742	5
8	785.415194	393.211235	768.388645	384.697961	767.404629	384.205953	S	432.281660	216.644468	415.255111	208.131193	414.271095	207.639186	4
9	884.483608	442.745442	867.457059	434.232168	866.473043	433.740160	V	345.249632	173.128454	328.223083	164.615180			3
10	983.552022	492.279649	966.525473	483.766374	965.541457	483.274366	V	***246.181218***	123.594247	229.154669	115.080973			2
11							K	147.112804	74.060040	130.086255	65.546766			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.4	1128.650269	0.004979	VLSQQAASVVK
5.5	1128.665512	-0.010264	VPLALFALNR
4.3	1128.657639	-0.002391	VIIMILNGEK
2.3	1128.665527	-0.010279	VLEVTVRWK

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

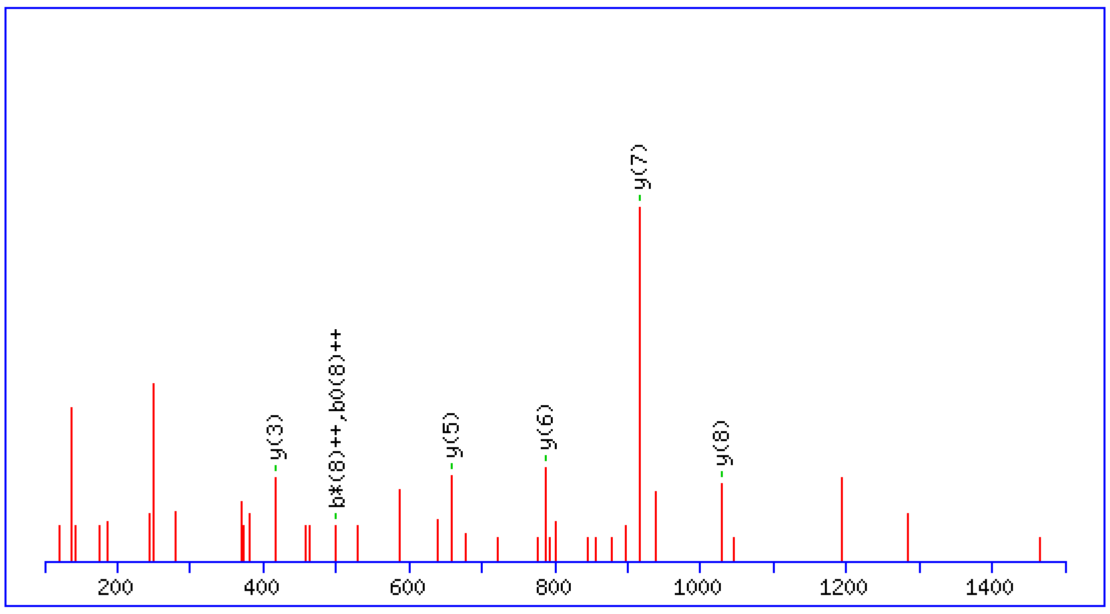
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YIEEQLLQR**
Found in **AR2BP_HUMAN**, ADP-ribosylation factor-like protein 2-binding protein OS=Homo sapiens GN=ARL2BP PE=1 SV=1

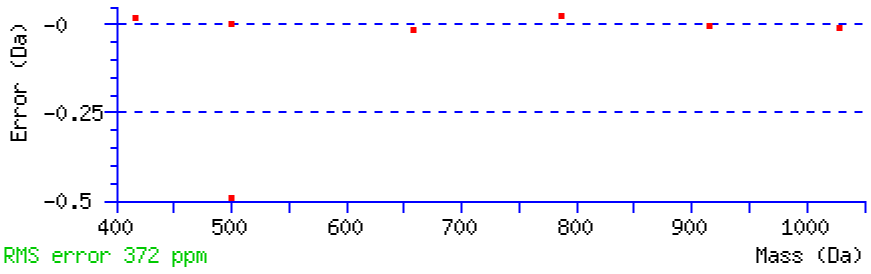
Match to Query 29076: 1190.634868 from(596.324710,2+) rtinseconds(2360) index(26472)
Title: Locus:1.1.1.2166.38
Data file 2011-11-10 - TFD - EP 3-6.mgf

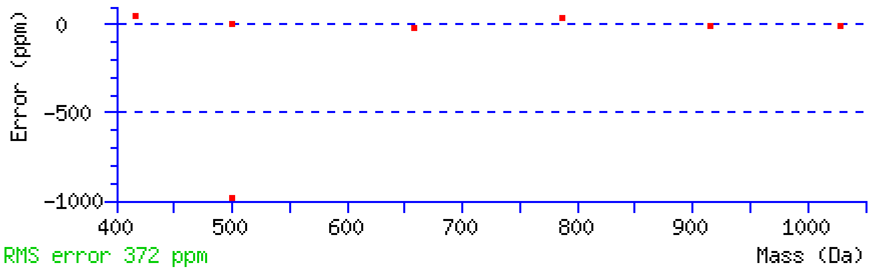
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1190.629501
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.0059
Matches : 7/74 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.070605	82.538940					**Y**							9
2	277.154669	139.080973					**I**	***1028.573486***	514.790381	1011.546937	506.277107	1010.562921	505.785099	8
3	406.197262	203.602269			388.186697	194.596987	**E**	***915.489422***	458.248349	898.462873	449.735075	897.478857	449.243067	7
4	535.239855	268.123566			517.229290	259.118283	**E**	***786.446829***	393.727053	769.420280	385.213778	768.436264	384.721770	6
5	663.298433	332.152855	646.271884	323.639580	645.287868	323.147572	**Q**	***657.404236***	329.205756	640.377687	320.692482			5
6	776.382497	388.694887	759.355948	380.181612	758.371932	379.689604	**L**	529.345658	265.176467	512.319109	256.663193			4
7	889.466561	445.236919	872.440012	436.723644	871.455996	436.231636	**L**	***416.261594***	208.634435	399.235045	200.121160			3
8	1017.525139	509.266208	1000.498590	500.752933	999.514574	500.260925	**Q**	303.177530	152.092403	286.150981	143.579128			2
9							**R**	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.4	1190.629501	0.005367	YIEEQLLQR
9.9	1190.640762	-0.005894	APSPAGPLHKGK
8.3	1190.644806	-0.009938	DRPFFPGLVK
8.3	1190.644135	-0.009267	VLMASVQGSKR
6.2	1190.629517	0.005351	SSPQAAVPYKK
1.5	1190.640747	-0.005879	AARQAADFTLK
1.3	1190.629532	0.005336	YLPVTKEGPR
0.6	1190.632889	0.001979	VINSLSMGINK
0.5	1190.629517	0.005351	ALPKSYQQPK

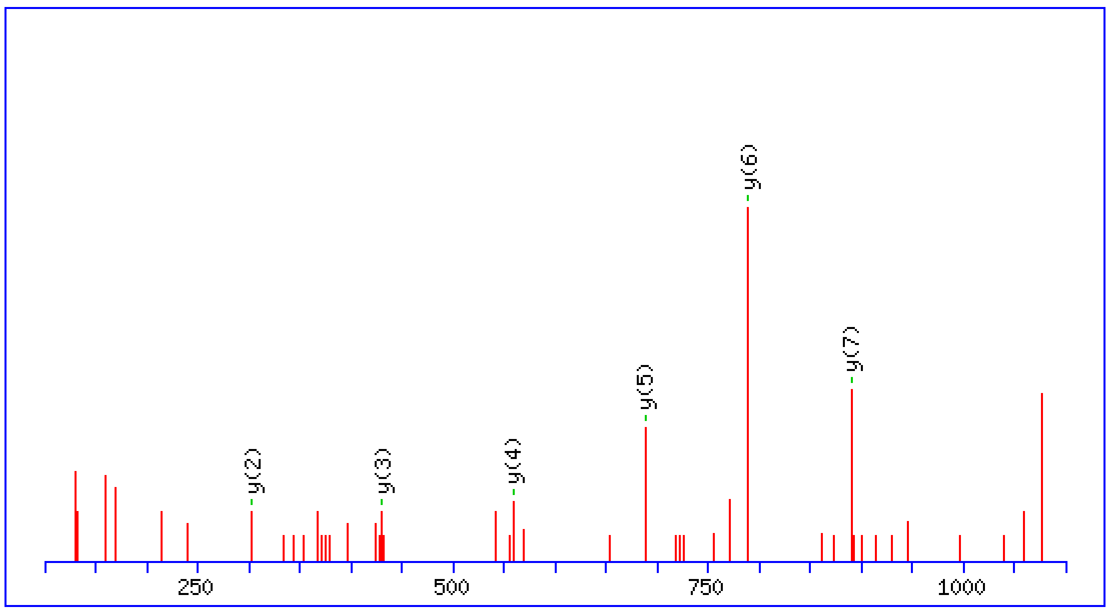
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **WTTEQQQR**
Found in **AR6P1_HUMAN**, ADP-ribosylation factor-like protein 6-interacting protein 1 OS=Homo sapiens GN=ARL6IP1 PE=1 SV=2

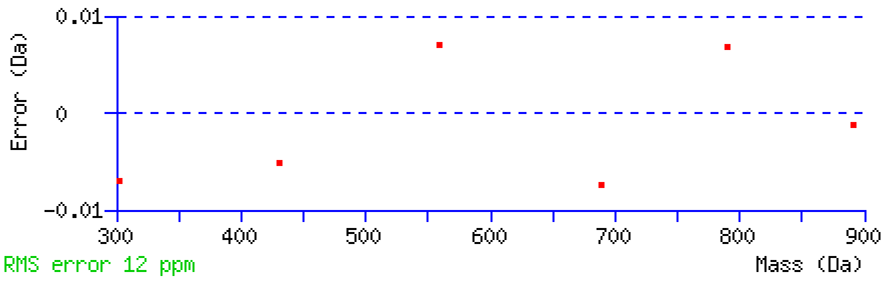
Match to Query 21770: 1075.505748 from(538.760150,2+) rtinseconds(991) index(1492)
Title: Locus:1.1.1.1645.25
Data file 2011-11-10 - TFD - EP 3-6.mgf

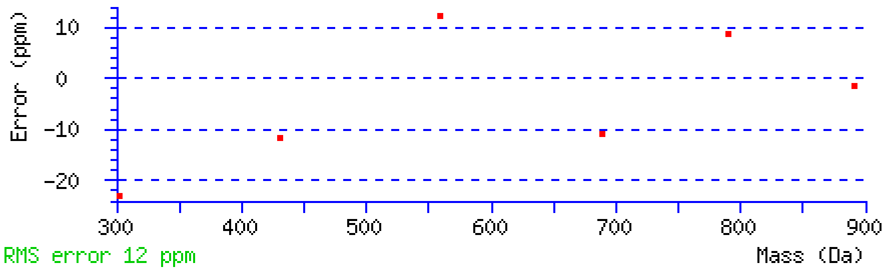
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1075.504669
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 49 **Expect:** 0.00015
Matches : 6/66 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	187.086589	94.046932					W							8
2	288.134268	144.570772			270.123703	135.565490	T	*890.432637*	445.719957	873.406088	437.206682	872.422072	436.714674	7
3	389.181947	195.094612			371.171382	186.089329	T	*789.384958*	395.196117	772.358409	386.682843	771.374393	386.190835	6
4	518.224540	259.615908			500.213975	250.610626	E	*688.337279*	344.672278	671.310730	336.159003	670.326714	335.666995	5
5	646.283118	323.645197	629.256569	315.131923	628.272553	314.639915	Q	*559.294686*	280.150981	542.268137	271.637707			4
6	774.341696	387.674486	757.315147	379.161212	756.331131	378.669204	Q	*431.236108*	216.121692	414.209559	207.608418			3
7	902.400274	451.703775	885.373725	443.190501	884.389709	442.698493	Q	*303.177530*	152.092403	286.150981	143.579129			2
8							R	175.118952	88.063114	158.092403	79.549840			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.8	1075.504669	0.001079	WTTEQQQR
8.1	1075.507996	-0.002248	EQMEKANAR
5.8	1075.514526	-0.008778	RDASEEELK
5.0	1075.508026	-0.002278	MAAADSVQQR
5.0	1075.508026	-0.002278	MSPQEGQKR
1.6	1075.508026	-0.002278	SAGKSCPPSR
0.3	1075.496811	0.008937	EGQLTPMPR

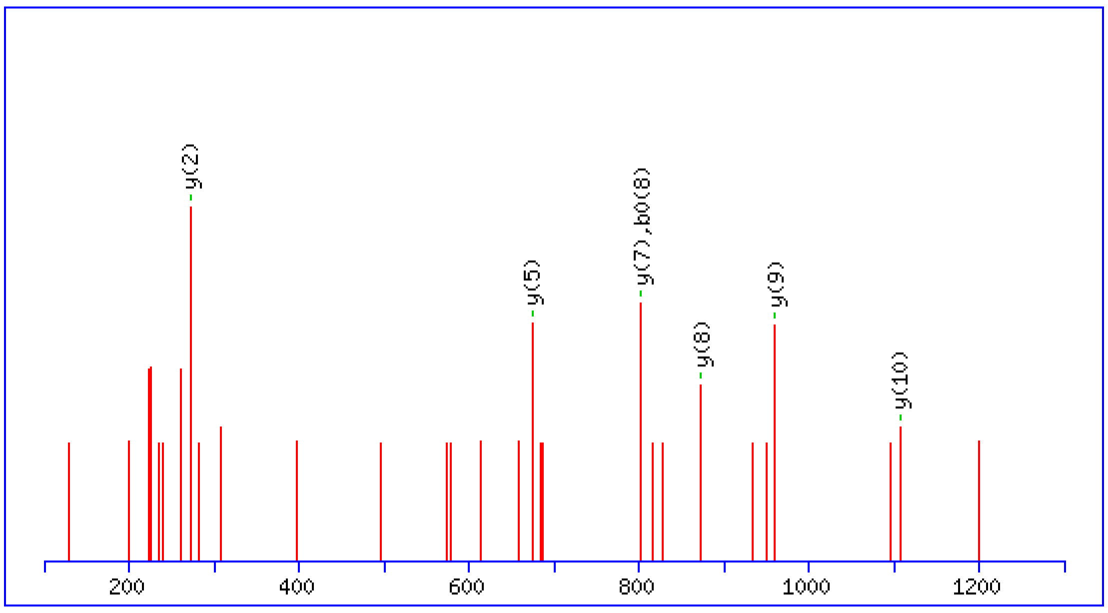
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AEFSAGAWSEPR**
Found in **AR6P6_HUMAN**, ADP-ribosylation factor-like protein 6-interacting protein 6 OS=Homo sapiens GN=ARL6IP6 PE=1 SV=1

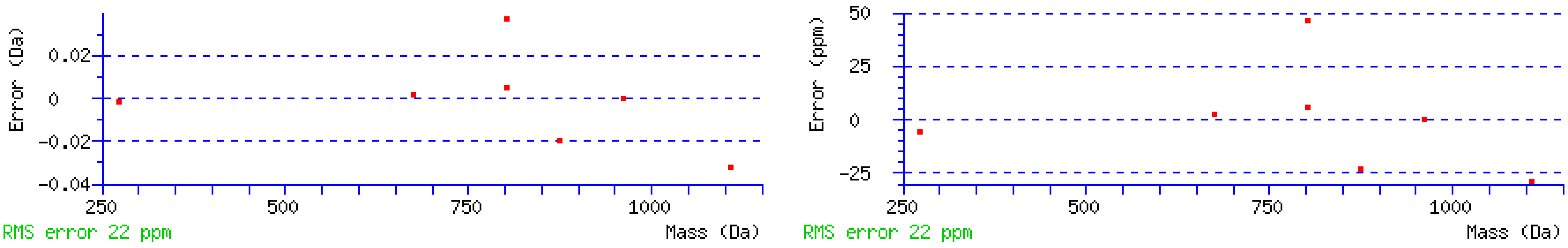
Match to Query 35229: 1306.600268 from(654.307410,2+) rtinseconds(2397) index(27182)
Title: Locus:1.1.1.2180.48
Data file 2011-11-10 - TFD - EP 3-6.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1306.594193
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 38  Expect: 0.0037
Matches : 7/104 fragment ions using 11 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			A							12
2	201.086983	101.047130	183.076418	92.041847	E	1236.564377	618.785827	1219.537828	610.272552	1218.553812	609.780544	11
3	348.155397	174.581336	330.144832	165.576054	F	*1107.521784*	554.264530	1090.495235	545.751256	1089.511219	545.259248	10
4	435.187425	218.097351	417.176860	209.092068	S	*960.453370*	480.730323	943.426821	472.217049	942.442805	471.725041	9
5	506.224539	253.615907	488.213974	244.610625	A	*873.421342*	437.214309	856.394793	428.701035	855.410777	428.209027	8
6	563.246003	282.126640	545.235438	273.121357	G	*802.384228*	401.695752	785.357679	393.182478	784.373663	392.690470	7
7	634.283117	317.645197	616.272552	308.639914	A	745.362764	373.185020	728.336215	364.671746	727.352199	364.179738	6
8	820.362430	410.684853	802.351865	401.679571	W	*674.325650*	337.666463	657.299101	329.153189	656.315085	328.661181	5
9	907.394458	454.200867	889.383893	445.195585	S	488.246337	244.626806	471.219788	236.113532	470.235772	235.621524	4
10	1036.437051	518.722164	1018.426486	509.716881	E	401.214309	201.110792	384.187760	192.597518	383.203744	192.105510	3
11	1133.489815	567.248546	1115.479250	558.243263	P	*272.171716*	136.589496	255.145167	128.076221			2
12					R	175.118952	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.2	1306.594193	0.006075	AEFSAGAWSEPR

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

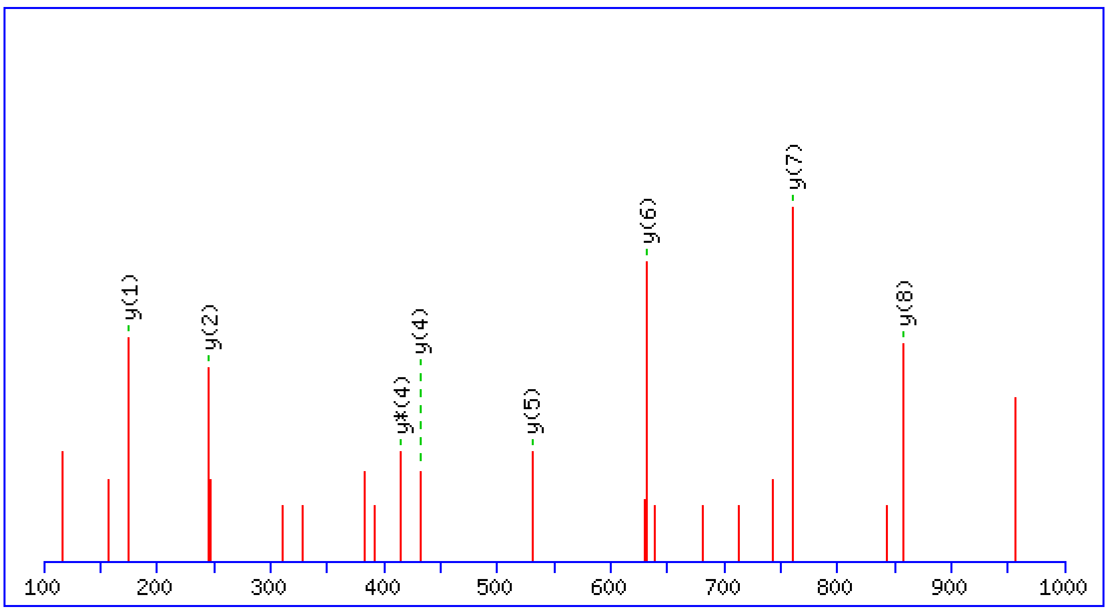
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VPETVADAR**
Found in **ADX_HUMAN**, Adrenodoxin, mitochondrial OS=Homo sapiens GN=FDX1 PE=1 SV=1

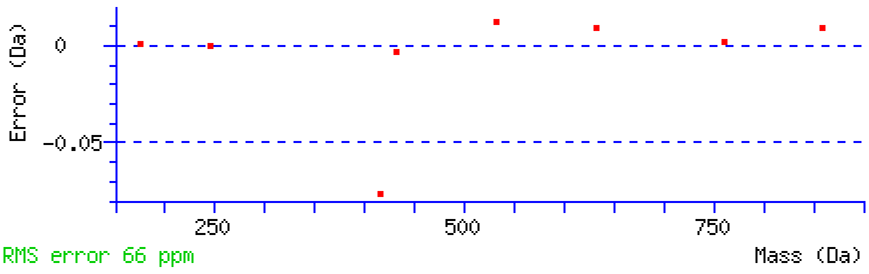
Match to Query 12511: 956.495168 from(479.254860,2+) rtinseconds(1179) index(3115)
Title: Locus:1.1.1.1855.8
Data file 2011-11-10 - TFD - EP 3-7.mgf

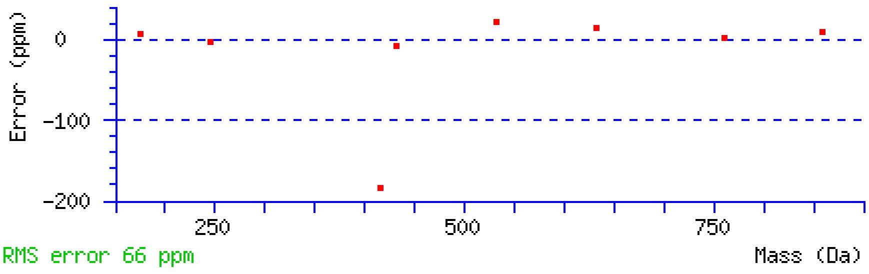
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 956.492706
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 81 **Expect:** 2.8e-007
Matches : 8/72 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483			**V**							9
2	197.128454	99.067865			**P**	***858.431573***	429.719425	841.405024	421.206150	840.421008	420.714142	8
3	326.171047	163.589161	308.160482	154.583879	**E**	***761.378809***	381.193042	744.352260	372.679768	743.368244	372.187760	7
4	427.218726	214.113001	409.208161	205.107719	**T**	***632.336216***	316.671746	615.309667	308.158471	614.325651	307.666463	6
5	526.287140	263.647208	508.276575	254.641926	**V**	***531.288537***	266.147906	514.261988	257.634632	513.277972	257.142624	5
6	597.324254	299.165765	579.313689	290.160483	**A**	***432.220123***	216.613699	415.193574	208.100425	414.209558	207.608417	4
7	712.351197	356.679237	694.340632	347.673954	**D**	361.183009	181.095142	344.156460	172.581868	343.172444	172.089860	3
8	783.388311	392.197793	765.377746	383.192511	**A**	***246.156066***	123.581671	229.129517	115.068396			2
9					**R**	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
80.9	956.492706	0.002462	VPETVADAR
13.4	956.503922	-0.008754	LPDRTEAR
12.7	956.486816	0.008352	KSFYWAR
11.9	956.492691	0.002477	LPTPESAAR
11.5	956.492722	0.002446	VPPTTEGTR
11.2	956.503937	-0.008769	VIPNQQSR
10.8	956.492722	0.002446	LTLGGPDPR
10.5	956.490189	0.004979	VCFYKAR
7.9	956.503922	-0.008754	ILNGQEQR
7.5	956.486176	0.008992	MVHTGEKR

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

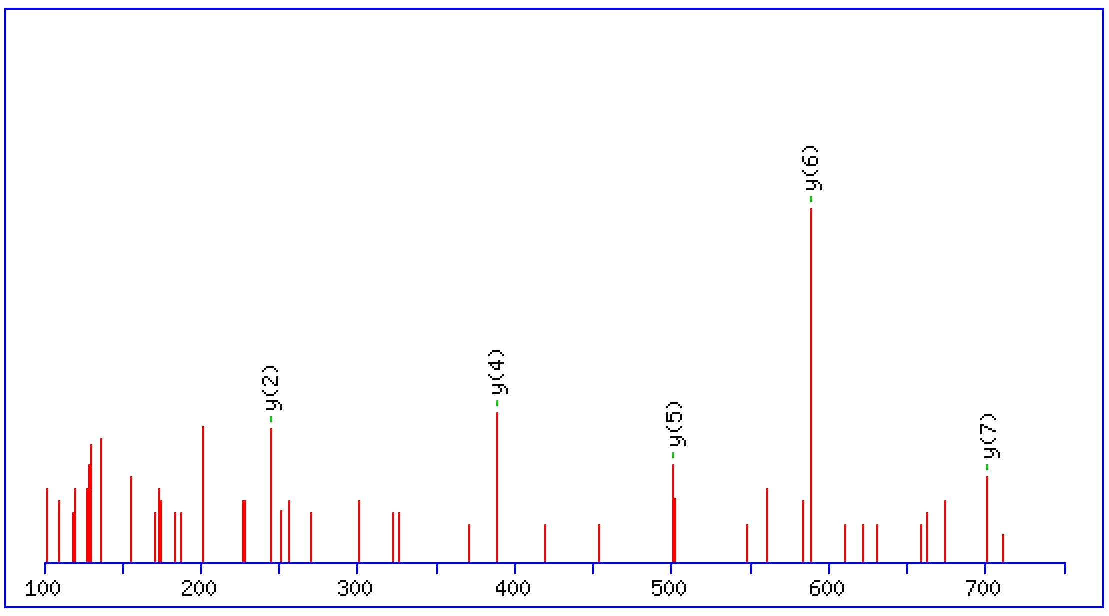
Mascot Search Results

Peptide View

MS/MS Fragmentation of **RPMEFEAALLSPGSPK**
Found in **AKIR1_HUMAN**, Akirin-1 OS=Homo sapiens GN=AKIRIN1 PE=1 SV=1

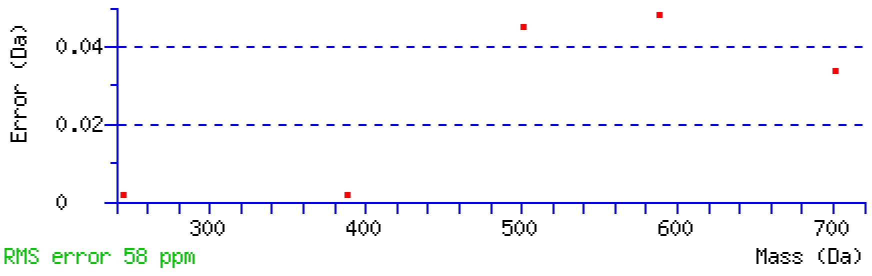
Match to Query 5806: 1744.890176 from(437.229820,4+) rtinseconds(1437) index(11305)
Title: Locus:1.1.1.1900.10
Data file 2011-11-10 - TFD - EP 4-1.mgf

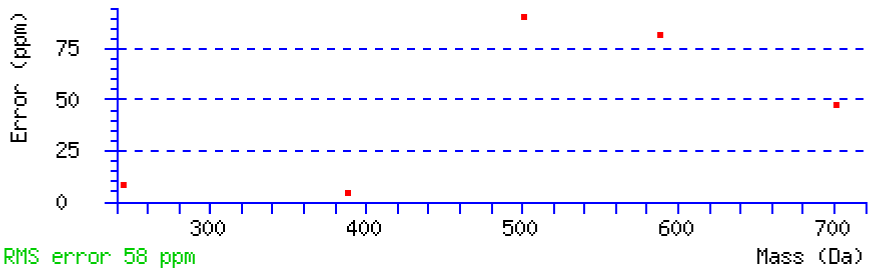
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1744.881775
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P12 : Oxidation (P)
Ions Score: 33 **Expect:** 0.0087
Matches : 5/170 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	157.108387	79.057831	140.081838	70.544557			R							16
2	254.161151	127.584213	237.134602	119.070939			P	1589.787972	795.397624	1572.761423	786.884350	1571.777407	786.392342	15
3	385.201636	193.104456	368.175087	184.591181			M	1492.735208	746.871242	1475.708659	738.357968	1474.724643	737.865960	14
4	514.244229	257.625753	497.217680	249.112478	496.233664	248.620470	E	1361.694723	681.351000	1344.668174	672.837725	1343.684158	672.345717	13
5	661.312643	331.159960	644.286094	322.646685	643.302078	322.154677	F	1232.652130	616.829703	1215.625581	608.316429	1214.641565	607.824421	12
6	790.355236	395.681256	773.328687	387.167982	772.344671	386.675974	E	1085.583716	543.295496	1068.557167	534.782222	1067.573151	534.290214	11
7	861.392350	431.199813	844.365801	422.686538	843.381785	422.194530	A	956.541123	478.774200	939.514574	470.260925	938.530558	469.768917	10
8	932.429464	466.718370	915.402915	458.205095	914.418899	457.713087	A	885.504009	443.255643	868.477460	434.742368	867.493444	434.250360	9
9	1045.513528	523.260402	1028.486979	514.747128	1027.502963	514.255119	L	814.466895	407.737086	797.440346	399.223811	796.456330	398.731803	8
10	1158.597592	579.802434	1141.571043	571.289159	1140.587027	570.797151	L	***701.382831***	351.195054	684.356282	342.681779	683.372266	342.189771	7
11	1245.629620	623.318448	1228.603071	614.805174	1227.619055	614.313165	S	***588.298767***	294.653022	571.272218	286.139747	570.288202	285.647739	6
12	1358.677299	679.842288	1341.650750	671.329013	1340.666734	670.837005	P	***501.266739***	251.137008	484.240190	242.623733	483.256174	242.131725	5
13	1415.698763	708.353019	1398.672214	699.839745	1397.688198	699.347737	G	***388.219060***	194.613168	371.192511	186.099894	370.208495	185.607886	4
14	1502.730791	751.869034	1485.704242	743.355759	1484.720226	742.863751	S	331.197596	166.102436	314.171047	157.589162	313.187031	157.097154	3
15	1599.783555	800.395416	1582.757006	791.882141	1581.772990	791.390133	P	***244.165568***	122.586422	227.139019	114.073148			2
16							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.8	1744.881775	0.008401	RPMEFEAALLSPGSPK
10.2	1744.881775	0.008401	RPMEFEAALLSPGSPK
10.2	1744.881775	0.008401	RPMEFEAALLSPGSPK
8.6	1744.881775	0.008401	RPMEFEAALLSPGSPK
7.5	1744.889664	0.000512	DQHFLEQHPLLQPK
7.3	1744.888336	0.001840	VPEPGYTKVPEPGSIK
7.0	1744.893707	-0.003531	GVSRSLWDVFAFSFK
5.6	1744.889648	0.000528	EEDVRPIFWASRPK
5.3	1744.899567	-0.009391	GESPPTPPGQPPISPKK
4.9	1744.903580	-0.013404	DKGPEPTFKPYLPPK

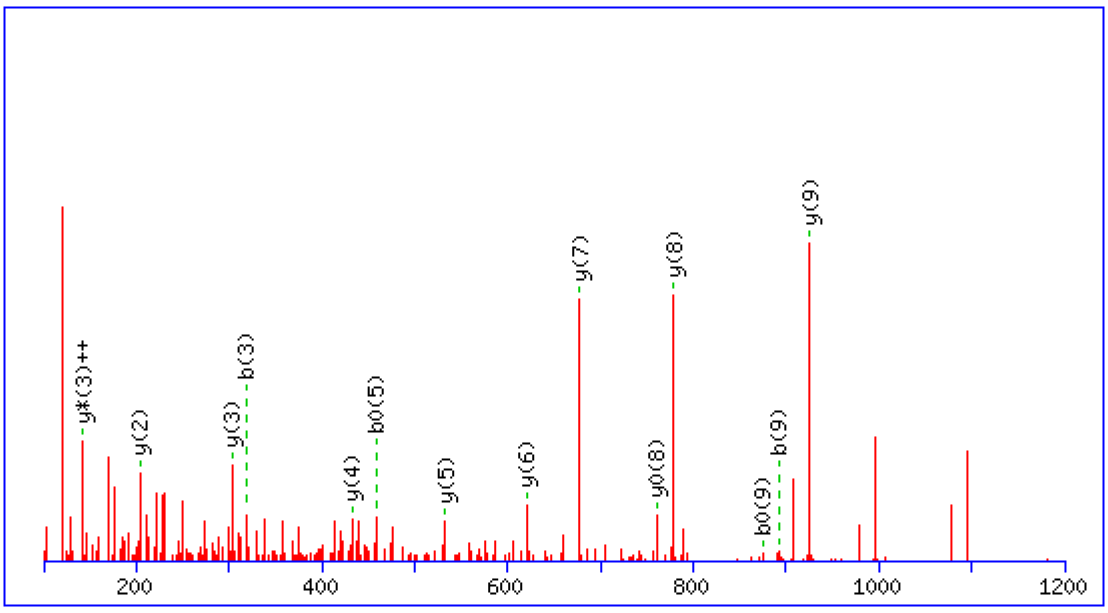
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IGFTGSTEVGK**
Found in **AL1L1_HUMAN**, Aldehyde dehydrogenase family 1 member L1 OS=Homo sapiens GN=ALDH1L1 PE=1 SV=2

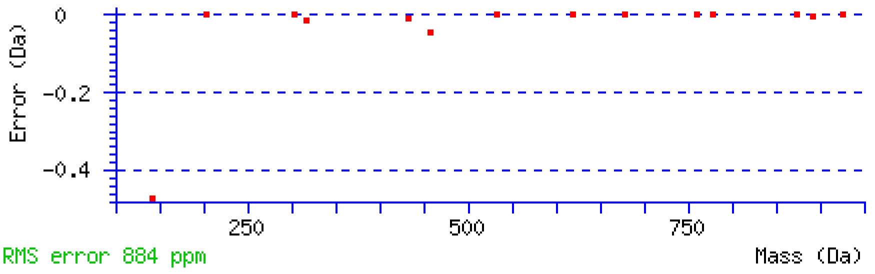
Match to Query 15514: 1094.561068 from(548.287810,2+) rtinseconds(1495) index(12514)
Title: Locus:1.1.1.2083.27
Data file 2011-11-12 - TFD - EP 5-3.mgf

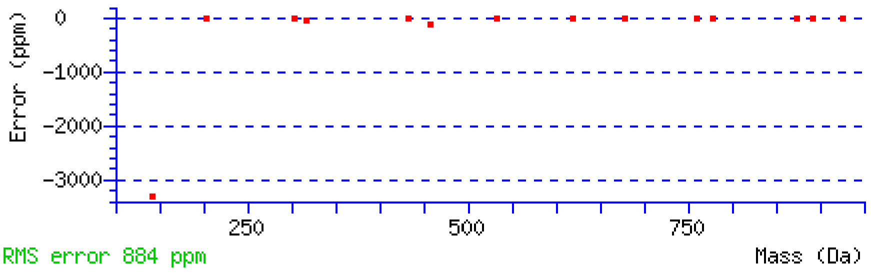
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1094.560806
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 69 **Expect:** 1.2e-006
Matches : 14/88 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							11
2	171.112804	86.060040			G	982.484003	491.745640	965.457454	483.232365	964.473438	482.740357	10
3	**318.181218**	159.594247			F	***925.462539***	463.234908	908.435990	454.721633	907.451974	454.229625	9
4	419.228897	210.118087	401.218332	201.112804	T	***778.394125***	389.700701	761.367576	381.187426	760.383560	380.695418	8
5	476.250361	238.628818	458.239796	229.623536	G	***677.346446***	339.176861	660.319897	330.663587	659.335881	330.171579	7
6	563.282389	282.144833	545.271824	273.139550	S	***620.324982***	310.666129	603.298433	302.152855	602.314417	301.660847	6
7	664.330068	332.668672	646.319503	323.663390	T	***533.292954***	267.150115	516.266405	258.636841	515.282389	258.144833	5
8	793.372661	397.189969	775.362096	388.184686	E	***432.245275***	216.626275	415.218726	208.113001	414.234710	207.620993	4
9	**892.441075**	446.724176	874.430510	437.718893	V	***303.202682***	152.104979	286.176133	143.591704			3
10	949.462539	475.234908	931.451974	466.229625	G	***204.134268***	102.570772	187.107719	94.057498			2
11					K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
86.0	1094.560806	0.000262	VAFTGSTEVGK
68.8	1094.560806	0.000262	IGFTGSTEVGK
8.0	1094.560791	0.000277	VPQSPAPTEGI

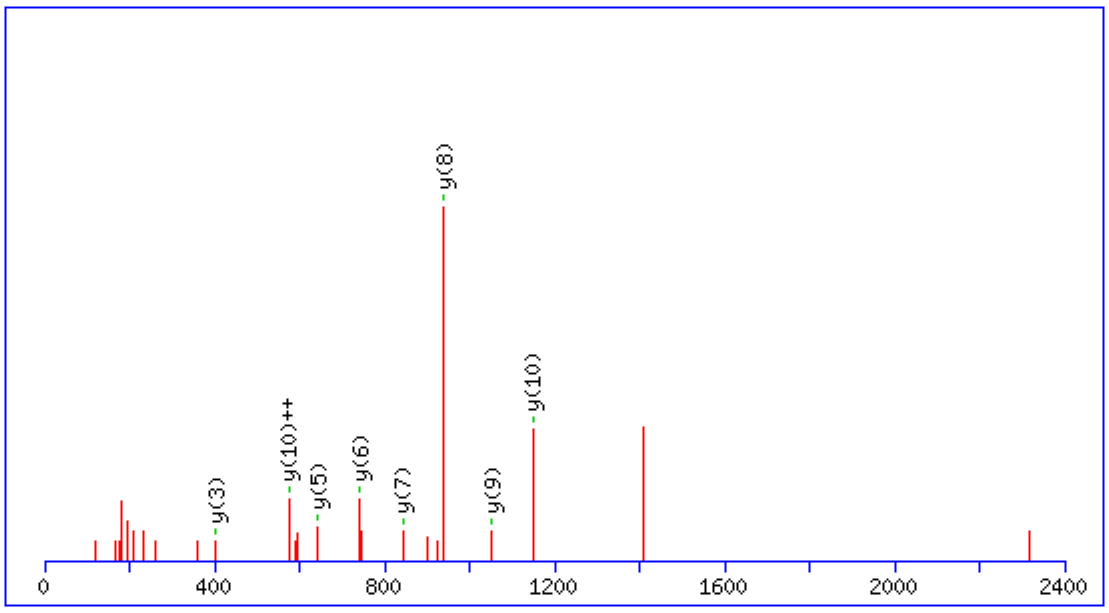
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FLPLPVVQLLDR**
Found in **RETST_HUMAN**, All-trans-retinol 13,14-reductase OS=Homo sapiens GN=RETSAT PE=2 SV=2

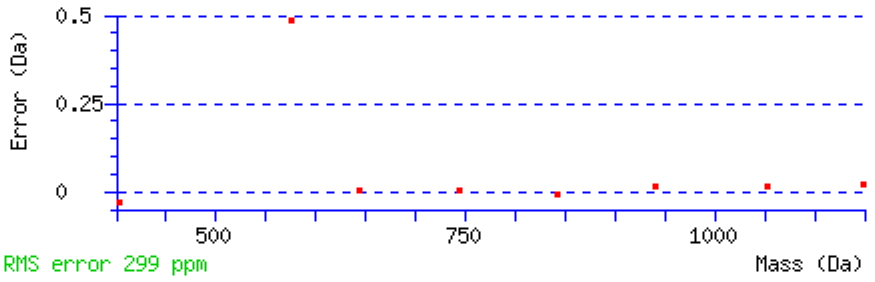
Match to Query 39577: 1408.853008 from(705.433780,2+) rtinseconds(4381) index(67596)
Title: Locus:1.1.1.3038.18
Data file 2011-11-12 - TFD - EP 6-3.mgf

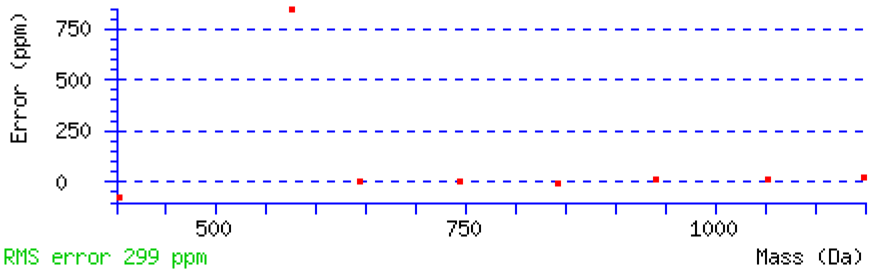
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1408.844223
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 58 **Expect:** 2.9e-006
Matches : 8/96 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.075690	74.541483					F							12
2	261.159754	131.083515					L	1262.783085	631.895181	1245.756536	623.381906	1244.772520	622.889898	11
3	358.212518	179.609897					P	***1149.699021***	575.353149	1132.672472	566.839874	1131.688456	566.347866	10
4	471.296582	236.151929					L	***1052.646257***	526.826767	1035.619708	518.313492	1034.635692	517.821484	9
5	568.349346	284.678311					P	***939.562193***	470.284735	922.535644	461.771460	921.551628	461.279452	8
6	667.417760	334.212518					V	***842.509429***	421.758353	825.482880	413.245078	824.498864	412.753070	7
7	766.486174	383.746725					V	***743.441015***	372.224146	726.414466	363.710871	725.430450	363.218863	6
8	894.544752	447.776014	877.518203	439.262740			Q	***644.372601***	322.689939	627.346052	314.176664	626.362036	313.684656	5
9	1007.628816	504.318046	990.602267	495.804772			L	516.314023	258.660650	499.287474	250.147375	498.303458	249.655367	4
10	1120.712880	560.860078	1103.686331	552.346804			L	***403.229959***	202.118618	386.203410	193.605343	385.219394	193.113335	3
11	1235.739823	618.373550	1218.713274	609.860275	1217.729258	609.368267	D	290.145895	145.576585	273.119346	137.063311	272.135330	136.571303	2
12							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
57.6	1408.844223	0.008785	FLPLPVVQLLDR

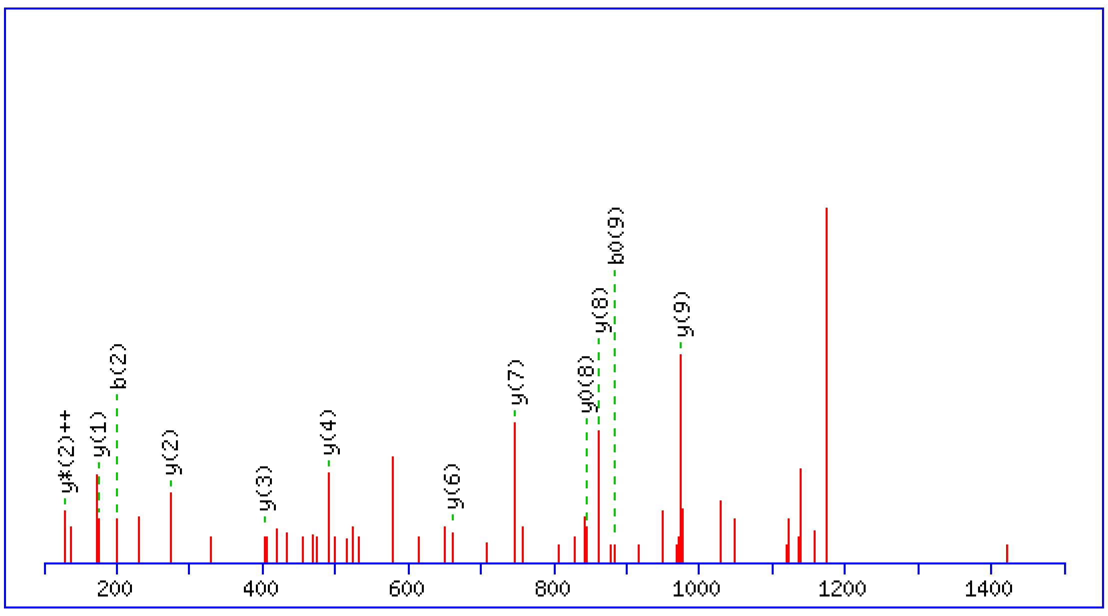
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TVLDSGISEVR**
Found in **CRYAA_HUMAN**, Alpha-crystallin A chain OS=Homo sapiens GN=CRYAA PE=1 SV=2

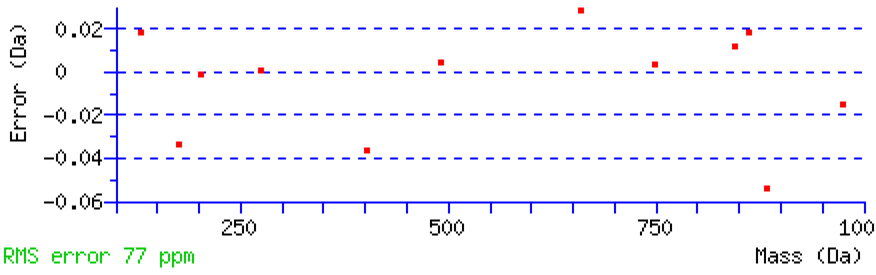
Match to Query 33370: 1174.614048 from(588.314300,2+) rtinseconds(2175) index(24181)
Title: Locus:1.1.1.2085.34
Data file 2011-11-10 - TFD - EP 4-6.mgf

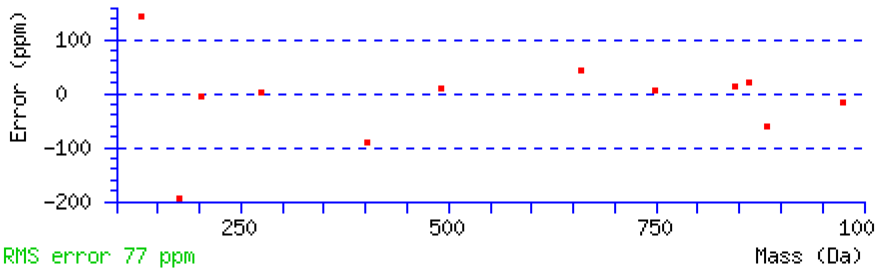
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1174.619370
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.0057
Matches : 12/96 fragment ions using 42 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116	84.044390	42.525833	T							11
2	201.123369	101.065322	183.112804	92.060040	V	1074.578964	537.793120	1057.552415	529.279846	1056.568399	528.787838	10
3	314.207433	157.607354	296.196868	148.602072	L	***975.510550***	488.258913	958.484001	479.745639	957.499985	479.253631	9
4	429.234376	215.120826	411.223811	206.115544	D	***862.426486***	431.716881	845.399937	423.203607	844.415921	422.711599	8
5	516.266404	258.636840	498.255839	249.631558	S	***747.399543***	374.203410	730.372994	365.690135	729.388978	365.198127	7
6	573.287868	287.147572	555.277303	278.142290	G	***660.367515***	330.687396	643.340966	322.174121	642.356950	321.682113	6
7	686.371932	343.689604	668.361367	334.684322	I	603.346051	302.176664	586.319502	293.663389	585.335486	293.171381	5
8	773.403960	387.205618	755.393395	378.200336	S	***490.261987***	245.634631	473.235438	237.121357	472.251422	236.629349	4
9	902.446553	451.726915	884.435988	442.721632	E	***403.229959***	202.118617	386.203410	193.605343	385.219394	193.113335	3
10	1001.514967	501.261122	983.504402	492.255839	V	***274.187366***	137.597321	257.160817	129.084046			2
11					R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.1	1174.619370	-0.005322	TVLDSGISEVR
8.6	1174.608093	0.005955	SLLDASEEAIK
7.0	1174.619354	-0.005306	LLSDLSVDSAR
6.3	1174.619354	-0.005306	TATGLGSKEAPK
4.8	1174.609436	0.004612	QPDNAKALYR
2.0	1174.612839	0.001209	KPPMATTKGGR
2.0	1174.609467	0.004581	QPAPPTSQPPR
0.5	1174.608124	0.005924	EADLDVATITK
0.0	1174.619339	-0.005291	SLIEKNQTDK

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

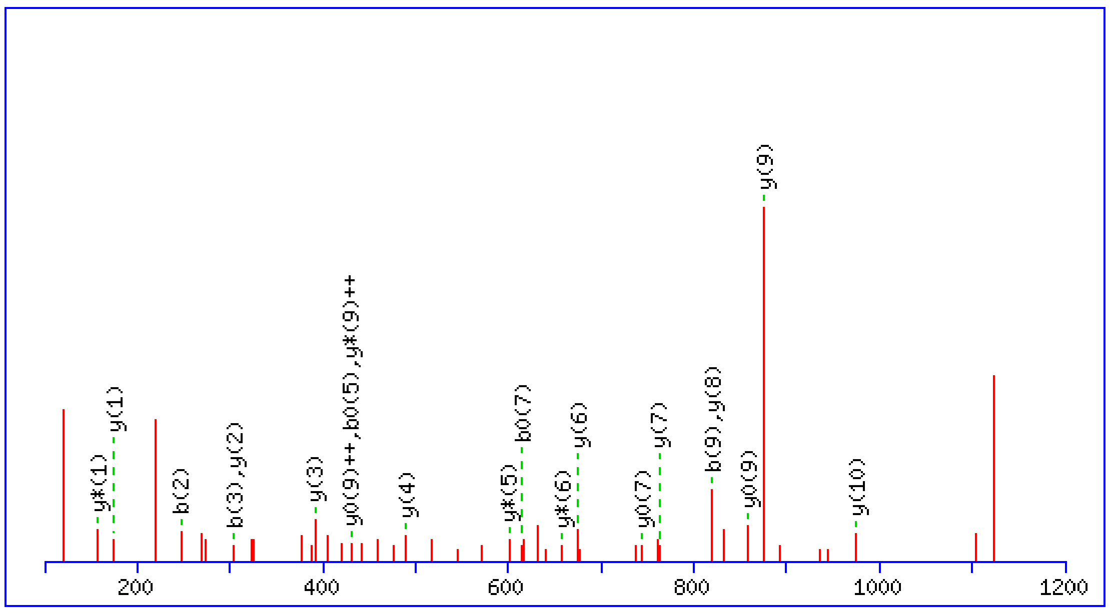
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FVGGSGQVSER**
Found in **AOFA_HUMAN**, Amine oxidase [flavin-containing] A OS=Homo sapiens GN=MAOA PE=1 SV=1

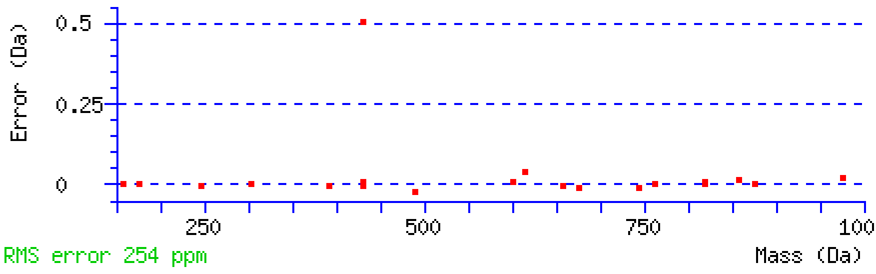
Match to Query 422366: 1121.544948 from(561.779750,2+) rtinseconds(1146) index(331421)
Title: Locus:1.1.1.770.30
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

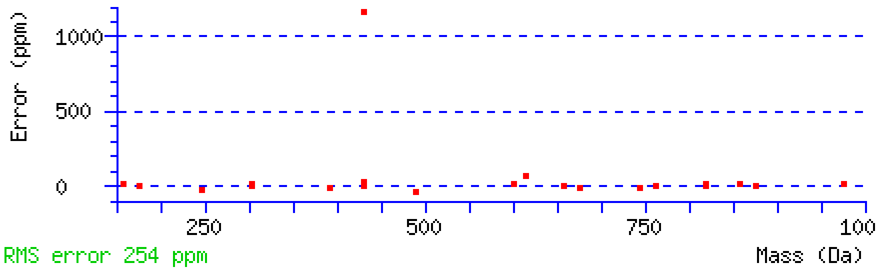
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1121.546555
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 56  Expect: 2.2e-005
Matches : 21/98 fragment ions using 41 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.075690	74.541483					F							11
2	**247.144104**	124.075690					V	***975.485399***	488.246338	958.458850	479.733063	957.474834	479.241055	10
3	**304.165568**	152.586422					G	***876.416985***	438.712131	859.390436	430.198856	858.406420	429.706848	9
4	361.187032	181.097154					G	***819.395521***	410.201399	802.368972	401.688124	801.384956	401.196116	8
5	448.219060	224.613168			430.208495	215.607885	S	***762.374057***	381.690667	745.347508	373.177392	744.363492	372.685384	7
6	505.240524	253.123900			487.229959	244.118617	G	***675.342029***	338.174653	658.315480	329.661378	657.331464	329.169370	6
7	633.299102	317.153189	616.272553	308.639914	615.288537	308.147906	Q	618.320565	309.663921	601.294016	301.150646	600.310000	300.658638	5
8	732.367516	366.687396	715.340967	358.174121	714.356951	357.682113	V	***490.261987***	245.634631	473.235438	237.121357	472.251422	236.629349	4
9	**819.399544**	410.203410	802.372995	401.690135	801.388979	401.198127	S	***391.193573***	196.100425	374.167024	187.587150	373.183008	187.095142	3
10	948.442137	474.724706	931.415588	466.211432	930.431572	465.719424	E	***304.161545***	152.584411	287.134996	144.071136	286.150980	143.579128	2
11							R	***175.118952***	88.063114	158.092403	79.549840			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.1	1121.546555	-0.001607	FVGGSGQVSER
6.0	1121.538681	0.006267	VTSLPAMTDR
0.7	1121.538666	0.006282	DSLGGNSKTIM
0.4	1121.542725	0.002223	FPQSVVTTPM
0.4	1121.542694	0.002254	FVKTPEAAPM
0.4	1121.542694	0.002254	FVKTPEAAPM
0.4	1121.542694	0.002254	FVKTPEAAPM
0.4	1121.535309	0.009639	FVPGSSQSEGK

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

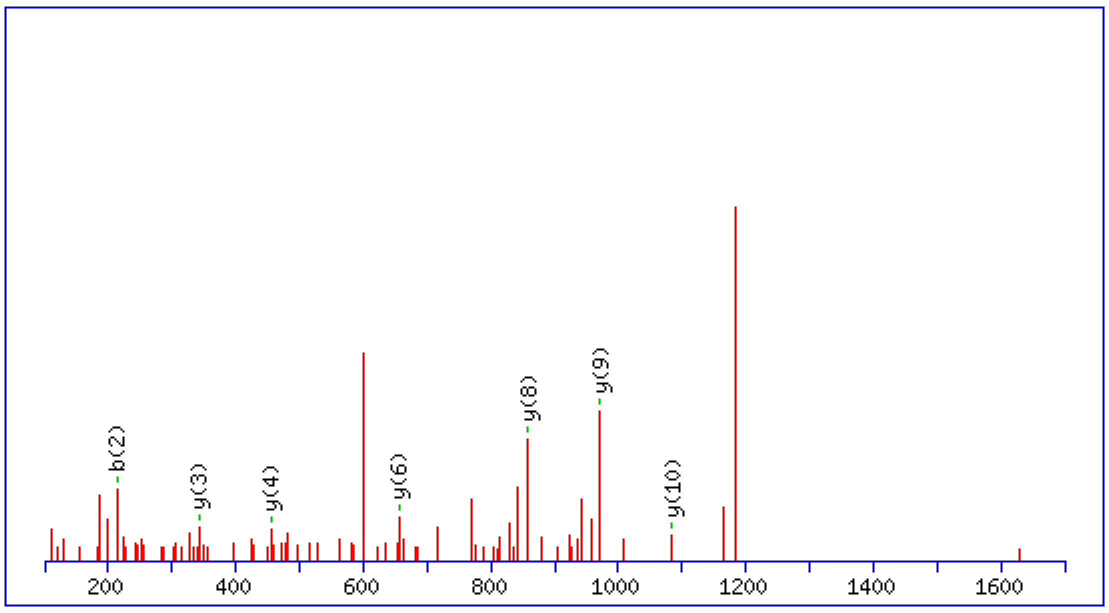
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLLSDSNLHDA**
Found in **CPIN1_HUMAN**, Anamorsin OS=Homo sapiens GN=CIAPIN1 PE=1 SV=2

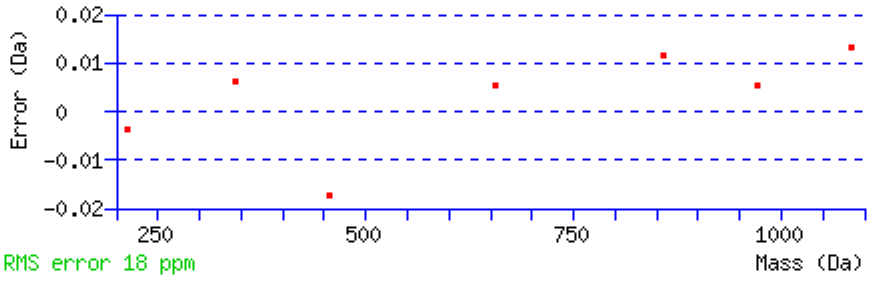
Match to Query 28395: 1182.596628 from(592.305590,2+) rtinseconds(2050) index(23025)
Title: Locus:1.1.1.2198.39
Data file 2011-11-12 - TFD - EP 5-4.mgf

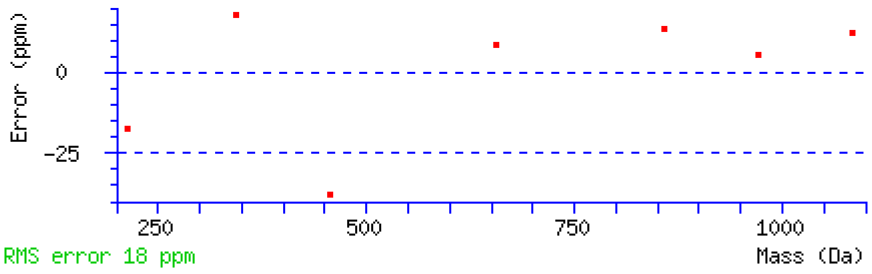
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1182.588058
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 42 **Expect:** 0.00072
Matches : 7/92 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							11
2	213.159754	107.083515					L	***1084.526928***	542.767102	1067.500379	534.253827	1066.516363	533.761819	10
3	326.243818	163.625547					L	***971.442864***	486.225070	954.416315	477.711795	953.432299	477.219787	9
4	413.275846	207.141561			395.265281	198.136278	S	***858.358800***	429.683038	841.332251	421.169763	840.348235	420.677755	8
5	528.302789	264.655033			510.292224	255.649750	D	771.326772	386.167024	754.300223	377.653749	753.316207	377.161741	7
6	615.334817	308.171046			597.324252	299.165764	S	***656.299829***	328.653552	639.273280	320.140278	638.289264	319.648270	6
7	729.377744	365.192510	712.351195	356.679235	711.367179	356.187227	N	569.267801	285.137539	552.241252	276.624264	551.257236	276.132256	5
8	842.461808	421.734542	825.435259	413.221267	824.451243	412.729259	L	***455.224874***	228.116075			437.214309	219.110792	4
9	979.520720	490.263998	962.494171	481.750723	961.510155	481.258715	H	***342.140810***	171.574043			324.130245	162.568760	3
10	1094.547663	547.777469	1077.521114	539.264195	1076.537098	538.772187	D	205.081898	103.044587			187.071333	94.039304	2
11							A	90.054955	45.531115					1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.0	1182.588058	0.008570	VLLSDSNLHDA

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

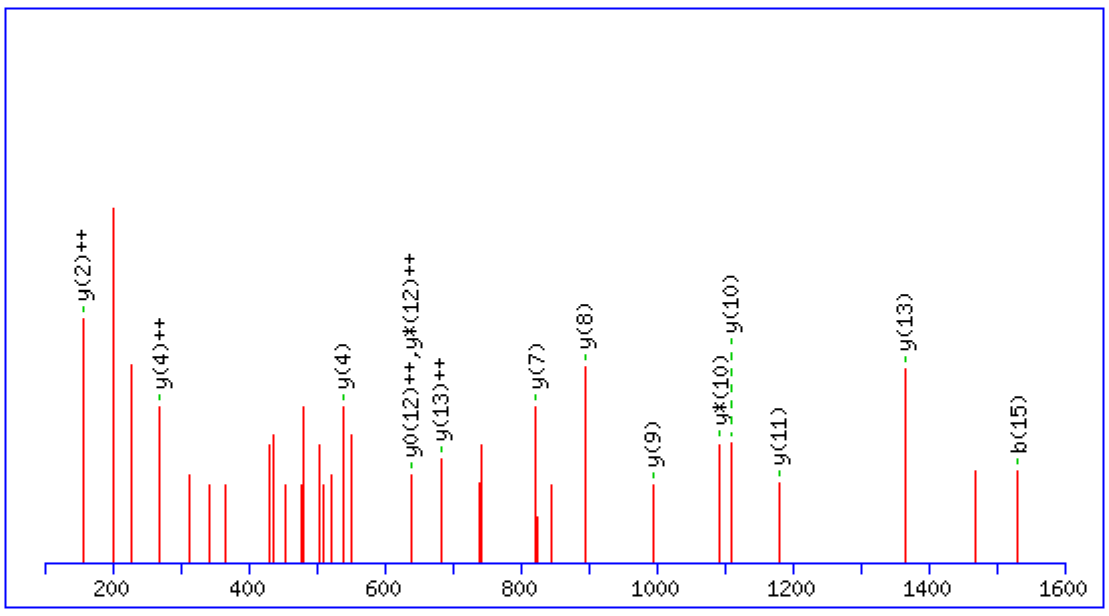
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **DLIALANTAGEVLLHR**
Found in **APC4_HUMAN**, Anaphase-promoting complex subunit 4 OS=Homo sapiens GN=ANAPC4 PE=1 SV=2

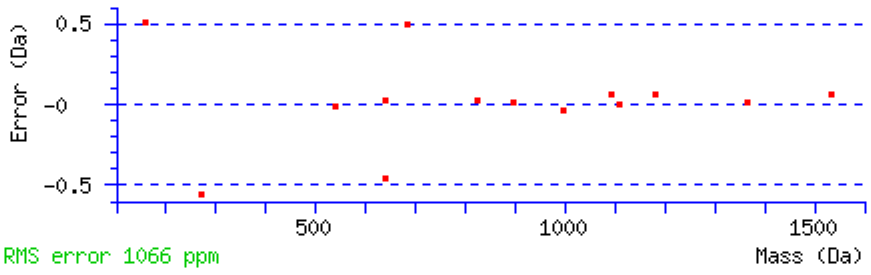
Match to Query 25771: 1704.947742 from(569.323190,3+) rtinseconds(4372) index(65895)
Title: Locus:1.1.1.3039.9
Data file 2011-11-12 - TFD - EP 6-2.mgf

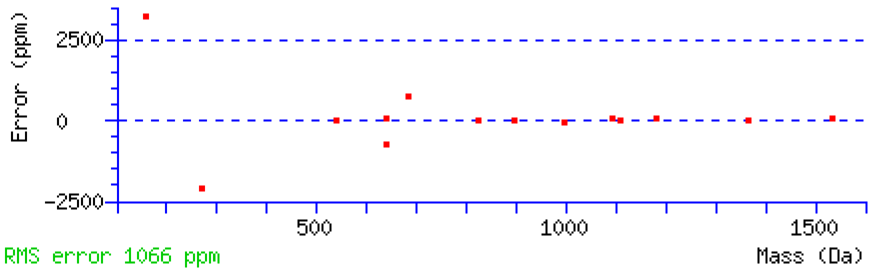
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1704.952240
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 41  Expect: 0.00026
Matches : 14/158 fragment ions using 22 most intense peaks   (help)
```

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	116.034219	58.520748			98.023654	49.515465	D							16
2	229.118283	115.062779			211.107718	106.057497	L	1590.932603	795.969939	1573.906054	787.456665	1572.922038	786.964657	15
3	342.202347	171.604811			324.191782	162.599529	I	1477.848539	739.427907	1460.821990	730.914633	1459.837974	730.422625	14
4	413.239461	207.123368			395.228896	198.118086	A	***1364.764475***	682.885875	1347.737926	674.372601	1346.753910	673.880593	13
5	526.323525	263.665401			508.312960	254.660118	L	1293.727361	647.367319	1276.700812	638.854044	1275.716796	638.362036	12
6	597.360639	299.183958			579.350074	290.178675	A	***1180.643297***	590.825286	1163.616748	582.312012	1162.632732	581.820004	11
7	711.403566	356.205421	694.377017	347.692146	693.393001	347.200138	N	***1109.606183***	555.306729	1092.579634	546.793455	1091.595618	546.301447	10
8	812.451245	406.729261	795.424696	398.215986	794.440680	397.723978	T	***995.563256***	498.285266	978.536707	489.771991	977.552691	489.279983	9
9	883.488359	442.247818	866.461810	433.734543	865.477794	433.242535	A	***894.515577***	447.761426	877.489028	439.248152	876.505012	438.756144	8
10	940.509823	470.758550	923.483274	462.245275	922.499258	461.753267	G	***823.478463***	412.242869	806.451914	403.729595	805.467898	403.237587	7
11	1069.552416	535.279846	1052.525867	526.766572	1051.541851	526.274564	E	766.456999	383.732137	749.430450	375.218863	748.446434	374.726855	6
12	1168.620830	584.814053	1151.594281	576.300779	1150.610265	575.808771	V	637.414406	319.210841	620.387857	310.697566			5
13	1281.704894	641.356085	1264.678345	632.842811	1263.694329	632.350802	L	***538.345992***	269.676634	521.319443	261.163359			4
14	1394.788958	697.898117	1377.762409	689.384842	1376.778393	688.892834	L	425.261928	213.134602	408.235379	204.621327			3
15	1531.847870	766.427573	1514.821321	757.914298	1513.837305	757.422290	H	312.177864	156.592570	295.151315	148.079295			2
16							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of DLIALANTAGEVLLHR
(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	1704.952240	-0.004498	DLIALANTAGEVLLHR
2.7	1704.938324	0.009418	AQISSPNLRTRPPPR
2.7	1704.938324	0.009418	AQISSPNLRTRPPPR
2.7	1704.938324	0.009418	AQISSPNLRTRPPPR
1.1	1704.941025	0.006717	LLGQPSLDSLPIPAPR
1.1	1704.941025	0.006717	LLGQPSLDSLPIPAPR

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

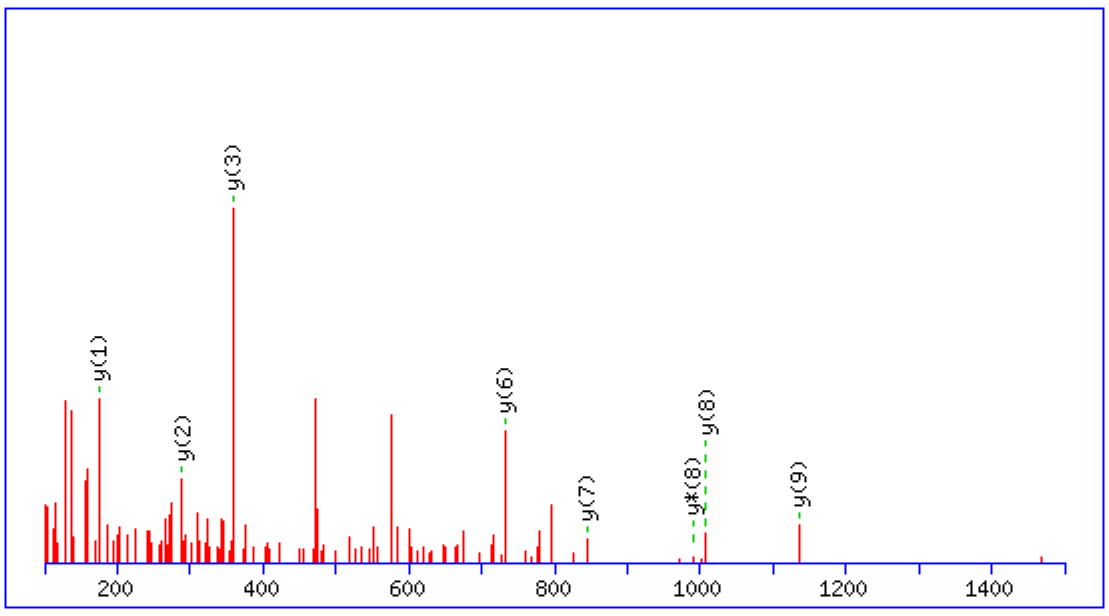
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MQYIERSALR**
Found in **ANKK1_HUMAN**, Ankyrin repeat and protein kinase domain-containing protein 1 OS=Homo sapiens GN=ANKK1 PE=1 SV=1

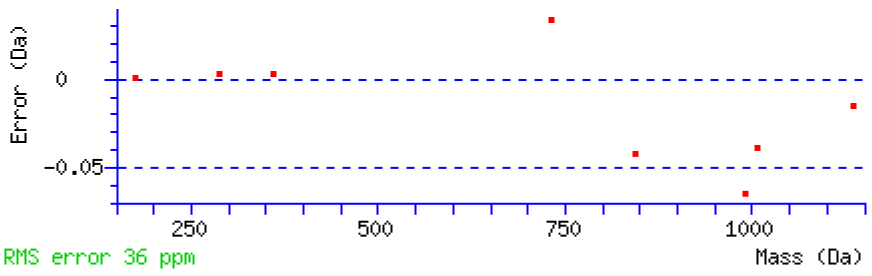
Match to Query 34402: 1265.645652 from(422.889160,3+) rtinseconds(1965) index(21924)
Title: Locus:1.1.1.2092.5
Data file 2011-11-10 - TFD - EP 3-4.mgf

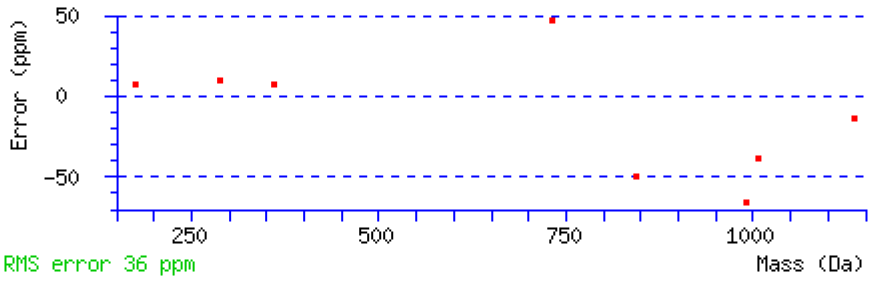
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1265.654999
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 56  Expect: 2.8e-005
Matches : 8/92 fragment ions using 11 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	132.047761	66.527518					M							10
2	260.106339	130.556807	243.079790	122.043533			Q	***1135.621833***	568.314554	1118.595284	559.801280	1117.611268	559.309272	9
3	423.169668	212.088472	406.143119	203.575198			Y	***1007.563255***	504.285265	990.536706	495.771991	989.552690	495.279983	8
4	536.253732	268.630504	519.227183	260.117230			I	***844.499926***	422.753601	827.473377	414.240326	826.489361	413.748318	7
5	665.296325	333.151801	648.269776	324.638526	647.285760	324.146518	E	***731.415862***	366.211569	714.389313	357.698294	713.405297	357.206286	6
6	821.397436	411.202356	804.370887	402.689081	803.386871	402.197073	R	602.373269	301.690272	585.346720	293.176998	584.362704	292.684990	5
7	908.429464	454.718370	891.402915	446.205095	890.418899	445.713087	S	446.272158	223.639717	429.245609	215.126442	428.261593	214.634434	4
8	979.466578	490.236927	962.440029	481.723652	961.456013	481.231644	A	***359.240130***	180.123703	342.213581	171.610428			3
9	1092.550642	546.778959	1075.524093	538.265685	1074.540077	537.773676	L	***288.203016***	144.605146	271.176467	136.091871			2
10							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
66.0	1265.643753	0.001899	MKYENELALR
55.9	1265.654999	-0.009347	MQYIERSALR
27.1	1265.643768	0.001884	EFKMNIEALR
9.4	1265.643799	0.001853	YLQAVVSSMPR
7.1	1265.636414	0.009238	APDALSHTPSVR
6.6	1265.643814	0.001838	YPVGVSNMVLR
6.5	1265.643799	0.001853	YLQAVVSSMPR
5.8	1265.651672	-0.006020	WHQVETTPLR
4.3	1265.651169	-0.005517	AGLYMKMEPVK
2.5	1265.655014	-0.009362	MQTAYGIKAQR

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

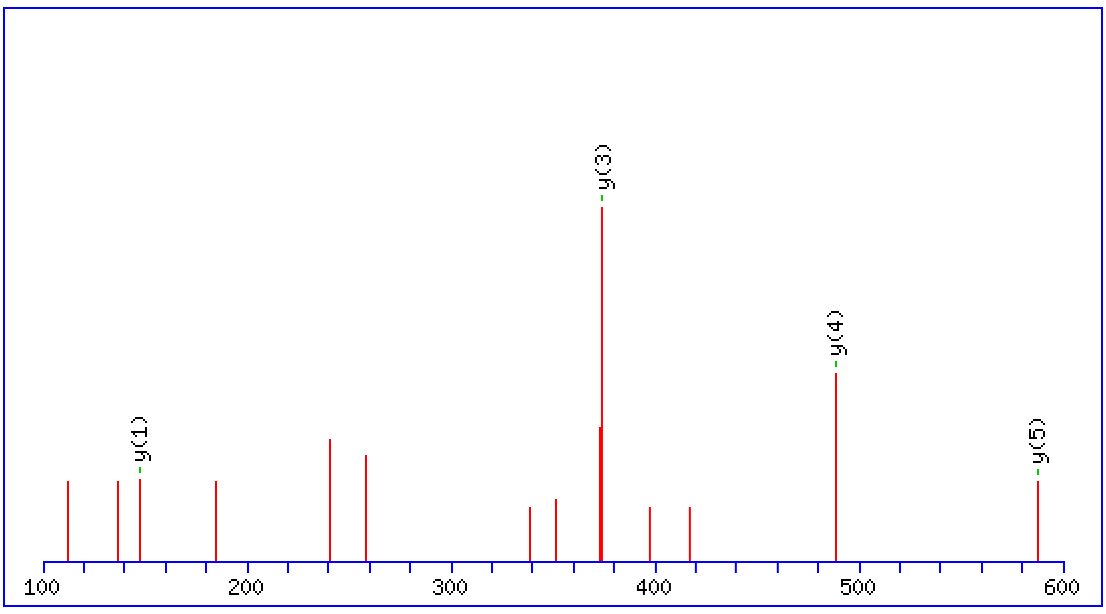
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **KPVNLNK**
Found in **AN30B_HUMAN**, Ankyrin repeat domain-containing protein 30B OS=Homo sapiens GN=ANKRD30B PE=2 SV=2

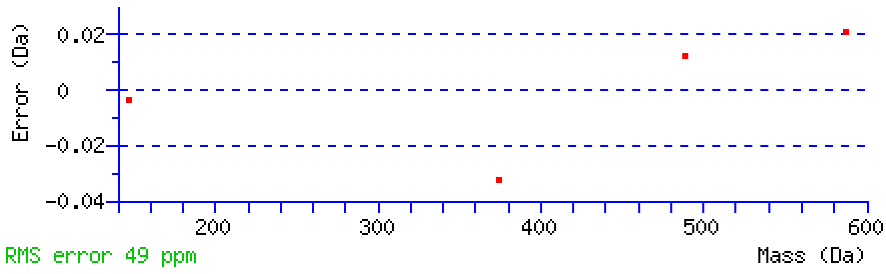
Match to Query 35547: 827.481948 from(414.748250,2+) rtinseconds(2429) index(185076)
Title: Locus:1.1.1.1614.4
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

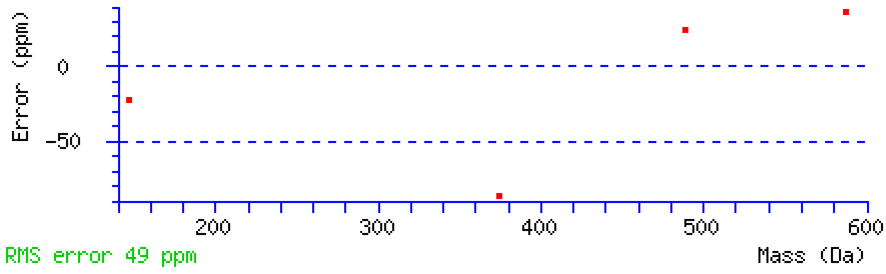
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 827.486481
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
P2      : Oxidation (P)
Ions Score: 34  Expect: 0.0053
Matches : 4/48 fragment ions using 5 most intense peaks   (help)
```

#	b	b^{++}	b*	b*$^{++}$	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	129.102239	65.054757	112.075690	56.541483	K					7
2	242.149918	121.578597	225.123369	113.065322	P	700.398815	350.703046	683.372266	342.189771	6
3	341.218332	171.112804	324.191783	162.599529	V	*587.351136*	294.179206	570.324587	285.665932	5
4	455.261259	228.134267	438.234710	219.620993	N	*488.282722*	244.644999	471.256173	236.131724	4
5	568.345323	284.676300	551.318774	276.163025	L	*374.239795*	187.623535	357.213246	179.110261	3
6	682.388250	341.697763	665.361701	333.184488	N	261.155731	131.081503	244.129182	122.568229	2
7					K	*147.112804*	74.060040	130.086255	65.546765	1

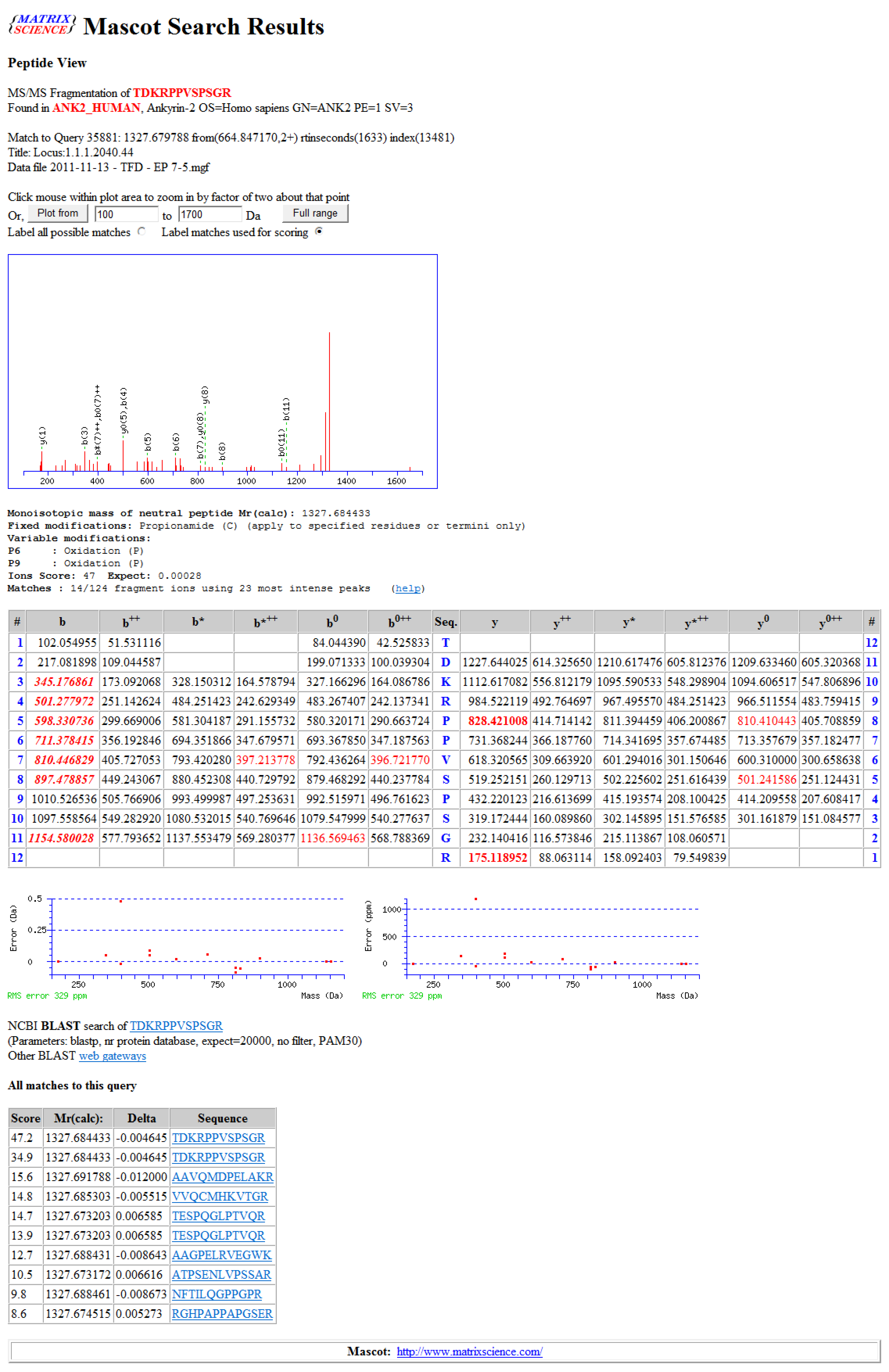




NCBI **BLAST** search of KPVNLNK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.3	827.486481	-0.004533	KPVNLNK
21.5	827.475266	0.006682	LQVDPLK
19.0	827.486481	-0.004533	VIQNNLK
9.6	827.486481	-0.004533	KAPVQAAK
8.6	827.475250	0.006698	LQTIEPK
7.3	827.486481	-0.004533	QLALQQK
6.2	827.475250	0.006698	SPAPSILK
2.8	827.486481	-0.004533	ANVGLNLK
2.8	827.475266	0.006682	DLPPVKK
2.8	827.475266	0.006682	IPVEVQK



MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **TDKRPPVSPSGR**
Found in **ANK2_HUMAN**, Ankyrin-2 OS=Homo sapiens GN=ANK2 PE=1 SV=3

Match to Query 35881: 1327.679788 from(664.847170,2+) rtinseconds(1633) index(13481)
Title: Locus:1.1.1.2040.44
Data file 2011-11-13 - TFD - EP 7-5.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●

```
Monoisotopic mass of neutral peptide Mr(calc): 1327.684433
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P6      : Oxidation (P)
P9      : Oxidation (P)
Ions Score: 47  Expect: 0.00028
Matches : 14/124 fragment ions using 23 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							12
2	217.081898	109.044587			199.071333	100.039304	D	1227.644025	614.325650	1210.617476	605.812376	1209.633460	605.320368	11
3	***345.176861***	173.092068	328.150312	164.578794	327.166296	164.086786	K	1112.617082	556.812179	1095.590533	548.298904	1094.606517	547.806896	10
4	***501.277972***	251.142624	484.251423	242.629349	483.267407	242.137341	R	984.522119	492.764697	967.495570	484.251423	966.511554	483.759415	9
5	***598.330736***	299.669006	581.304187	291.155732	580.320171	290.663724	P	**828.421008**	414.714142	811.394459	406.200867	810.410443	405.708859	8
6	***711.378415***	356.192846	694.351866	347.679571	693.367850	347.187563	P	731.368244	366.187760	714.341695	357.674485	713.357679	357.182477	7
7	***810.446829***	405.727053	793.420280	397.213778	792.436264	396.721770	V	618.320565	309.663920	601.294016	301.150646	600.310000	300.658638	6
8	***897.478857***	449.243067	880.452308	440.729792	879.468292	440.237784	S	519.252151	260.129713	502.225602	251.616439	501.241586	251.124431	5
9	1010.526536	505.766906	993.499987	497.253631	992.515971	496.761623	P	432.220123	216.613699	415.193574	208.100425	414.209558	207.608417	4
10	1097.558564	549.282920	1080.532015	540.769646	1079.547999	540.277637	S	319.172444	160.089860	302.145895	151.576585	301.161879	151.084577	3
11	***1154.580028***	577.793652	1137.553479	569.280377	1136.569463	568.788369	G	232.140416	116.573846	215.113867	108.060571			2
12							R	**175.118952**	88.063114	158.092403	79.549839			1

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.2	1327.684433	-0.004645	TDKRPPVSPSGR
34.9	1327.684433	-0.004645	TDKRPPVSPSGR
15.6	1327.691788	-0.012000	AAVQMDPELAKR
14.8	1327.685303	-0.005515	VVQCMHKVTGR
14.7	1327.673203	0.006585	TESPQGLPTVQR
13.9	1327.673203	0.006585	TESPQGLPTVQR
12.7	1327.688431	-0.008643	AAGPELRVEGWK
10.5	1327.673172	0.006616	ATPSENLVPSSAR
9.8	1327.688461	-0.008673	NFTILQGPPGPR
8.6	1327.674515	0.005273	RGHPAPPAPGSER

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

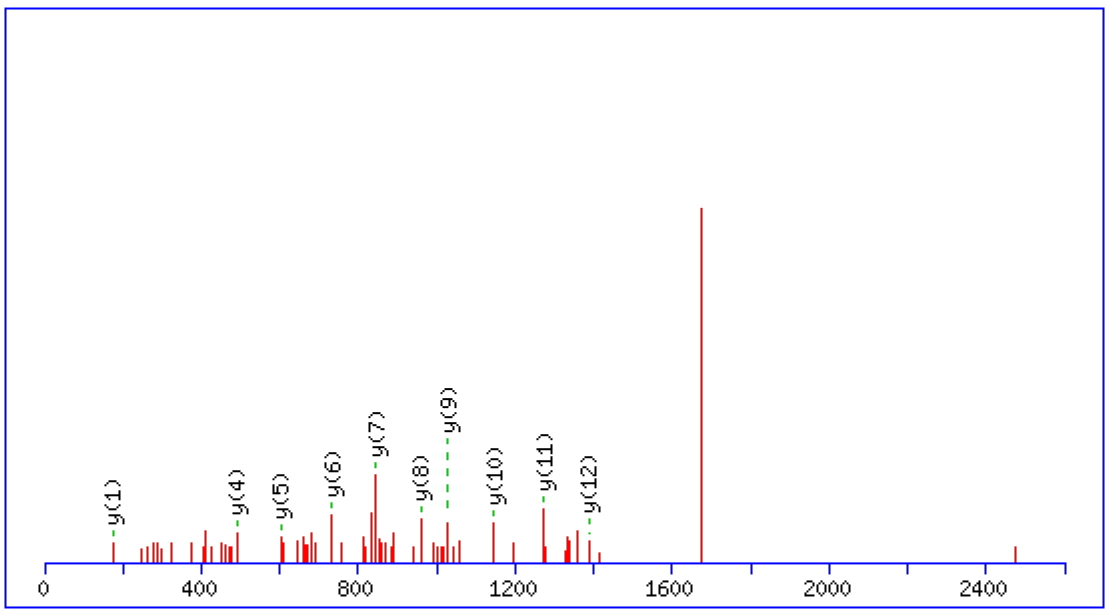
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GAGTNEDALIEILTTR**
Found in **ANXA3_HUMAN**, Annexin A3 OS=Homo sapiens GN=ANXA3 PE=1 SV=3

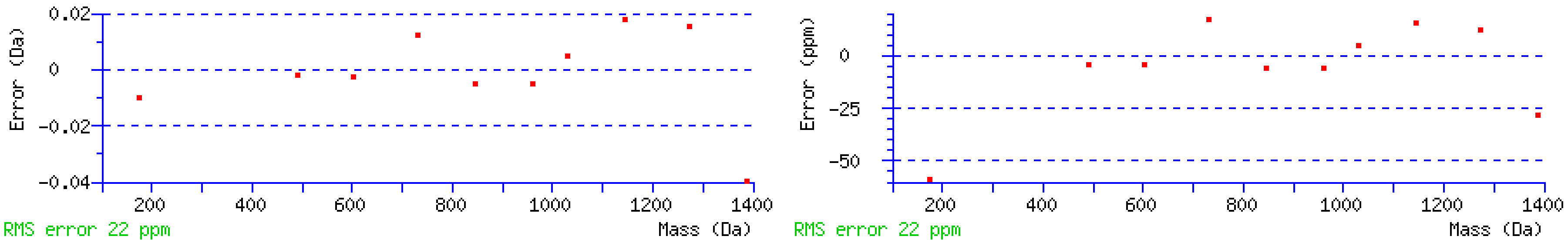
Match to Query 54713: 1672.862768 from(837.438660,2+) rtinseconds(3881) index(57470)
Title: Locus:1.1.1.2887.34
Data file 2011-11-12 - TFD - EP 5-4.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [0] to [2600] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1672.863159
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 88 **Expect:** 2.4e-008
Matches : 10/164 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							16
2	129.065854	65.036565					A	1616.848993	808.928134	1599.822444	800.414860	1598.838428	799.922852	15
3	186.087318	93.547297					G	1545.811879	773.409577	1528.785330	764.896303	1527.801314	764.404295	14
4	287.134997	144.071136			269.124432	135.065854	T	1488.790415	744.898845	1471.763866	736.385571	1470.779850	735.893563	13
5	401.177924	201.092600	384.151375	192.579326	383.167359	192.087318	N	***1387.742736***	694.375006	1370.716187	685.861731	1369.732171	685.369723	12
6	530.220517	265.613897	513.193968	257.100622	512.209952	256.608614	E	***1273.699809***	637.353542	1256.673260	628.840268	1255.689244	628.348260	11
7	645.247460	323.127368	628.220911	314.614094	627.236895	314.122086	D	***1144.657216***	572.832246	1127.630667	564.318971	1126.646651	563.826963	10
8	716.284574	358.645925	699.258025	350.132651	698.274009	349.640643	A	***1029.630273***	515.318774	1012.603724	506.805500	1011.619708	506.313492	9
9	829.368638	415.187957	812.342089	406.674683	811.358073	406.182675	L	***958.593159***	479.800217	941.566610	471.286943	940.582594	470.794935	8
10	942.452702	471.729989	925.426153	463.216715	924.442137	462.724707	I	***845.509095***	423.258185	828.482546	414.744911	827.498530	414.252903	7
11	1071.495295	536.251285	1054.468746	527.738011	1053.484730	527.246003	E	***732.425031***	366.716153	715.398482	358.202879	714.414466	357.710871	6
12	1184.579359	592.793317	1167.552810	584.280043	1166.568794	583.788035	I	***603.382438***	302.194857	586.355889	293.681582	585.371873	293.189574	5
13	1297.663423	649.335349	1280.636874	640.822075	1279.652858	640.330067	L	***490.298374***	245.652825	473.271825	237.139550	472.287809	236.647542	4
14	1398.711102	699.859189	1381.684553	691.345914	1380.700537	690.853906	T	377.214310	189.110793	360.187761	180.597518	359.203745	180.105510	3
15	1499.758781	750.383028	1482.732232	741.869754	1481.748216	741.377746	T	276.166631	138.586953	259.140082	130.073679	258.156066	129.581671	2
16							R	***175.118952***	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
87.5	1672.863159	-0.000391	GAGTNEDALIEILTTR
18.3	1672.878433	-0.015665	DGNDNVTLLFAPLLR
10.8	1672.856628	0.006140	SLEAINGSGLQMGLQR
2.4	1672.849472	0.013296	GDPGPPGPPPVILPGMK
0.4	1672.849472	0.013296	GDPGPPGPPPVILPGMK
0.4	1672.849472	0.013296	GDPGPPGPPPVILPGMK

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

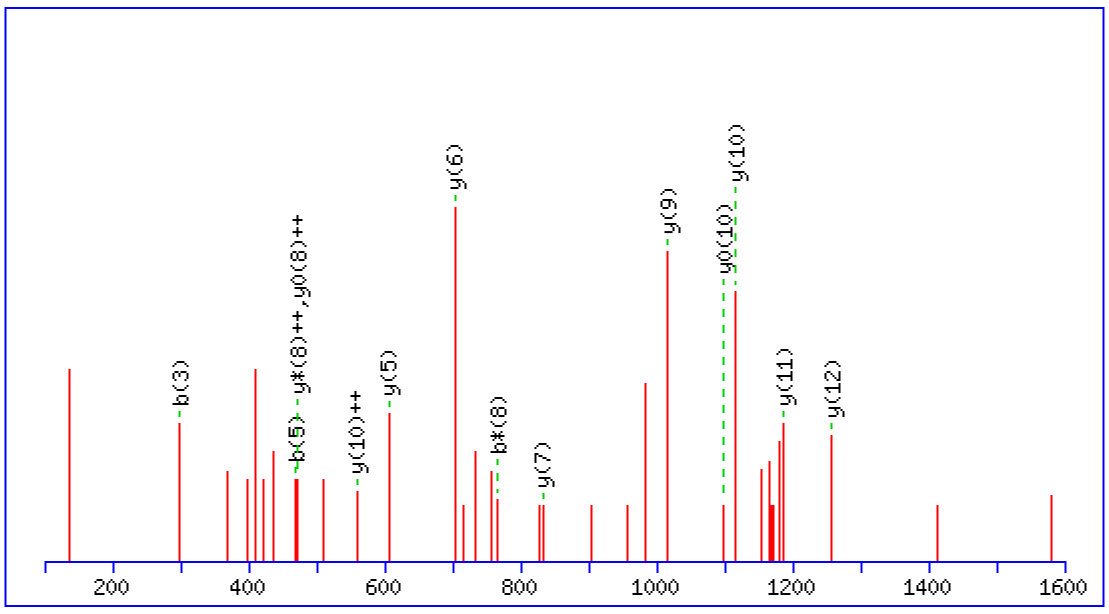
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QVAAVGQEPQVFGR**
Found in **TAP1_HUMAN**, Antigen peptide transporter 1 OS=Homo sapiens GN=TAP1 PE=1 SV=2

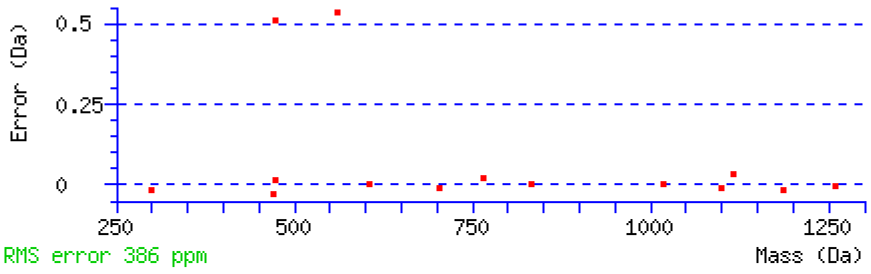
Match to Query 825999: 1484.766028 from(743.390290,2+) rtinseconds(2212) index(515985)
Title: Locus:1.1.1.1176.43
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

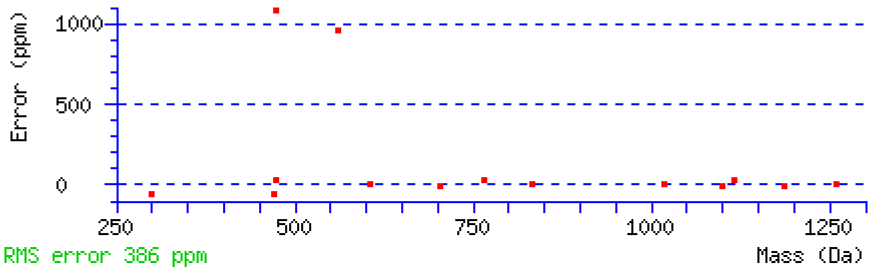
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1484.773590
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 37  Expect: 0.00065
Matches : 14/130 fragment ions using 27 most intense peaks   (help)
```

#	b	b^{++}	b*	b*$^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^0	y^{0++}	#
1	129.065854	65.036565	112.039305	56.523291			Q							14
2	228.134268	114.570772	211.107719	106.057498			V	1357.722277	679.364777	1340.695728	670.851502	1339.711712	670.359494	13
3	**299.171382**	150.089329	282.144833	141.576055			A	***1258.653863***	629.830570	1241.627314	621.317295	1240.643298	620.825287	12
4	370.208496	185.607886	353.181947	177.094612			A	***1187.616749***	594.312013	1170.590200	585.798738	1169.606184	585.306730	11
5	**469.276910**	235.142093	452.250361	226.628819			V	***1116.579635***	558.793456	1099.553086	550.280181	1098.569070	549.788173	10
6	526.298374	263.652825	509.271825	255.139551			G	***1017.511221***	509.259249	1000.484672	500.745974	999.500656	500.253966	9
7	654.356952	327.682114	637.330403	319.168840			Q	960.489757	480.748517	943.463208	472.235242	942.479192	471.743234	8
8	783.399545	392.203411	766.372996	383.690136	765.388980	383.198128	E	***832.431179***	416.719228	815.404630	408.205953	814.420614	407.713945	7
9	880.452309	440.729793	863.425760	432.216518	862.441744	431.724510	P	***703.388586***	352.197931	686.362037	343.684657			6
10	1008.510887	504.759082	991.484338	496.245807	990.500322	495.753799	Q	***606.335822***	303.671549	589.309273	295.158275			5
11	1107.579301	554.293289	1090.552752	545.780014	1089.568736	545.288006	V	478.277244	239.642260	461.250695	231.128986			4
12	1254.647715	627.827496	1237.621166	619.314221	1236.637150	618.822213	F	379.208830	190.108053	362.182281	181.594778			3
13	1311.669179	656.338228	1294.642630	647.824953	1293.658614	647.332945	G	232.140416	116.573846	215.113867	108.060571			2
14							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of QVAAVGQEPQVFGR
(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	1484.773590	-0.007562	QVAAVGQEPQVFGR
2.6	1484.776932	-0.010904	GLQAVMAGLANGEVR
0.9	1484.752441	0.013587	SPSPPRAGPFGYPR

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

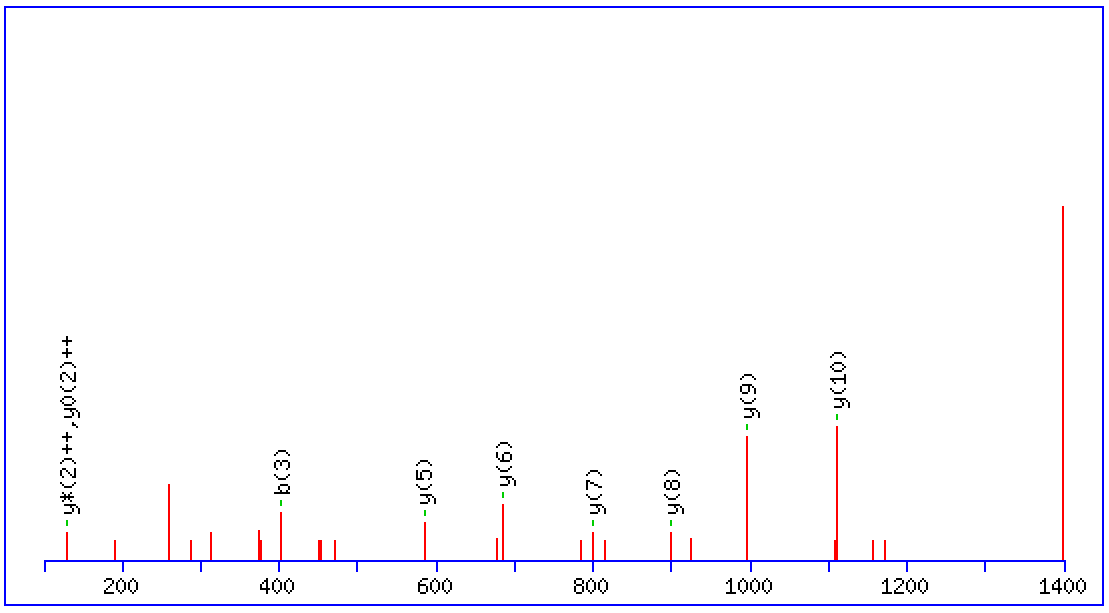
Mascot Search Results

Peptide View

MS/MS Fragmentation of **CLDPVDTPNPTR**
Found in **SLPI_HUMAN**, Antileukoproteinase OS=Homo sapiens GN=SLPI PE=1 SV=2

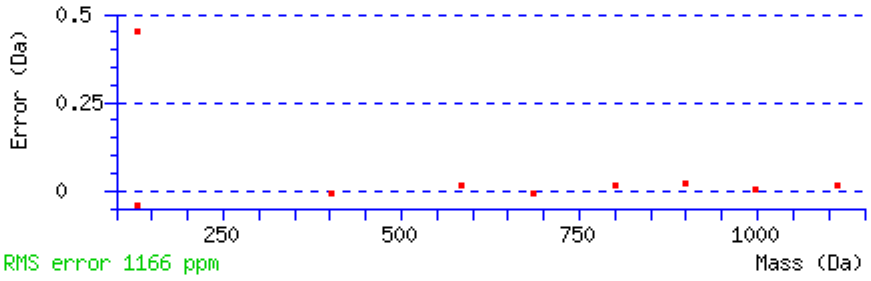
Match to Query 34959: 1397.661328 from(699.837940,2+) rtinseconds(1870) index(14597)
Title: Locus:1.1.1.2118.50
Data file 2011-11-10 - TFD - EP 3-7.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●

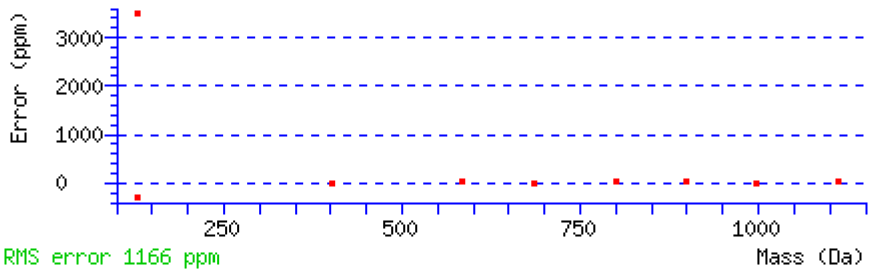


Monoisotopic mass of neutral peptide Mr(calc): 1397.660919
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 43 **Expect:** 0.00052
Matches : 9/110 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	175.053575	88.030425					C							12
2	288.137639	144.572457					L	1224.621893	612.814585	1207.595344	604.301310	1206.611328	603.809302	11
3	403.164582	202.085929			385.154017	193.080647	D	*1111.537829*	556.272553	1094.511280	547.759278	1093.527264	547.267270	10
4	500.217346	250.612311			482.206781	241.607028	P	*996.510886*	498.759081	979.484337	490.245807	978.500321	489.753799	9
5	599.285760	300.146518			581.275195	291.141235	V	*899.458122*	450.232699	882.431573	441.719425	881.447557	441.227417	8
6	714.312703	357.659989			696.302138	348.654707	D	*800.389708*	400.698492	783.363159	392.185218	782.379143	391.693210	7
7	815.360382	408.183829			797.349817	399.178546	T	*685.362765*	343.185021	668.336216	334.671746	667.352200	334.179738	6
8	912.413146	456.710211			894.402581	447.704928	P	*584.315086*	292.661181	567.288537	284.147907	566.304521	283.655899	5
9	1026.456073	513.731675	1009.429524	505.218400	1008.445508	504.726392	N	487.262322	244.134799	470.235773	235.621525	469.251757	235.129517	4
10	1123.508837	562.258057	1106.482288	553.744782	1105.498272	553.252774	P	373.219395	187.113335	356.192846	178.600061	355.208830	178.108053	3
11	1224.556516	612.781896	1207.529967	604.268622	1206.545951	603.776614	T	276.166631	138.586953	259.140082	130.073679	258.156066	129.581671	2
12							R	175.118952	88.063114	158.092403	79.549839			1



RMS error 1166 ppm



RMS error 1166 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.8	1397.660919	0.000409	CLDPVDTPNPTR

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

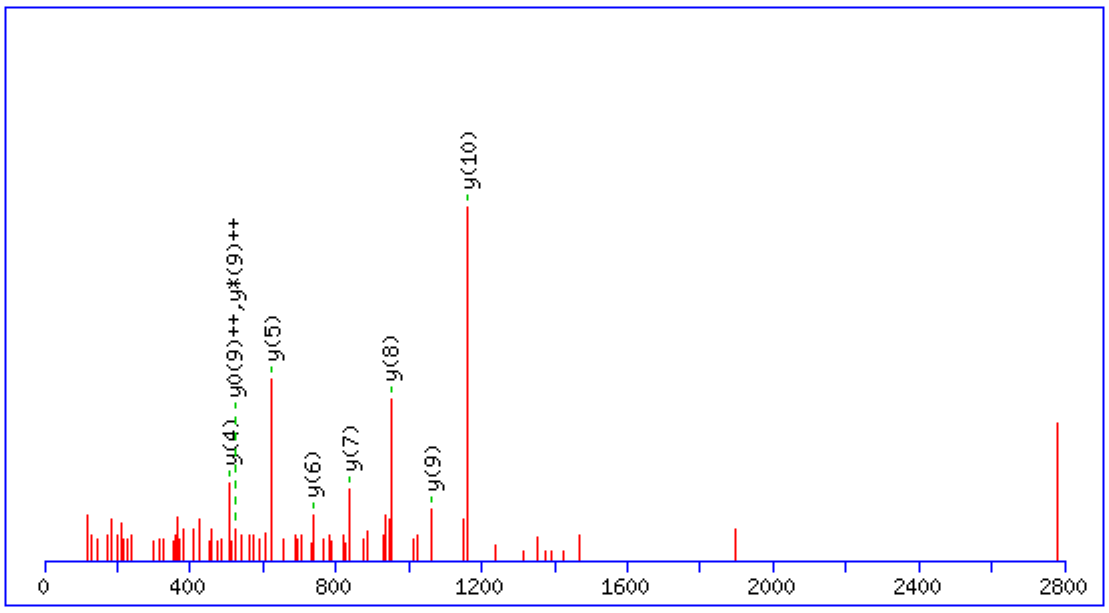
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EVPLNTIIFMGR**
Found in **ANT3_HUMAN**, Antithrombin-III OS=Homo sapiens GN=SERPINC1 PE=1 SV=1

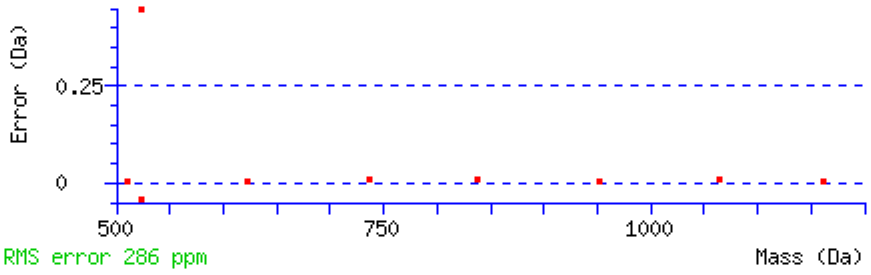
Match to Query 38861: 1388.756588 from(695.385570,2+) rtinseconds(3588) index(53470)
Title: Locus:1.1.1.2784.26
Data file 2011-11-10 - TFD - EP 3-3.mgf

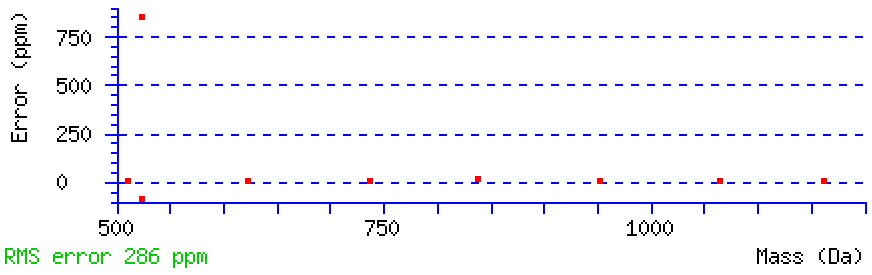
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1388.748596
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 50 **Expect:** 3.6e-005
Matches : 9/112 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	E							12
2	229.118283	115.062780			211.107718	106.057497	V	1260.713291	630.860283	1243.686742	622.347009	1242.702726	621.855001	11
3	326.171047	163.589161			308.160482	154.583879	P	***1161.644877***	581.326077	1144.618328	572.812802	1143.634312	572.320794	10
4	439.255111	220.131193			421.244546	211.125911	L	***1064.592113***	532.799694	1047.565564	524.286420	1046.581548	523.794412	9
5	553.298038	277.152657	536.271489	268.639383	535.287473	268.147375	N	***951.508049***	476.257662	934.481500	467.744388	933.497484	467.252380	8
6	654.345717	327.676497	637.319168	319.163222	636.335152	318.671214	T	***837.465122***	419.236199	820.438573	410.722924	819.454557	410.230916	7
7	767.429781	384.218529	750.403232	375.705254	749.419216	375.213246	I	***736.417443***	368.712359	719.390894	360.199085			6
8	880.513845	440.760561	863.487296	432.247286	862.503280	431.755278	I	***623.333379***	312.170327	606.306830	303.657053			5
9	1027.582259	514.294768	1010.555710	505.781493	1009.571694	505.289485	F	***510.249315***	255.628295	493.222766	247.115021			4
10	1158.622744	579.815010	1141.596195	571.301736	1140.612179	570.809728	M	363.180901	182.094088	346.154352	173.580814			3
11	1215.644208	608.325742	1198.617659	599.812468	1197.633643	599.320459	G	232.140416	116.573846	215.113867	108.060571			2
12							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.9	1388.748596	0.007992	EVPLNTIIFMGR
2.6	1388.769699	-0.013111	KLQAMVIEISNK

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

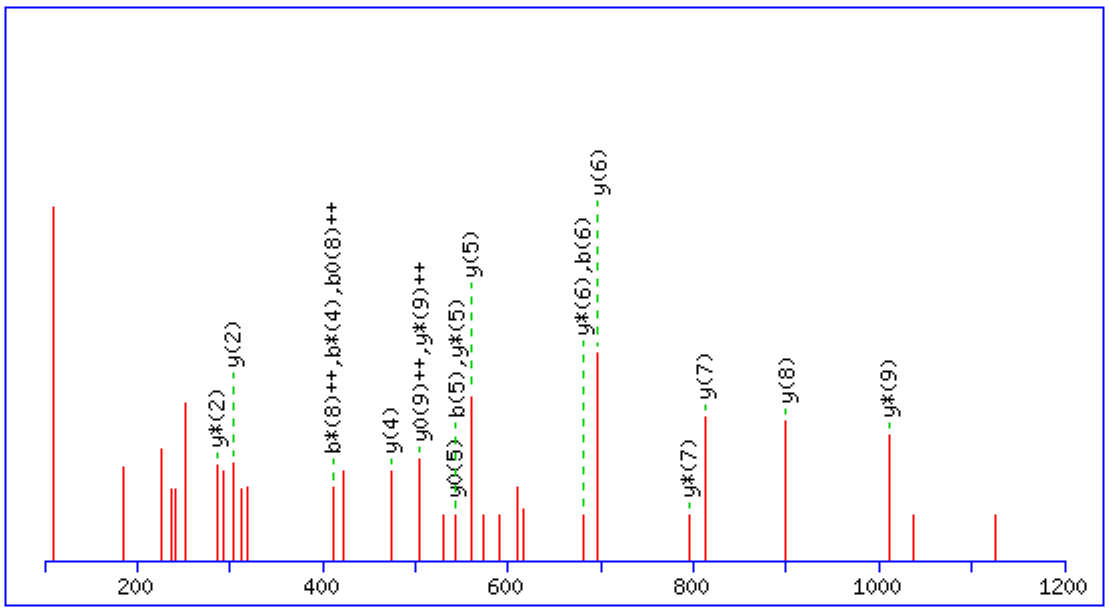
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LVQSDHSAVQR**
Found in **AP1G2_HUMAN**, AP-1 complex subunit gamma-like 2 OS=Homo sapiens GN=AP1G2 PE=1 SV=1

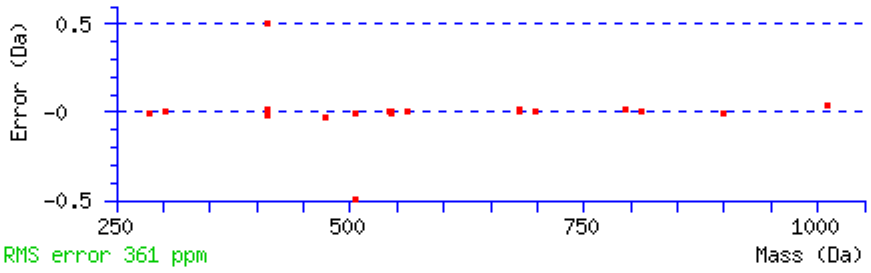
Match to Query 32805: 1238.637852 from(413.886560,3+) rtinseconds(769) index(204)
Title: Locus:1.1.1.1740.2
Data file 2011-11-10 - TFD - EP 3-2.mgf

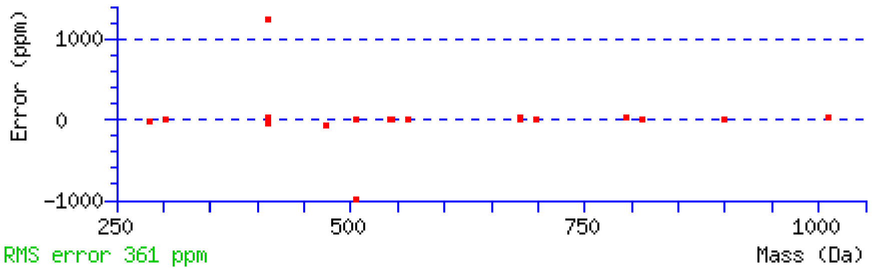
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1238.636749
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 32  Expect: 0.0084
Matches : 19/102 fragment ions using 27 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							11
2	213.159754	107.083515					V	1126.559961	563.783618	1109.533412	555.270344	1108.549396	554.778336	10
3	341.218332	171.112804	324.191783	162.599529			Q	1027.491547	514.249411	1010.464998	505.736137	1009.480982	505.244129	9
4	428.250360	214.628818	411.223811	206.115543	410.239795	205.623535	S	***899.432969***	450.220122	882.406420	441.706848	881.422404	441.214840	8
5	**543.277303**	272.142290	526.250754	263.629015	525.266738	263.137007	D	***812.400941***	406.704108	795.374392	398.190834	794.390376	397.698826	7
6	**680.336215**	340.671745	663.309666	332.158471	662.325650	331.666463	H	***697.373998***	349.190637	680.347449	340.677362	679.363433	340.185354	6
7	767.368243	384.187759	750.341694	375.674485	749.357678	375.182477	S	***560.315086***	280.661181	543.288537	272.147906	542.304521	271.655898	5
8	838.405357	419.706316	821.378808	411.193042	820.394792	410.701034	A	***473.283058***	237.145167	456.256509	228.631892			4
9	937.473771	469.240523	920.447222	460.727249	919.463206	460.235241	V	402.245944	201.626610	385.219395	193.113335			3
10	1065.532349	533.269812	1048.505800	524.756538	1047.521784	524.264530	Q	***303.177530***	152.092403	286.150981	143.579128			2
11							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LVQSDHSAVQR
(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	1238.636749	0.001103	LVQSDHSAVQR

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

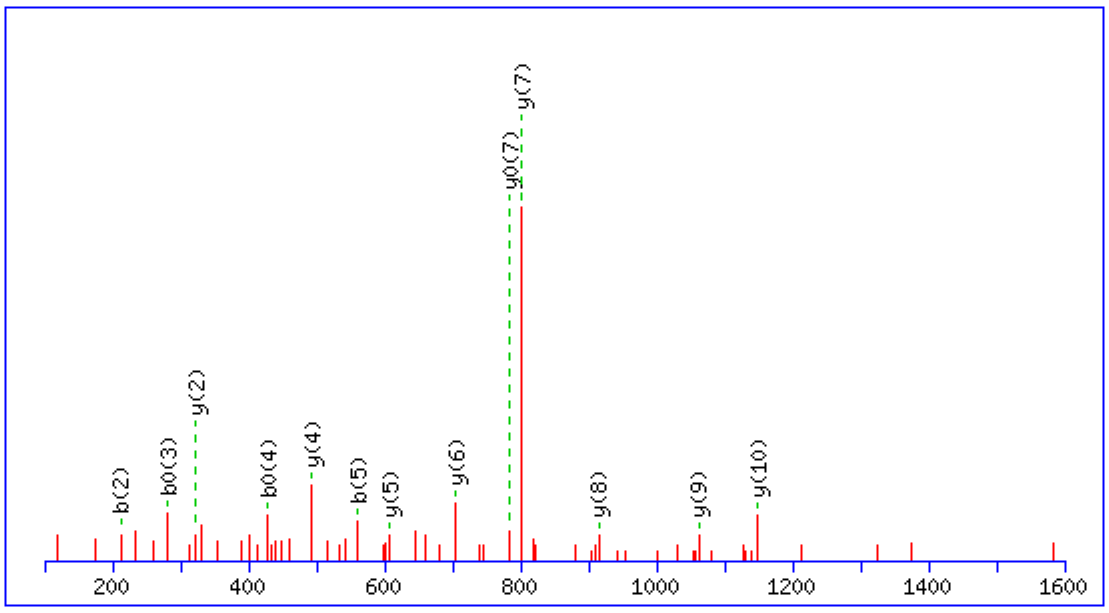
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLSFIPPDGNFR**
Found in **AP3M1_HUMAN**, AP-3 complex subunit mu-1 OS=Homo sapiens GN=AP3M1 PE=1 SV=1

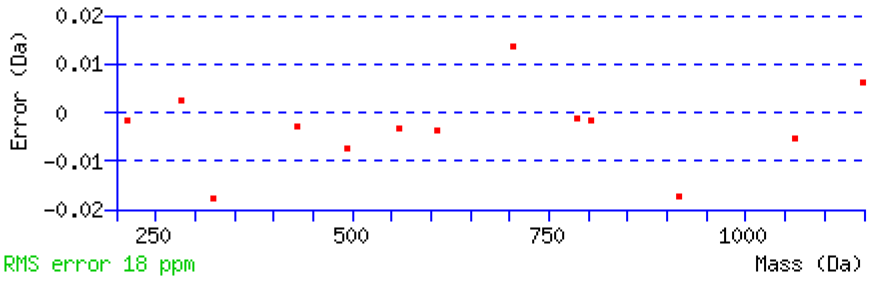
Match to Query 39709: 1360.722588 from(681.368570,2+) rtinseconds(3105) index(43446)
Title: Locus:1.1.1.2522.27
Data file 2011-11-10 - TFD - EP 3-4.mgf

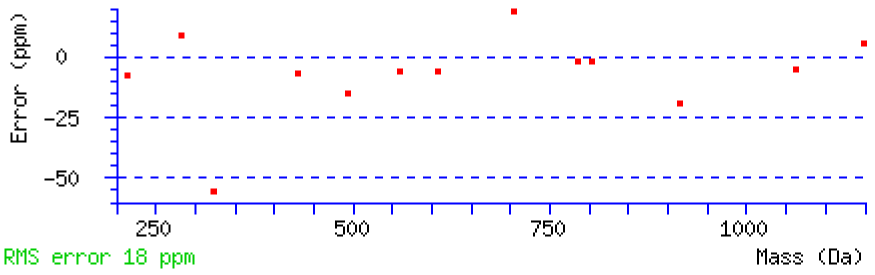
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1360.713943
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 56 **Expect:** 9.8e-006
Matches : 13/102 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							12
2	**213.159754**	107.083515					L	1262.652798	631.830037	1245.626249	623.316763	1244.642233	622.824755	11
3	300.191782	150.599529			282.181217	141.594247	S	***1149.568734***	575.288005	1132.542185	566.774731	1131.558169	566.282723	10
4	447.260196	224.133736			429.249631	215.128454	F	***1062.536706***	531.771991	1045.510157	523.258717	1044.526141	522.766709	9
5	**560.344260**	280.675768			542.333695	271.670486	I	***915.468292***	458.237784	898.441743	449.724510	897.457727	449.232502	8
6	657.397024	329.202150			639.386459	320.196868	P	***802.384228***	401.695752	785.357679	393.182478	784.373663	392.690470	7
7	754.449788	377.728532			736.439223	368.723250	P	***705.331464***	353.169370	688.304915	344.656096	687.320899	344.164088	6
8	869.476731	435.242004			851.466166	426.236721	D	***608.278700***	304.642988	591.252151	296.129714	590.268135	295.637706	5
9	926.498195	463.752736			908.487630	454.747453	G	***493.251757***	247.129516	476.225208	238.616242			4
10	1040.541122	520.774199	1023.514573	512.260924	1022.530557	511.768917	N	436.230293	218.618784	419.203744	210.105510			3
11	1187.609536	594.308406	1170.582987	585.795132	1169.598971	585.303124	F	***322.187366***	161.597321	305.160817	153.084047			2
12							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.4	1360.713943	0.008645	VLSFIPPDGNFR

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

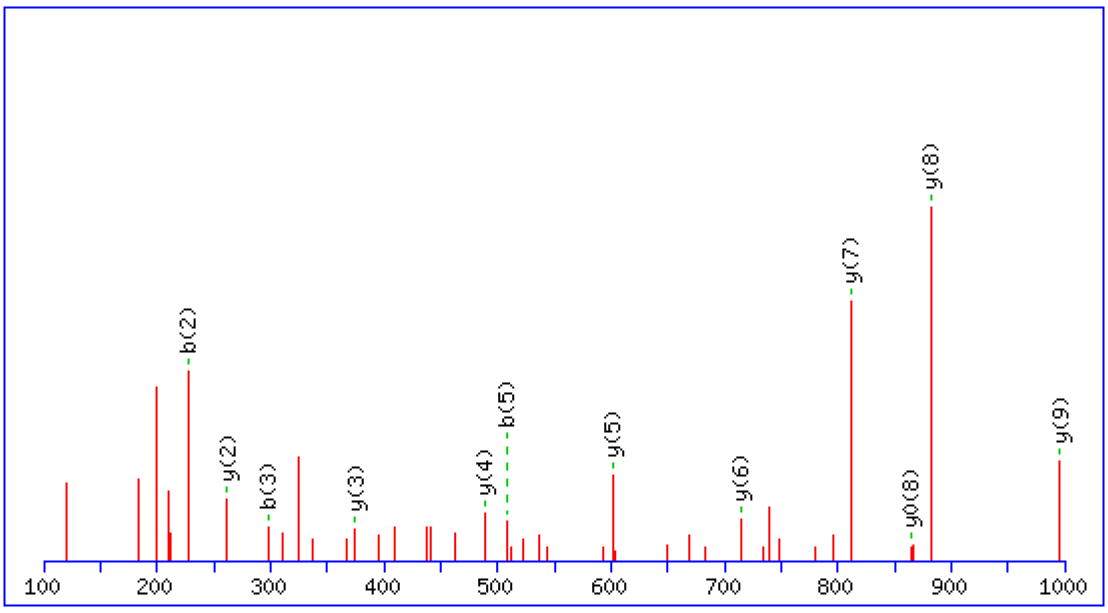
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILAPLLILDK**
Found in **AP4S1_HUMAN**, AP-4 complex subunit sigma-1 OS=Homo sapiens GN=AP4S1 PE=2 SV=1

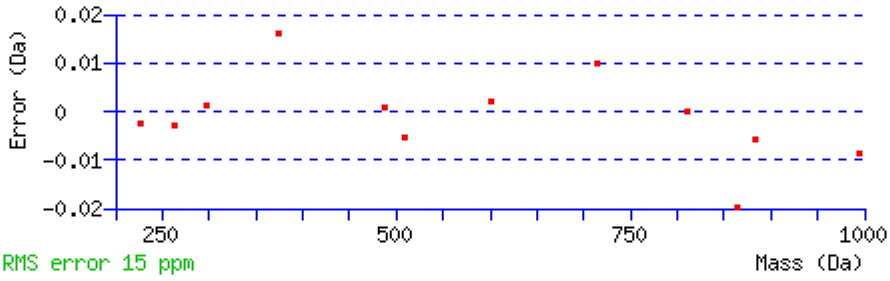
Match to Query 22303: 1107.727648 from(554.871100,2+) rtinseconds(3790) index(41143)
Title: Locus:1.1.1.2773.6
Data file 2011-11-12 - TFD - EP 6-7.mgf

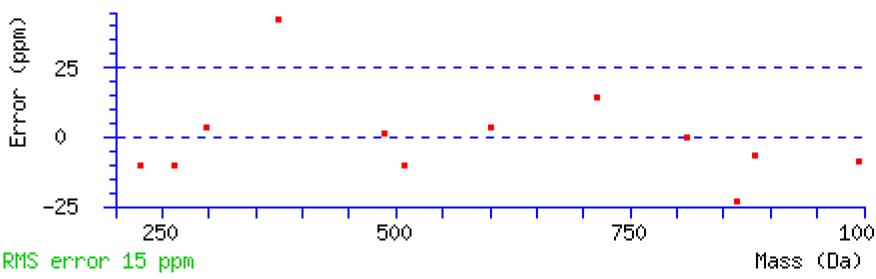
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1107.726700
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 57 **Expect:** 1.8e-006
Matches : 12/72 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							10
2	**227.175404**	114.091340			L	***995.649945***	498.328611	978.623396	489.815336	977.639380	489.323328	9
3	**298.212518**	149.609897			A	***882.565881***	441.786579	865.539332	433.273304	864.555316	432.781296	8
4	395.265282	198.136279			P	***811.528767***	406.268022	794.502218	397.754747	793.518202	397.262739	7
5	**508.349346**	254.678311			L	***714.476003***	357.741640	697.449454	349.228365	696.465438	348.736357	6
6	621.433410	311.220343			L	***601.391939***	301.199608	584.365390	292.686333	583.381374	292.194325	5
7	734.517474	367.762375			I	***488.307875***	244.657575	471.281326	236.144301	470.297310	235.652293	4
8	847.601538	424.304407			L	***375.223811***	188.115543	358.197262	179.602269	357.213246	179.110261	3
9	962.628481	481.817879	944.617916	472.812596	D	***262.139747***	131.573511	245.113198	123.060237	244.129182	122.568229	2
10					K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
57.4	1107.726700	0.000948	ILAPLLILDK
0.4	1107.737946	-0.010298	LLVPQVAIKK

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

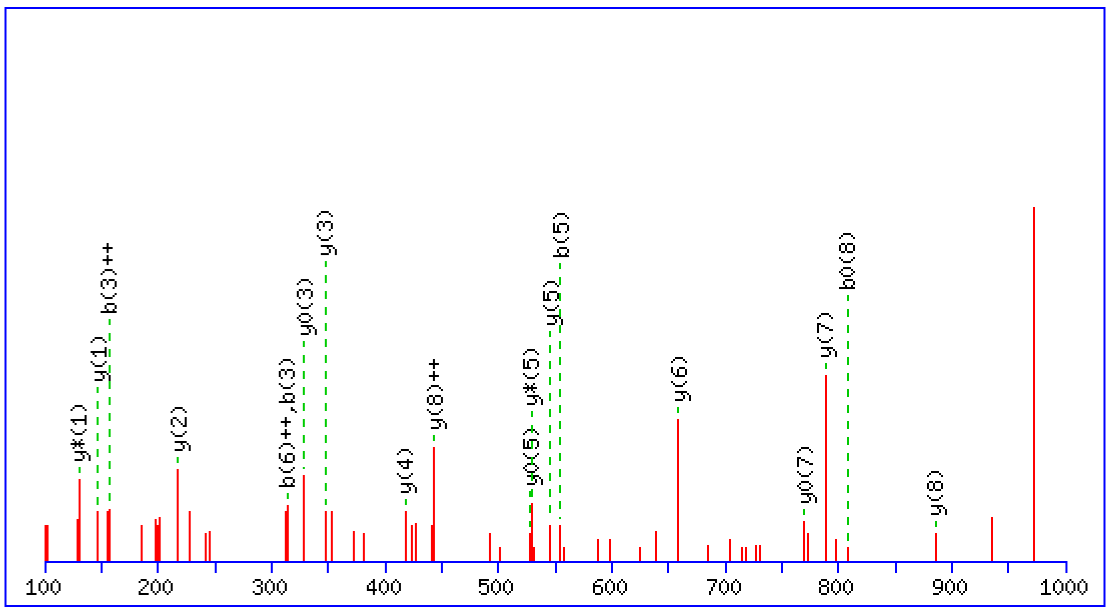
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SPELQAEAK**
Found in **APOA2_HUMAN**, Apolipoprotein A-II OS=Homo sapiens GN=APOA2 PE=1 SV=1

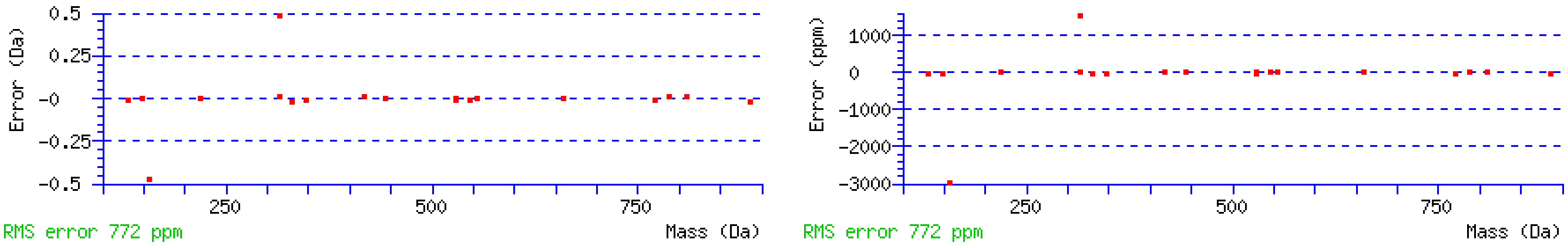
Match to Query 222039: 971.493468 from(486.754010,2+) rtinseconds(1042) index(244557)
Title: Locus:1.1.1.838.10
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 971.492340
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 60 **Expect:** 9.5e-006
Matches : 19/84 fragment ions using 31 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							9
2	185.092068	93.049672			167.081503	84.044389	P	***885.467624***	443.237450	868.441075	434.724176	867.457059	434.232168	8
3	**314.134661**	**157.570968**			296.124096	148.565686	E	***788.414860***	394.711068	771.388311	386.197794	770.404295	385.705786	7
4	427.218725	214.113001			409.208160	205.107718	L	***659.372267***	330.189772	642.345718	321.676497	641.361702	321.184489	6
5	**555.277303**	278.142290	538.250754	269.629015	537.266738	269.137007	Q	***546.288203***	273.647740	529.261654	265.134465	528.277638	264.642457	5
6	626.314417	**313.660847**	609.287868	305.147572	608.303852	304.655564	A	***418.229625***	209.618450	401.203076	201.105176	400.219060	200.613168	4
7	755.357010	378.182143	738.330461	369.668869	737.346445	369.176861	E	***347.192511***	174.099893	330.165962	165.586619	329.181946	165.094611	3
8	826.394124	413.700700	809.367575	405.187426	808.383559	404.695418	A	***218.149918***	109.578597	201.123369	101.065322			2
9							K	***147.112804***	74.060040	130.086255	65.546765			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
59.6	971.492340	0.001128	SPELQAEAK
10.6	971.492371	0.001097	SPEAATPVGK
9.3	971.492371	0.001097	VNDPETAVK
8.2	971.492371	0.001097	SPDSPKTPK
7.6	971.492355	0.001113	APEINISVN
5.1	971.492371	0.001097	SPDSPKTPK
4.3	971.492371	0.001097	EKPTGPPAK
4.1	971.489853	0.003615	LAEHMFPK
3.1	971.492355	0.001113	SPSPAPEKK
1.7	971.492386	0.001082	DVPVPTNAK

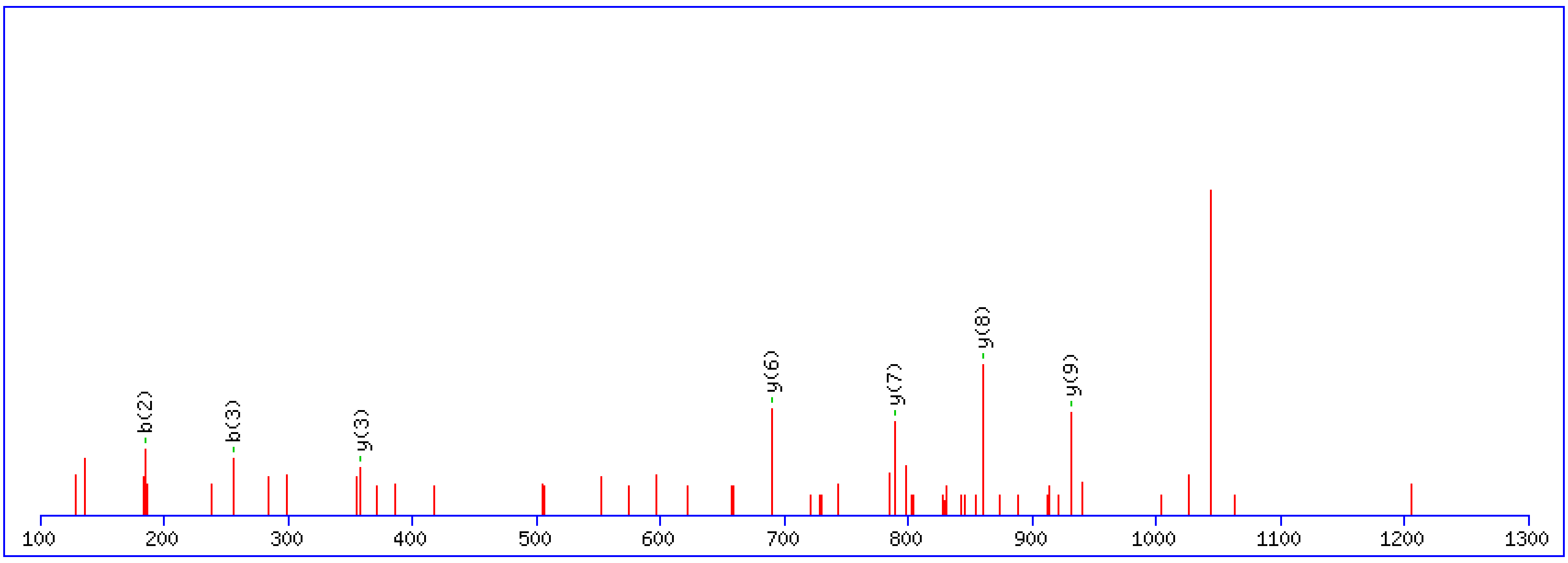
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **IAAVDTDSPR**
Found in **BAX_HUMAN**, Apoptosis regulator BAX OS=Homo sapiens GN=BAX PE=1 SV=1

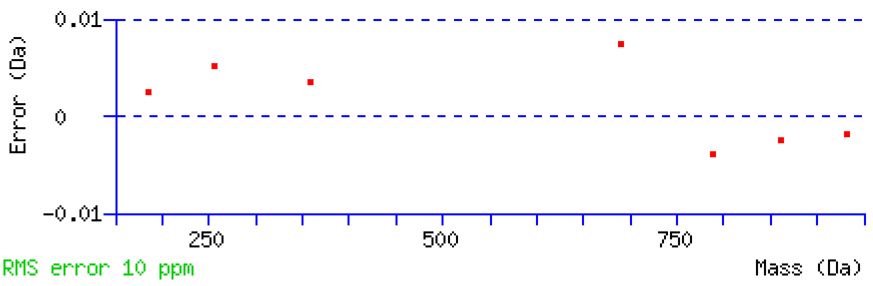
Match to Query 11582: 1043.528808 from(522.771680,2+) rtinseconds(1066) index(4976)
Title: Locus:1.1.1.789.17
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 2.mgf

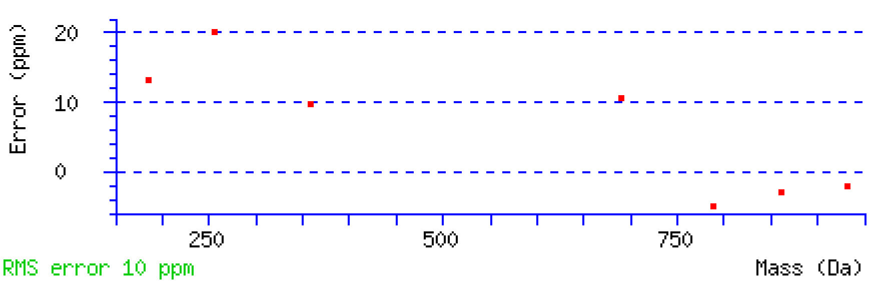
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1043.524734
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 44 **Expect:** 0.00029
Matches : 7/78 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308			I							10
2	**185.128454**	93.067865			A	***931.447951***	466.227614	914.421402	457.714339	913.437386	457.222331	9
3	**256.165568**	128.586422			A	***860.410837***	430.709057	843.384288	422.195782	842.400272	421.703774	8
4	355.233982	178.120629			V	***789.373723***	395.190500	772.347174	386.677225	771.363158	386.185217	7
5	470.260925	235.634100	452.250360	226.628818	D	***690.305309***	345.656293	673.278760	337.143018	672.294744	336.651010	6
6	571.308604	286.157940	553.298039	277.152658	T	575.278366	288.142821	558.251817	279.629547	557.267801	279.137539	5
7	686.335547	343.671412	668.324982	334.666129	D	474.230687	237.618981	457.204138	229.105707	456.220122	228.613699	4
8	773.367575	387.187426	755.357010	378.182143	S	***359.203744***	180.105510	342.177195	171.592235	341.193179	171.100227	3
9	870.420339	435.713808	852.409774	426.708525	P	272.171716	136.589496	255.145167	128.076221			2
10					R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
43.8	1043.524734	0.004074	IAAVDTDSPR
6.0	1043.535965	-0.007157	SPARTQSPGK

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

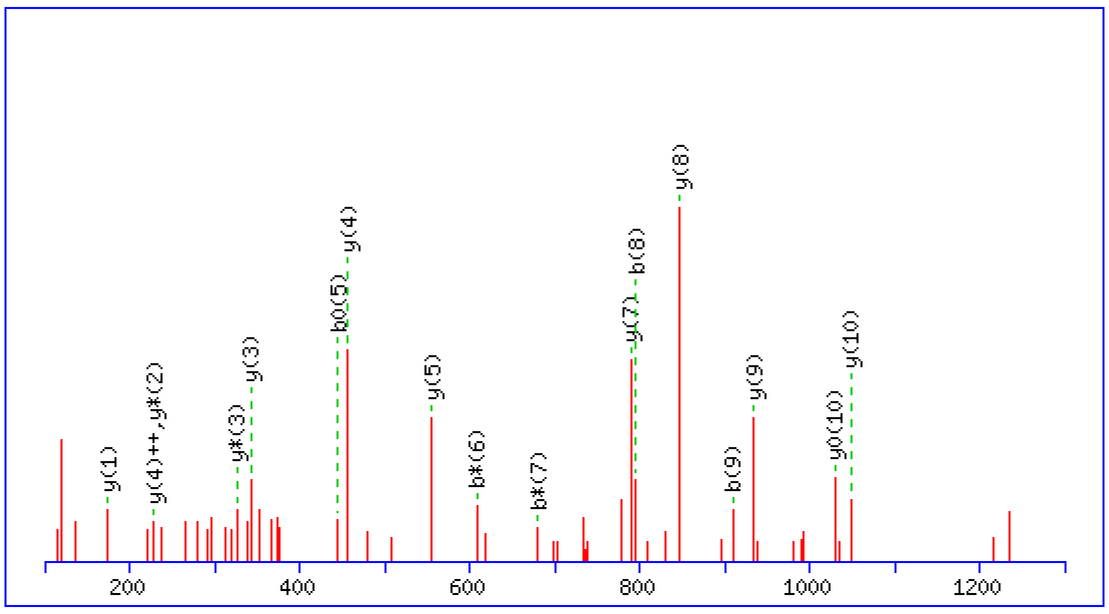
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GFNSGYAVNPAR**
Found in **AQP3_HUMAN**, Aquaporin-3 OS=Homo sapiens GN=AQP3 PE=2 SV=2

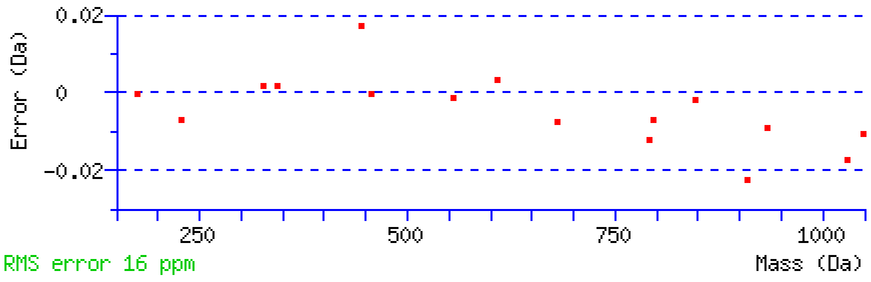
Match to Query 583083: 1251.597208 from(626.805880,2+) rtinseconds(1795) index(508024)
Title: Locus:1.1.1.1014.37
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

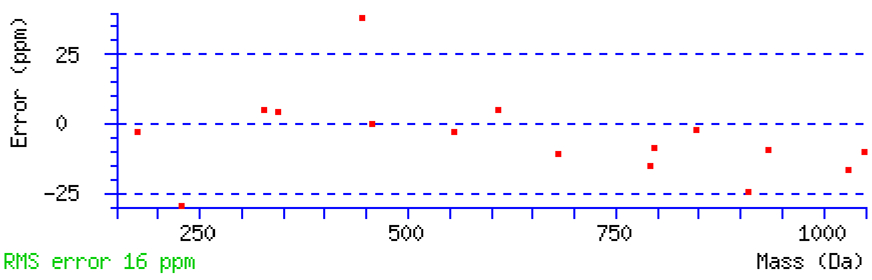
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1251.599625
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 72 **Expect:** 7.3e-007
Matches : 17/106 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							12
2	205.097154	103.052215					F	1195.585447	598.296362	1178.558898	589.783087	1177.574882	589.291079	11
3	319.140081	160.073679	302.113532	151.560404			N	***1048.517033***	524.762155	1031.490484	516.248880	1030.506468	515.756872	10
4	406.172109	203.589693	389.145560	195.076418	388.161544	194.584410	S	***934.474106***	467.740691	917.447557	459.227417	916.463541	458.735409	9
5	463.193573	232.100425	446.167024	223.587150	445.183008	223.095142	G	***847.442078***	424.224677	830.415529	415.711403			8
6	626.256902	313.632089	609.230353	305.118815	608.246337	304.626807	Y	***790.420614***	395.713945	773.394065	387.200671			7
7	697.294016	349.150646	680.267467	340.637372	679.283451	340.145364	A	627.357285	314.182281	610.330736	305.669006			6
8	**796.362430**	398.684853	779.335881	390.171579	778.351865	389.679571	V	***556.320171***	278.663724	539.293622	270.150449			5
9	**910.405357**	455.706317	893.378808	447.193042	892.394792	446.701034	N	***457.251757***	229.129516	440.225208	220.616242			4
10	1007.458121	504.232699	990.431572	495.719424	989.447556	495.227416	P	***343.208830***	172.108053	326.182281	163.594779			3
11	1078.495235	539.751256	1061.468686	531.237981	1060.484670	530.745973	A	246.156066	123.581671	229.129517	115.068397			2
12							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
71.8	1251.599625	-0.002417	GFNSGYAVNPAR
9.1	1251.603012	-0.005804	TPKNGPPPCPR
8.9	1251.603012	-0.005804	TPKNGPPPCPR
6.4	1251.603012	-0.005804	TPKNGPPPCPR
6.4	1251.603012	-0.005804	TPKNGPPPCPR
5.7	1251.602982	-0.005774	NEGMVLEHPAR

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

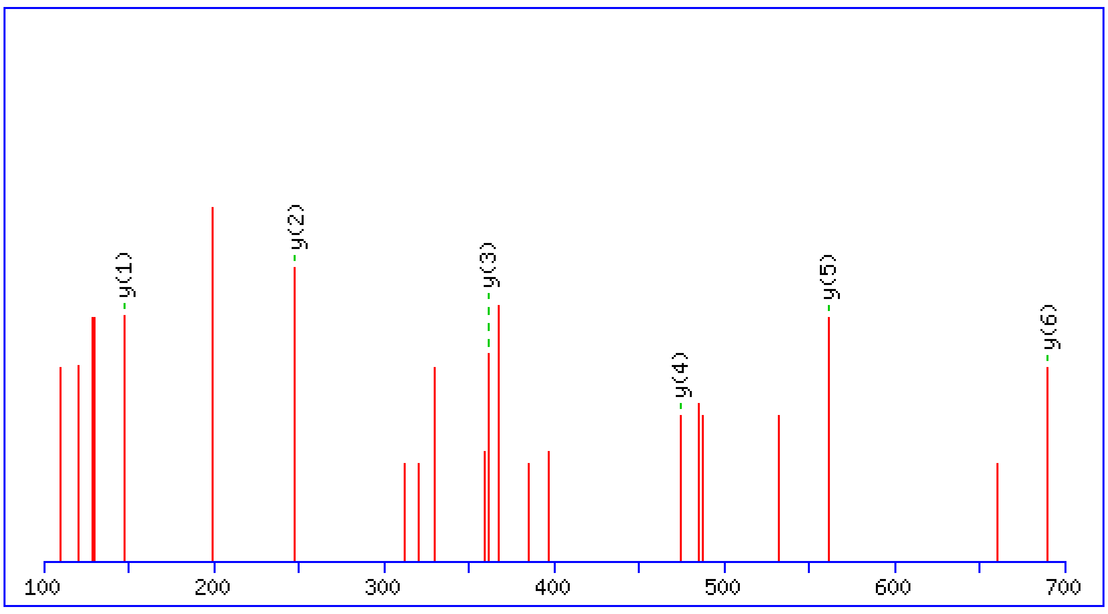
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IESLITK**
Found in **ARAP2_HUMAN**, Arf-GAP with Rho-GAP domain, ANK repeat and PH domain-containing protein 2 OS=Homo sapiens GN=ARAP2 PE=1 SV=3

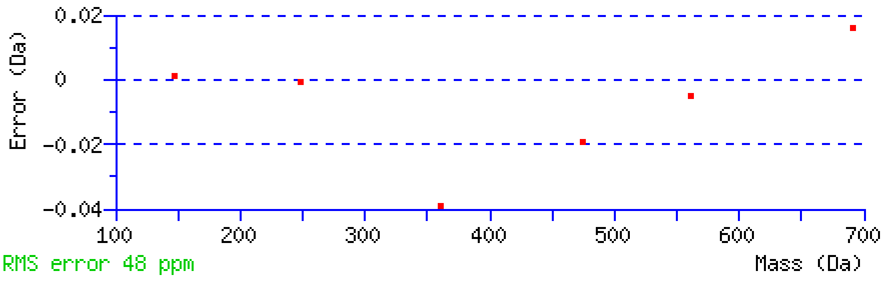
Match to Query 414: 802.485508 from(402.250030,2+) rtinseconds(1562) index(14408)
Title: Locus:1.1.1.1962.3
Data file 2011-11-12 - TFD - EP 6-3.mgf

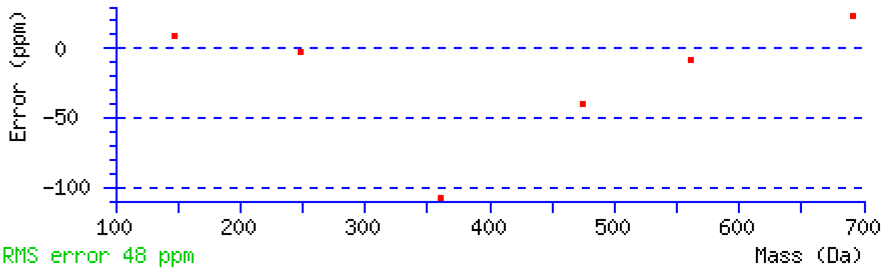
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 802.479996
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 45 **Expect:** 0.00019
Matches : 6/56 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							7
2	243.133933	122.070605	225.123368	113.065322	E	***690.403232***	345.705254	673.376683	337.191980	672.392667	336.699972	6
3	330.165961	165.586618	312.155396	156.581336	S	***561.360639***	281.183958	544.334090	272.670683	543.350074	272.178675	5
4	443.250025	222.128650	425.239460	213.123368	L	***474.328611***	237.667944	457.302062	229.154669	456.318046	228.662661	4
5	556.334089	278.670683	538.323524	269.665400	I	***361.244547***	181.125912	344.217998	172.612637	343.233982	172.120629	3
6	657.381768	329.194522	639.371203	320.189240	T	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.578597	2
7					K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.1	802.479996	0.005512	IESLITK
10.9	802.491226	-0.005718	SNKLTLK
9.5	802.479996	0.005512	ELSTLLK
7.1	802.480011	0.005497	ITVLETK
7.1	802.480011	0.005497	IVTLETK
7.1	802.480011	0.005497	LVTLETK
6.9	802.492569	-0.007061	IHRHLK
6.7	802.480011	0.005497	TLEVLTK
5.9	802.491226	-0.005718	ISALKGSK
5.0	802.491226	-0.005718	ALSSKGLK

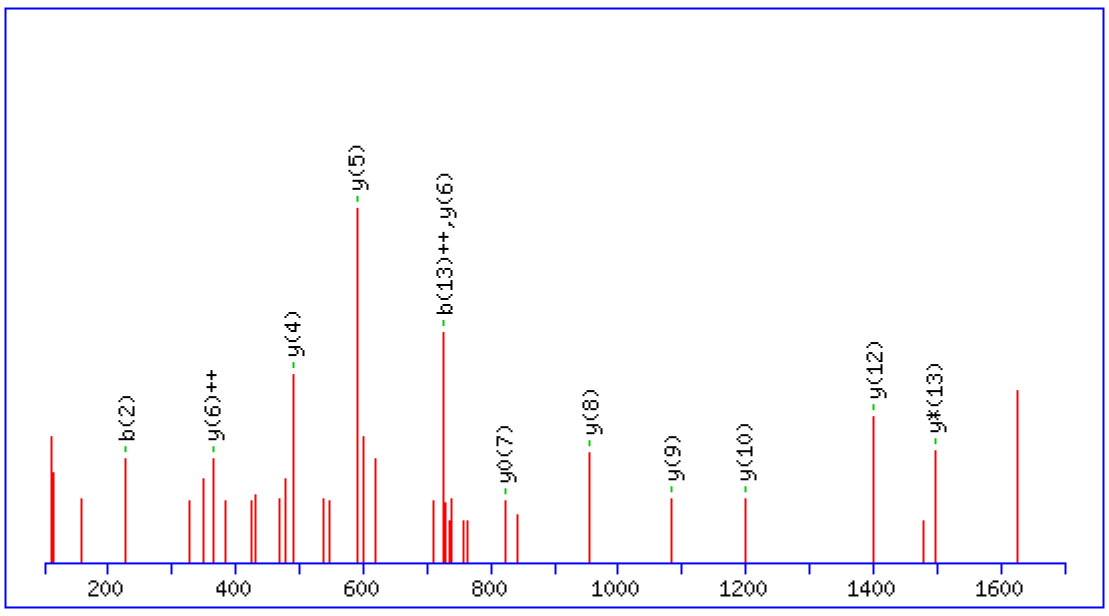
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LNSNDEDIHTANER**
Found in **ARLY_HUMAN**, Argininosuccinate lyase OS=Homo sapiens GN=ASL PE=1 SV=4

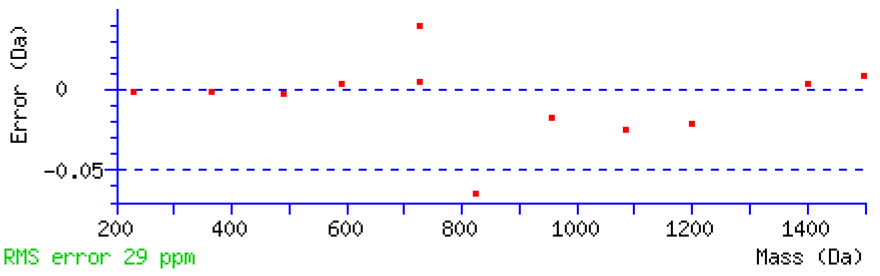
Match to Query 925105: 1626.724302 from(543.248710,3+) rtinseconds(1063) index(412795)
Title: Locus:1.1.1.740.39
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

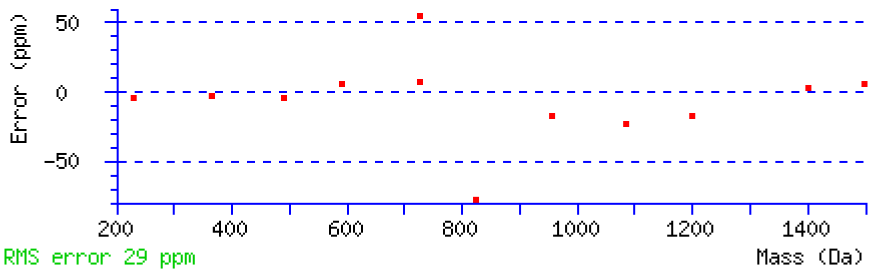
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1626.723358
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 52 **Expect:** 4.2e-005
Matches : 12/148 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^0	y^{0++}	#
1	114.091340	57.549308					L							14
2	228.134267	114.570771	211.107718	106.057497			N	1514.646602	757.826939	1497.620053	749.313665	1496.636037	748.821657	13
3	315.166295	158.086785	298.139746	149.573511	297.155730	149.081503	S	***1400.603675***	700.805476	1383.577126	692.292201	1382.593110	691.800193	12
4	429.209222	215.108249	412.182673	206.594975	411.198657	206.102967	N	1313.571647	657.289462	1296.545098	648.776187	1295.561082	648.284179	11
5	544.236165	272.621721	527.209616	264.108446	526.225600	263.616438	D	***1199.528720***	600.267998	1182.502171	591.754724	1181.518155	591.262716	10
6	673.278758	337.143017	656.252209	328.629743	655.268193	328.137735	E	***1084.501777***	542.754527	1067.475228	534.241252	1066.491212	533.749244	9
7	788.305701	394.656489	771.279152	386.143214	770.295136	385.651206	D	***955.459184***	478.233230	938.432635	469.719956	937.448619	469.227948	8
8	901.389765	451.198521	884.363216	442.685246	883.379200	442.193238	I	840.432241	420.719759	823.405692	412.206484	822.421676	411.714476	7
9	1038.448677	519.727977	1021.422128	511.214702	1020.438112	510.722694	H	***727.348177***	364.177727	710.321628	355.664452	709.337612	355.172444	6
10	1139.496356	570.251816	1122.469807	561.738542	1121.485791	561.246534	T	***590.289265***	295.648271	573.262716	287.134996	572.278700	286.642988	5
11	1210.533470	605.770373	1193.506921	597.257099	1192.522905	596.765091	A	***489.241586***	245.124431	472.215037	236.611156	471.231021	236.119148	4
12	1324.576397	662.791837	1307.549848	654.278562	1306.565832	653.786554	N	418.204472	209.605874	401.177923	201.092600	400.193907	200.600592	3
13	1453.618990	727.313133	1436.592441	718.799859	1435.608425	718.307851	E	304.161545	152.584411	287.134996	144.071136	286.150980	143.579128	2
14							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.9	1626.723358	0.000944	LNSNDEDIHTANER
9.3	1626.716171	0.008131	LNEEEPPGGQDPWK
6.8	1626.735489	-0.011187	QVCNERNCPIHGK
2.3	1626.713486	0.010816	GGPEHRSAWGEADSR
1.6	1626.719559	0.004743	LTPNPDGPPSQAAAPM
0.6	1626.713013	0.011289	VKEFCENLSADCR
0.2	1626.726929	-0.002627	NLDCPELISEFMK

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

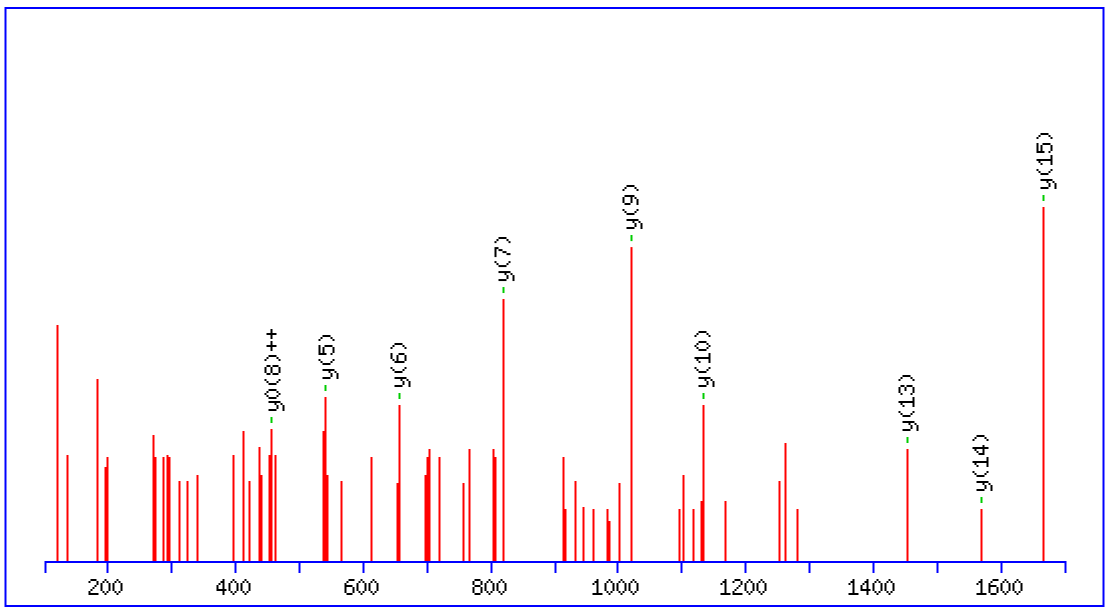
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AQVDSSFLSLYDSHVAK**
Found in **ARM10_HUMAN**, Armadillo repeat-containing protein 10 OS=Homo sapiens GN=ARMC10 PE=1 SV=1

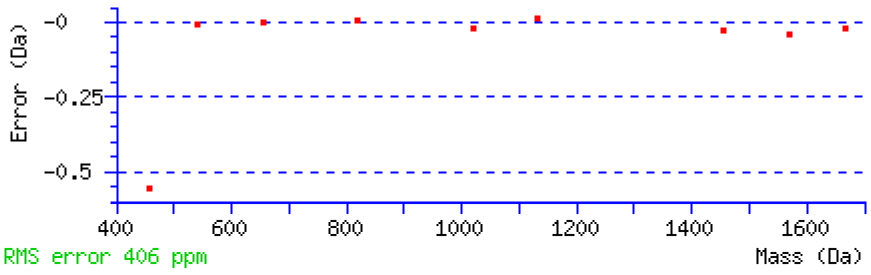
Match to Query 53170: 1865.912712 from(622.978180,3+) rtinseconds(3010) index(39509)
Title: Locus:1.1.1.2563.22
Data file 2011-11-13 - TFD - EP 7-5.mgf

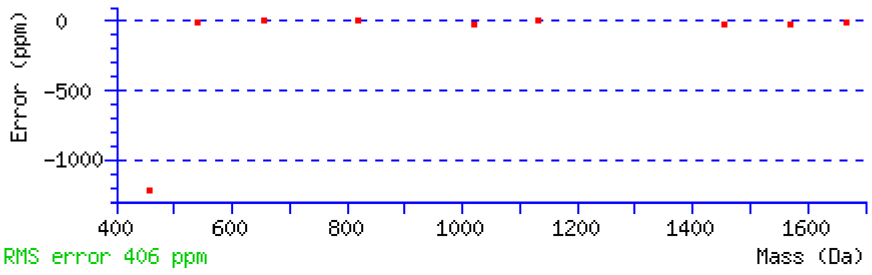
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1865.915939
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 52 **Expect:** 0.0001
Matches : 9/176 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							17
2	200.102968	100.555122	183.076419	92.041848			Q	1795.886105	898.446691	1778.859556	889.933416	1777.875540	889.441408	16
3	299.171382	150.089329	282.144833	141.576055			V	***1667.827527***	834.417402	1650.800978	825.904127	1649.816962	825.412119	15
4	414.198325	207.602801	397.171776	199.089526	396.187760	198.597518	D	***1568.759113***	784.883195	1551.732564	776.369920	1550.748548	775.877912	14
5	501.230353	251.118814	484.203804	242.605540	483.219788	242.113532	S	***1453.732170***	727.369723	1436.705621	718.856449	1435.721605	718.364441	13
6	588.262381	294.634829	571.235832	286.121554	570.251816	285.629546	S	1366.700142	683.853709	1349.673593	675.340435	1348.689577	674.848427	12
7	735.330795	368.169036	718.304246	359.655761	717.320230	359.163753	F	1279.668114	640.337695	1262.641565	631.824421	1261.657549	631.332413	11
8	848.414859	424.711068	831.388310	416.197793	830.404294	415.705785	L	***1132.599700***	566.803488	1115.573151	558.290214	1114.589135	557.798206	10
9	935.446887	468.227082	918.420338	459.713807	917.436322	459.221799	S	***1019.515636***	510.261456	1002.489087	501.748182	1001.505071	501.256174	9
10	1048.530951	524.769114	1031.504402	516.255839	1030.520386	515.763831	L	932.483608	466.745442	915.457059	458.232168	914.473043	457.740160	8
11	1211.594280	606.300778	1194.567731	597.787504	1193.583715	597.295496	Y	***819.399544***	410.203410	802.372995	401.690136	801.388979	401.198128	7
12	1326.621223	663.814250	1309.594674	655.300975	1308.610658	654.808967	D	***656.336215***	328.671746	639.309666	320.158471	638.325650	319.666463	6
13	1413.653251	707.330264	1396.626702	698.816989	1395.642686	698.324981	S	***541.309272***	271.158274	524.282723	262.645000	523.298707	262.152992	5
14	1550.712163	775.859720	1533.685614	767.346445	1532.701598	766.854437	H	454.277244	227.642260	437.250695	219.128986			4
15	1649.780577	825.393927	1632.754028	816.880652	1631.770012	816.388644	V	317.218332	159.112804	300.191783	150.599530			3
16	1720.817691	860.912484	1703.791142	852.399209	1702.807126	851.907201	A	218.149918	109.578597	201.123369	101.065322			2
17							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.6	1865.915939	-0.003227	AQVDSSFLSLYDSHVAK

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

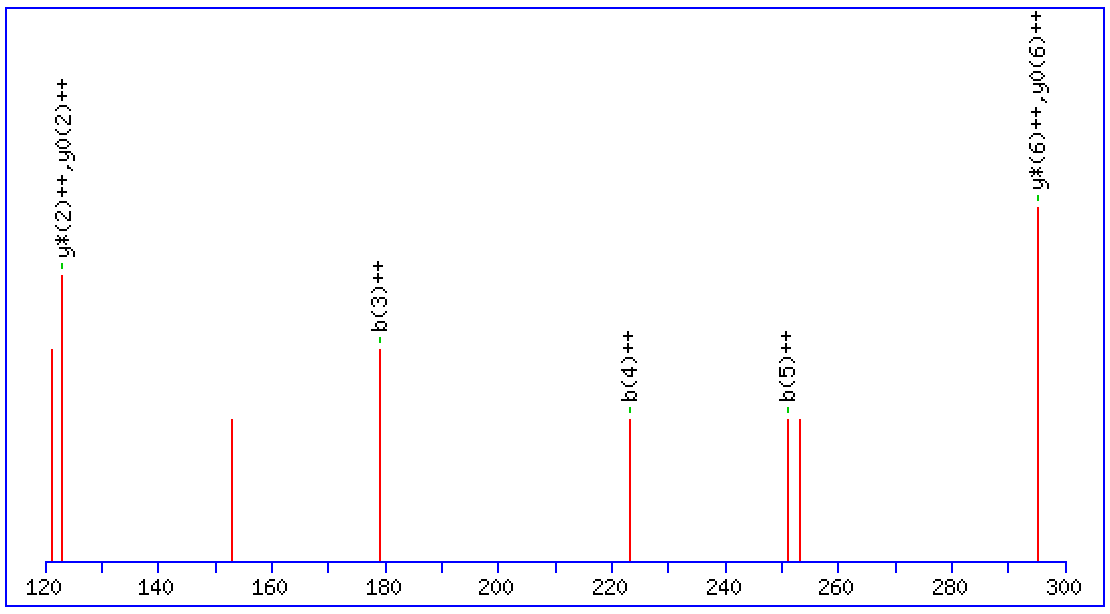
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of KDISGSDK
Found in ARMC4_HUMAN, Armadillo repeat-containing protein 4 OS=Homo sapiens GN=ARMC4 PE=2 SV=1

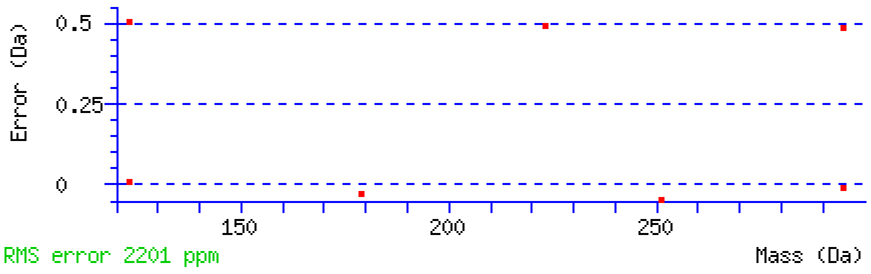
Match to Query 61542: 848.418188 from(425.216370,2+) rtinseconds(4879) index(968293)
Title: Locus:1.1.1.2254.3
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

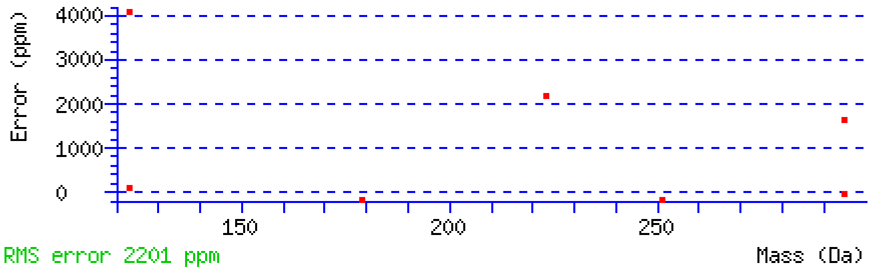
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 120 to 300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 848.423950
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 49 **Expect:** 0.00061
Matches : 9/80 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	129.102239	65.054757	112.075690	56.541483			K							8
2	244.129182	***122.568229***	227.102633	114.054955	226.118617	113.562947	D	721.336274	361.171775	704.309725	352.658501	703.325709	352.166493	7
3	357.213246	***179.110261***	340.186697	170.596987	339.202681	170.104979	I	606.309331	303.658304	589.282782	295.145029	588.298766	294.653021	6
4	444.245274	***222.626275***	427.218725	214.113001	426.234709	213.620993	S	493.225267	247.116271	476.198718	238.602997	475.214702	238.110989	5
5	501.266738	***251.137007***	484.240189	242.623733	483.256173	242.131725	G	406.193239	203.600257	389.166690	195.086983	388.182674	194.594975	4
6	588.298766	***294.653021***	571.272217	286.139747	570.288201	285.647739	S	349.171775	175.089525	332.145226	166.576251	331.161210	166.084243	3
7	703.325709	352.166493	686.299160	343.653218	685.315144	343.161210	D	262.139747	131.573511	245.113198	123.060237	244.129182	122.568229	2
8							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.9	848.423950	-0.005762	KDISGSDK
31.5	848.410034	0.008154	RSSPGSSR
15.2	848.424820	-0.006632	MPIVMAR
15.2	848.417419	0.000769	MPQSKSR
15.2	848.417419	0.000769	MPQSKSR
8.2	848.421448	-0.003260	QMGSWLK
8.2	848.423965	-0.005777	TKTDGSPK
7.8	848.423965	-0.005777	ISGSVSGDK
7.5	848.413559	0.004629	LMAEALAM
2.3	848.413589	0.004599	MLLDQVM

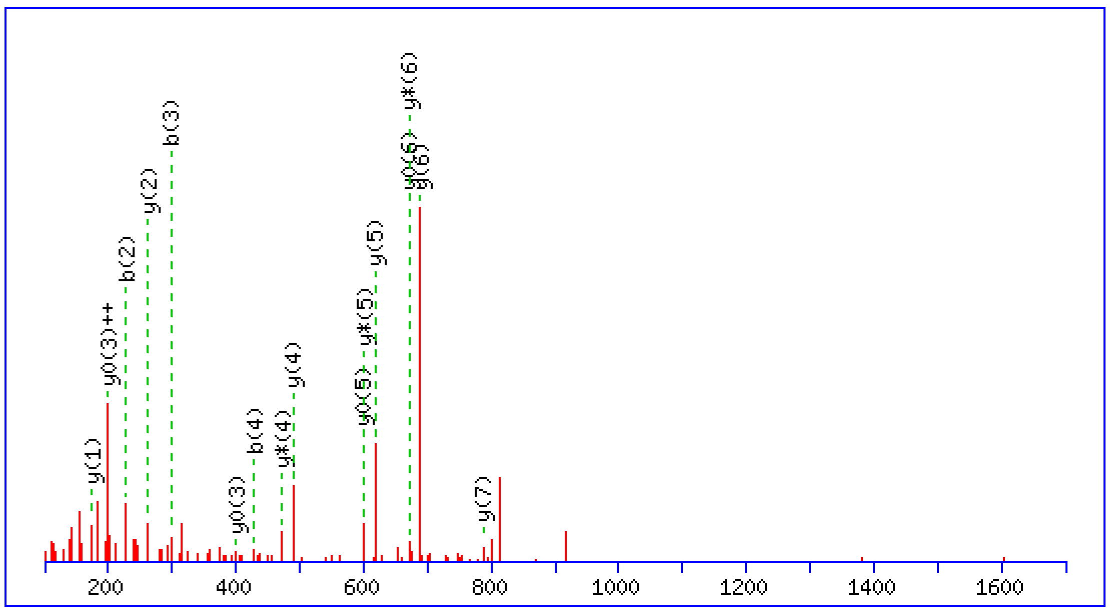
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QVAEARSR**
Found in **ARMC7_HUMAN**, Armadillo repeat-containing protein 7 OS=Homo sapiens GN=ARMC7 PE=2 SV=1

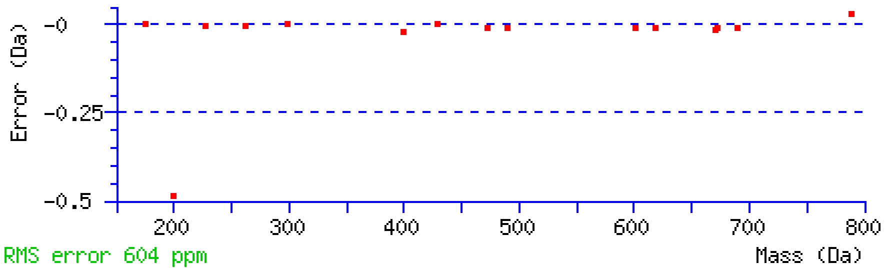
Match to Query 9363: 915.479888 from(458.747220,2+) rtinseconds(1422) index(11527)
Title: Locus:1.1.1.1986.10
Data file 2011-11-10 - TFD - EP 3-2.mgf

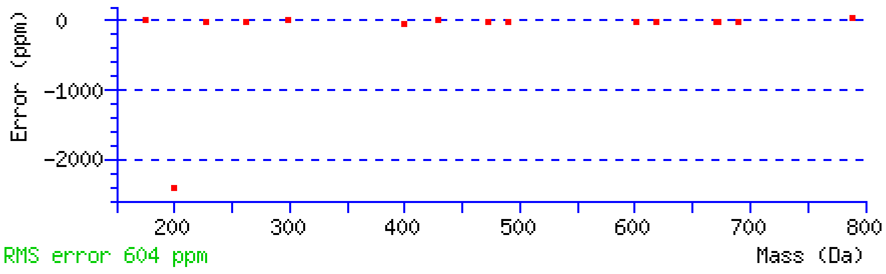
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 915.488602
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.0041
Matches : 16/76 fragment ions using 31 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	129.065854	65.036565	112.039305	56.523291			Q							8
2	**228.134268**	114.570772	211.107719	106.057498			V	***788.437326***	394.722301	771.410777	386.209027	770.426761	385.717019	7
3	**299.171382**	150.089329	282.144833	141.576055			A	***689.368912***	345.188094	672.342363	336.674820	671.358347	336.182812	6
4	**428.213975**	214.610626	411.187426	206.097351	410.203410	205.605343	E	***618.331798***	309.669537	601.305249	301.156263	600.321233	300.664255	5
5	499.251089	250.129183	482.224540	241.615908	481.240524	241.123900	A	***489.289205***	245.148240	472.262656	236.634966	471.278640	236.142958	4
6	655.352200	328.179738	638.325651	319.666464	637.341635	319.174456	R	418.252091	209.629683	401.225542	201.116409	400.241526	200.624401	3
7	742.384228	371.695752	725.357679	363.182478	724.373663	362.690470	S	***262.150980***	131.579128	245.124431	123.065854	244.140415	122.573846	2
8							R	***175.118952***	88.063114	158.092403	79.549840			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.6	915.477356	0.002532	NLAENISR
35.6	915.488602	-0.008714	QVAEARSR
18.3	915.477356	0.002532	ARAELNDK
12.6	915.488617	-0.008729	GGLPSASRR
8.3	915.477356	0.002532	LNENAISR
7.7	915.477371	0.002517	QVADAREK
6.6	915.484756	-0.004868	IMLSPEAR
4.9	915.488617	-0.008729	NISTPRGR
3.2	915.488617	-0.008729	AQRVSSPR
3.1	915.470840	0.009048	CRPNLSR

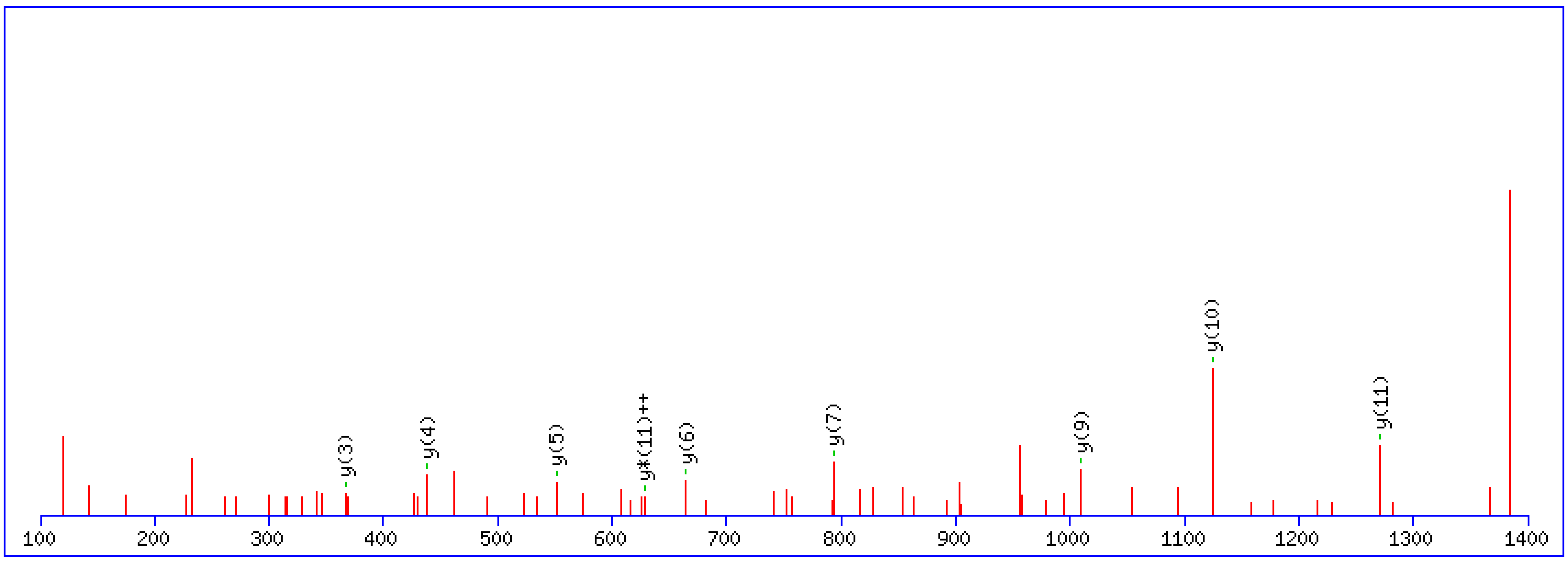
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IFDSEEILAGYK**
Found in **SYNC_HUMAN**, Asparaginyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=NARS PE=1 SV=1

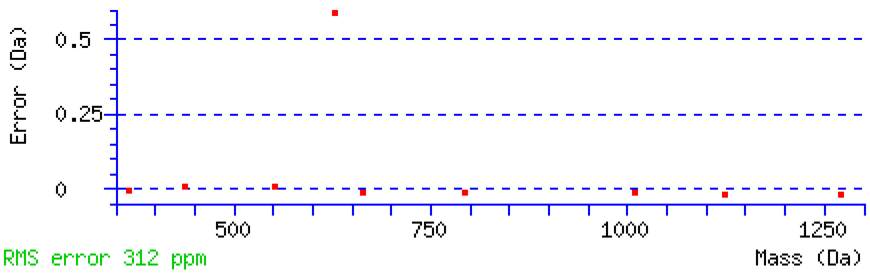
Match to Query 35313: 1383.683948 from(692.849250,2+) rtinseconds(2977) index(41089)
Title: Locus:1.1.1.1511.30
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 2.mgf

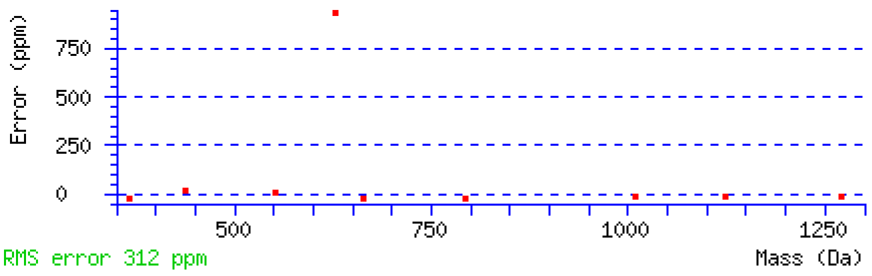
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1383.692169
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 41  Expect: 0.00023
Matches : 9/94 fragment ions using 25 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							12
2	261.159754	131.083515			F	***1271.615410***	636.311343	1254.588861	627.798069	1253.604845	627.306061	11
3	376.186697	188.596986	358.176132	179.591704	D	***1124.546996***	562.777136	1107.520447	554.263862	1106.536431	553.771854	10
4	463.218725	232.113001	445.208160	223.107718	S	***1009.520053***	505.263665	992.493504	496.750390	991.509488	496.258382	9
5	592.261318	296.634297	574.250753	287.629015	E	922.488025	461.747651	905.461476	453.234376	904.477460	452.742368	8
6	721.303911	361.155594	703.293346	352.150311	E	***793.445432***	397.226354	776.418883	388.713080	775.434867	388.221072	7
7	834.387975	417.697626	816.377410	408.692343	I	***664.402839***	332.705058	647.376290	324.191783			6
8	947.472039	474.239658	929.461474	465.234375	L	***551.318775***	276.163026	534.292226	267.649751			5
9	1018.509153	509.758215	1000.498588	500.752932	A	***438.234711***	219.620994	421.208162	211.107719			4
10	1075.530617	538.268947	1057.520052	529.263664	G	***367.197597***	184.102437	350.171048	175.589162			3
11	1238.593946	619.800611	1220.583381	610.795329	Y	310.176133	155.591705	293.149584	147.078430			2
12					K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.4	1383.692169	-0.008221	IFDSEEILAGYK
2.6	1383.681641	0.002307	LPSAPSGGAPIRDM

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

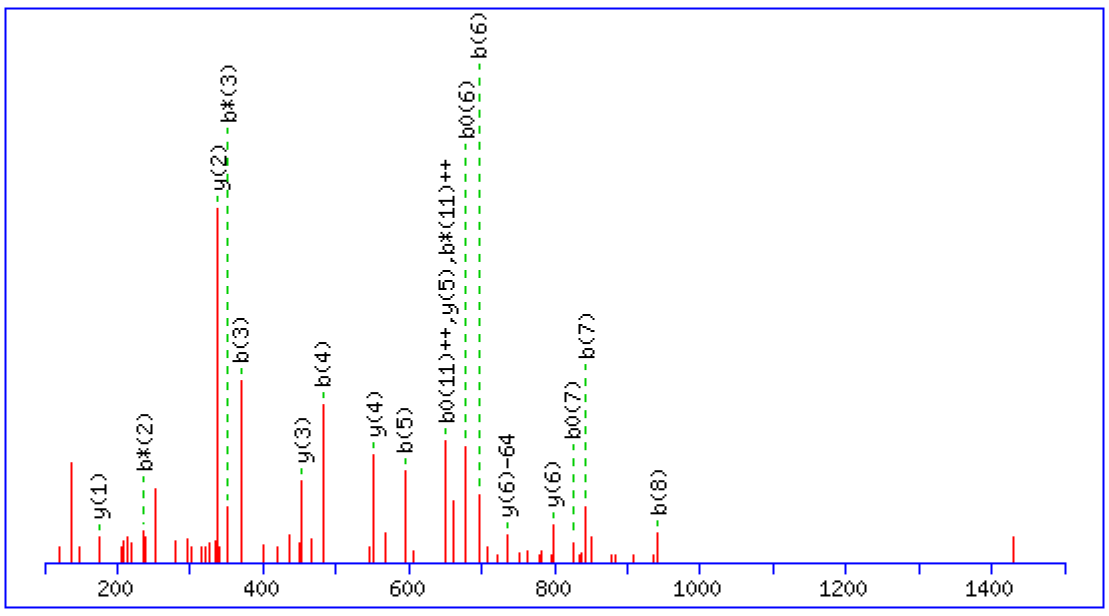
Mascot Search Results

Peptide View

MS/MS Fragmentation of **RPDLLTMVVDYR**
Found in **PEA15_HUMAN**, Astrocytic phosphoprotein PEA-15 OS=Homo sapiens GN=PEA15 PE=1 SV=2

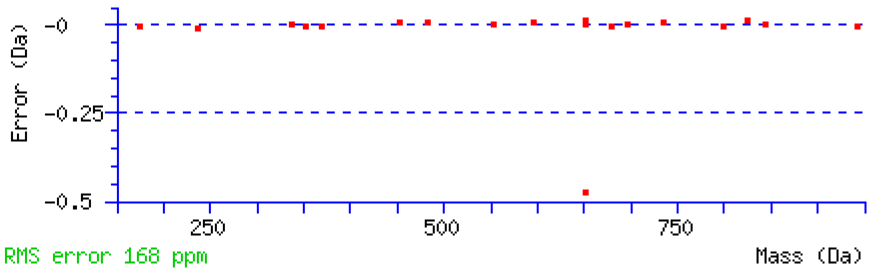
Match to Query 40316: 1492.769622 from(498.597150,3+) rtinseconds(2911) index(32415)
Title: Locus:1.1.1.2444.8
Data file 2011-11-12 - TFD - EP 6-7.mgf

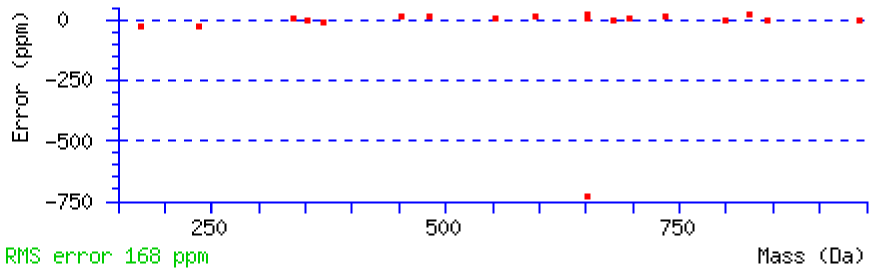
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1492.770798
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M7 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 48 **Expect:** 4.2e-005
Matches : 19/190 fragment ions using 28 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	157.108387	79.057831	140.081838	70.544557			R							12
2	254.161151	127.584213	237.134602	119.070939			P	1337.676966	669.342121	1320.650417	660.828847	1319.666401	660.336839	11
3	***369.188094***	185.097685	352.161545	176.584410	351.177529	176.092402	D	1240.624202	620.815739	1223.597653	612.302465	1222.613637	611.810457	10
4	***482.272158***	241.639717	465.245609	233.126443	464.261593	232.634435	L	1125.597259	563.302268	1108.570710	554.788993	1107.586694	554.296985	9
5	***595.356222***	298.181749	578.329673	289.668475	577.345657	289.176467	L	1012.513195	506.760236	995.486646	498.246961	994.502630	497.754953	8
6	***696.403901***	348.705589	679.377352	340.192314	678.393336	339.700306	T	899.429131	450.218204	882.402582	441.704929	881.418566	441.212921	7
7	***843.439301***	422.223289	826.412752	413.710014	825.428736	413.218006	M	***798.381452***	399.694364	781.354903	391.181090	780.370887	390.689082	6
8	***942.507715***	471.757496	925.481166	463.244221	924.497150	462.752213	V	***651.346052***	326.176664	634.319503	317.663390	633.335487	317.171382	5
9	1041.576129	521.291703	1024.549580	512.778428	1023.565564	512.286420	V	***552.277638***	276.642457	535.251089	268.129183	534.267073	267.637175	4
10	1156.603072	578.805174	1139.576523	570.291900	1138.592507	569.799892	D	***453.209224***	227.108250	436.182675	218.594976	435.198659	218.102968	3
11	1319.666401	660.336839	1302.639852	651.823564	1301.655836	651.331556	Y	***338.182281***	169.594778	321.155732	161.081504			2
12							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.7	1492.770798	-0.001176	RPDLLTMVVDYR
21.7	1492.770798	-0.001176	RPDLLTMVVDYR
1.0	1492.762894	0.006728	EMISSNIQAMIIK
0.9	1492.760895	0.008727	QFRGPMAAISFPR
0.3	1492.770782	-0.001160	ECGKAFISLPSVR
0.3	1492.777267	-0.007645	SLAYALEKNLEDK
0.1	1492.777313	-0.007691	TNLTTFNPSILEK

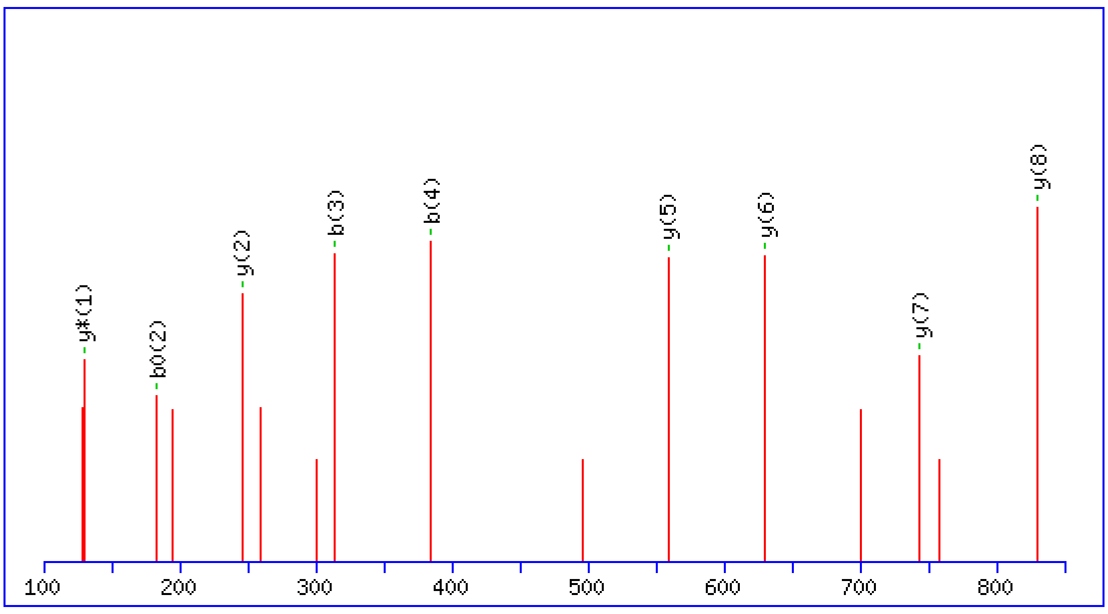
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ISLAPTDVK**
Found in **ATX2L_HUMAN**, Ataxin-2-like protein OS=Homo sapiens GN=ATXN2L PE=1 SV=2

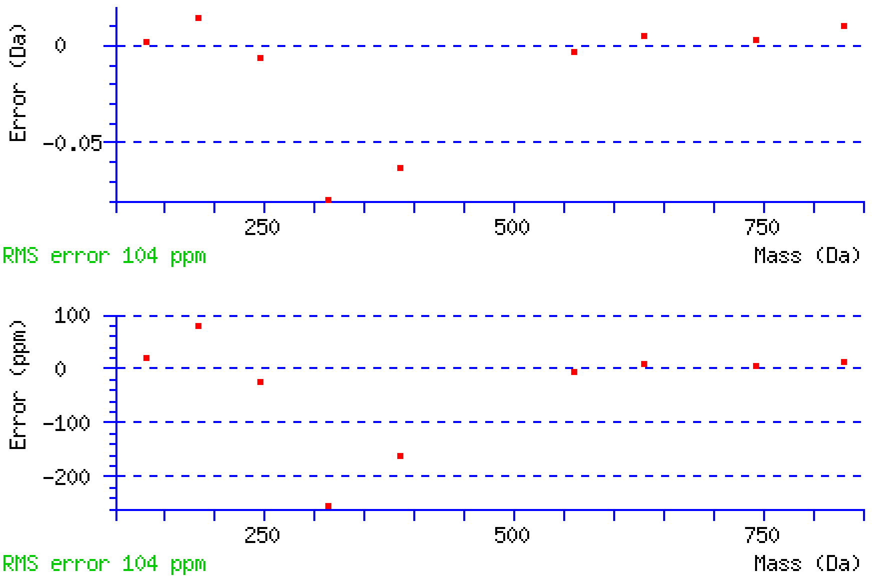
Match to Query 183813: 942.544508 from(472.279530,2+) rtinseconds(1894) index(427775)
Title: Locus:1.1.1.1064.6
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 942.538589
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 42 **Expect:** 0.0013
Matches : 9/74 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							9
2	201.123368	101.065322	183.112803	92.060039	S	***830.461810***	415.734543	813.435261	407.221269	812.451245	406.729261	8
3	**314.207432**	157.607354	296.196867	148.602071	L	***743.429782***	372.218529	726.403233	363.705255	725.419217	363.213247	7
4	**385.244546**	193.125911	367.233981	184.120628	A	***630.345718***	315.676497	613.319169	307.163223	612.335153	306.671215	6
5	482.297310	241.652293	464.286745	232.647010	P	***559.308604***	280.157940	542.282055	271.644666	541.298039	271.152658	5
6	583.344989	292.176133	565.334424	283.170850	T	462.255840	231.631558	445.229291	223.118283	444.245275	222.626275	4
7	698.371932	349.689604	680.361367	340.684322	D	361.208161	181.107718	344.181612	172.594444	343.197596	172.102436	3
8	797.440346	399.223811	779.429781	390.218528	V	***246.181218***	123.594247	229.154669	115.080972			2
9					K	147.112804	74.060040	130.086255	65.546765			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.8	942.538589	0.005919	ISLAPTDVK
14.9	942.549820	-0.005312	LSPVQKQK
13.0	942.549820	-0.005312	LSIIGPTSR
13.0	942.549805	-0.005297	LSLKTPER
11.5	942.538559	0.005949	EALEAVLAK
10.3	942.538589	0.005919	LAEGVLDVK
10.3	942.538559	0.005949	ALEAALVEK
9.9	942.538559	0.005949	IEAQELLK
9.4	942.549789	-0.005281	NAKEALAVK
8.8	942.549835	-0.005327	ISGVQVNVK

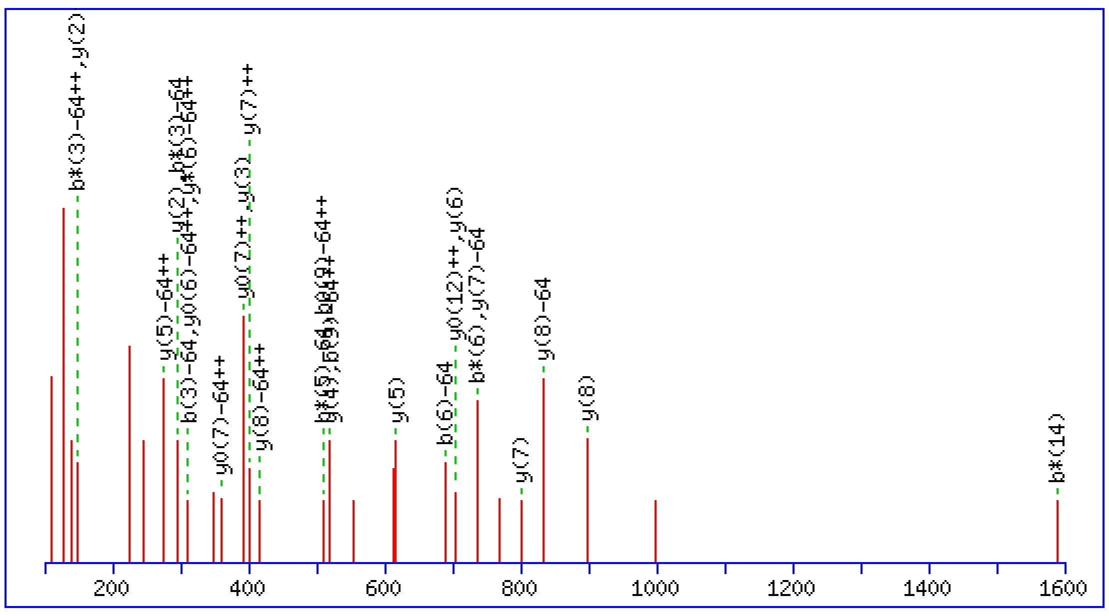
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MLNTNYHLPPSPKPMK**
Found in **ATP8_HUMAN**, ATP synthase protein 8 OS=Homo sapiens GN=MT-ATP8 PE=1 SV=1

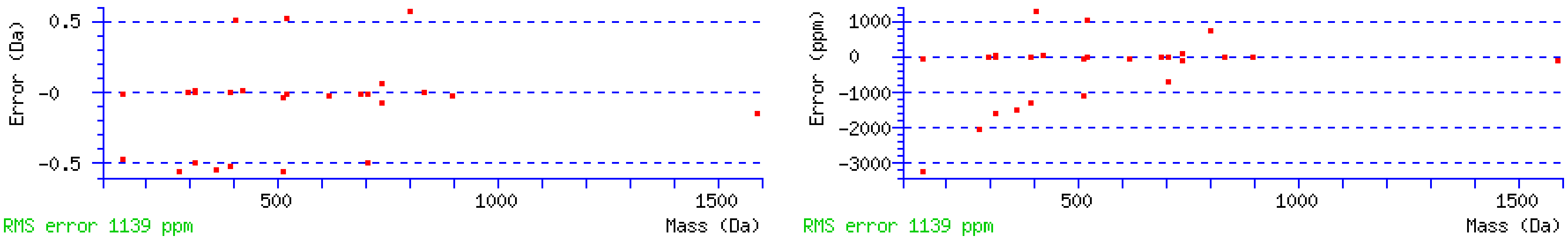
Match to Query 24876: 1898.944296 from(475.743350,4+) rtinseconds(1773) index(7048)
Title: Locus:1.1.1.2397.14
Data file 2011-11-14 - TFD - EP 8-8.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1898.938248
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M1      : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
M15     : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 36  Expect: 0.00066
Matches : 28/316 fragment ions using 32 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	148.042676	74.524976					M							16
2	261.126740	131.067008					L	1752.910153	876.958715	1735.883604	868.445440	1734.899588	867.953432	15
3	375.169667	188.088472	358.143118	179.575197			N	1639.826089	820.416683	1622.799540	811.903408	1621.815524	811.411400	14
4	476.217346	238.612311	459.190797	230.099037	458.206781	229.607029	T	1525.783162	763.395219	1508.756613	754.881945	1507.772597	754.389937	13
5	590.260273	295.633775	573.233724	287.120500	572.249708	286.628492	N	1424.735483	712.871380	1407.708934	704.358105	1406.724918	703.866097	12
6	753.323602	377.165439	736.297053	368.652165	735.313037	368.160157	Y	1310.692556	655.849916	1293.666007	647.336642	1292.681991	646.844634	11
7	890.382514	445.694895	873.355965	437.181621	872.371949	436.689613	H	1147.629227	574.318252	1130.602678	565.804977	1129.618662	565.312969	10
8	1003.466578	502.236927	986.440029	493.723653	985.456013	493.231645	L	1010.570315	505.788796	993.543766	497.275521	992.559750	496.783513	9
9	1100.519342	550.763309	1083.492793	542.250035	1082.508777	541.758027	P	***897.486251***	449.246764	880.459702	440.733489	879.475686	440.241481	8
10	1197.572106	599.289691	1180.545557	590.776417	1179.561541	590.284409	P	***800.433487***	400.720382	783.406938	392.207107	782.422922	391.715099	7
11	1284.604134	642.805705	1267.577585	634.292431	1266.593569	633.800423	S	***703.380723***	352.194000	686.354174	343.680725	685.370158	343.188717	6
12	1381.656898	691.332087	1364.630349	682.818813	1363.646333	682.326805	P	***616.348695***	308.677986	599.322146	300.164711			5
13	1509.751861	755.379569	1492.725312	746.866294	1491.741296	746.374286	K	***519.295931***	260.151604	502.269382	251.638329			4
14	1606.804625	803.905951	1589.778076	795.392676	1588.794060	794.900668	P	***391.200968***	196.104122	374.174419	187.590848			3
15	1753.840025	877.423651	1736.813476	868.910376	1735.829460	868.418368	M	***294.148204***	147.577740	277.121655	139.064465			2
16							K	***147.112804***	74.060040	130.086255	65.546765			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.2	1898.938248	0.006048	MLNTNYHLPPSPKPMK
30.0	1898.938248	0.006048	MLNTNYHLPPSPKPMK
26.3	1898.938248	0.006048	MLNTNYHLPPSPKPMK
17.0	1898.938248	0.006048	MLNTNYHLPPSPKPMK
13.8	1898.938248	0.006048	MLNTNYHLPPSPKPMK
13.7	1898.938248	0.006048	MLNTNYHLPPSPKPMK
3.0	1898.938248	0.006048	MLNTNYHLPPSPKPMK
2.2	1898.949509	-0.005213	QQRPKVGCFSQMIFK
1.8	1898.938248	0.006048	MLNTNYHLPPSPKPMK
1.8	1898.952164	-0.007868	GAIGLVPKAYIMEMYDI

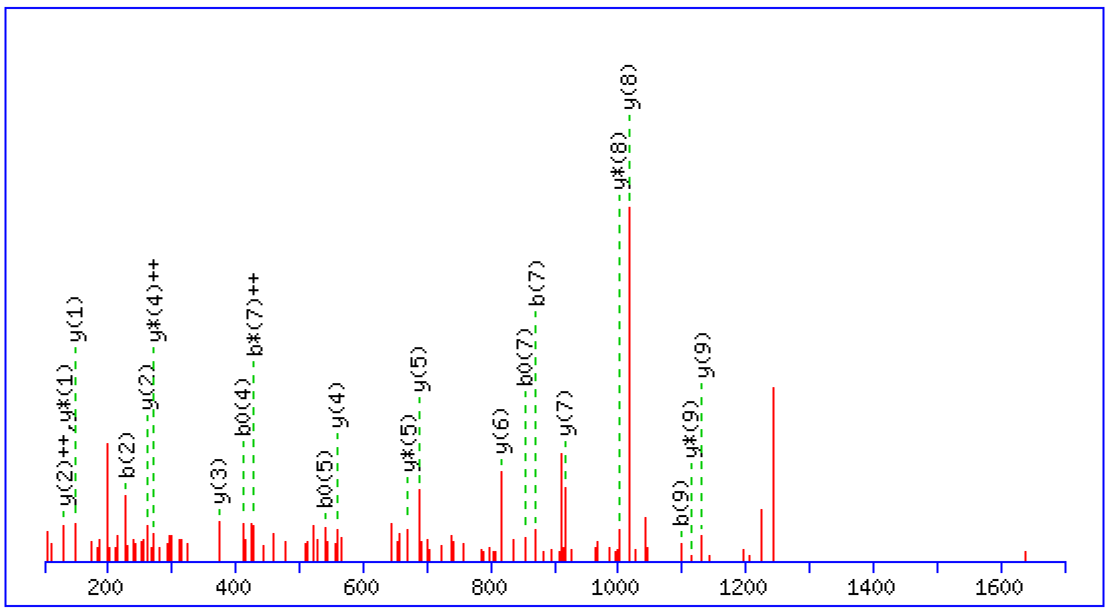
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LITTQQWLIK**
Found in **ATP6_HUMAN**, ATP synthase subunit a OS=Homo sapiens GN=MT-ATP6 PE=1 SV=1

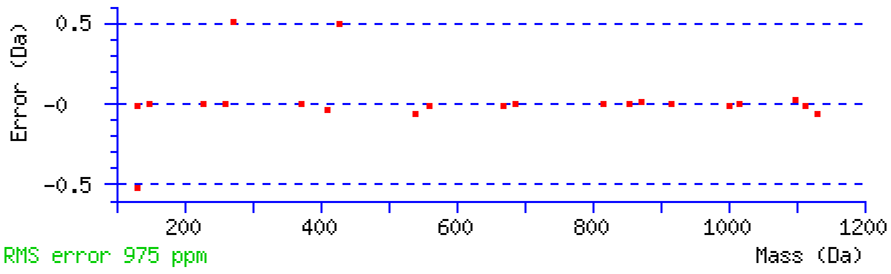
Match to Query 32289: 1242.734468 from(622.374510,2+) rtinseconds(2939) index(39800)
Title: Locus:1.1.1.2520.27
Data file 2011-11-14 - TFD - EP 8-1.mgf

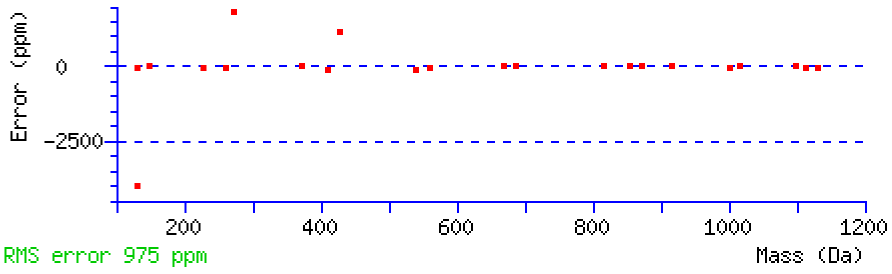
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1242.733597
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 66 **Expect:** 1.1e-006
Matches : 22/84 fragment ions using 35 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					**L**							10
2	**227.175404**	114.091340					**I**	***1130.656823***	565.832050	1113.630274	557.318775	1112.646258	556.826767	9
3	328.223083	164.615179			310.212518	155.609897	**T**	***1017.572759***	509.290018	1000.546210	500.776743	999.562194	500.284735	8
4	429.270762	215.139019			411.260197	206.133737	**T**	***916.525080***	458.766178	899.498531	450.252904	898.514515	449.760896	7
5	557.329340	279.168308	540.302791	270.655034	539.318775	270.163026	**Q**	***815.477401***	408.242339	798.450852	399.729064			6
6	685.387918	343.197597	668.361369	334.684323	667.377353	334.192315	**Q**	***687.418823***	344.213050	670.392274	335.699775			5
7	**871.467231**	436.237254	854.440682	427.723979	853.456666	427.231971	**W**	***559.360245***	280.183761	542.333696	271.670486			4
8	984.551295	492.779286	967.524746	484.266011	966.540730	483.774003	**L**	***373.280932***	187.144104	356.254383	178.630830			3
9	**1097.635359**	549.321318	1080.608810	540.808043	1079.624794	540.316035	**I**	***260.196868***	130.602072	243.170319	122.088798			2
10							**K**	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
65.5	1242.733597	0.000871	LITTQQWLIK
8.1	1242.727066	0.007402	ILFIRMLHGK
6.8	1242.733582	0.000886	IIREIFPDIK
4.8	1242.736954	-0.002486	AIPIKQGMLLK
4.5	1242.744812	-0.010344	IIAILLDAHHK
1.6	1242.729553	0.004915	KSSAQGKPLALK
1.0	1242.733597	0.000871	QLSALGFVIPAK

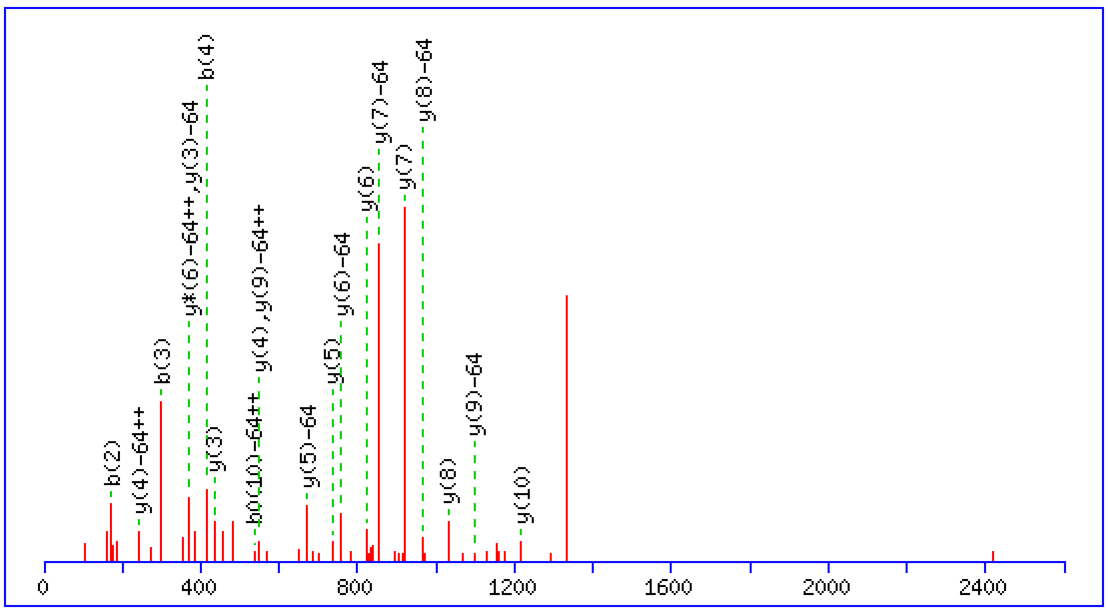
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGELPSWILMR**
Found in **ATPK_HUMAN**, ATP synthase subunit f, mitochondrial OS=Homo sapiens GN=ATP5J2 PE=1 SV=3

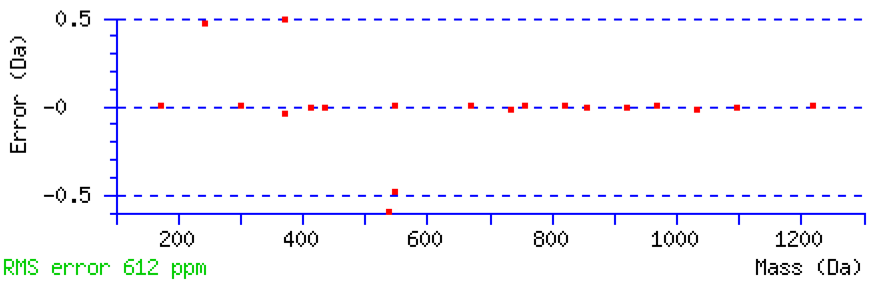
Match to Query 32783: 1329.710208 from(665.862380,2+) rtinseconds(3596) index(38246)
Title: Locus:1.1.1.2822.6
Data file 2011-11-13 - TFD - EP 7-7.mgf

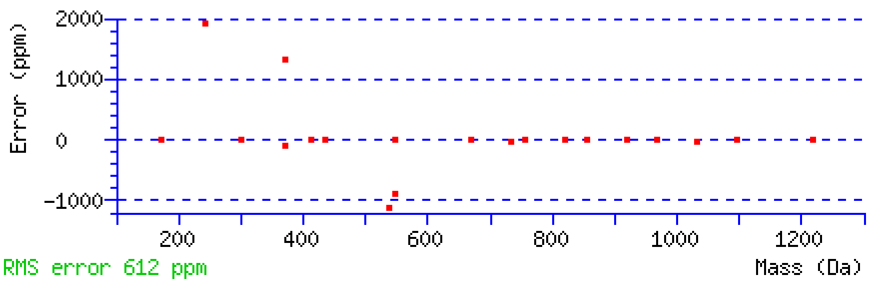
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1329.711472
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M10 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 55 **Expect:** 2e-005
Matches : 20/136 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							11
2	**171.112804**	86.060040			G	***1217.634706***	609.320991	1200.608157	600.807717	1199.624141	600.315709	10
3	**300.155397**	150.581336	282.144832	141.576054	E	1160.613242	580.810259	1143.586693	572.296985	1142.602677	571.804976	9
4	**413.239461**	207.123369	395.228896	198.118086	L	***1031.570649***	516.288963	1014.544100	507.775688	1013.560084	507.283680	8
5	510.292225	255.649750	492.281660	246.644468	P	***918.486585***	459.746930	901.460036	451.233656	900.476020	450.741648	7
6	597.324253	299.165765	579.313688	290.160482	S	***821.433821***	411.220549	804.407272	402.707274	803.423256	402.215266	6
7	783.403566	392.205421	765.393001	383.200138	W	***734.401793***	367.704535	717.375244	359.191260			5
8	896.487630	448.747453	878.477065	439.742170	I	***548.322480***	274.664878	531.295931	266.151604			4
9	1009.571694	505.289485	991.561129	496.284202	L	***435.238416***	218.122846	418.211867	209.609571			3
10	1156.607094	578.807185	1138.596529	569.801902	M	322.154352	161.580814	305.127803	153.067539			2
11					R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.5	1329.711472	-0.001264	LGELPSWILMR
15.2	1329.711472	-0.001264	LGELPSWILMR
5.2	1329.715332	-0.005124	VTAIHIDPATHR
4.4	1329.707458	0.002750	LSVSNMVHTAKK
2.1	1329.707458	0.002750	LLSVLNQMPQR
1.2	1329.707474	0.002734	GTPVNRVPIMAK

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

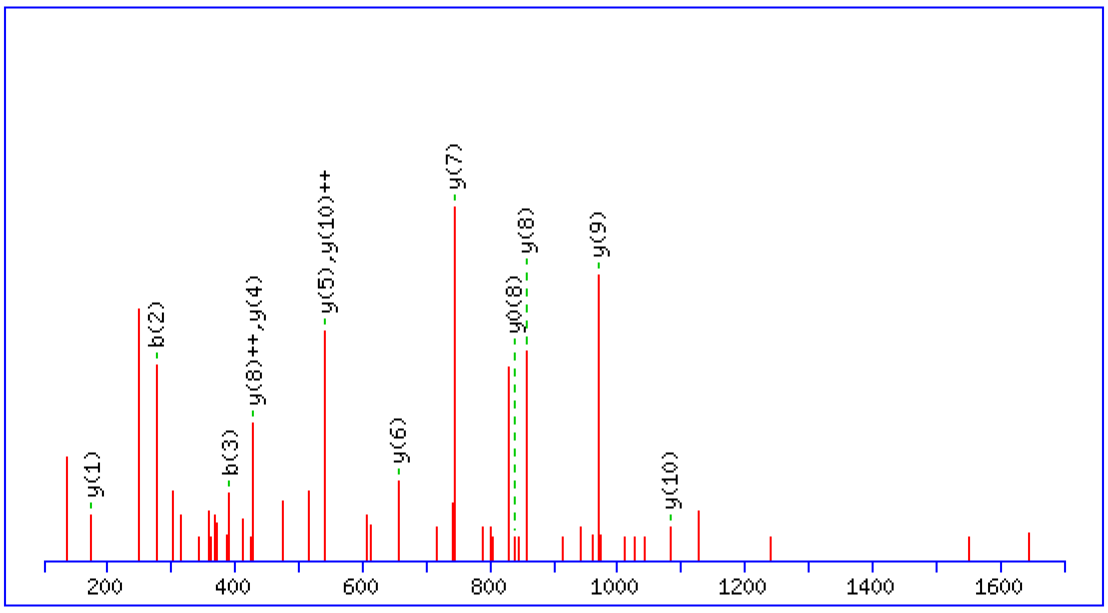
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YLLLSDLPGVR**
Found in **ATP5S_HUMAN**, ATP synthase subunit s, mitochondrial OS=Homo sapiens GN=ATP5S PE=1 SV=3

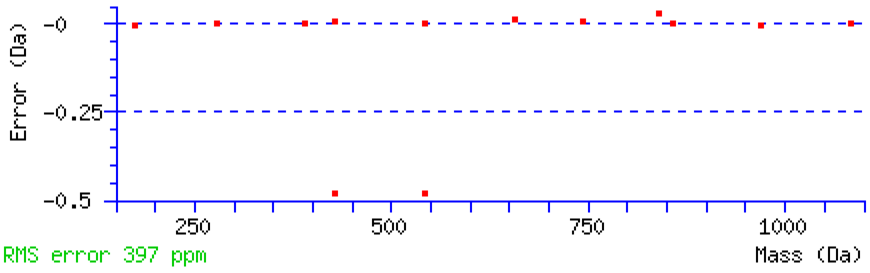
Match to Query 32872: 1244.716688 from(623.365620,2+) rtinseconds(3495) index(46210)
Title: Locus:1.1.1.2602.21
Data file 2011-11-14 - TFD - EP 8-6.mgf

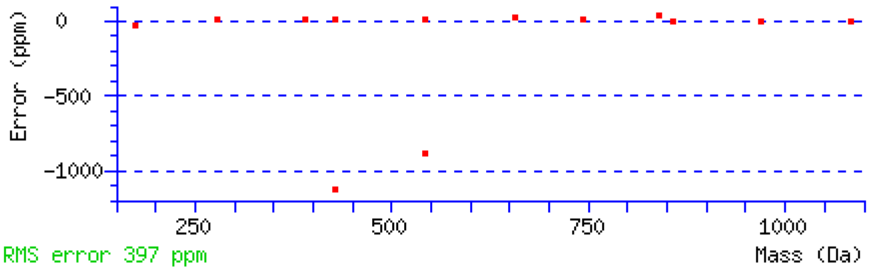
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1700] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1244.712860
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 57 **Expect:** 9e-006
Matches : 13/82 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.070605	82.538940			Y							11
2	**277.154669**	139.080973			L	***1082.656821***	541.832049	1065.630272	533.318774	1064.646256	532.826766	10
3	**390.238733**	195.623005			L	***969.572757***	485.290017	952.546208	476.776742	951.562192	476.284734	9
4	503.322797	252.165037			L	***856.488693***	428.747985	839.462144	420.234710	838.478128	419.742702	8
5	590.354825	295.681051	572.344260	286.675768	S	***743.404629***	372.205953	726.378080	363.692678	725.394064	363.200670	7
6	705.381768	353.194522	687.371203	344.189240	D	***656.372601***	328.689939	639.346052	320.176664	638.362036	319.684656	6
7	818.465832	409.736554	800.455267	400.731272	L	***541.345658***	271.176467	524.319109	262.663193			5
8	915.518596	458.262936	897.508031	449.257654	P	***428.261594***	214.634435	411.235045	206.121160			4
9	972.540060	486.773668	954.529495	477.768386	G	331.208830	166.108053	314.182281	157.594778			3
10	1071.608474	536.307875	1053.597909	527.302593	V	274.187366	137.597321	257.160817	129.084046			2
11					R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
57.1	1244.712860	0.003828	YLLLSDLPGVR
4.7	1244.716248	0.000440	LVPGGKATLVMK
4.4	1244.727463	-0.010775	VARMGLTKPLK

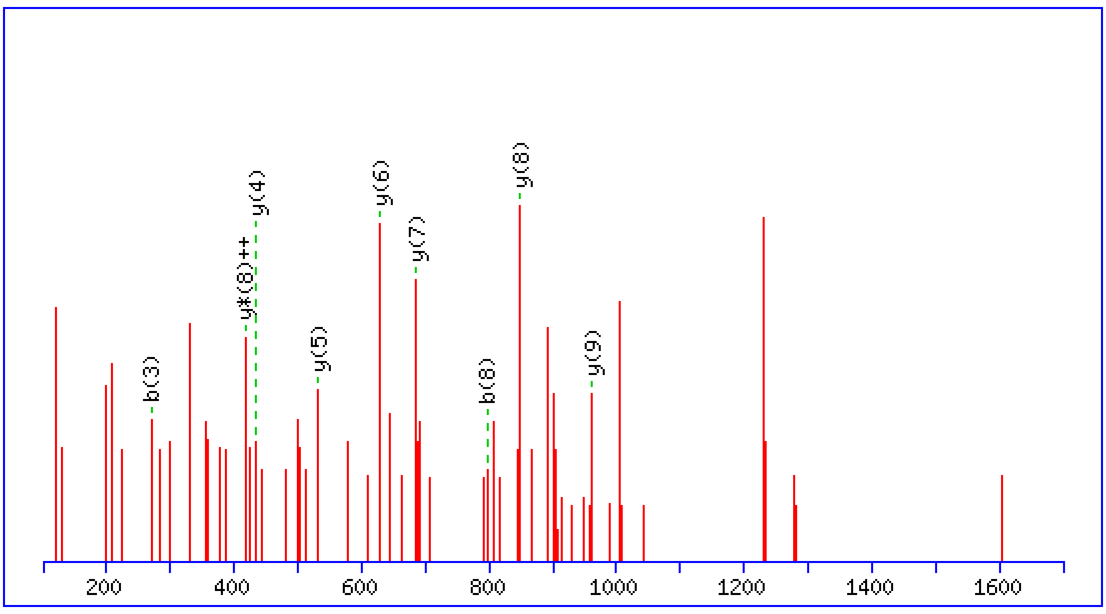
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GVLLYGPPGCGK**
Found in **ATAD1_HUMAN**, ATPase family AAA domain-containing protein 1 OS=Homo sapiens GN=ATAD1 PE=1 SV=1

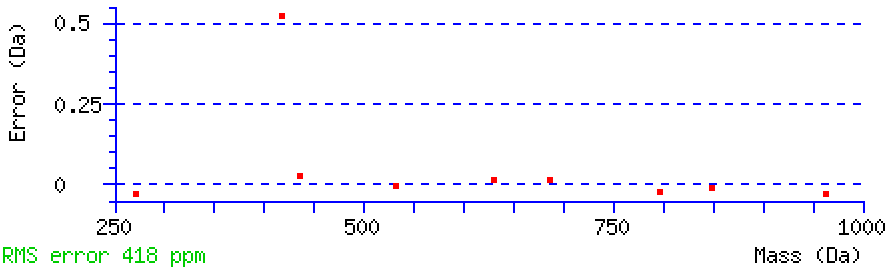
Match to Query 33085: 1230.645788 from(616.330170,2+) rtinseconds(2264) index(27741)
Title: Locus:1.1.1.2248.36
Data file 2011-11-14 - TFD - EP 8-4.mgf

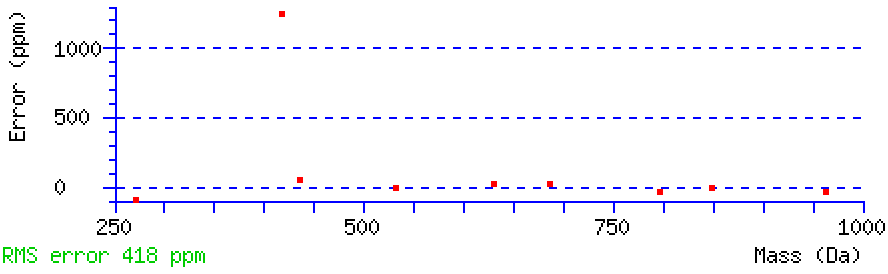
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1700] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1230.643082
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 30  Expect: 0.0026
Matches : 9/66 fragment ions using 19 most intense peaks   (help)
```

#	b	b^{++}	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	58.028740	29.518008	G					12
2	157.097154	79.052215	V	1174.628894	587.818085	1157.602345	579.304811	11
3	**270.181218**	135.594247	L	1075.560480	538.283878	1058.533931	529.770604	10
4	383.265282	192.136279	L	***962.476416***	481.741846	945.449867	473.228572	9
5	546.328611	273.667944	Y	***849.392352***	425.199814	832.365803	**416.686540**	8
6	603.350075	302.178676	G	***686.329023***	343.668150	669.302474	335.154875	7
7	700.402839	350.705058	P	***629.307559***	315.157418	612.281010	306.644143	6
8	**797.455603**	399.231440	P	***532.254795***	266.631036	515.228246	258.117761	5
9	854.477067	427.742172	G	***435.202031***	218.104654	418.175482	209.591379	4
10	1028.523366	514.765321	C	378.180567	189.593921	361.154018	181.080647	3
11	1085.544830	543.276053	G	204.134268	102.570772	187.107719	94.057497	2
12			K	147.112804	74.060040	130.086255	65.546765	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.3	1230.643082	0.002706	GVLLYGPPGCGK
2.6	1230.635681	0.010107	RLPGPDELFR
1.3	1230.645569	0.000219	VLGVTSEELER

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

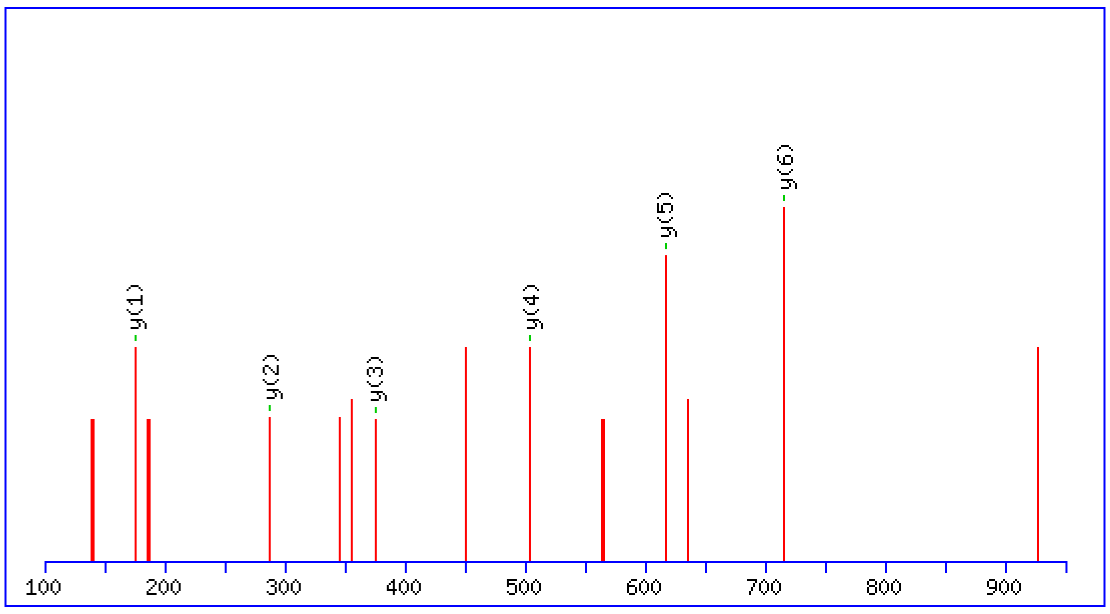
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QTVLESIR**
Found in **ATD3A_HUMAN**, ATPase family AAA domain-containing protein 3A OS=Homo sapiens GN=ATAD3A PE=1 SV=2

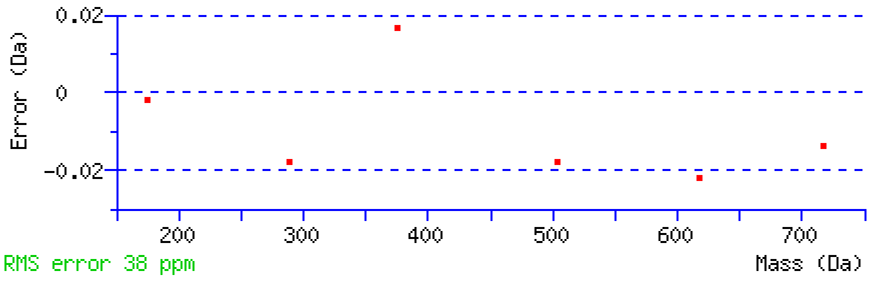
Match to Query 188109: 944.526048 from(473.270300,2+) rtinseconds(2025) index(755943)
Title: Locus:1.1.1.1116.13
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●

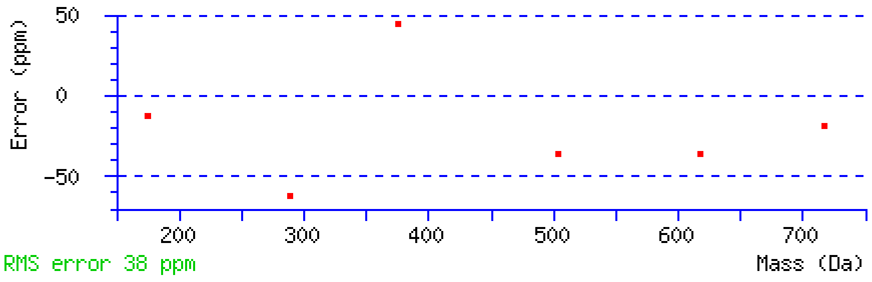


Monoisotopic mass of neutral peptide Mr(calc): 944.529083
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.0014
Matches : 6/78 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	129.065854	65.036565	112.039305	56.523291			Q							8
2	230.113533	115.560405	213.086984	107.047130	212.102968	106.555122	T	817.477794	409.242535	800.451245	400.729261	799.467229	400.237253	7
3	329.181947	165.094612	312.155398	156.581337	311.171382	156.089329	V	*716.430115*	358.718696	699.403566	350.205421	698.419550	349.713413	6
4	442.266011	221.636644	425.239462	213.123369	424.255446	212.631361	L	*617.361701*	309.184489	600.335152	300.671214	599.351136	300.179206	5
5	571.308604	286.157940	554.282055	277.644666	553.298039	277.152658	E	*504.277637*	252.642456	487.251088	244.129182	486.267072	243.637174	4
6	658.340632	329.673954	641.314083	321.160680	640.330067	320.668672	S	*375.235044*	188.121160	358.208495	179.607885	357.224479	179.115877	3
7	771.424696	386.215986	754.398147	377.702712	753.414131	377.210704	I	*288.203016*	144.605146	271.176467	136.091871			2
8							R	*175.118952*	88.063114	158.092403	79.549839			1



RMS error 38 ppm



RMS error 38 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.2	944.529083	-0.003035	QTVLESIR
20.1	944.529083	-0.003035	SLKPTDLR
17.9	944.529053	-0.003005	EKLAESLR
15.3	944.529083	-0.003035	TKPSDIIR
15.0	944.529068	-0.003020	LTNSEIIR
9.7	944.529053	-0.003005	EKLASLER
9.7	944.529068	-0.003020	KIPSSELR
8.9	944.529099	-0.003051	QIVTTDLR
7.1	944.522552	0.003496	IVCRELR
7.1	944.519196	0.006852	VWREVTR

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

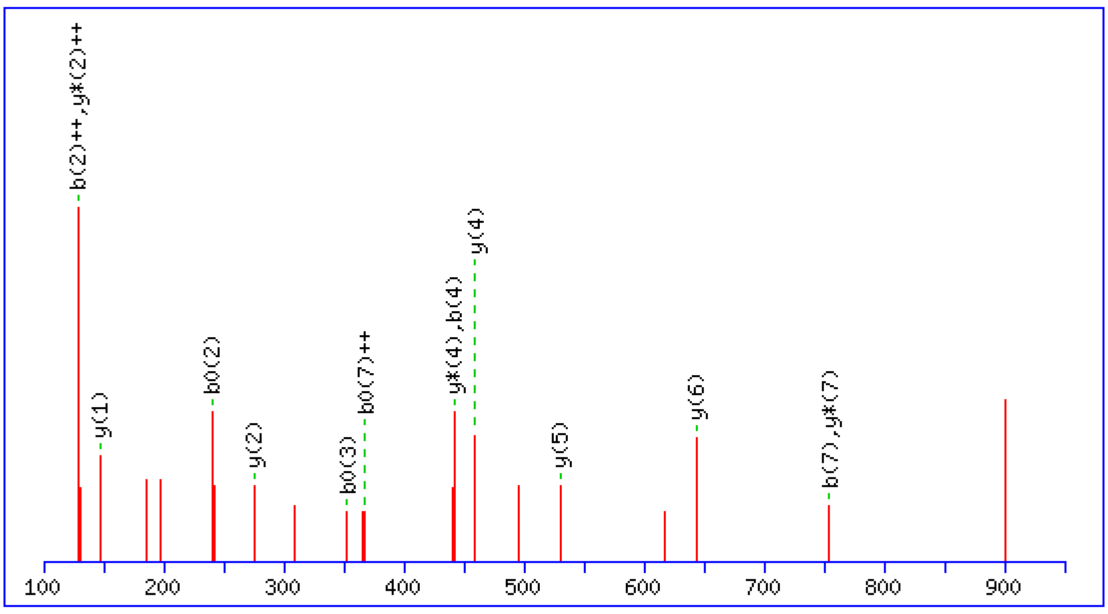
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EQLAALKK**
Found in **ATIF1_HUMAN**, ATPase inhibitor, mitochondrial OS=Homo sapiens GN=ATPIF1 PE=1 SV=1

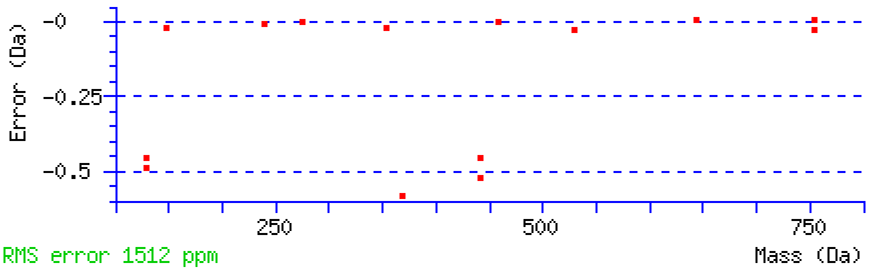
Match to Query 126418: 899.544008 from(450.779280,2+) rtinseconds(1063) index(577660)
Title: Locus:1.1.1.723.10
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

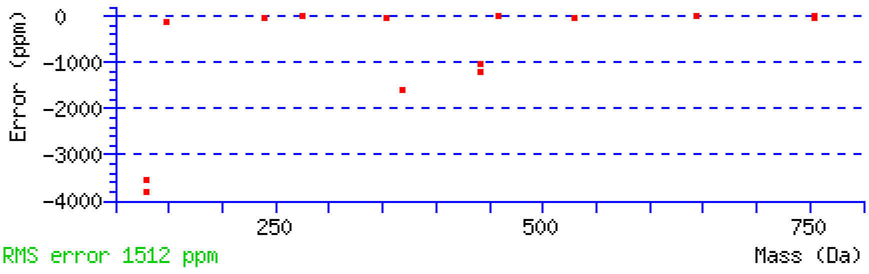
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [950] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 899.543976
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 48 **Expect:** 9.7e-005
Matches : 14/68 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	130.049869	65.528572			112.039304	56.523290	E					8
2	258.108447	129.557862	241.081898	121.044587	240.097882	120.552579	Q	771.508701	386.257989	754.482152	377.744714	7
3	371.192511	186.099894	354.165962	177.586619	353.181946	177.094611	L	***643.450123***	322.228700	626.423574	313.715425	6
4	**442.229625**	221.618450	425.203076	213.105176	424.219060	212.613168	A	***530.366059***	265.686668	513.339510	257.173393	5
5	513.266739	257.137008	496.240190	248.623733	495.256174	248.131725	A	***459.328945***	230.168110	442.302396	221.654836	4
6	626.350803	313.679040	609.324254	305.165765	608.340238	304.673757	L	388.291831	194.649554	371.265282	186.136279	3
7	**754.445766**	377.726521	737.419217	369.213247	736.435201	368.721239	K	***275.207767***	138.107521	258.181218	129.594247	2
8							K	***147.112804***	74.060040	130.086255	65.546765	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.1	899.543976	0.000032	EQLAALKK
22.7	899.543976	0.000032	QIEAKALK
22.1	899.543976	0.000032	QEALAKLK
19.5	899.544006	0.000002	KPKATPVK
15.3	899.544006	0.000002	VAVATPAKK
12.6	899.544006	0.000002	ALVATPGKK
11.5	899.544006	0.000002	LLGDVQKK
11.3	899.543976	0.000032	KIALEAQK
8.3	899.543976	0.000032	IALEAQKK
8.2	899.543976	0.000032	KEIEILR

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

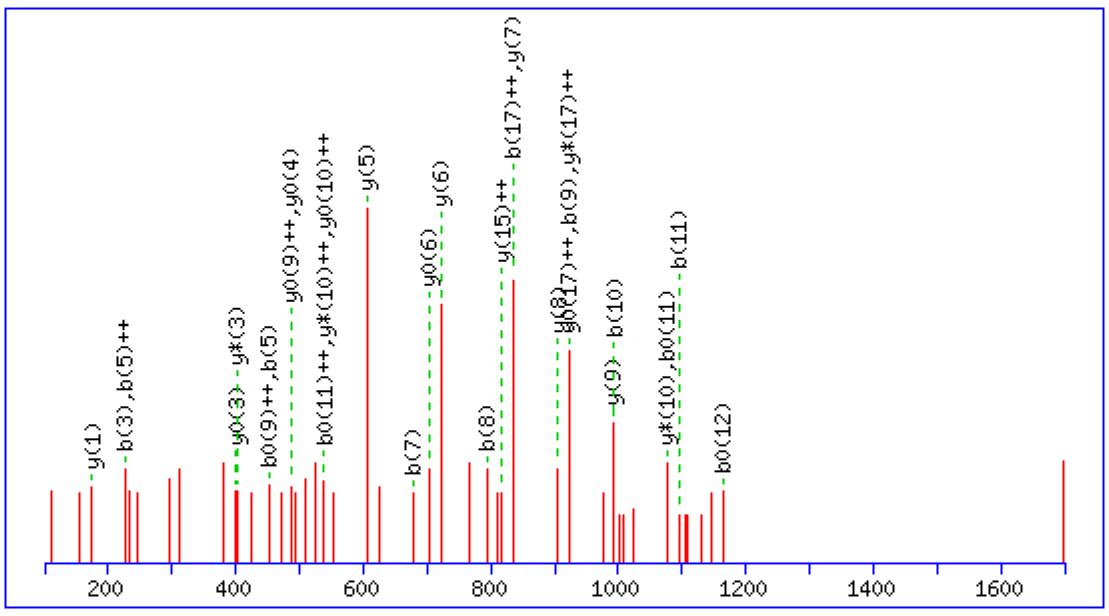
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **APGIILLDEATSALDTSNER**
Found in **ABCB6_HUMAN**, ATP-binding cassette sub-family B member 6, mitochondrial OS=Homo sapiens GN=ABCB6 PE=1 SV=1

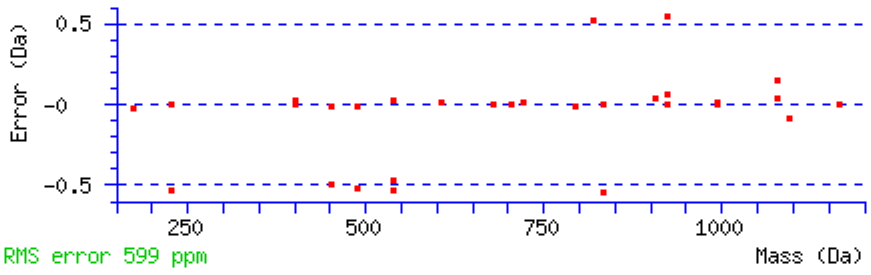
Match to Query 60891: 2085.064932 from(696.028920,3+) rtinseconds(3940) index(55495)
Title: Locus:1.1.1.3039.22
Data file 2011-11-12 - TFD - EP 5-1.mgf

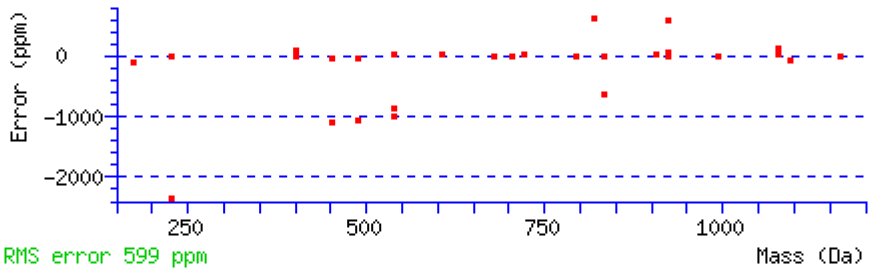
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2085.058945
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 44 **Expect:** 0.00037
Matches : 30/178 fragment ions using 40 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							20
2	169.097154	85.052215					P	2015.029141	1008.018209	1998.002592	999.504934	1997.018576	999.012926	19
3	***226.118618***	113.562947					G	1917.976377	959.491827	1900.949828	950.978552	1899.965812	950.486544	18
4	339.202682	170.104979					I	1860.954913	930.981095	1843.928364	922.467820	1842.944348	921.975812	17
5	***452.286746***	226.647011					I	1747.870849	874.439062	1730.844300	865.925788	1729.860284	865.433780	16
6	565.370810	283.189043					L	1634.786785	817.897031	1617.760236	809.383756	1616.776220	808.891748	15
7	***678.454874***	339.731075					L	1521.702721	761.354998	1504.676172	752.841724	1503.692156	752.349716	14
8	***793.481817***	397.244547			775.471252	388.239264	D	1408.618657	704.812967	1391.592108	696.299692	1390.608092	695.807684	13
9	***922.524410***	461.765843			904.513845	452.760561	E	1293.591714	647.299495	1276.565165	638.786221	1275.581149	638.294212	12
10	***993.561524***	497.284400			975.550959	488.279117	A	1164.549121	582.778199	1147.522572	574.264924	1146.538556	573.772916	11
11	***1094.609203***	547.808240			1076.598638	538.802957	T	1093.512007	547.259642	1076.485458	538.746367	1075.501442	538.254359	10
12	1181.641231	591.324254			1163.630666	582.318971	S	***992.464328***	496.735802	975.437779	488.222528	974.453763	487.730520	9
13	1252.678345	626.842811			1234.667780	617.837528	A	***905.432300***	453.219788	888.405751	444.706513	887.421735	444.214505	8
14	1365.762409	683.384842			1347.751844	674.379560	L	***834.395186***	417.701231	817.368637	409.187956	816.384621	408.695948	7
15	1480.789352	740.898314			1462.778787	731.893032	D	***721.311122***	361.159199	704.284573	352.645925	703.300557	352.153917	6
16	1581.837031	791.422154			1563.826466	782.416871	T	***606.284179***	303.645728	589.257630	295.132453	588.273614	294.640445	5
17	1668.869059	834.938168			1650.858494	825.932885	S	505.236500	253.121888	488.209951	244.608613	487.225935	244.116605	4
18	1782.911986	891.959631	1765.885437	883.446357	1764.901421	882.954349	N	418.204472	209.605874	401.177923	201.092599	400.193907	200.600591	3
19	1911.954579	956.480928	1894.928030	947.967653	1893.944014	947.475645	E	304.161545	152.584410	287.134996	144.071136	286.150980	143.579128	2
20							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.2	2085.058945	0.005987	APGIILLDEATSALDTSNER
7.2	2085.081604	-0.016672	IVALMDTYSPSLPKSLYR
2.9	2085.081604	-0.016672	IVALMDTYSPSLPKSLYR
0.7	2085.060272	0.004660	IQLPDLENQRNFNELSR

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

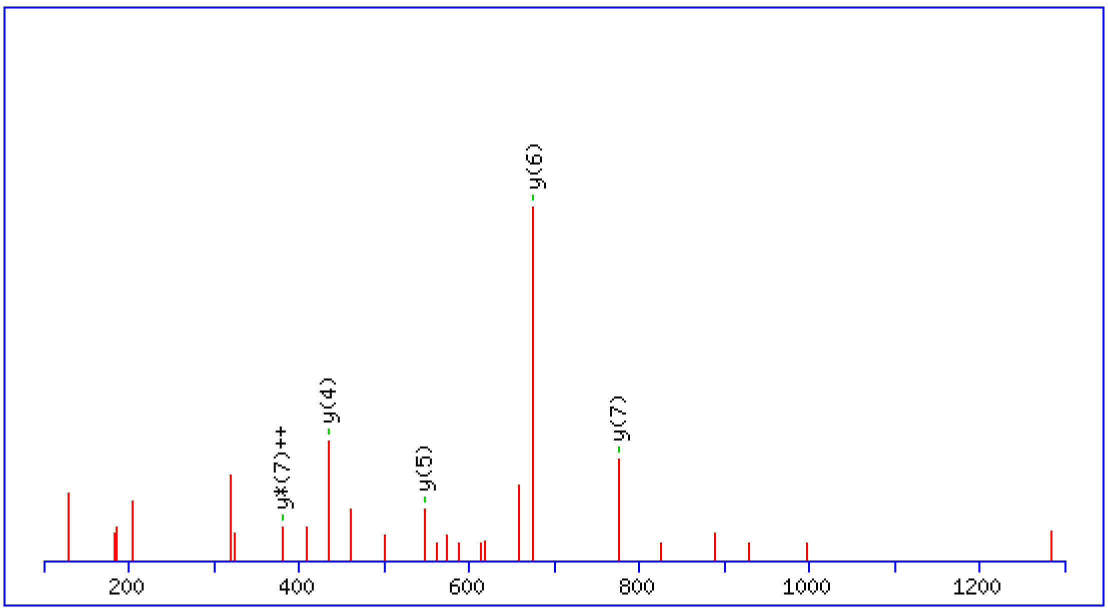
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LVEPMAGR**
Found in **ABCCB_HUMAN**, ATP-binding cassette sub-family C member 11 OS=Homo sapiens GN=ABCC11 PE=1 SV=1

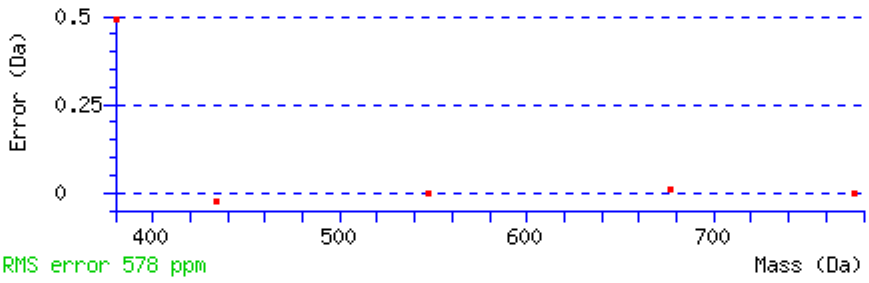
Match to Query 7135: 887.461068 from(444.737810,2+) rtinseconds(1379) index(10160)
Title: Locus:1.1.1.1921.8
Data file 2011-11-12 - TFD - EP 6-2.mgf

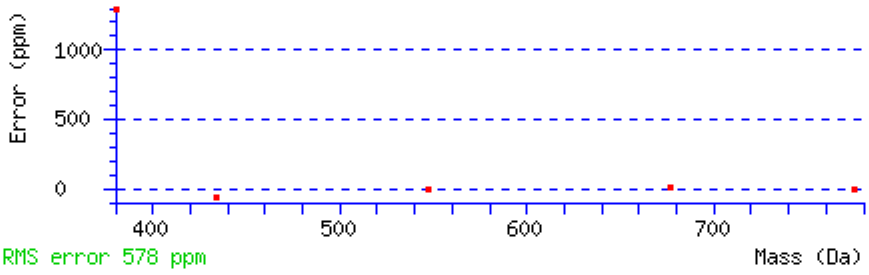
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 887.453476
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P4      : Oxidation (P)
Ions Score: 32  Expect: 0.0078
Matches : 5/56 fragment ions using 7 most intense peaks   (help)
```

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308			L							8
2	213.159754	107.083515			V	***775.376701***	388.191989	758.350152	379.678714	757.366136	379.186706	7
3	342.202347	171.604811	324.191782	162.599529	E	***676.308287***	338.657782	659.281738	330.144507	658.297722	329.652499	6
4	455.250026	228.128651	437.239461	219.123369	P	***547.265694***	274.136485	530.239145	265.623211			5
5	586.290511	293.648894	568.279946	284.643611	M	***434.218015***	217.612645	417.191466	209.099371			4
6	657.327625	329.167451	639.317060	320.162168	A	303.177530	152.092403	286.150981	143.579128			3
7	714.349089	357.678183	696.338524	348.672900	G	232.140416	116.573846	215.113867	108.060571			2
8					R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.7	887.453476	0.007592	LVEPMAGR
17.5	887.453476	0.007592	LVEPMAGR
6.3	887.461334	-0.000266	IYHRDGK
3.1	887.464706	-0.003638	QLLQCGR

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

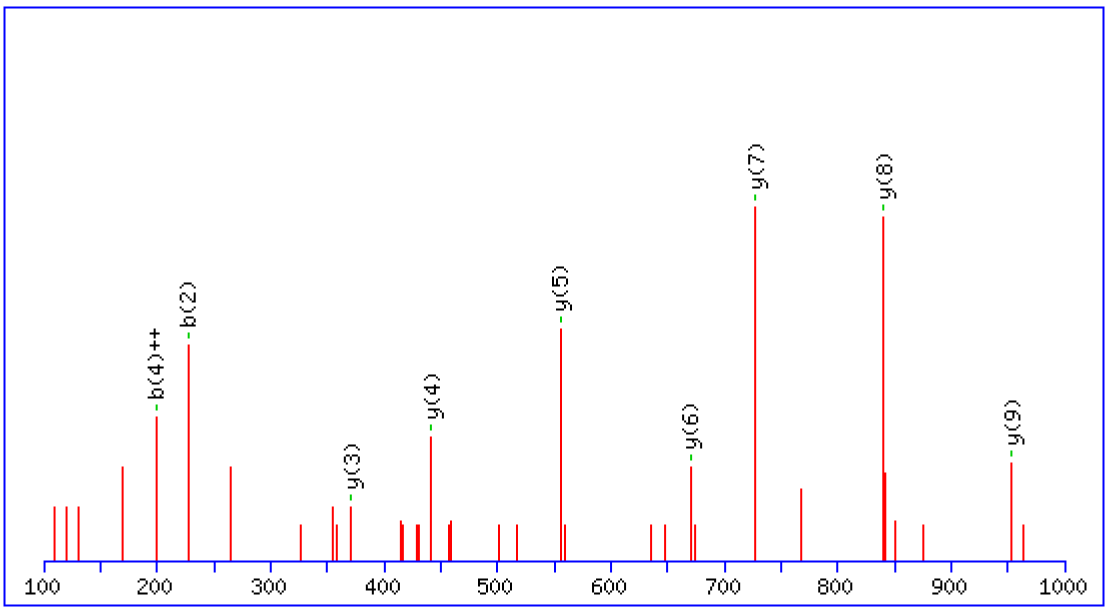
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLLGDLAPVR**
Found in **ABCF3_HUMAN**, ATP-binding cassette sub-family F member 3 OS=Homo sapiens GN=ABCF3 PE=1 SV=2

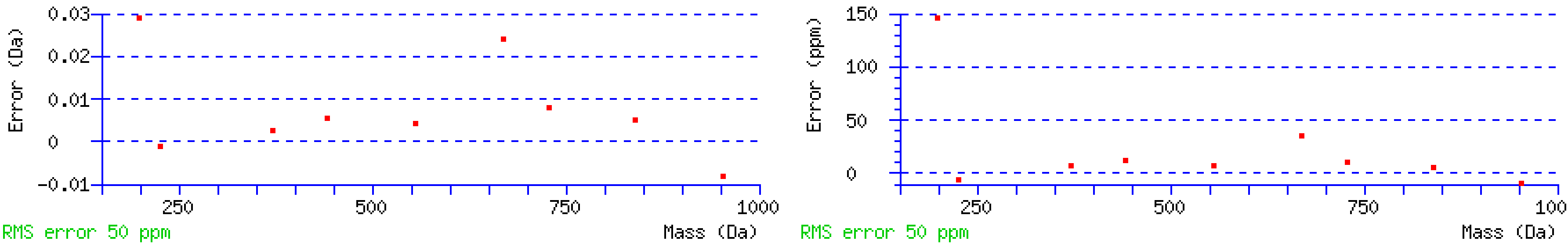
Match to Query 21285: 1065.653428 from(533.833990,2+) rtinseconds(3023) index(40918)
Title: Locus:1.1.1.2638.8
Data file 2011-11-10 - TFD - EP 4-2.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1065.654617
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 67 **Expect:** 2.4e-007
Matches : 9/72 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							10
2	227.175404	114.091340			L	***953.577843***	477.292559	936.551294	468.779285	935.567278	468.287277	9
3	340.259468	170.633372			L	***840.493779***	420.750527	823.467230	412.237253	822.483214	411.745245	8
4	397.280932	199.144104			G	***727.409715***	364.208496	710.383166	355.695221	709.399150	355.203213	7
5	512.307875	256.657576	494.297310	247.652293	D	***670.388251***	335.697764	653.361702	327.184489	652.377686	326.692481	6
6	625.391939	313.199608	607.381374	304.194325	L	***555.361308***	278.184292	538.334759	269.671018			5
7	696.429053	348.718165	678.418488	339.712882	A	***442.277244***	221.642260	425.250695	213.128985			4
8	793.481817	397.244547	775.471252	388.239264	P	***371.240130***	186.123703	354.213581	177.610428			3
9	892.550231	446.778753	874.539666	437.773471	V	274.187366	137.597321	257.160817	129.084046			2
10					R	175.118952	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
66.5	1065.654617	-0.001189	LLLGDLAPVR
10.1	1065.643387	0.010041	ILPTPPATLK
0.8	1065.654617	-0.001189	EPLVIQVLR
0.6	1065.643387	0.010041	IGLLPLLNPT

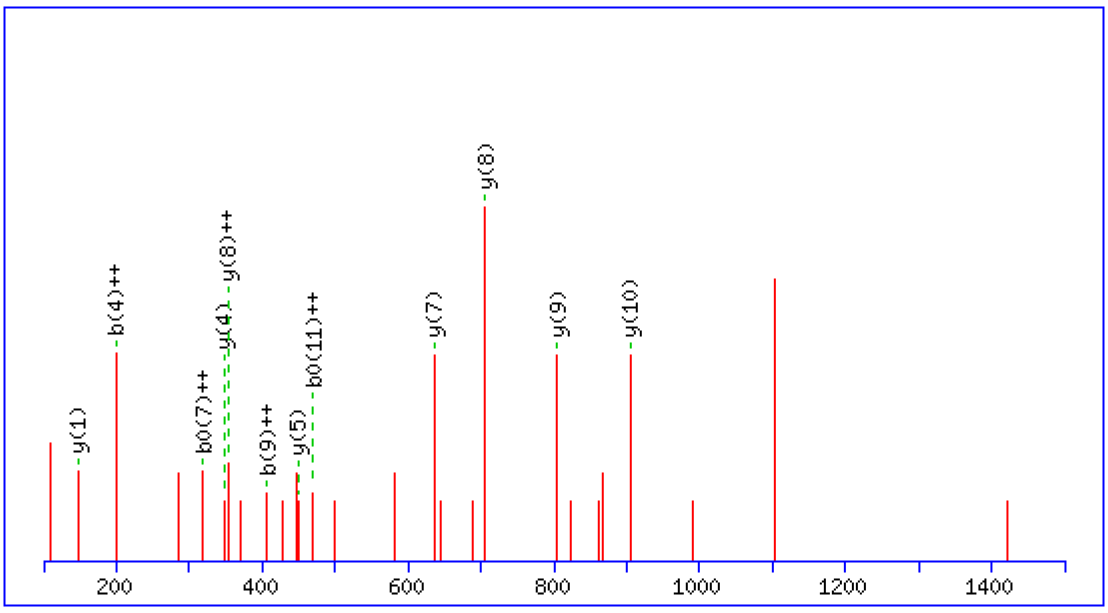
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVVVAGETGSGK**
Found in **DHX29_HUMAN**, ATP-dependent RNA helicase DHX29 OS=Homo sapiens GN=DHX29 PE=1 SV=2

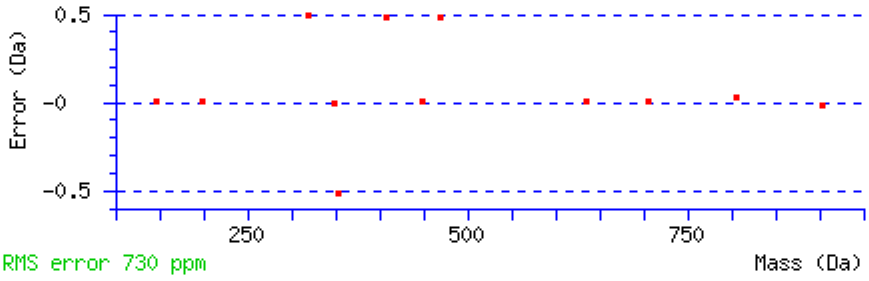
Match to Query 20347: 1101.596648 from(551.805600,2+) rtinseconds(1156) index(3762)
Title: Locus:1.1.1.2004.39
Data file 2011-11-12 - TFD - EP 5-1.mgf

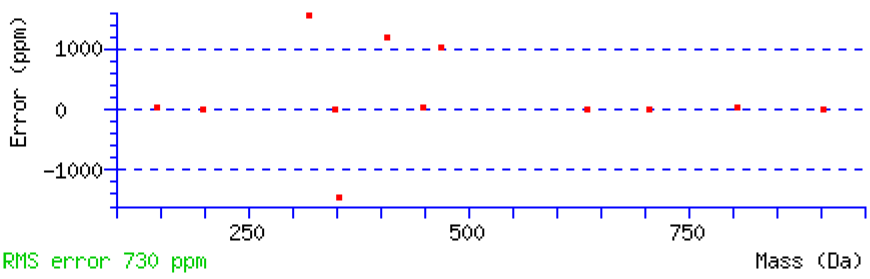
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1101.603012
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 37 **Expect:** 0.0019
Matches : 13/94 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483			V							12
2	199.144104	100.075690			V	1003.541852	502.274564	986.515303	493.761290	985.531287	493.269282	11
3	298.212518	149.609897			V	***904.473438***	452.740357	887.446889	444.227083	886.462873	443.735075	10
4	397.280932	**199.144104**			V	***805.405024***	403.206150	788.378475	394.692876	787.394459	394.200868	9
5	468.318046	234.662661			A	***706.336610***	353.671943	689.310061	345.158669	688.326045	344.666661	8
6	525.339510	263.173393			G	***635.299496***	318.153386	618.272947	309.640112	617.288931	309.148104	7
7	654.382103	327.694690	636.371538	318.689407	E	578.278032	289.642654	561.251483	281.129380	560.267467	280.637372	6
8	755.429782	378.218529	737.419217	369.213247	T	***449.235439***	225.121358	432.208890	216.608083	431.224874	216.116075	5
9	812.451246	**406.729261**	794.440681	397.723979	G	***348.187760***	174.597518	331.161211	166.084244	330.177195	165.592236	4
10	899.483274	450.245275	881.472709	441.239993	S	291.166296	146.086786	274.139747	137.573512	273.155731	137.081504	3
11	956.504738	478.756007	938.494173	469.750725	G	204.134268	102.570772	187.107719	94.057498			2
12					K	***147.112804***	74.060040	130.086255	65.546766			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.0	1101.603012	-0.006364	VVVVAGETGSGK
7.9	1101.606995	-0.010347	LEQPFLDLK

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

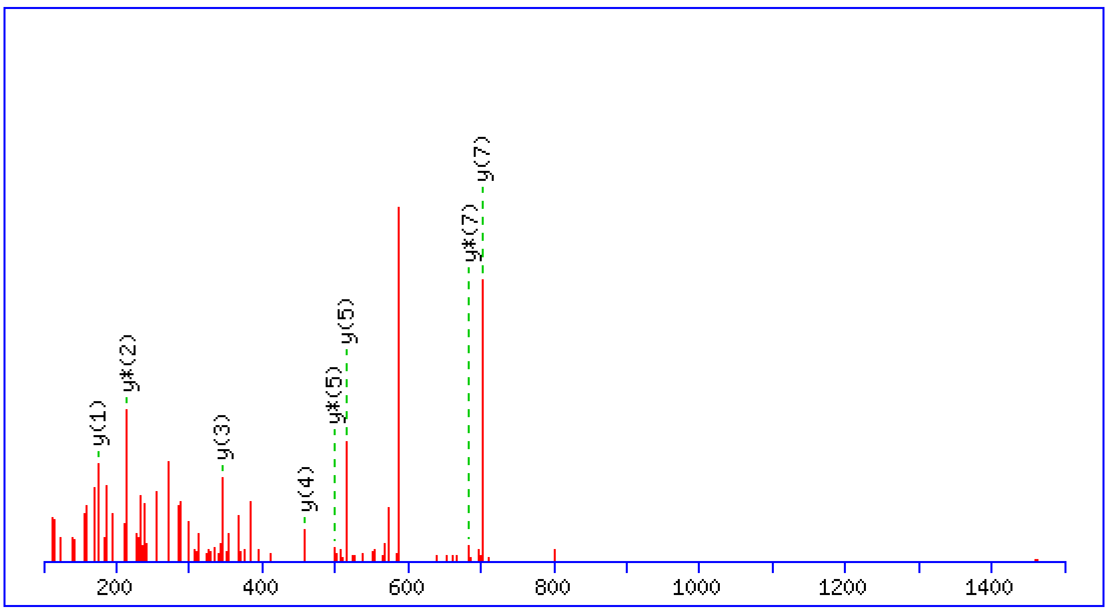
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVSGLPGR**
Found in **ANPRB_HUMAN**, Atrial natriuretic peptide receptor 2 OS=Homo sapiens GN=NPR2 PE=1 SV=1

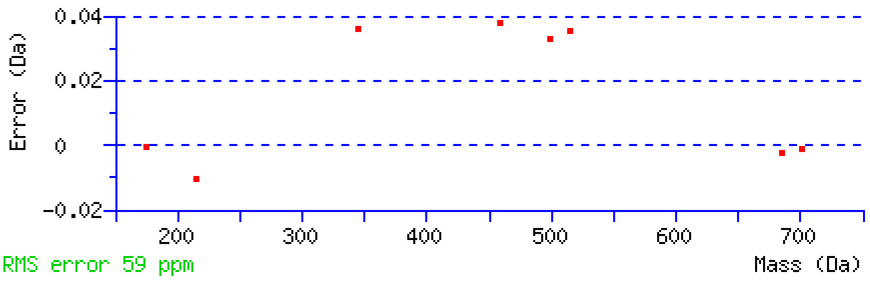
Match to Query 1309: 799.456748 from(400.735650,2+) rtinseconds(1406) index(500978)
Title: Locus:1.1.1.863.2
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

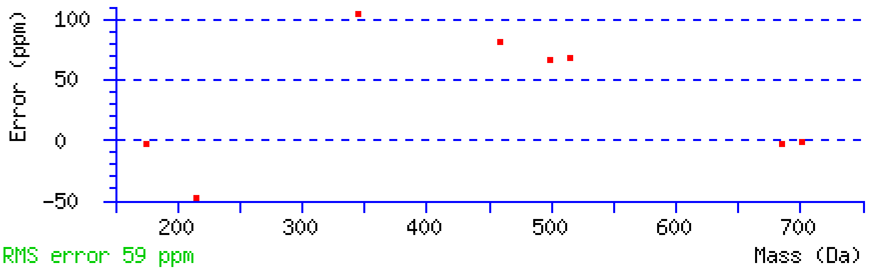
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 799.455215
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
P6 : Oxidation (P)
Ions Score: 37 **Expect:** 0.0027
Matches : 8/56 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483			V							8
2	199.144104	100.075690			V	***701.394065***	351.200671	684.367516	342.687396	683.383500	342.195388	7
3	286.176132	143.591704	268.165567	134.586422	S	602.325651	301.666464	585.299102	293.153189	584.315086	292.661181	6
4	343.197596	172.102436	325.187031	163.097153	G	***515.293623***	258.150450	498.267074	249.637175			5
5	456.281660	228.644468	438.271095	219.639186	L	***458.272159***	229.639717	441.245610	221.126443			4
6	569.329339	285.168308	551.318774	276.163025	P	***345.188095***	173.097685	328.161546	164.584411			3
7	626.350803	313.679040	608.340238	304.673757	G	232.140416	116.573846	215.113867	108.060571			2
8					R	***175.118952***	88.063114	158.092403	79.549839			1

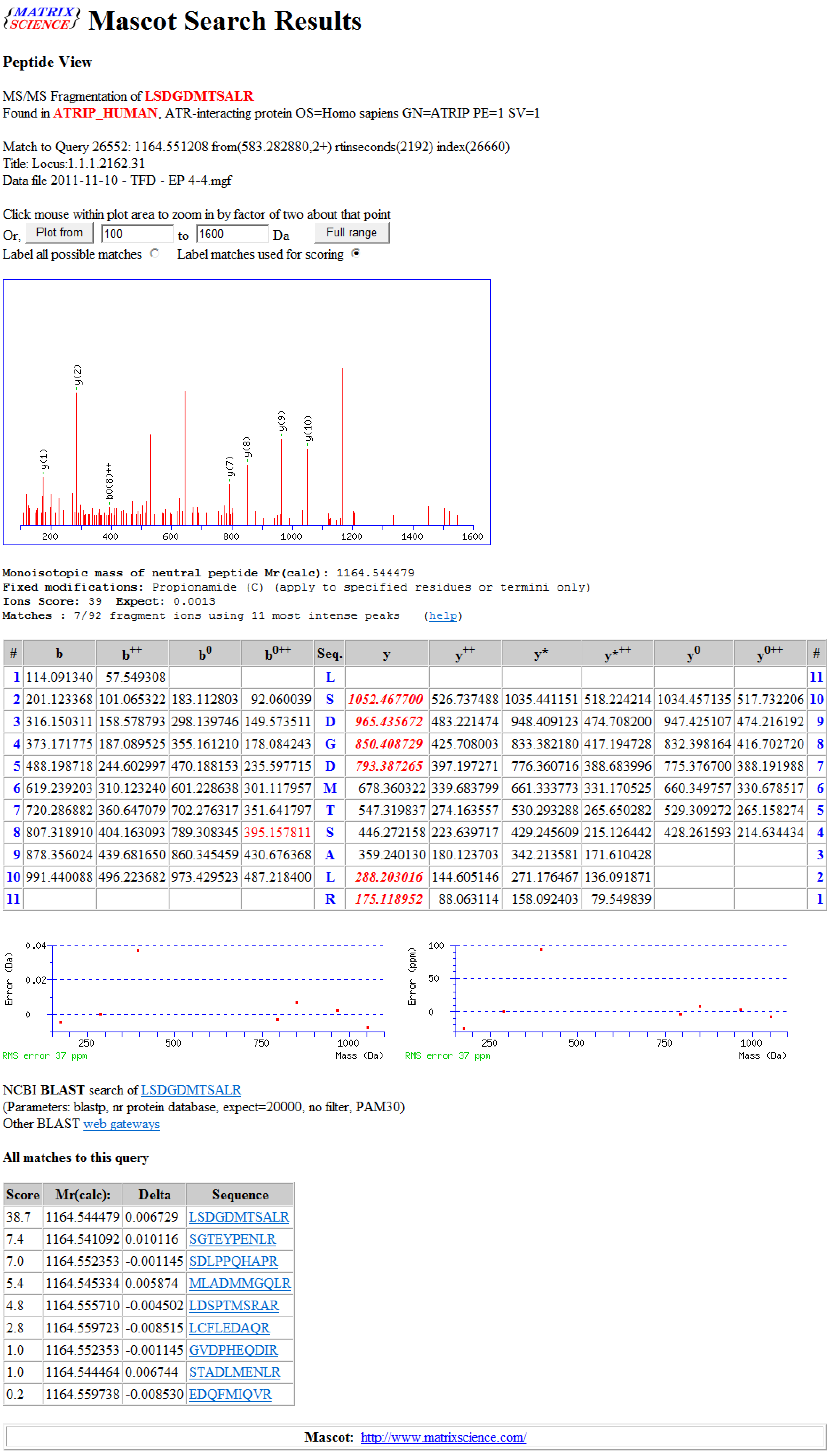




NCBI **BLAST** search of VVSGLPGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.8	799.455215	0.001533	VVSGLPGR
32.5	799.455200	0.001548	TLKPPGR
27.5	799.455185	0.001563	VDAILNR
20.0	799.455200	0.001548	TPAVIQR
17.2	799.455200	0.001548	VLKDPGR
16.3	799.455200	0.001548	LTQVSPR
15.9	799.455185	0.001563	VDNLALR
15.2	799.455200	0.001548	VADLVAGR
14.9	799.455185	0.001563	AALSPLGR
14.9	799.455185	0.001563	DLNILGR



Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSDGDMTSALR**
Found in **ATRIP_HUMAN**, ATR-interacting protein OS=Homo sapiens GN=ATRIP PE=1 SV=1

Match to Query 26552: 1164.551208 from(583.282880,2+) rtinseconds(2192) index(26660)
Title: Locus:1.1.1.2162.31
Data file 2011-11-10 - TFD - EP 4-4.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●

```
Monoisotopic mass of neutral peptide Mr(calc): 1164.544479
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 39  Expect: 0.0013
Matches : 7/92 fragment ions using 11 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							11
2	201.123368	101.065322	183.112803	92.060039	S	***1052.467700***	526.737488	1035.441151	518.224214	1034.457135	517.732206	10
3	316.150311	158.578793	298.139746	149.573511	D	***965.435672***	483.221474	948.409123	474.708200	947.425107	474.216192	9
4	373.171775	187.089525	355.161210	178.084243	G	***850.408729***	425.708003	833.382180	417.194728	832.398164	416.702720	8
5	488.198718	244.602997	470.188153	235.597715	D	***793.387265***	397.197271	776.360716	388.683996	775.376700	388.191988	7
6	619.239203	310.123240	601.228638	301.117957	M	678.360322	339.683799	661.333773	331.170525	660.349757	330.678517	6
7	720.286882	360.647079	702.276317	351.641797	T	547.319837	274.163557	530.293288	265.650282	529.309272	265.158274	5
8	807.318910	404.163093	789.308345	395.157811	S	446.272158	223.639717	429.245609	215.126442	428.261593	214.634434	4
9	878.356024	439.681650	860.345459	430.676368	A	359.240130	180.123703	342.213581	171.610428			3
10	991.440088	496.223682	973.429523	487.218400	L	***288.203016***	144.605146	271.176467	136.091871			2
11					R	***175.118952***	88.063114	158.092403	79.549839			1

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.7	1164.544479	0.006729	LSDGDMTSALR
7.4	1164.541092	0.010116	SGTEYPENLR
7.0	1164.552353	-0.001145	SDLPPQHAPR
5.4	1164.545334	0.005874	MLADMMGQLR
4.8	1164.555710	-0.004502	LDSPTMSRAR
2.8	1164.559723	-0.008515	LCFLEDAQR
1.0	1164.552353	-0.001145	GVDPHEQDIR
1.0	1164.544464	0.006744	STADLMENLR
0.2	1164.559738	-0.008530	EDQFMIQVR

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

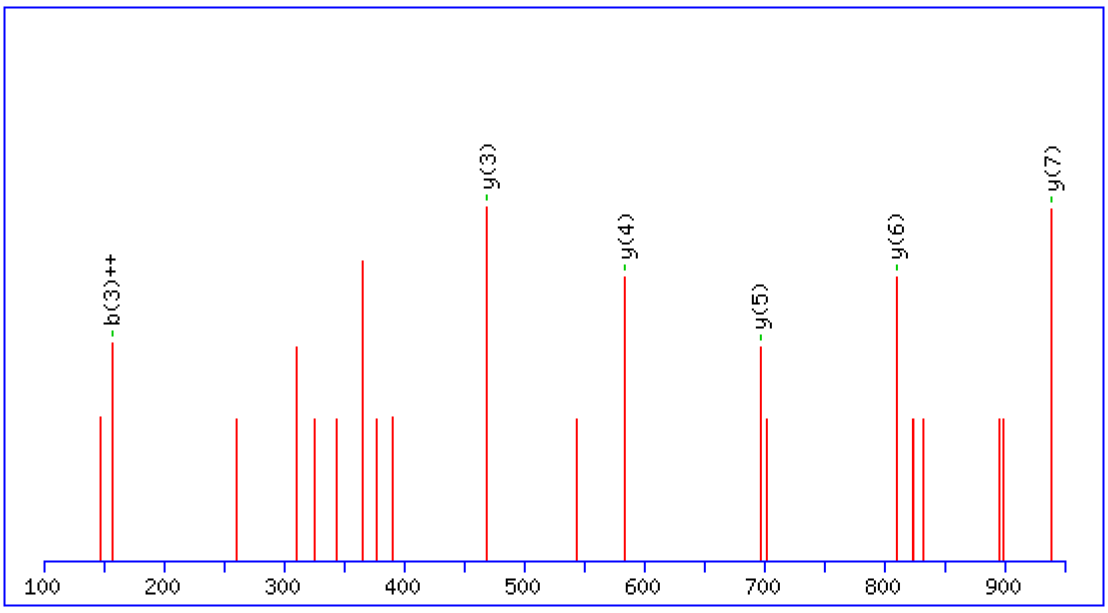
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALEIIDFFR**
Found in **ATG9A_HUMAN**, Autophagy-related protein 9A OS=Homo sapiens GN=ATG9A PE=1 SV=3

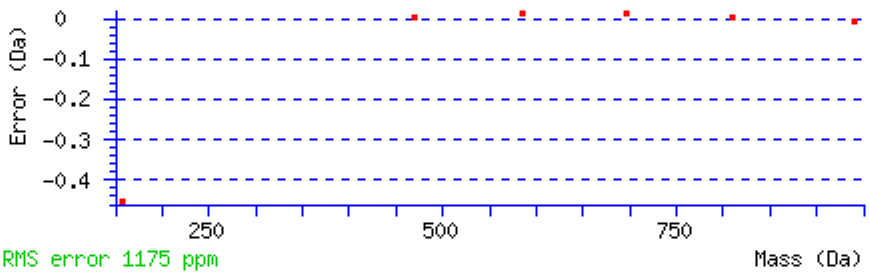
Match to Query 23638: 1122.608308 from(562.311430,2+) rtinseconds(4151) index(61267)
Title: Locus:1.1.1.3001.10
Data file 2011-11-14 - TFD - EP 7-1.mgf

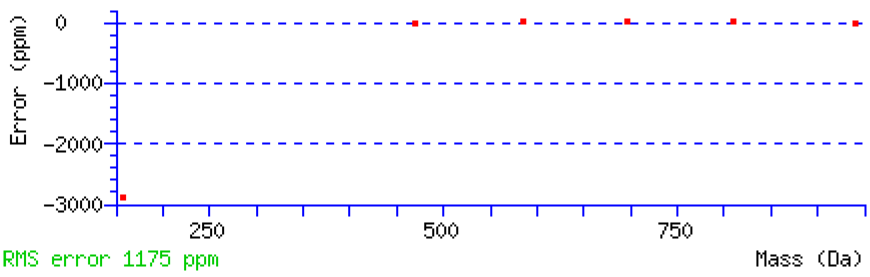
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1122.607330
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 35 **Expect:** 0.0022
Matches : 6/70 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			A							9
2	185.128454	93.067865			L	1052.577508	526.792392	1035.550959	518.279118	1034.566943	517.787110	8
3	314.171047	157.589161	296.160482	148.583879	E	*939.493444*	470.250360	922.466895	461.737086	921.482879	461.245078	7
4	427.255111	214.131193	409.244546	205.125911	I	*810.450851*	405.729064	793.424302	397.215789	792.440286	396.723781	6
5	540.339175	270.673226	522.328610	261.667943	I	*697.366787*	349.187032	680.340238	340.673757	679.356222	340.181749	5
6	655.366118	328.186697	637.355553	319.181415	D	*584.282723*	292.645000	567.256174	284.131725	566.272158	283.639717	4
7	802.434532	401.720904	784.423967	392.715622	F	*469.255780*	235.131528	452.229231	226.618253			3
8	949.502946	475.255111	931.492381	466.249828	F	322.187366	161.597321	305.160817	153.084047			2
9					R	175.118952	88.063114	158.092403	79.549840			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.2	1122.607330	0.000978	ALEIIDFFR
4.8	1122.607346	0.000962	SVFVGNLPYK
1.7	1122.603287	0.005021	NILYTRSEK
0.8	1122.603302	0.005006	NKAPQEPPVK

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

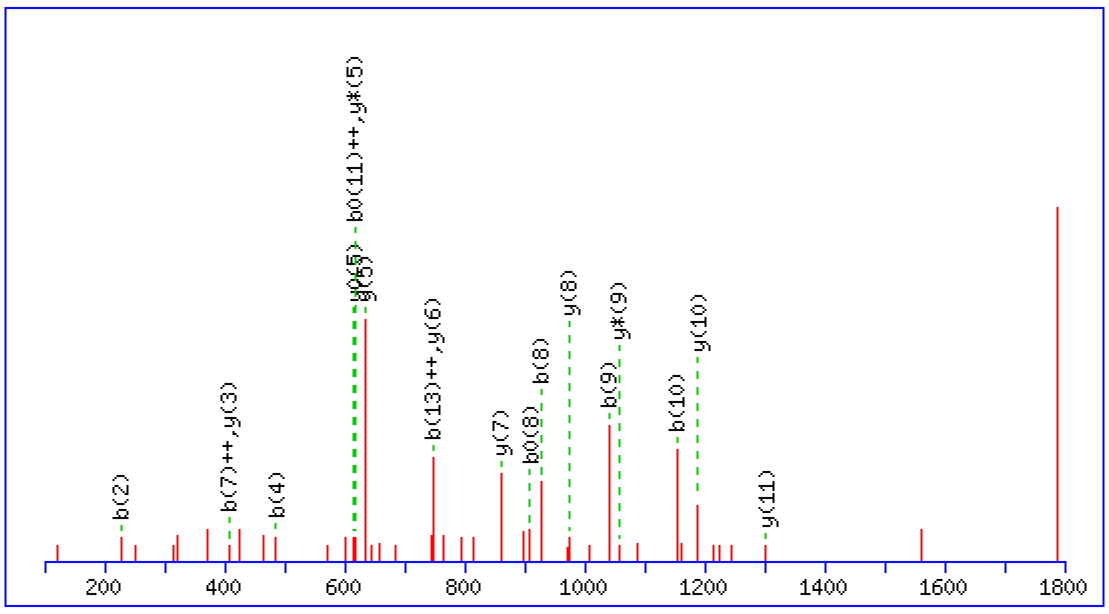
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILEEIDTLILPENFK**
Found in **BAG1_HUMAN**, BAG family molecular chaperone regulator 1 OS=Homo sapiens GN=BAG1 PE=1 SV=4

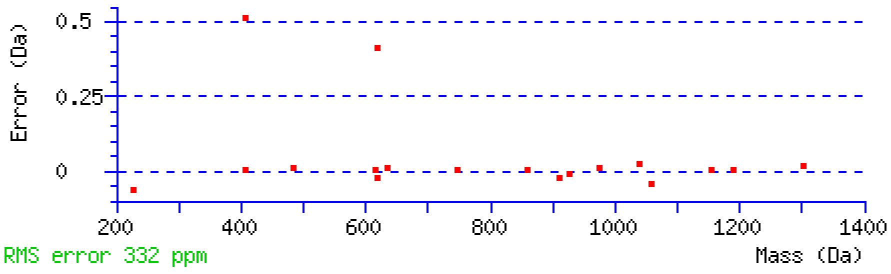
Match to Query 58533: 1785.985368 from(893.999960,2+) rtinseconds(3968) index(59563)
Title: Locus:1.1.1.2889.44
Data file 2011-11-14 - TFD - EP 8-4.mgf

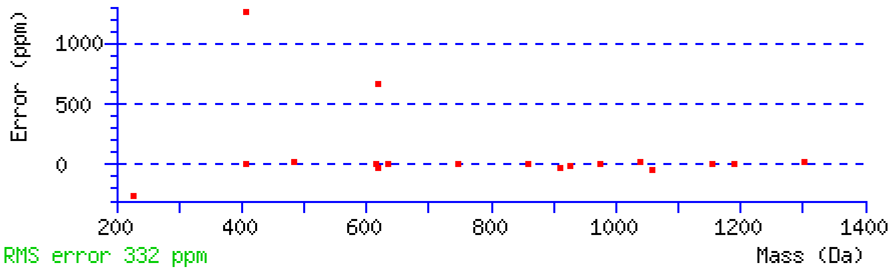
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1785.976379
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 31  Expect: 0.0046
Matches : 19/134 fragment ions using 35 most intense peaks   (help)
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.091340	57.549308					I							15
2	**227.175404**	114.091340					L	1673.899630	837.453453	1656.873081	828.940179	1655.889065	828.448171	14
3	356.217997	178.612637			338.207432	169.607354	E	1560.815566	780.911421	1543.789017	772.398147	1542.805001	771.906139	13
4	**485.260590**	243.133933			467.250025	234.128651	E	1431.772973	716.390124	1414.746424	707.876850	1413.762408	707.384842	12
5	598.344654	299.675965			580.334089	290.670683	I	***1302.730380***	651.868828	1285.703831	643.355554	1284.719815	642.863545	11
6	713.371597	357.189437			695.361032	348.184154	D	***1189.646316***	595.326796	1172.619767	586.813522	1171.635751	586.321514	10
7	814.419276	**407.713276**			796.408711	398.707994	T	1074.619373	537.813325	1057.592824	529.300050	1056.608808	528.808042	9
8	**927.503340**	464.255308			909.492775	455.250026	L	***973.571694***	487.289485	956.545145	478.776210	955.561129	478.284202	8
9	**1040.587404**	520.797340			1022.576839	511.792058	I	***860.487630***	430.747453	843.461081	422.234178	842.477065	421.742170	7
10	**1153.671468**	577.339372			1135.660903	568.334090	L	***747.403566***	374.205421	730.377017	365.692146	729.393001	365.200138	6
11	1250.724232	625.865754			1232.713667	616.860472	P	***634.319502***	317.663389	617.292953	309.150115	616.308937	308.658107	5
12	1379.766825	690.387050			1361.756260	681.381768	E	537.266738	269.137007	520.240189	260.623733	519.256173	260.131725	4
13	1493.809752	**747.408514**	1476.783203	738.895240	1475.799187	738.403231	N	***408.224145***	204.615711	391.197596	196.102436			3
14	1640.878166	820.942721	1623.851617	812.429447	1622.867601	811.937438	F	294.181218	147.594247	277.154669	139.080973			2
15							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.8	1785.976379	0.008989	ILEEIDTLILPENFK

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

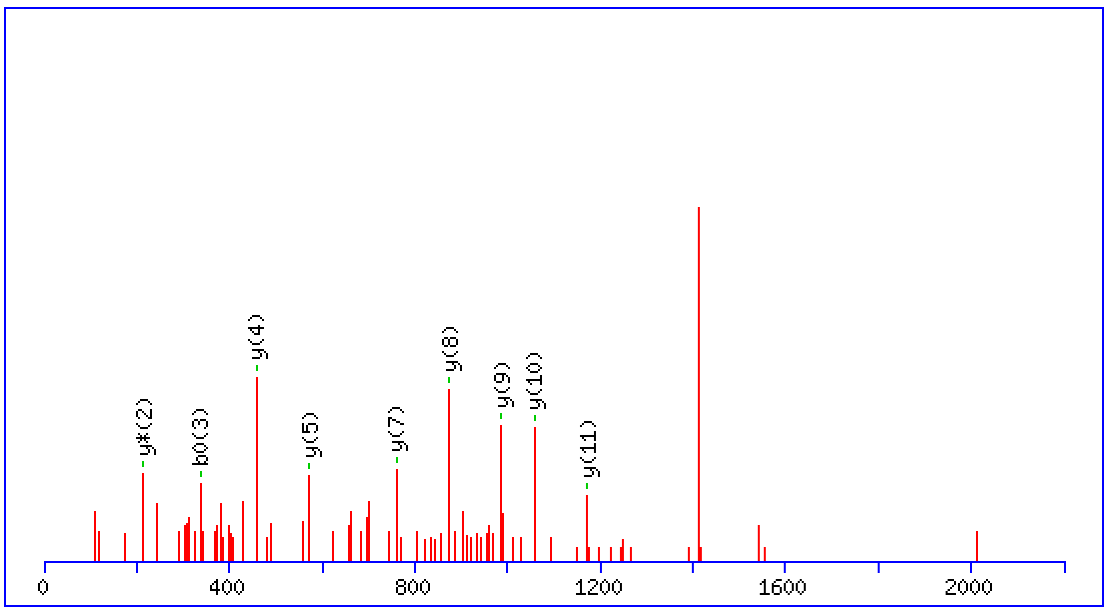
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELLALDSVDPEGR**
Found in **BAG3_HUMAN**, BAG family molecular chaperone regulator 3 OS=Homo sapiens GN=BAG3 PE=1 SV=3

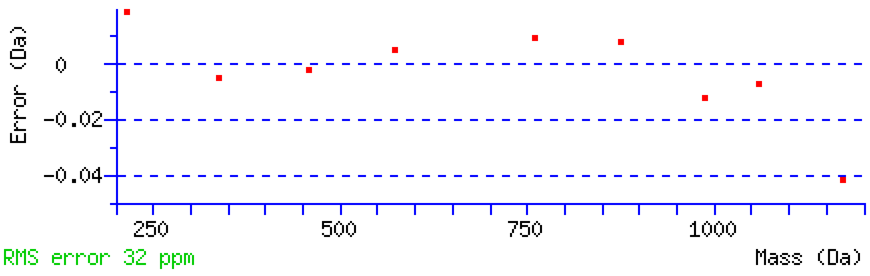
Match to Query 40419: 1412.711848 from(707.363200,2+) rtinseconds(2870) index(35380)
Title: Locus:1.1.1.2730.33
Data file 2011-11-12 - TFD - EP 5-2.mgf

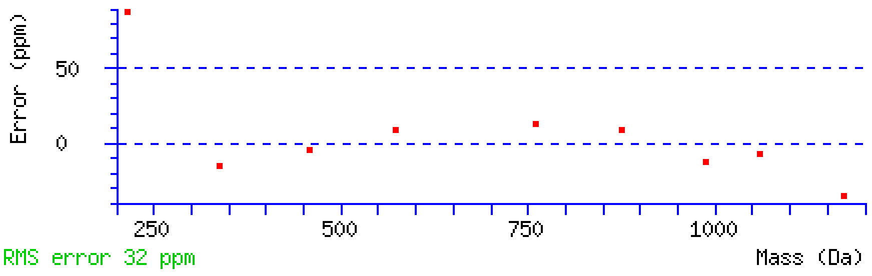
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [0] to [2200] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1412.714706
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 50  Expect: 8.9e-005
Matches : 9/116 fragment ions using 13 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572	112.039304	56.523290	E							13
2	243.133933	122.070605	225.123368	113.065322	L	1284.679407	642.843341	1267.652858	634.330067	1266.668842	633.838059	12
3	356.217997	178.612637	338.207432	169.607354	L	***1171.595343***	586.301310	1154.568794	577.788035	1153.584778	577.296027	11
4	427.255111	214.131193	409.244546	205.125911	A	***1058.511279***	529.759278	1041.484730	521.246003	1040.500714	520.753995	10
5	540.339175	270.673226	522.328610	261.667943	L	***987.474165***	494.240721	970.447616	485.727446	969.463600	485.235438	9
6	655.366118	328.186697	637.355553	319.181415	D	***874.390101***	437.698689	857.363552	429.185414	856.379536	428.693406	8
7	742.398146	371.702711	724.387581	362.697429	S	***759.363158***	380.185217	742.336609	371.671943	741.352593	371.179935	7
8	841.466560	421.236918	823.455995	412.231635	V	672.331130	336.669203	655.304581	328.155929	654.320565	327.663921	6
9	956.493503	478.750389	938.482938	469.745107	D	***573.262716***	287.134996	556.236167	278.621722	555.252151	278.129714	5
10	1053.546267	527.276772	1035.535702	518.271489	P	***458.235773***	229.621524	441.209224	221.108250	440.225208	220.616242	4
11	1182.588860	591.798068	1164.578295	582.792786	E	361.183009	181.095142	344.156460	172.581868	343.172444	172.089860	3
12	1239.610324	620.308800	1221.599759	611.303518	G	232.140416	116.573846	215.113867	108.060571			2
13					R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.7	1412.714706	-0.002858	ELLALDSVDPEGR
2.5	1412.708176	0.003672	ALSLCPSPAQSPR

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

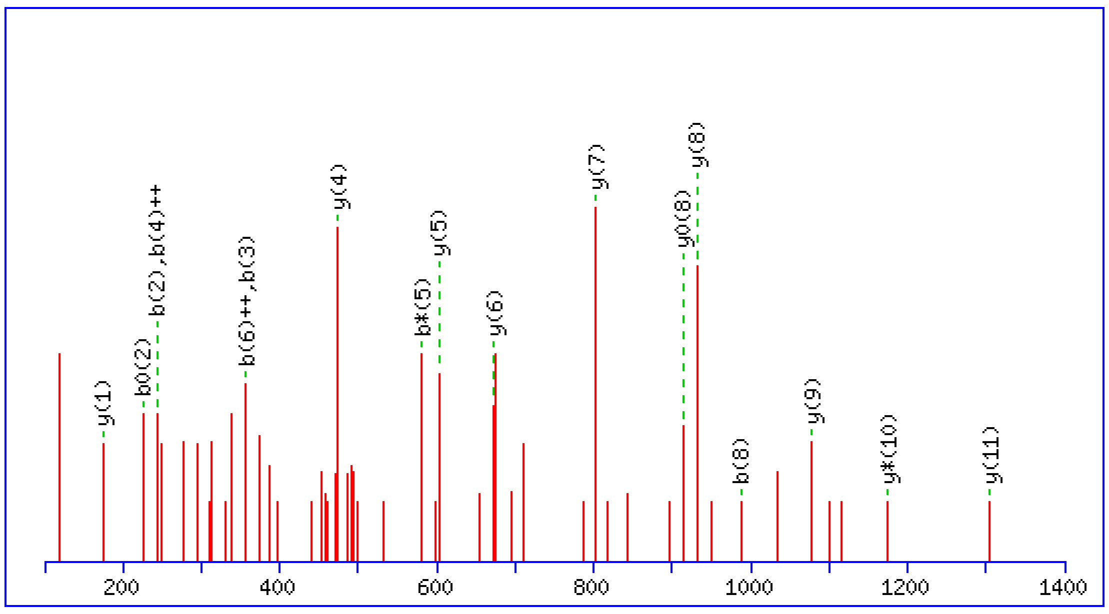
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IEIQNIFEEAQSLVR**
Found in **BAG5_HUMAN**, BAG family molecular chaperone regulator 5 OS=Homo sapiens GN=BAG5 PE=1 SV=1

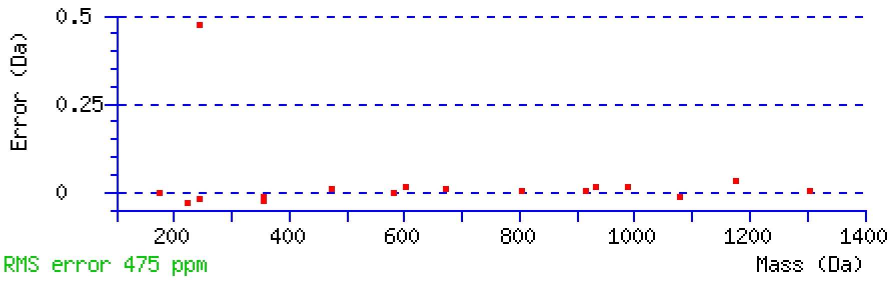
Match to Query 53581: 1787.938032 from(596.986620,3+) rtinseconds(4408) index(68523)
Title: Locus:1.1.1.3165.7
Data file 2011-11-10 - TFD - EP 4-3.mgf

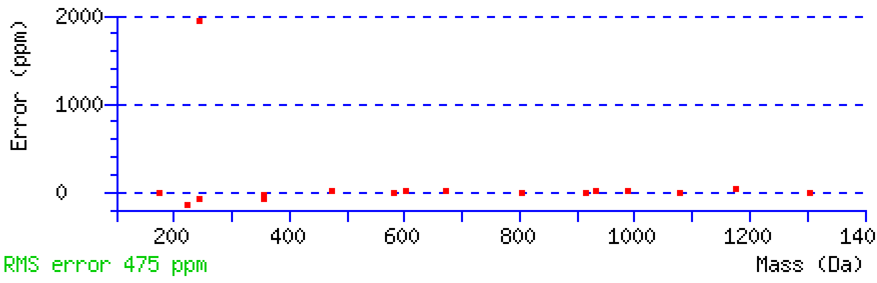
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1787.941727
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 54 **Expect:** 3.9e-005
Matches : 17/154 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					I							15
2	**243.133933**	122.070605			225.123368	113.065322	E	1675.864976	838.436126	1658.838427	829.922852	1657.854411	829.430844	14
3	**356.217997**	178.612637			338.207432	169.607354	I	1546.822383	773.914830	1529.795834	765.401555	1528.811818	764.909547	13
4	484.276575	**242.641926**	467.250026	234.128651	466.266010	233.636643	Q	1433.738319	717.372798	1416.711770	708.859523	1415.727754	708.367515	12
5	598.319502	299.663389	581.292953	291.150115	580.308937	290.658107	N	***1305.679741***	653.343509	1288.653192	644.830234	1287.669176	644.338226	11
6	711.403566	**356.205421**	694.377017	347.692147	693.393001	347.200139	I	1191.636814	596.322045	1174.610265	587.808771	1173.626249	587.316763	10
7	858.471980	429.739628	841.445431	421.226354	840.461415	420.734346	F	***1078.552750***	539.780013	1061.526201	531.266739	1060.542185	530.774731	9
8	**987.514573**	494.260925	970.488024	485.747650	969.504008	485.255642	E	***931.484336***	466.245806	914.457787	457.732532	913.473771	457.240524	8
9	1116.557166	558.782221	1099.530617	550.268947	1098.546601	549.776939	E	***802.441743***	401.724510	785.415194	393.211235	784.431178	392.719227	7
10	1187.594280	594.300778	1170.567731	585.787504	1169.583715	585.295496	A	***673.399150***	337.203213	656.372601	328.689939	655.388585	328.197931	6
11	1315.652858	658.330067	1298.626309	649.816793	1297.642293	649.324785	Q	***602.362036***	301.684656	585.335487	293.171382	584.351471	292.679374	5
12	1402.684886	701.846081	1385.658337	693.332807	1384.674321	692.840799	S	***474.303458***	237.655367	457.276909	229.142092	456.292893	228.650084	4
13	1515.768950	758.388113	1498.742401	749.874839	1497.758385	749.382831	L	387.271430	194.139353	370.244881	185.626078			3
14	1614.837364	807.922320	1597.810815	799.409046	1596.826799	798.917038	V	274.187366	137.597321	257.160817	129.084047			2
15							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.5	1787.941727	-0.003695	IEIQNIFEEAQSLVR
9.3	1787.937714	0.000318	EQLAQGSQLTERLTSK
3.4	1787.945114	-0.007082	LTAIDILTTCAADIQR
0.6	1787.945145	-0.007113	SVLLDVSAGQLLMVDGR

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

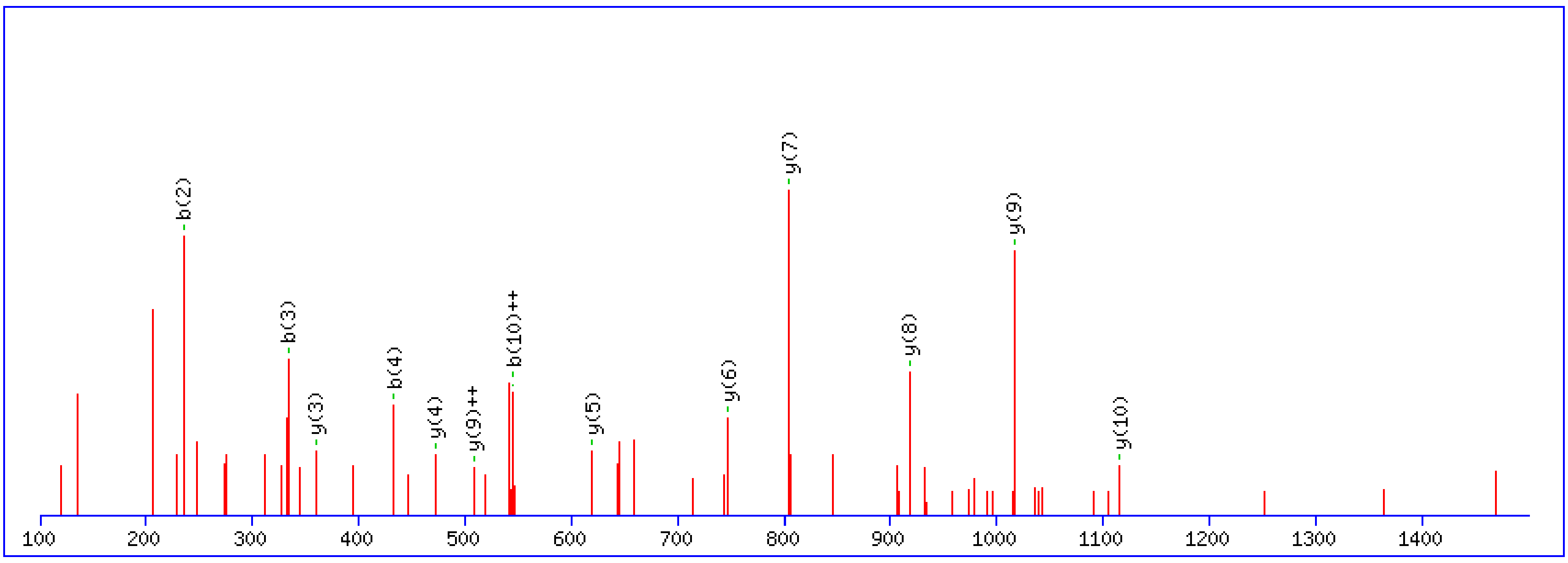
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **AYVVLGQFLVLK**
Found in **BAF_HUMAN**, Barrier-to-autointegration factor OS=Homo sapiens GN=BANF1 PE=1 SV=1

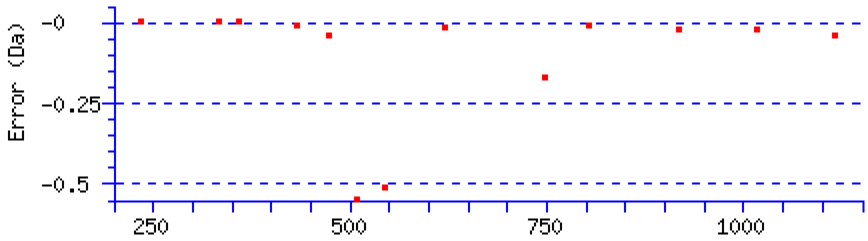
Match to Query 35121: 1348.799828 from(675.407190,2+) rtinseconds(3883) index(57987)
Title: Locus:1.1.1.1915.17
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 3.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●

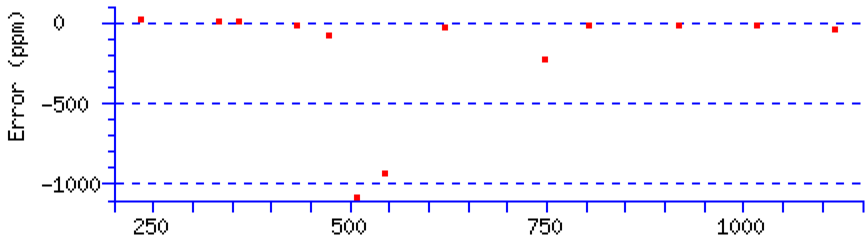


Monoisotopic mass of neutral peptide Mr(calc): 1348.811859
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 40 **Expect:** 0.00015
Matches : 13/76 fragment ions using 31 most intense peaks (help)

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	72.044390	36.525833			A					12
2	**235.107719**	118.057498			Y	1278.782023	639.894650	1261.755474	631.381375	11
3	**334.176133**	167.591704			V	***1115.718694***	558.362985	1098.692145	549.849711	10
4	**433.244547**	217.125912			V	***1016.650280***	508.828778	999.623731	500.315503	9
5	546.328611	273.667944			L	***917.581866***	459.294571	900.555317	450.781297	8
6	603.350075	302.178676			G	***804.497802***	402.752539	787.471253	394.239264	7
7	731.408653	366.207965	714.382104	357.694690	Q	***747.476338***	374.241807	730.449789	365.728532	6
8	878.477067	439.742172	861.450518	431.228897	F	***619.417760***	310.212518	602.391211	301.699243	5
9	991.561131	496.284204	974.534582	487.770929	L	***472.349346***	236.678311	455.322797	228.165036	4
10	1090.629545	545.818411	1073.602996	537.305136	V	***359.265282***	180.136279	342.238733	171.623004	3
11	1203.713609	602.360442	1186.687060	593.847168	L	260.196868	130.602072	243.170319	122.088797	2
12					K	147.112804	74.060040	130.086255	65.546765	1



RMS error 401 ppm



RMS error 401 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.1	1348.811859	-0.012031	AYVVLGQFLVLK

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

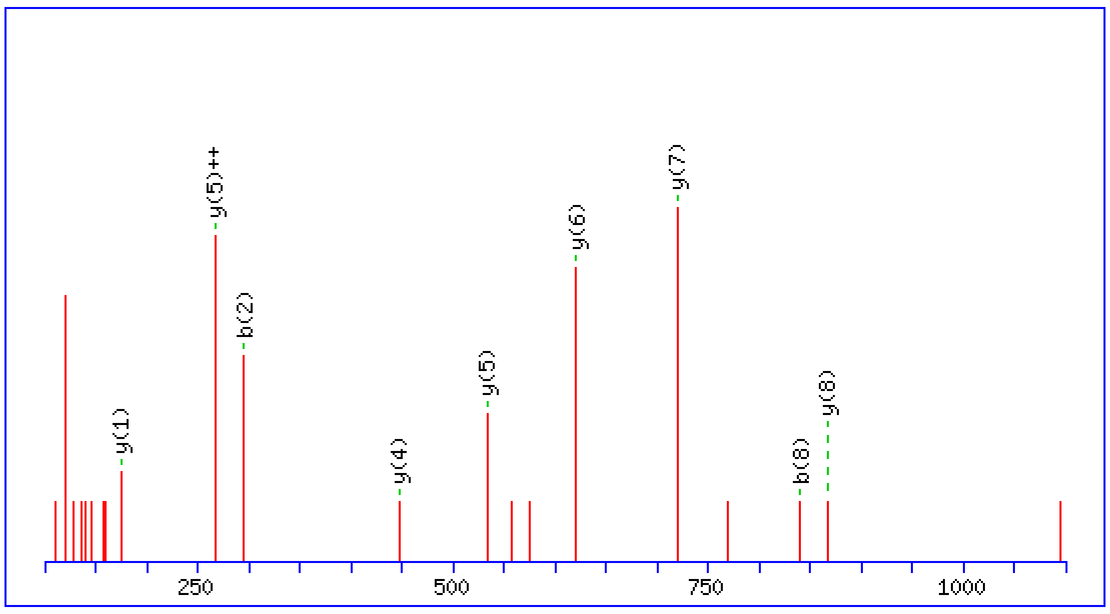
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FFVSSSQGR**
Found in **BASI_HUMAN**, Basigin OS=Homo sapiens GN=BSG PE=1 SV=2

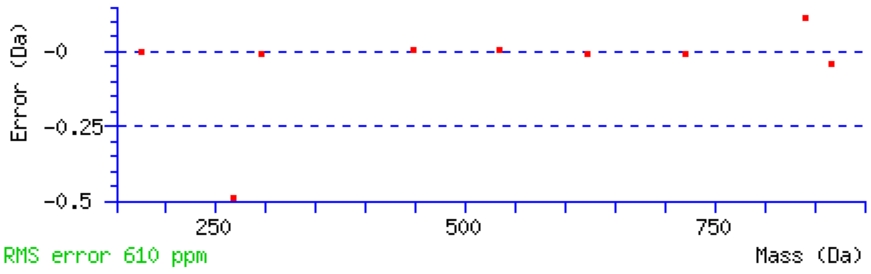
Match to Query 279038: 1013.493148 from(507.753850,2+) rtinseconds(1683) index(830505)
Title: Locus:1.1.1.1187.20
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

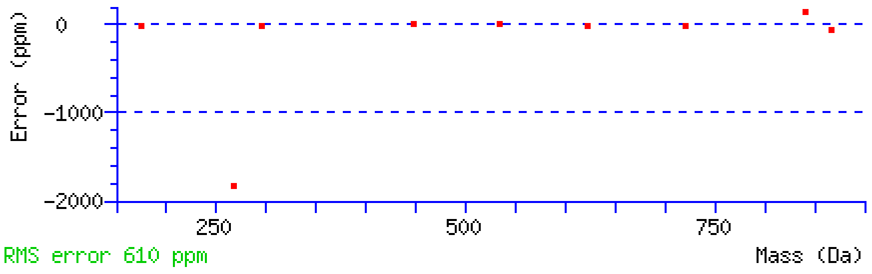
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1100] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1013.493057
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 48 **Expect:** 0.00038
Matches : 9/72 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.075690	74.541483					F							9
2	**295.144104**	148.075690					F	***867.431906***	434.219591	850.405357	425.706317	849.421341	425.214309	8
3	394.212518	197.609897					V	***720.363492***	360.685384	703.336943	352.172110	702.352927	351.680102	7
4	481.244546	241.125911			463.233981	232.120628	S	***621.295078***	311.151177	604.268529	302.637903	603.284513	302.145895	6
5	568.276574	284.641925			550.266009	275.636642	S	***534.263050***	267.635163	517.236501	259.121889	516.252485	258.629881	5
6	655.308602	328.157939			637.298037	319.152656	S	***447.231022***	224.119149	430.204473	215.605875	429.220457	215.113867	4
7	783.367180	392.187228	766.340631	383.673953	765.356615	383.181945	Q	360.198994	180.603135	343.172445	172.089861			3
8	**840.388644**	420.697960	823.362095	412.184686	822.378079	411.692678	G	232.140416	116.573846	215.113867	108.060572			2
9							R	***175.118952***	88.063114	158.092403	79.549840			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.3	1013.493057	0.000091	FFVSSSQGR
13.5	1013.485168	0.007980	EHLPKVEM
4.5	1013.496399	-0.003251	NMPDPITAR
3.1	1013.488998	0.004150	QEAEPPRR
1.3	1013.493011	0.000137	NLNPEWNK
1.1	1013.489227	0.003921	FFGLPITGM

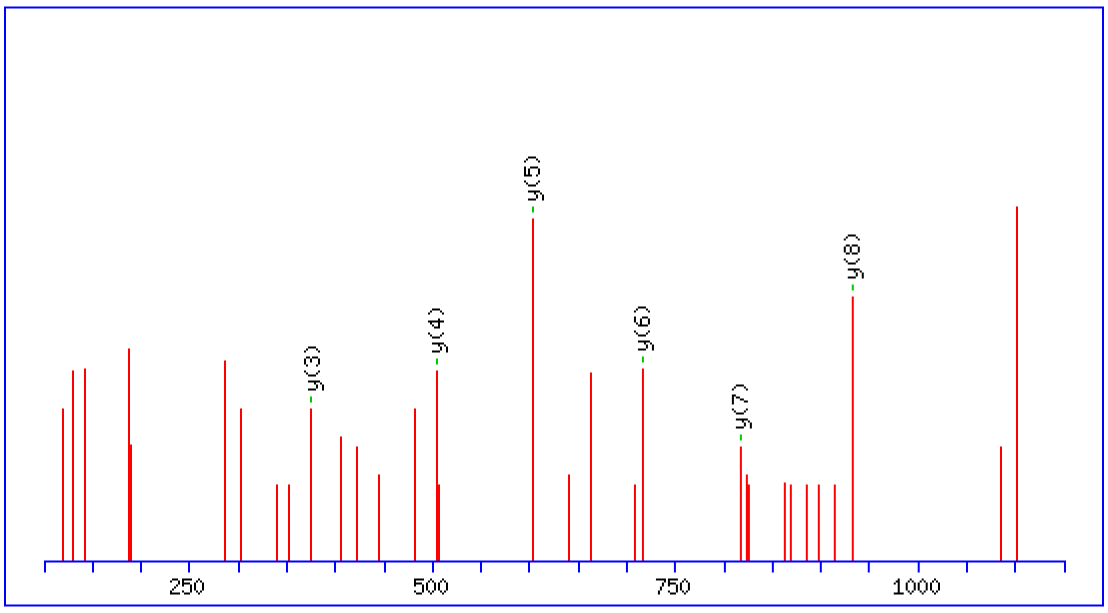
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLDTLVESIR**
Found in **BCL10_HUMAN**, B-cell lymphoma/leukemia 10 OS=Homo sapiens GN=BCL10 PE=1 SV=1

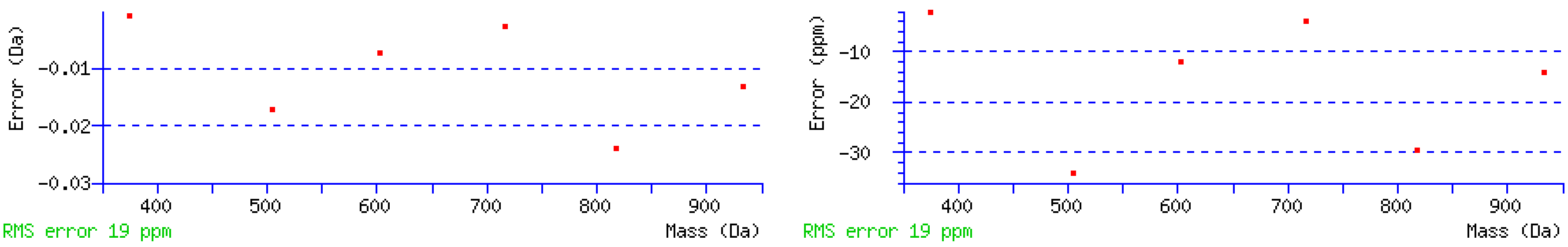
Match to Query 23547: 1101.597828 from(551.806190,2+) rtinseconds(3076) index(41398)
Title: Locus:1.1.1.2485.23
Data file 2011-11-10 - TFD - EP 4-5.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1101.602982
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 47 **Expect:** 0.00021
Matches : 6/82 fragment ions using 10 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	58.028740	29.518008			G							10
2	171.112804	86.060040			L	1045.588801	523.298039	1028.562252	514.784764	1027.578236	514.292756	9
3	286.139747	143.573512	268.129182	134.568229	D	*932.504737*	466.756007	915.478188	458.242732	914.494172	457.750724	8
4	387.187426	194.097351	369.176861	185.092069	T	*817.477794*	409.242535	800.451245	400.729261	799.467229	400.237253	7
5	500.271490	250.639383	482.260925	241.634101	L	*716.430115*	358.718696	699.403566	350.205421	698.419550	349.713413	6
6	599.339904	300.173590	581.329339	291.168308	V	*603.346051*	302.176664	586.319502	293.663389	585.335486	293.171381	5
7	728.382497	364.694887	710.371932	355.689604	E	*504.277637*	252.642456	487.251088	244.129182	486.267072	243.637174	4
8	815.414525	408.210901	797.403960	399.205618	S	*375.235044*	188.121160	358.208495	179.607885	357.224479	179.115877	3
9	928.498589	464.752933	910.488024	455.747650	I	288.203016	144.605146	271.176467	136.091871			2
10					R	175.118952	88.063114	158.092403	79.549839			1



RMS error 19 ppm RMS error 19 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.5	1101.602982	-0.005154	GLDTLVESIR

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

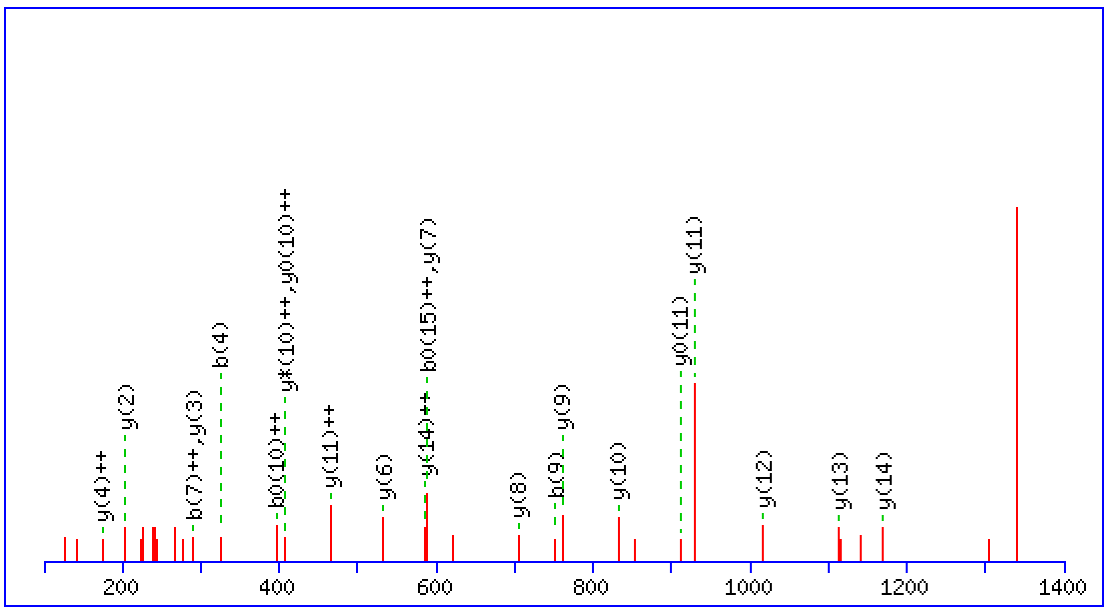
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLGPSPAGDGPSGSGK**
Found in **BAD_HUMAN**, Bcl2 antagonist of cell death OS=Homo sapiens GN=BAD PE=1 SV=3

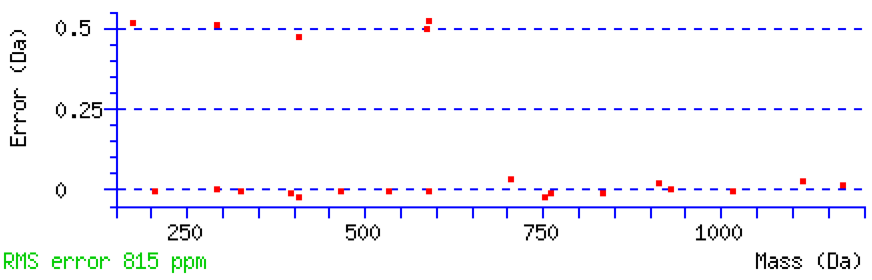
Match to Query 38936: 1339.637788 from(670.826170,2+) rtinseconds(1260) index(7166)
Title: Locus:1.1.1.1800.51
Data file 2011-11-14 - TFD - EP 8-5.mgf

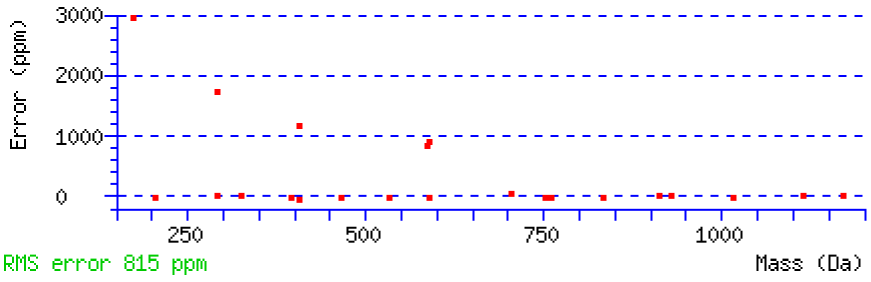
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1400] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1339.636826
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 85 **Expect:** 3.2e-008
Matches : 22/138 fragment ions using 32 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008			G							16
2	171.112804	86.060040			L	1283.622621	642.314949	1266.596072	633.801674	1265.612056	633.309666	15
3	228.134268	114.570772			G	***1170.538557***	585.772917	1153.512008	577.259642	1152.527992	576.767634	14
4	**325.187032**	163.097154			P	***1113.517093***	557.262185	1096.490544	548.748910	1095.506528	548.256902	13
5	412.219060	206.613168	394.208495	197.607885	S	***1016.464329***	508.735803	999.437780	500.222528	998.453764	499.730520	12
6	509.271824	255.139550	491.261259	246.134267	P	***929.432301***	465.219789	912.405752	456.706514	911.421736	456.214506	11
7	580.308938	290.658107	562.298373	281.652825	A	***832.379537***	416.693407	815.352988	408.180132	814.368972	407.688124	10
8	637.330402	319.168839	619.319837	310.163557	G	***761.342423***	381.174850	744.315874	372.661575	743.331858	372.169567	9
9	**752.357345**	376.682311	734.346780	367.677028	D	***704.320959***	352.664118	687.294410	344.150843	686.310394	343.658835	8
10	809.378809	405.193043	791.368244	396.187760	G	***589.294016***	295.150646	572.267467	286.637372	571.283451	286.145364	7
11	906.431573	453.719425	888.421008	444.714142	P	***532.272552***	266.639914	515.246003	258.126640	514.261987	257.634632	6
12	993.463601	497.235439	975.453036	488.230156	S	435.219788	218.113532	418.193239	209.600258	417.209223	209.108250	5
13	1050.485065	525.746171	1032.474500	516.740888	G	348.187760	174.597518	331.161211	166.084244	330.177195	165.592236	4
14	1137.517093	569.262185	1119.506528	560.256902	S	***291.166296***	146.086786	274.139747	137.573512	273.155731	137.081504	3
15	1194.538557	597.772917	1176.527992	588.767634	G	***204.134268***	102.570772	187.107719	94.057497			2
16					K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
85.0	1339.636826	0.000962	GLGPSPAGDGPSGSGK
6.1	1339.626434	0.011354	VPNACLFTMNK

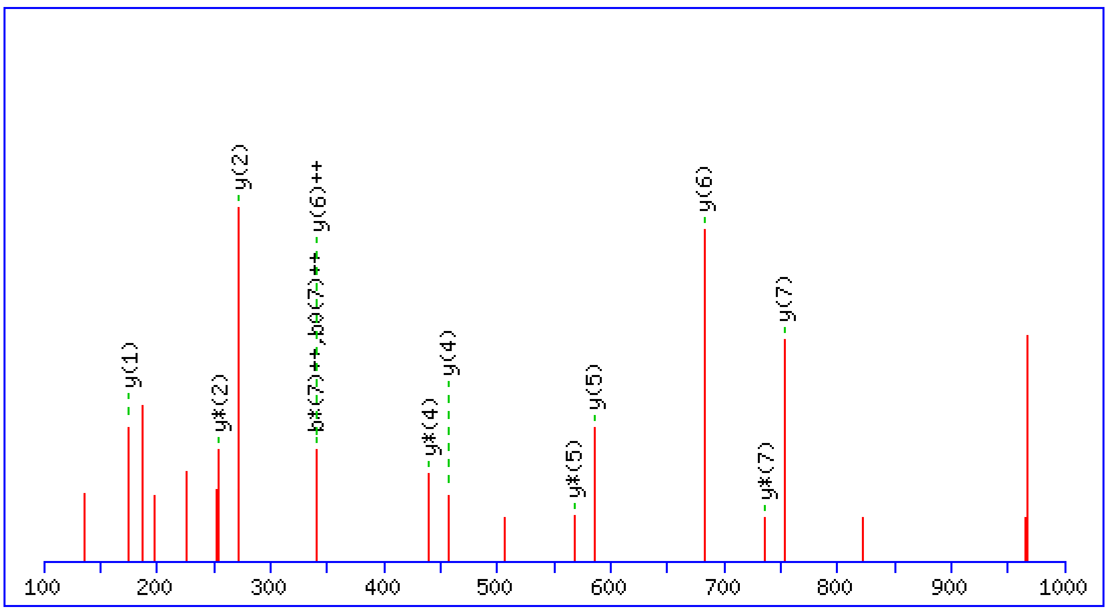
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TIAPQNAPR**
Found in **BCLF1_HUMAN**, Bcl-2-associated transcription factor 1 OS=Homo sapiens GN=BCLAF1 PE=1 SV=2

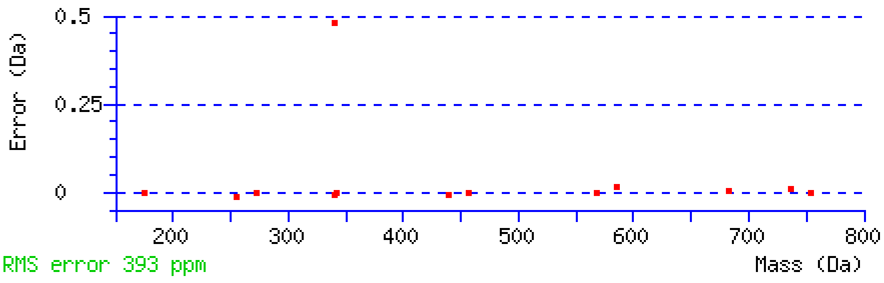
Match to Query 13202: 966.533868 from(484.274210,2+) rtinseconds(1010) index(4464)
Title: Locus:1.1.1.1709.25
Data file 2011-11-12 - TFD - EP 6-1.mgf

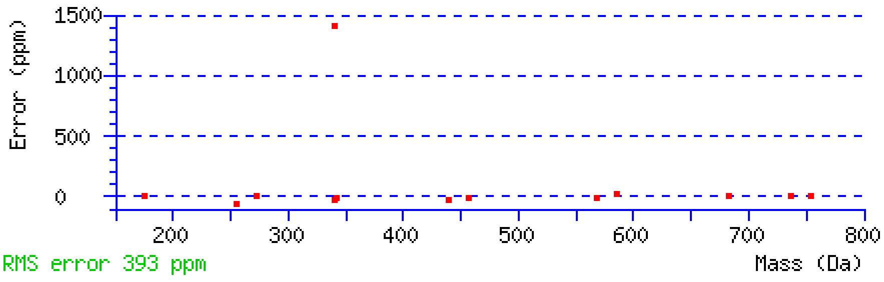
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 966.524658
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 51 **Expect:** 6.2e-005
Matches : 13/72 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	102.054955	51.531116			84.044390	42.525833	**T**					9
2	215.139019	108.073147			197.128454	99.067865	**I**	866.484277	433.745777	849.457728	425.232502	8
3	286.176133	143.591704			268.165568	134.586422	**A**	***753.400213***	377.203745	736.373664	368.690470	7
4	383.228897	192.118087			365.218332	183.112804	**P**	***682.363099***	341.685188	665.336550	333.171913	6
5	511.287475	256.147376	494.260926	247.634101	493.276910	247.142093	**Q**	***585.310335***	293.158806	568.283786	284.645531	5
6	625.330402	313.168839	608.303853	304.655565	607.319837	304.163557	**N**	***457.251757***	229.129516	440.225208	220.616242	4
7	696.367516	348.687396	679.340967	340.174122	678.356951	339.682114	**A**	343.208830	172.108053	326.182281	163.594778	3
8	793.420280	397.213778	776.393731	388.700504	775.409715	388.208496	**P**	***272.171716***	136.589496	255.145167	128.076221	2
9							**R**	***175.118952***	88.063114	158.092403	79.549839	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.3	966.524658	0.009210	TIAPQNAPR
11.8	966.539932	-0.006064	WPGKVPAGR
10.9	966.524658	0.009210	VEGPAKPNR
4.6	966.524673	0.009195	RLPAPPPR
4.4	966.535889	-0.002021	GSLERHLR
0.7	966.524658	0.009210	RLEPAPPR
0.3	966.538589	-0.004721	VDPAVPLEK

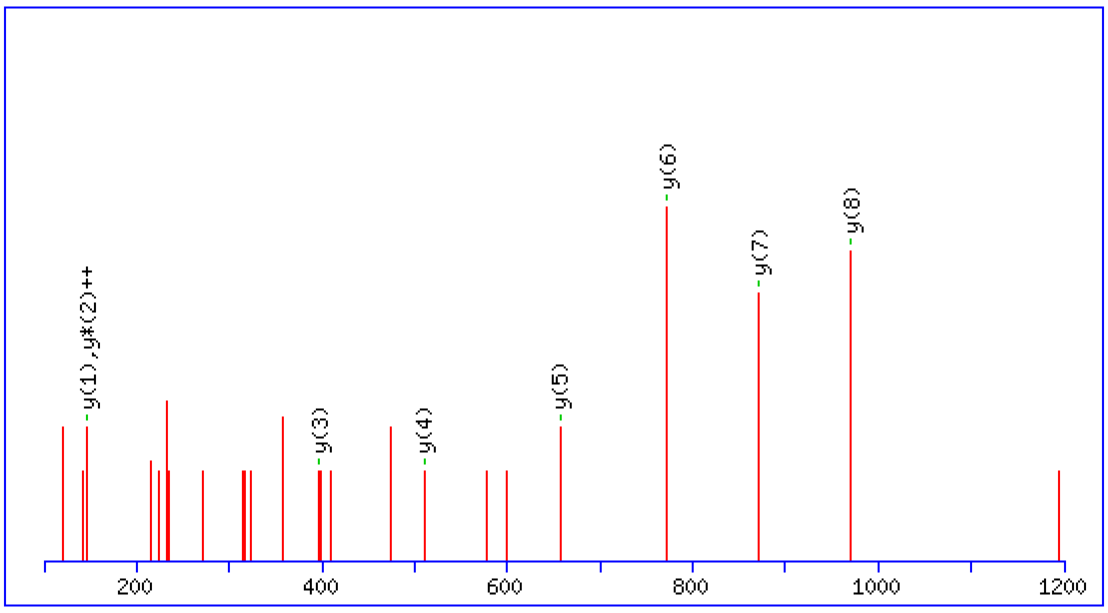
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELVVDFLSYK**
Found in **B2CL1_HUMAN**, Bcl-2-like protein 1 OS=Homo sapiens GN=BCL2L1 PE=1 SV=1

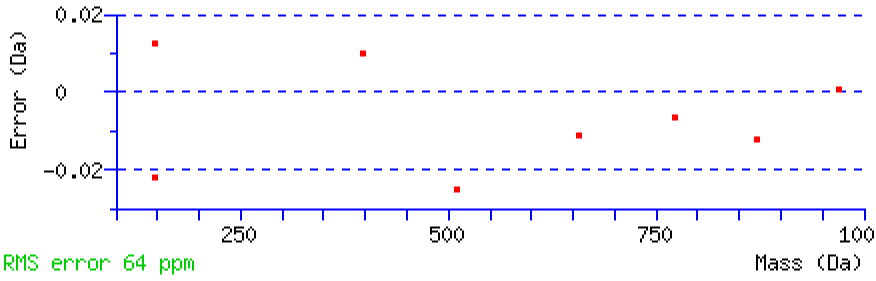
Match to Query 27043: 1211.645068 from(606.829810,2+) rtinseconds(3549) index(46590)
Title: Locus:1.1.1.2966.17
Data file 2011-11-10 - TFD - EP 3-5.mgf

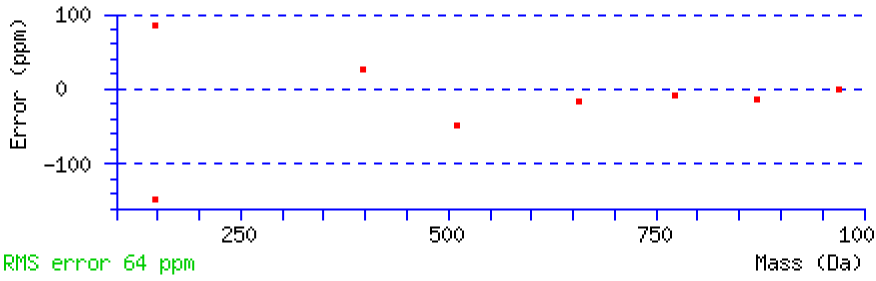
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1211.643784
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 49  Expect: 3.5e-005
Matches : 8/86 fragment ions using 15 most intense peaks   (help)
```

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	130.049869	65.528572	112.039304	56.523290	E							10
2	243.133933	122.070605	225.123368	113.065322	L	1083.608474	542.307875	1066.581925	533.794601	1065.597909	533.302592	9
3	342.202347	171.604812	324.191782	162.599529	V	***970.524410***	485.765843	953.497861	477.252569	952.513845	476.760561	8
4	441.270761	221.139019	423.260196	212.133736	V	***871.455996***	436.231636	854.429447	427.718361	853.445431	427.226353	7
5	556.297704	278.652490	538.287139	269.647208	D	***772.387582***	386.697429	755.361033	378.184154	754.377017	377.692146	6
6	703.366118	352.186697	685.355553	343.181415	F	***657.360639***	329.183958	640.334090	320.670683	639.350074	320.178675	5
7	816.450182	408.728729	798.439617	399.723447	L	***510.292225***	255.649750	493.265676	247.136476	492.281660	246.644468	4
8	903.482210	452.244743	885.471645	443.239461	S	***397.208161***	199.107718	380.181612	190.594444	379.197596	190.102436	3
9	1066.545539	533.776408	1048.534974	524.771125	Y	310.176133	155.591704	293.149584	147.078430			2
10					K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.0	1211.643784	0.001284	ELVVDFLSYK
1.5	1211.655716	-0.010648	VVHRPMGTRK
1.2	1211.654999	-0.009931	LEQAVEWPLK

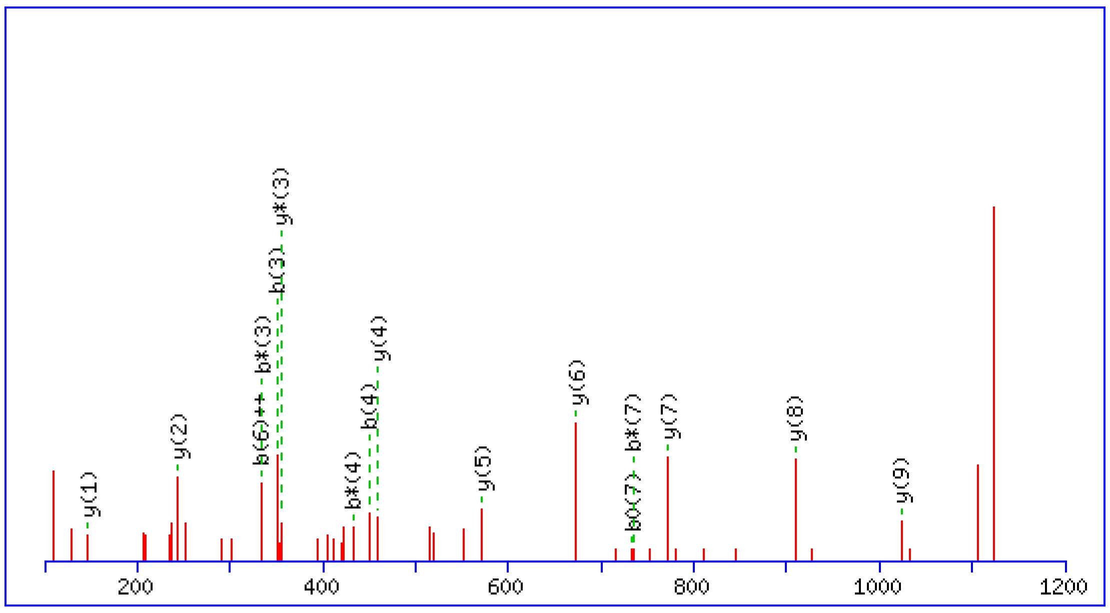
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VNHVTLSQPK**
Found in **B2MG_HUMAN**, Beta-2-microglobulin OS=Homo sapiens GN=B2M PE=1 SV=1

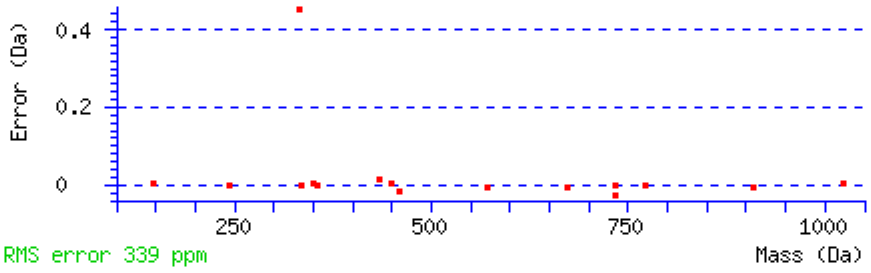
Match to Query 422842: 1121.622008 from(561.818280,2+) rtinseconds(1063) index(495213)
Title: Locus:1.1.1.729.33
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

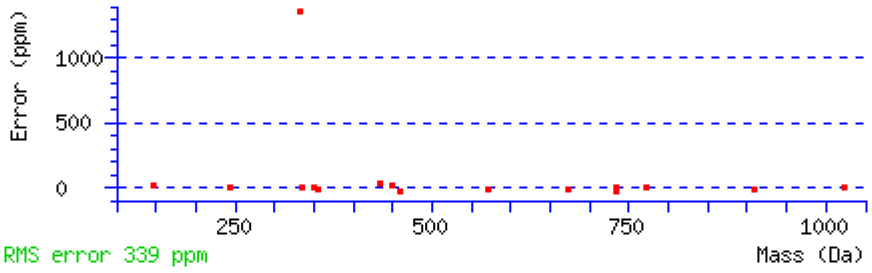
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1121.619308
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 53 **Expect:** 5e-005
Matches : 16/92 fragment ions using 32 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	100.075690	50.541483					**V**							10
2	214.118617	107.562947	197.092068	99.049672			**N**	***1023.558170***	512.282723	1006.531621	503.769449	1005.547605	503.277441	9
3	**351.177529**	176.092402	334.150980	167.579128			**H**	***909.515243***	455.261260	892.488694	446.747985	891.504678	446.255977	8
4	**450.245943**	225.626610	433.219394	217.113335			**V**	***772.456331***	386.731804	755.429782	378.218529	754.445766	377.726521	7
5	551.293622	276.150449	534.267073	267.637175	533.283057	267.145167	**T**	***673.387917***	337.197597	656.361368	328.684322	655.377352	328.192314	6
6	664.377686	332.692481	647.351137	324.179207	646.367121	323.687199	**L**	***572.340238***	286.673757	555.313689	278.160483	554.329673	277.668475	5
7	751.409714	376.208495	734.383165	367.695221	733.399149	367.203213	**S**	***459.256174***	230.131725	442.229625	221.618450	441.245609	221.126443	4
8	879.468292	440.237784	862.441743	431.724510	861.457727	431.232502	**Q**	372.224146	186.615711	355.197597	178.102437			3
9	976.521056	488.764166	959.494507	480.250892	958.510491	479.758884	**P**	***244.165568***	122.586422	227.139019	114.073148			2
10							**K**	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
53.1	1121.619308	0.002700	VNHVTLSQPK

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

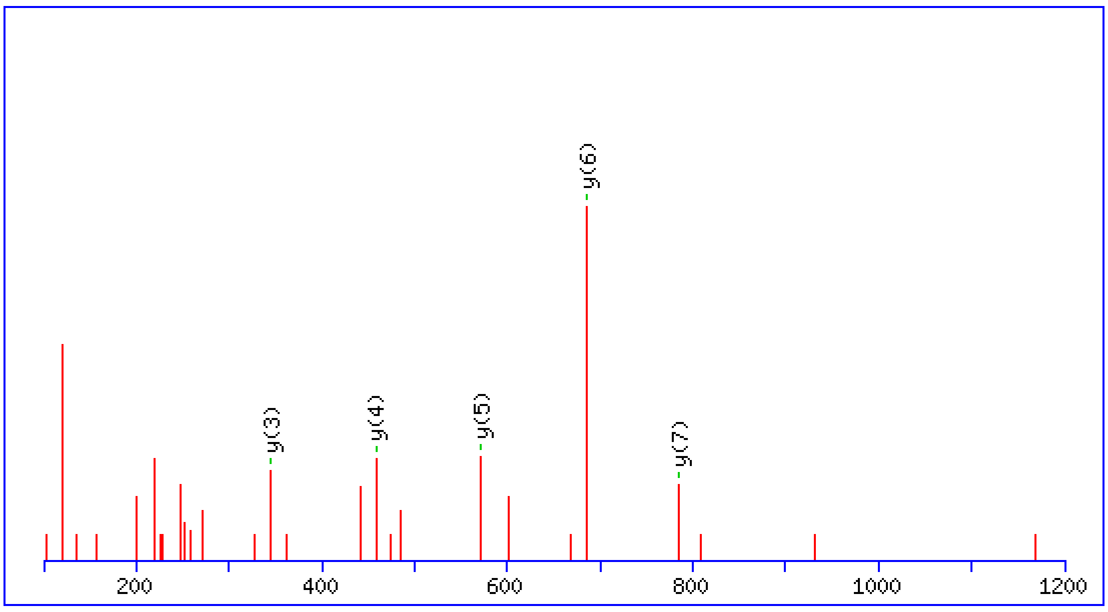
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FVDILGLR**
Found in **CTBL1_HUMAN**, Beta-catenin-like protein 1 OS=Homo sapiens GN=CTNNBL1 PE=1 SV=1

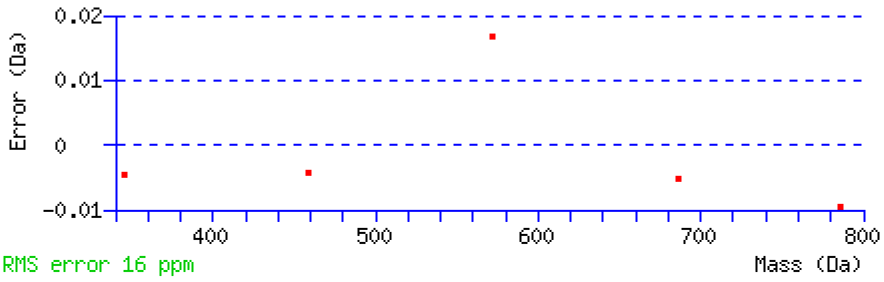
Match to Query 11446: 931.546908 from(466.780730,2+) rtinseconds(3269) index(45848)
Title: Locus:1.1.1.2665.3
Data file 2011-11-14 - TFD - EP 8-2.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●

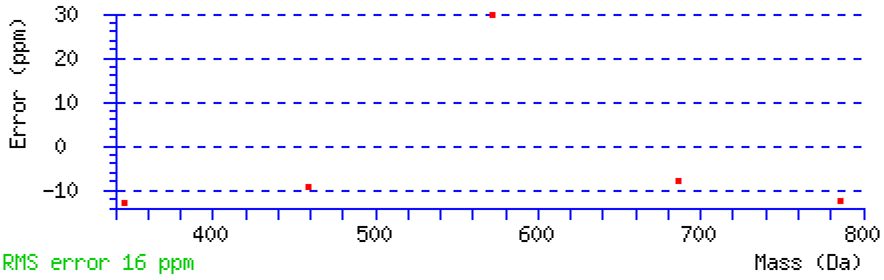


Monoisotopic mass of neutral peptide Mr(calc): 931.549103
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 37 **Expect:** 0.0006
Matches : 5/56 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.075690	74.541483			F							8
2	247.144104	124.075690			V	***785.487965***	393.247621	768.461416	384.734346	767.477400	384.242338	7
3	362.171047	181.589161	344.160482	172.583879	D	***686.419551***	343.713414	669.393002	335.200139	668.408986	334.708131	6
4	475.255111	238.131193	457.244546	229.125911	I	***571.392608***	286.199942	554.366059	277.686668			5
5	588.339175	294.673226	570.328610	285.667943	L	***458.308544***	229.657910	441.281995	221.144635			4
6	645.360639	323.183958	627.350074	314.178675	G	***345.224480***	173.115878	328.197931	164.602603			3
7	758.444703	379.725990	740.434138	370.720707	L	288.203016	144.605146	271.176467	136.091871			2
8					R	175.118952	88.063114	158.092403	79.549839			1



RMS error 16 ppm



RMS error 16 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.4	931.549103	-0.002195	FVDILGLR

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

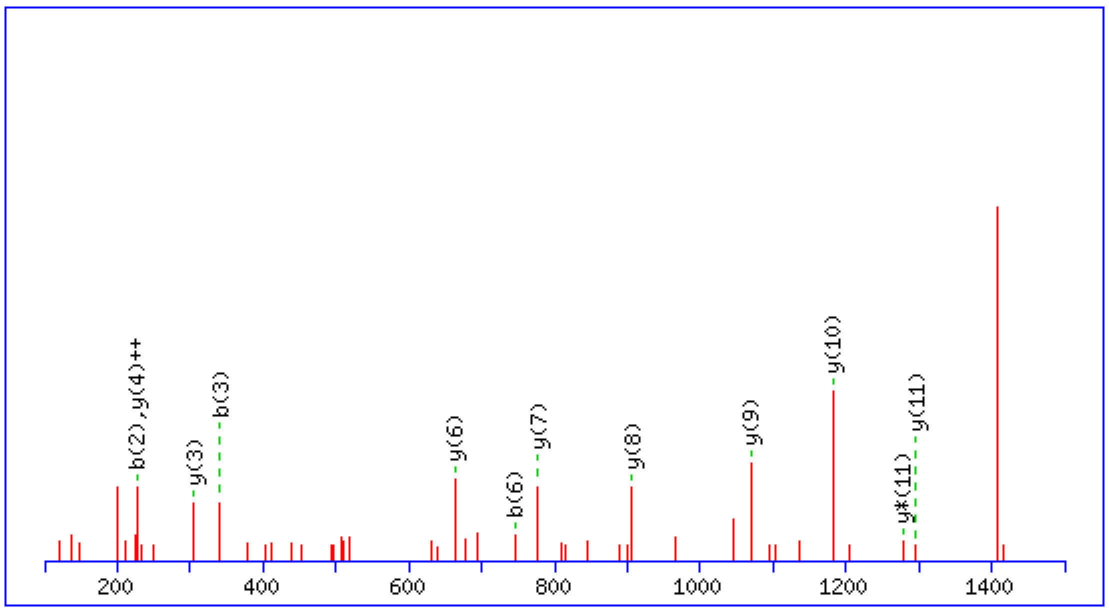
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IILYENPNFTGK**
Found in **CRBB2_HUMAN**, Beta-crystallin B2 OS=Homo sapiens GN=CRYBB2 PE=1 SV=2

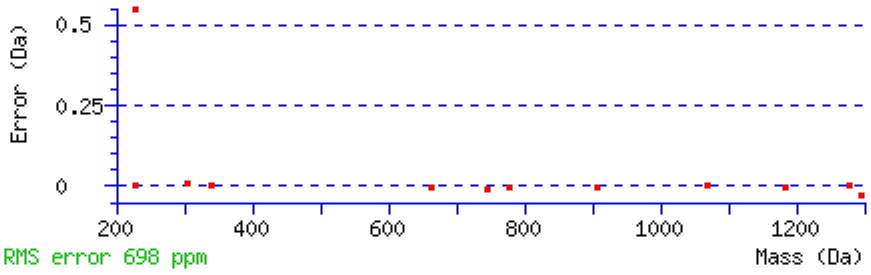
Match to Query 41431: 1407.732668 from(704.873610,2+) rtinseconds(2656) index(33474)
Title: Locus:1.1.1.2326.43
Data file 2011-11-10 - TFD - EP 4-5.mgf

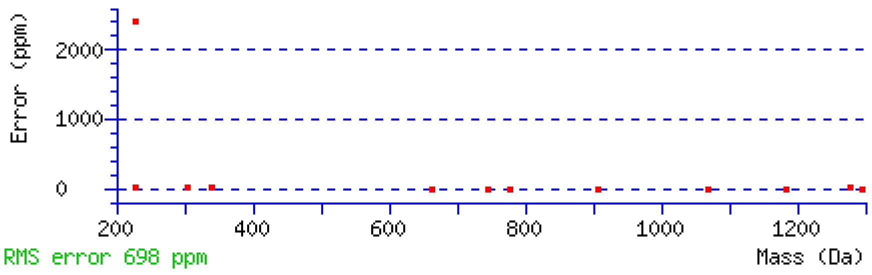
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1407.739792
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 45  Expect: 0.00028
Matches : 12/110 fragment ions using 21 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					I							12
2	**227.175404**	114.091340					I	***1295.663029***	648.335153	1278.636480	639.821878	1277.652464	639.329870	11
3	**340.259468**	170.633372					L	***1182.578965***	591.793120	1165.552416	583.279846	1164.568400	582.787838	10
4	503.322797	252.165036					Y	***1069.494901***	535.251089	1052.468352	526.737814	1051.484336	526.245806	9
5	632.365390	316.686333			614.354825	307.681051	E	***906.431572***	453.719424	889.405023	445.206149	888.421007	444.714141	8
6	**746.408317**	373.707797	729.381768	365.194522	728.397752	364.702514	N	***777.388979***	389.198128	760.362430	380.684853	759.378414	380.192845	7
7	843.461081	422.234179	826.434532	413.720904	825.450516	413.228896	P	***663.346052***	332.176664	646.319503	323.663389	645.335487	323.171382	6
8	957.504008	479.255642	940.477459	470.742368	939.493443	470.250360	N	566.293288	283.650282	549.266739	275.137007	548.282723	274.644999	5
9	1104.572422	552.789849	1087.545873	544.276575	1086.561857	543.784566	F	452.250361	226.628818	435.223812	218.115544	434.239796	217.623536	4
10	1205.620101	603.313689	1188.593552	594.800414	1187.609536	594.308406	T	***305.181947***	153.094611	288.155398	144.581337	287.171382	144.089329	3
11	1262.641565	631.824420	1245.615016	623.311146	1244.631000	622.819138	G	204.134268	102.570772	187.107719	94.057497			2
12							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.9	1407.739792	-0.007124	IILYENPNFTGK

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

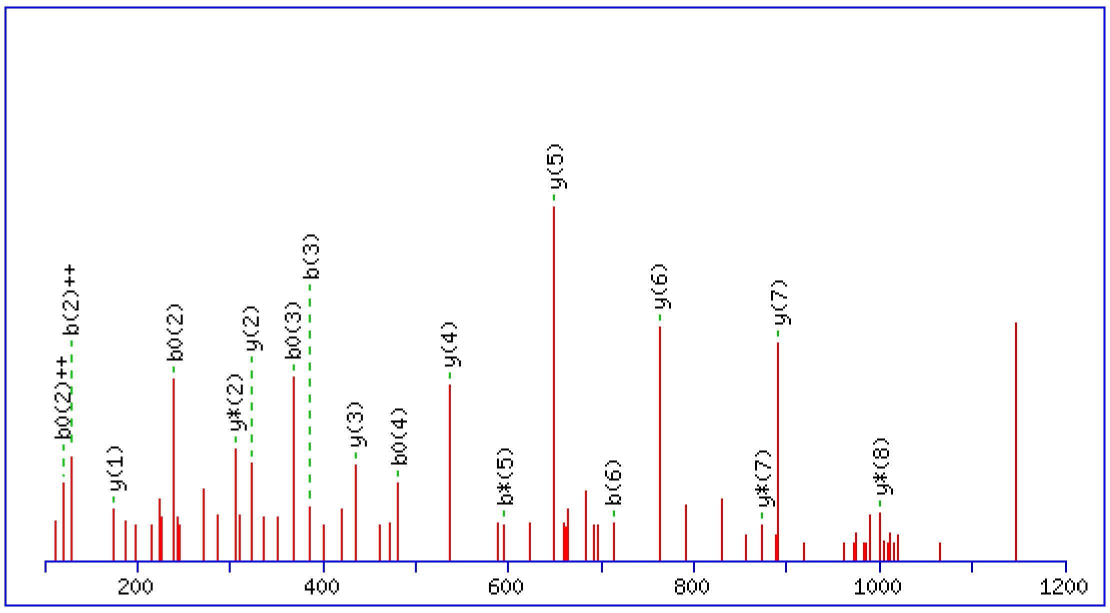
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EQQILTLFR**
Found in **LACB2_HUMAN**, Beta-lactamase-like protein 2 OS=Homo sapiens GN=LACTB2 PE=1 SV=2

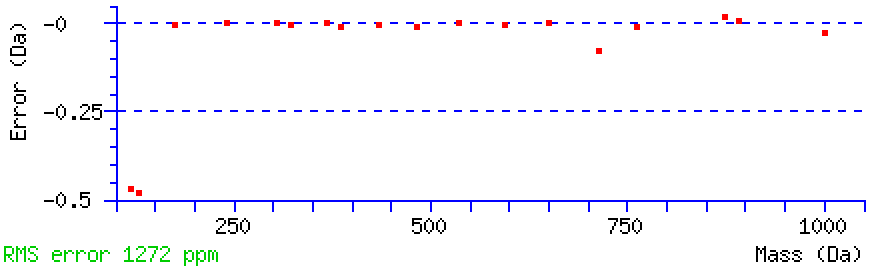
Match to Query 25475: 1146.643428 from(574.328990,2+) rtinseconds(3197) index(45637)
Title: Locus:1.1.1.2542.8
Data file 2011-11-10 - TFD - EP 4-4.mgf

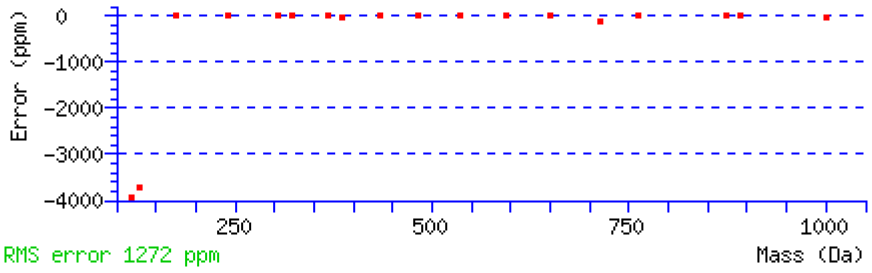
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1146.639694
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 45  Expect: 0.00017
Matches : 18/88 fragment ions using 30 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	E							9
2	258.108447	129.557862	241.081898	121.044587	240.097882	120.552579	Q	1018.604393	509.805835	1001.577844	501.292560	1000.593828	500.800552	8
3	**386.167025**	193.587151	369.140476	185.073876	368.156460	184.581868	Q	***890.545815***	445.776546	873.519266	437.263271	872.535250	436.771263	7
4	499.251089	250.129183	482.224540	241.615908	481.240524	241.123900	I	***762.487237***	381.747257	745.460688	373.233982	744.476672	372.741974	6
5	612.335153	306.671215	595.308604	298.157940	594.324588	297.665932	L	***649.403173***	325.205225	632.376624	316.691950	631.392608	316.199942	5
6	**713.382832**	357.195054	696.356283	348.681780	695.372267	348.189772	T	***536.319109***	268.663193	519.292560	260.149918	518.308544	259.657910	4
7	826.466896	413.737086	809.440347	405.223812	808.456331	404.731804	L	***435.271430***	218.139353	418.244881	209.626079			3
8	973.535310	487.271293	956.508761	478.758019	955.524745	478.266011	F	***322.187366***	161.597321	305.160817	153.084047			2
9							R	***175.118952***	88.063114	158.092403	79.549840			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.7	1146.639694	0.003734	EQQILTLFR
32.9	1146.639694	0.003734	KEQPLFTLR
3.9	1146.635681	0.007747	GTARTSKPTTK
1.6	1146.639679	0.003749	APGAAPPPALSAK
0.5	1146.639679	0.003749	EPHISLIPNK

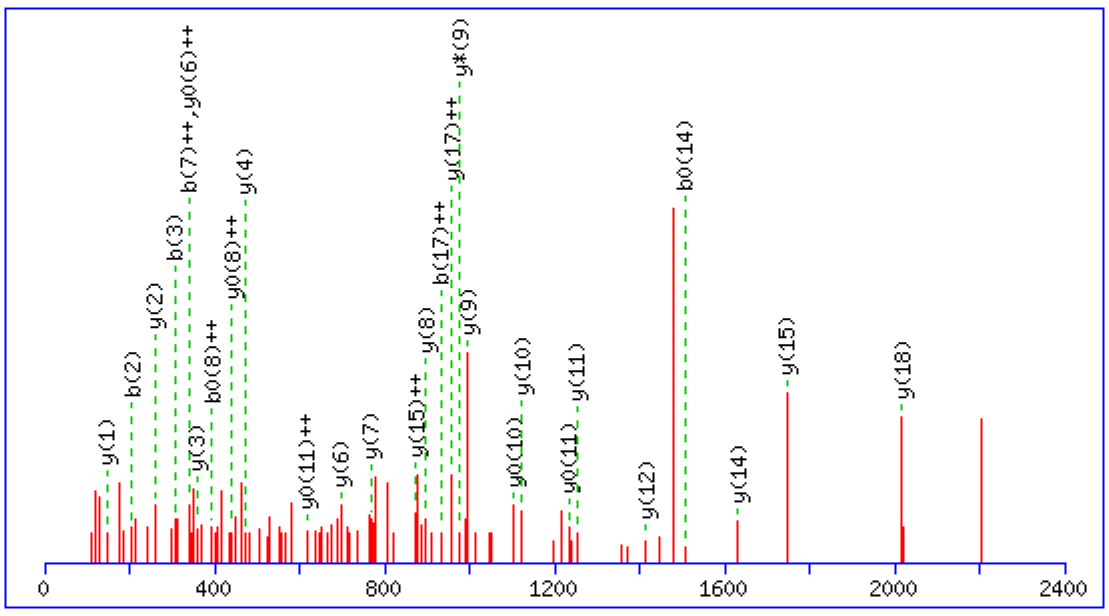
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GFTGIDSEYEKPEAPELVLK**
Found in **PAPS1_HUMAN**, Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 1 OS=Homo sapiens GN=PAPSS1 PE=1 SV=2

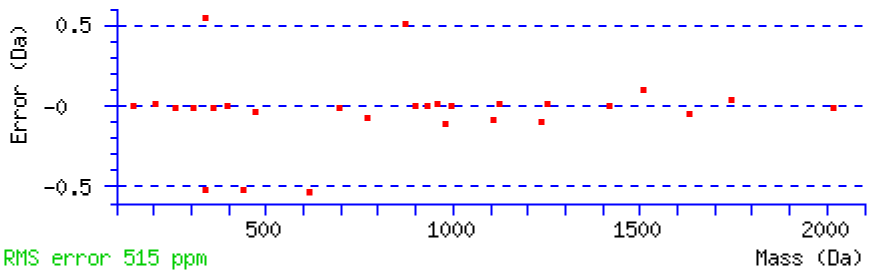
Match to Query 65396: 2221.120332 from(741.380720,3+) rtinseconds(2915) index(36236)
Title: Locus:1.1.1.2747.39
Data file 2011-11-12 - TFD - EP 5-2.mgf

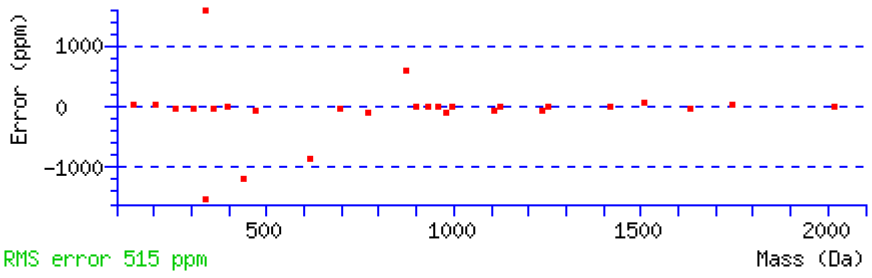
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [0] to [2400] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2221.115402
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 44  Expect: 0.0005
Matches : 28/196 fragment ions using 85 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	58.028740	29.518008					G							20
2	205.097154	103.052215					F	2165.101244	1083.054260	2148.074695	1074.540985	2147.090679	1074.048977	19
3	306.144833	153.576055			288.134268	144.570772	T	***2018.032830***	1009.520053	2001.006281	1001.006779	2000.022265	1000.514771	18
4	363.166297	182.086786			345.155732	173.081504	G	1916.985151	958.996214	1899.958602	950.482939	1898.974586	949.990931	17
5	476.250361	238.628818			458.239796	229.623536	I	1859.963687	930.485482	1842.937138	921.972207	1841.953122	921.480199	16
6	591.277304	296.142290			573.266739	287.137008	D	***1746.879623***	873.943450	1729.853074	865.430175	1728.869058	864.938167	15
7	678.309332	339.658304			660.298767	330.653022	S	***1631.852680***	816.429978	1614.826131	807.916704	1613.842115	807.424696	14
8	807.351925	404.179601			789.341360	395.174318	E	1544.820652	772.913964	1527.794103	764.400690	1526.810087	763.908682	13
9	970.415254	485.711265			952.404689	476.705983	Y	***1415.778059***	708.392668	1398.751510	699.879393	1397.767494	699.387385	12
10	1099.457847	550.232561			1081.447282	541.227279	E	***1252.714730***	626.861003	1235.688181	618.347729	1234.704165	617.855721	11
11	1227.552810	614.280043	1210.526261	605.766769	1209.542245	605.274760	K	***1123.672137***	562.339707	1106.645588	553.826432	1105.661572	553.334424	10
12	1324.605574	662.806425	1307.579025	654.293151	1306.595009	653.801142	P	***995.577174***	498.292225	978.550625	489.778951	977.566609	489.286943	9
13	1453.648167	727.327722	1436.621618	718.814447	1435.637602	718.322439	E	***898.524410***	449.765843	881.497861	441.252569	880.513845	440.760561	8
14	1524.685281	762.846279	1507.658732	754.333004	1506.674716	753.840996	A	***769.481817***	385.244547	752.455268	376.731272	751.471252	376.239264	7
15	1621.738045	811.372661	1604.711496	802.859386	1603.727480	802.367378	P	***698.444703***	349.725990	681.418154	341.212715	680.434138	340.720707	6
16	1750.780638	875.893957	1733.754089	867.380683	1732.770073	866.888674	E	601.391939	301.199608	584.365390	292.686333	583.381374	292.194325	5
17	1863.864702	932.435989	1846.838153	923.922714	1845.854137	923.430706	L	***472.349346***	236.678311	455.322797	228.165037			4
18	1962.933116	981.970196	1945.906567	973.456922	1944.922551	972.964913	V	***359.265282***	180.136279	342.238733	171.623005			3
19	2076.017180	1038.512228	2058.990631	1029.998953	2058.006615	1029.506945	L	***260.196868***	130.602072	243.170319	122.088798			2
20							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.4	2221.115402	0.004930	GFTGIDSEYEKPEAPELVLK

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

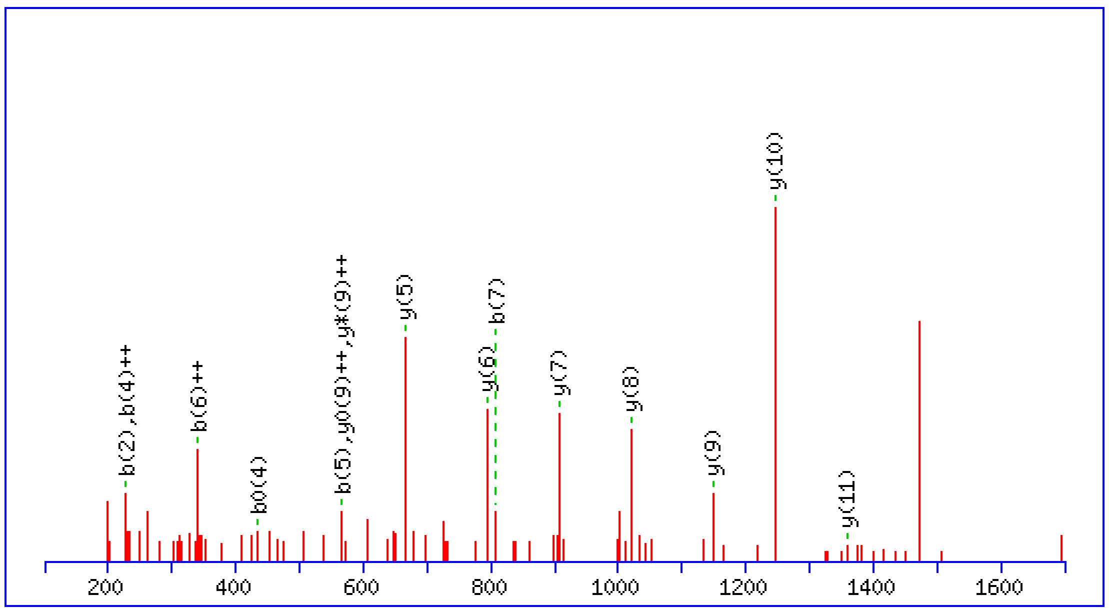
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLPELLQPYTER**
Found in **COASY_HUMAN**, Bifunctional coenzyme A synthase OS=Homo sapiens GN=COASY PE=1 SV=4

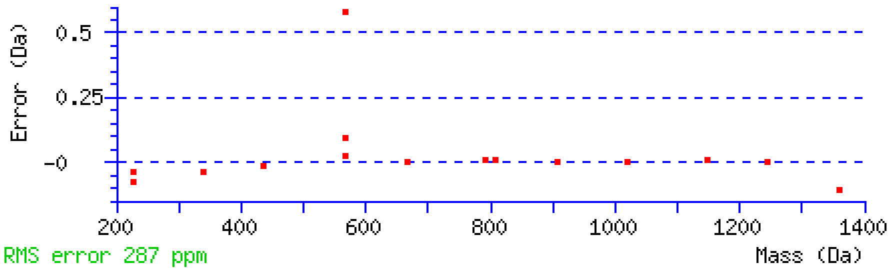
Match to Query 43743: 1470.813388 from(736.413970,2+) rtinseconds(3268) index(47008)
Title: Locus:1.1.1.2793.26
Data file 2011-11-13 - TFD - EP 7-3.mgf

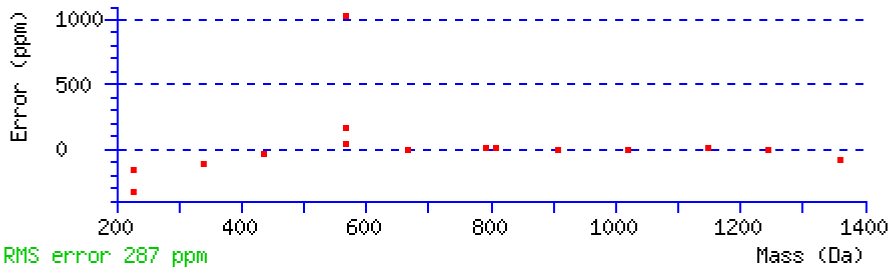
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1700] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1470.808197
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 65 **Expect:** 1.7e-006
Matches : 15/112 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					L							12
2	**227.175404**	114.091340					L	***1358.731444***	679.869360	1341.704895	671.356086	1340.720879	670.864078	11
3	324.228168	162.617722					P	***1245.647380***	623.327328	1228.620831	614.814054	1227.636815	614.322045	10
4	453.270761	**227.139018**			435.260196	218.133736	E	***1148.594616***	574.800946	1131.568067	566.287671	1130.584051	565.795663	9
5	**566.354825**	283.681051			548.344260	274.675768	L	***1019.552023***	510.279650	1002.525474	501.766375	1001.541458	501.274367	8
6	679.438889	**340.223083**			661.428324	331.217800	L	***906.467959***	453.737618	889.441410	445.224343	888.457394	444.732335	7
7	**807.497467**	404.252372	790.470918	395.739097	789.486902	395.247089	Q	***793.383895***	397.195585	776.357346	388.682311	775.373330	388.190303	6
8	904.550231	452.778754	887.523682	444.265479	886.539666	443.773471	P	***665.325317***	333.166296	648.298768	324.653022	647.314752	324.161014	5
9	1067.613560	534.310418	1050.587011	525.797144	1049.602995	525.305136	Y	568.272553	284.639914	551.246004	276.126640	550.261988	275.634632	4
10	1168.661239	584.834258	1151.634690	576.320983	1150.650674	575.828975	T	405.209224	203.108250	388.182675	194.594975	387.198659	194.102967	3
11	1297.703832	649.355554	1280.677283	640.842280	1279.693267	640.350271	E	304.161545	152.584410	287.134996	144.071136	286.150980	143.579128	2
12							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
65.0	1470.808197	0.005191	LLPELLQPYTER
7.1	1470.811584	0.001804	LLLDLPIQLMDR
3.7	1470.801697	0.011691	ILIVTQTPHYMR

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

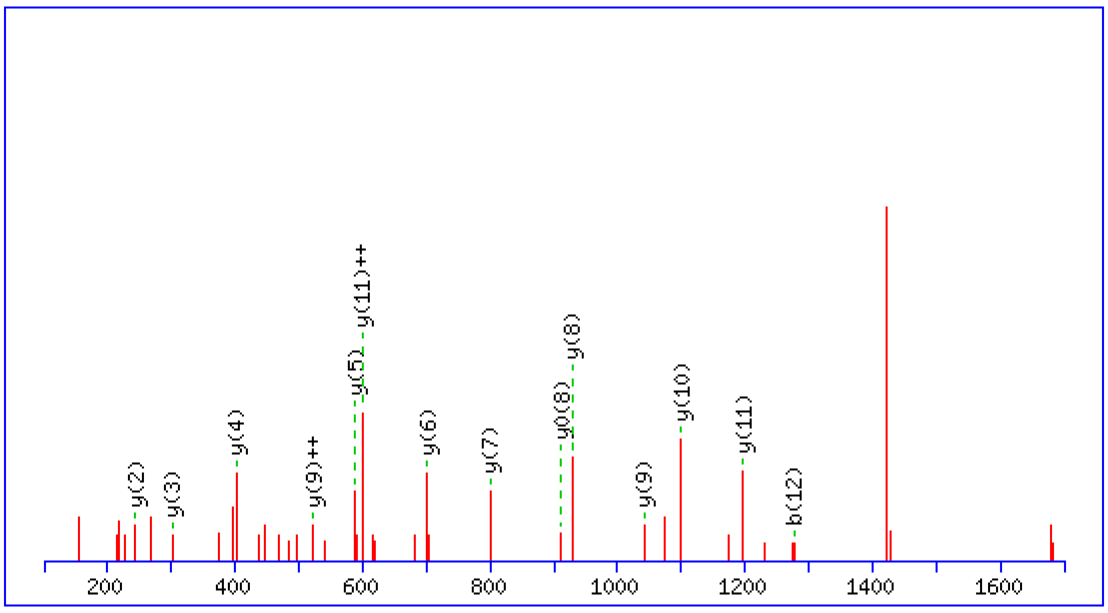
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLPGIEVLWTGPK**
Found in **NCOAT_HUMAN**, Bifunctional protein NCOAT OS=Homo sapiens GN=MGEA5 PE=1 SV=2

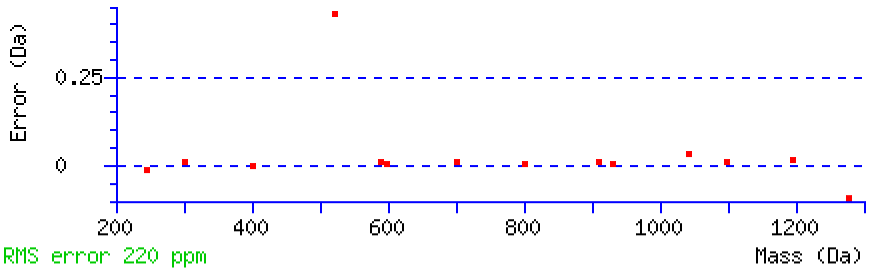
Match to Query 42606: 1421.824868 from(711.919710,2+) rtinseconds(3901) index(58269)
Title: Locus:1.1.1.2785.30
Data file 2011-11-12 - TFD - EP 6-1.mgf

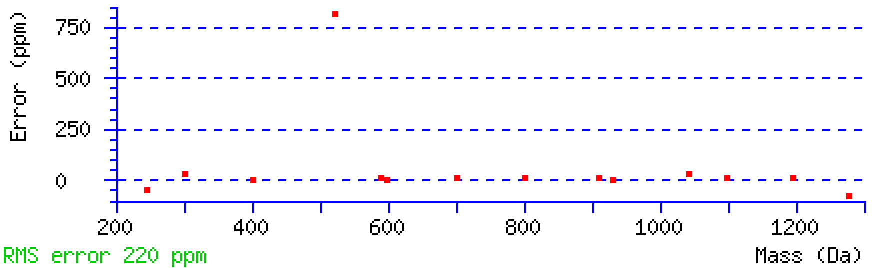
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1421.828232
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 68  Expect: 5.7e-007
Matches : 14/104 fragment ions using 31 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							13
2	227.175404	114.091340			L	1309.751451	655.379364	1292.724902	646.866089	1291.740886	646.374081	12
3	324.228168	162.617722			P	*1196.667387*	598.837332	1179.640838	590.324057	1178.656822	589.832049	11
4	381.249632	191.128454			G	*1099.614623*	550.310949	1082.588074	541.797675	1081.604058	541.305667	10
5	494.333696	247.670486			I	*1042.593159*	521.800218	1025.566610	513.286943	1024.582594	512.794935	9
6	623.376289	312.191783	605.365724	303.186500	E	*929.509095*	465.258186	912.482546	456.744911	911.498530	456.252903	8
7	722.444703	361.725990	704.434138	352.720707	V	*800.466502*	400.736889	783.439953	392.223615	782.455937	391.731607	7
8	835.528767	418.268022	817.518202	409.262739	L	*701.398088*	351.202682	684.371539	342.689408	683.387523	342.197400	6
9	1021.608080	511.307678	1003.597515	502.302395	W	*588.314024*	294.660650	571.287475	286.147376	570.303459	285.655368	5
10	1122.655759	561.831518	1104.645194	552.826235	T	*402.234711*	201.620993	385.208162	193.107719	384.224146	192.615711	4
11	1179.677223	590.342249	1161.666658	581.336967	G	*301.187032*	151.097154	284.160483	142.583879			3
12	1276.729987	638.868631	1258.719422	629.863349	P	*244.165568*	122.586422	227.139019	114.073148			2
13					K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
67.7	1421.828232	-0.003364	LLPGIEVLWTGPK

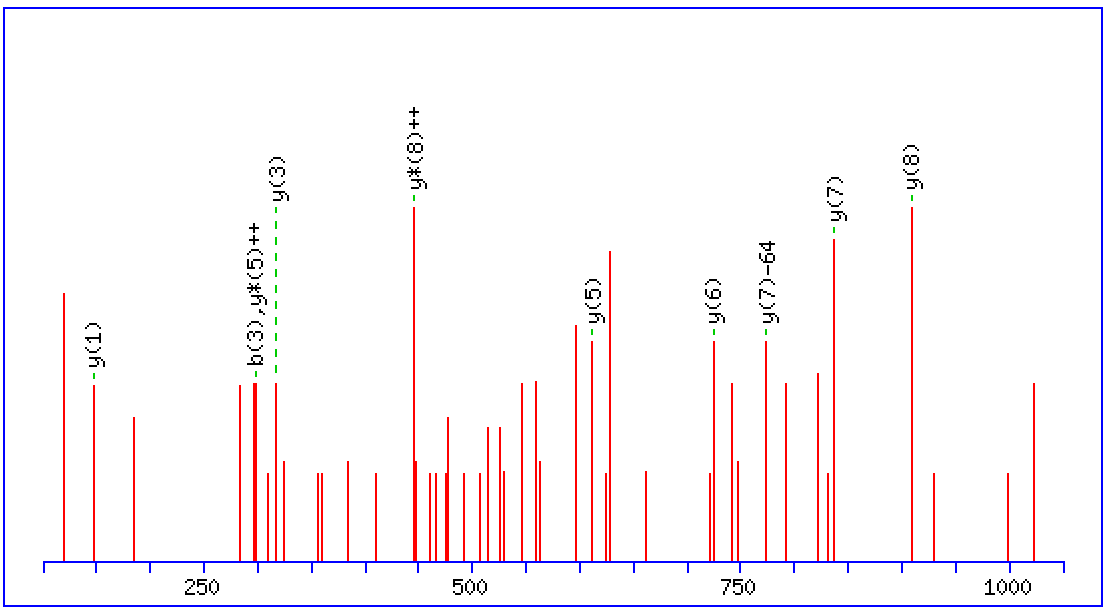
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LAPIMFGIK**
Found in **GLCNE_HUMAN**, Bifunctional UDP-N-acetylglucosamine 2-epimerase/N-acetylmannosamine kinase OS=Homo sapiens GN=GNE PE=1 SV=1

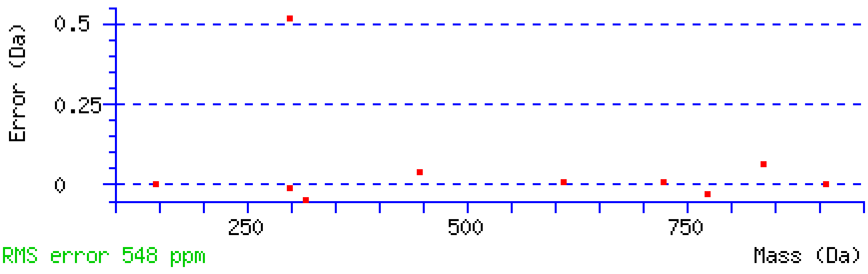
Match to Query 14377: 1020.577368 from(511.295960,2+) rtinseconds(3020) index(42651)
Title: Locus:1.1.1.2568.6
Data file 2011-11-10 - TFD - EP 3-3.mgf

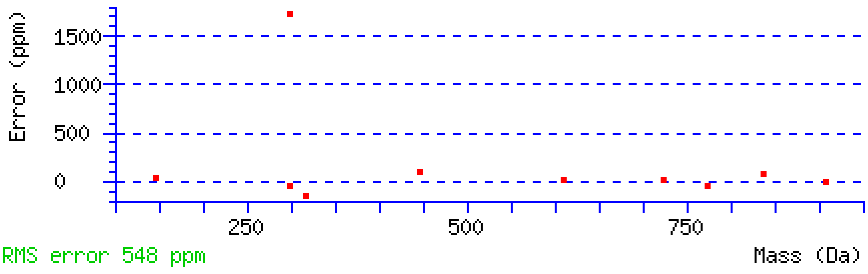
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1020.567780
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P3     : Oxidation (P)
M5     : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 35  Expect: 0.0018
Matches : 10/72 fragment ions using 18 most intense peaks    (help)
```

#	b	b^{++}	Seq.	y	y^{++}	y^*	y^{*++}	#
1	114.091340	57.549308	L					9
2	185.128454	93.067865	A	*908.491003*	454.749140	891.464454	446.235865	8
3	298.176133	149.591704	P	*837.453889*	419.230583	820.427340	410.717308	7
4	411.260197	206.133737	I	*724.406210*	362.706743	707.379661	354.193469	6
5	558.295597	279.651437	M	*611.322146*	306.164711	594.295597	297.651437	5
6	705.364011	353.185644	F	464.286746	232.647011	447.260197	224.133737	4
7	762.385475	381.696376	G	*317.218332*	159.112804	300.191783	150.599530	3
8	875.469539	438.238408	I	260.196868	130.602072	243.170319	122.088798	2
9			K	*147.112804*	74.060040	130.086255	65.546765	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.2	1020.567780	0.009588	LAPIMFGIK
11.8	1020.567764	0.009604	LAIYGMLPK
9.9	1020.567764	0.009604	LAIYGMLPK
6.6	1020.582855	-0.005487	LSPHKVQGR

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

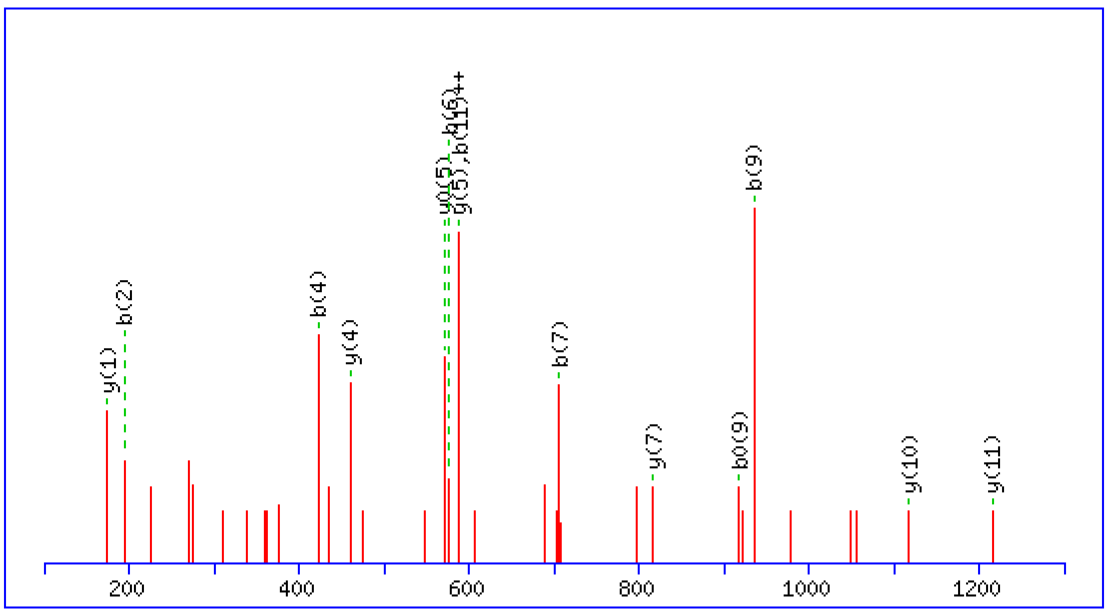
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GHVEPGEDDLETALR**
Found in **AP4A_HUMAN**, Bis(5'-nucleosyl)-tetraphosphatase [asymmetrical] OS=Homo sapiens GN=NUDT2 PE=1 SV=3

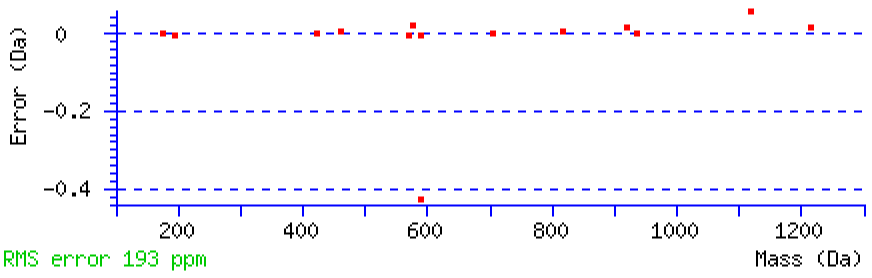
Match to Query 51737: 1636.766562 from(546.596130,3+) rtinseconds(2230) index(25329)
Title: Locus:1.1.1.2068.22
Data file 2011-11-12 - TFD - EP 5-6.mgf

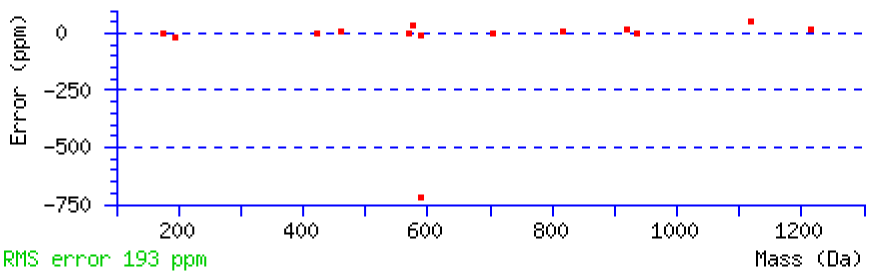
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1636.769272
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 52  Expect: 6.3e-005
Matches : 14/128 fragment ions using 20 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008			G							15
2	*195.087652*	98.047464			H	1580.755092	790.881184	1563.728543	782.367910	1562.744527	781.875901	14
3	294.156066	147.581671			V	1443.696180	722.351728	1426.669631	713.838453	1425.685615	713.346445	13
4	*423.198659*	212.102968	405.188094	203.097685	E	1344.627766	672.817521	1327.601217	664.304246	1326.617201	663.812238	12
5	520.251423	260.629350	502.240858	251.624067	P	*1215.585173*	608.296224	1198.558624	599.782950	1197.574608	599.290942	11
6	*577.272887*	289.140082	559.262322	280.134799	G	*1118.532409*	559.769842	1101.505860	551.256568	1100.521844	550.764560	10
7	*706.315480*	353.661378	688.304915	344.656096	E	1061.510945	531.259110	1044.484396	522.745836	1043.500380	522.253828	9
8	821.342423	411.174850	803.331858	402.169567	D	932.468352	466.737814	915.441803	458.224539	914.457787	457.732531	8
9	*936.369366*	468.688321	918.358801	459.683039	D	*817.441409*	409.224342	800.414860	400.711068	799.430844	400.219060	7
10	1049.453430	525.230353	1031.442865	516.225071	L	702.414466	351.710871	685.387917	343.197596	684.403901	342.705588	6
11	1178.496023	589.751649	1160.485458	580.746367	E	*589.330402*	295.168839	572.303853	286.655564	571.319837	286.163556	5
12	1279.543702	640.275489	1261.533137	631.270206	T	*460.287809*	230.647542	443.261260	222.134268	442.277244	221.642260	4
13	1350.580816	675.794046	1332.570251	666.788763	A	359.240130	180.123703	342.213581	171.610428			3
14	1463.664880	732.336078	1445.654315	723.330795	L	288.203016	144.605146	271.176467	136.091871			2
15					R	*175.118952*	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.7	1636.769272	-0.002710	GHVEPGEDDLETALR
10.2	1636.751511	0.015051	DPPPEPSPSKGSPCR
2.9	1636.751511	0.015051	DPPPEPSPSKGSPCR
0.8	1636.762741	0.003821	MNNGPVLGHEEEVGR
0.7	1636.769272	-0.002710	SRTAVDGFQSESPEK
0.2	1636.776642	-0.010080	ELTACIFPTESEAR

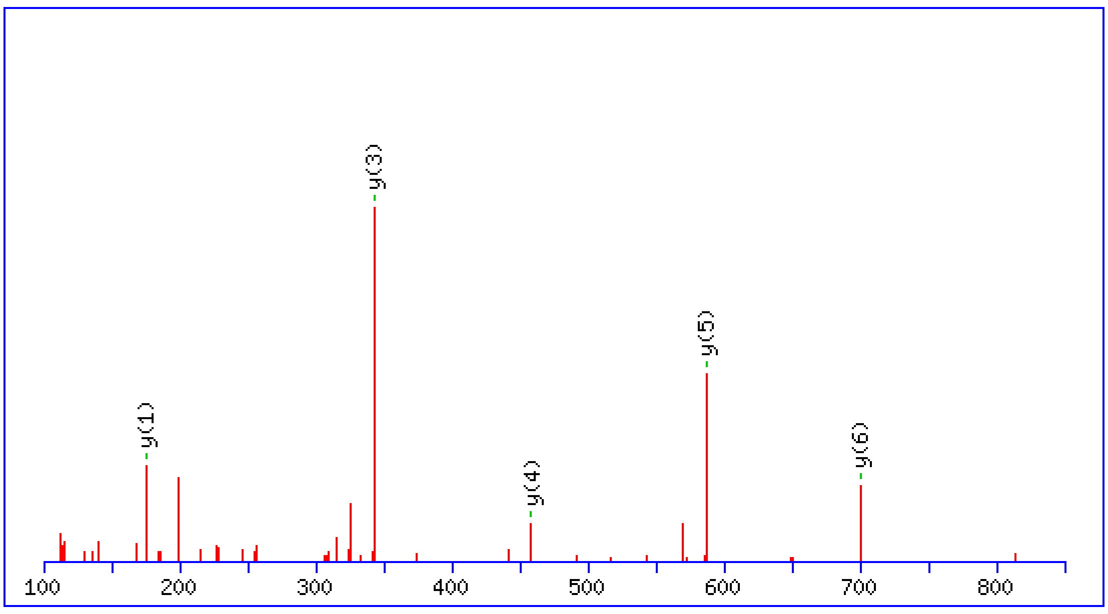
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IIEDPAR**
Found in **EMAL2_HUMAN**, Echinoderm microtubule-associated protein-like 2 OS=Homo sapiens GN=EML2 PE=2 SV=1

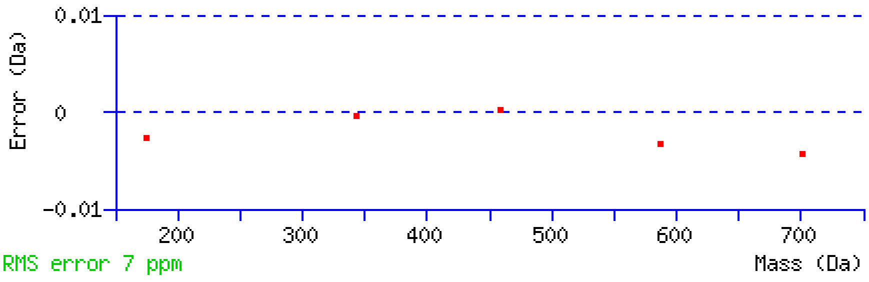
Match to Query 18545: 812.441168 from(407.227860,2+) rtinseconds(1111) index(413710)
Title: Locus:1.1.1.759.4
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

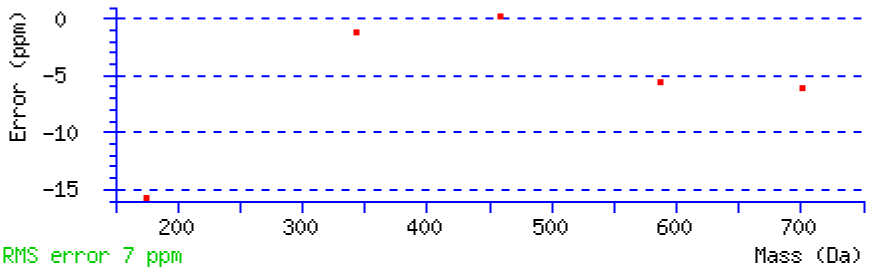
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 812.439194
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 48 **Expect:** 9e-005
Matches : 5/50 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							7
2	227.175404	114.091340			I	*700.362430*	350.684853	683.335881	342.171579	682.351865	341.679571	6
3	356.217997	178.612637	338.207432	169.607354	E	*587.278366*	294.142821	570.251817	285.629547	569.267801	285.137539	5
4	471.244940	236.126108	453.234375	227.120826	D	*458.235773*	229.621524	441.209224	221.108250	440.225208	220.616242	4
5	568.297704	284.652490	550.287139	275.647208	P	*343.208830*	172.108053	326.182281	163.594778			3
6	639.334818	320.171047	621.324253	311.165765	A	246.156066	123.581671	229.129517	115.068396			2
7					R	*175.118952*	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.2	812.439194	0.001974	IIEDPAR
48.2	812.439194	0.001974	LLEDAPR
28.9	812.439209	0.001959	LPEIPGR
23.3	812.439209	0.001959	LPVAPER
21.1	812.439209	0.001959	IPPLGER
15.2	812.439209	0.001959	IPVPAER
15.0	812.439194	0.001974	ILPAEDR
15.0	812.439209	0.001959	LPPDALR
13.1	812.439194	0.001974	EPVELAR
8.5	812.439194	0.001974	IDLPEAR

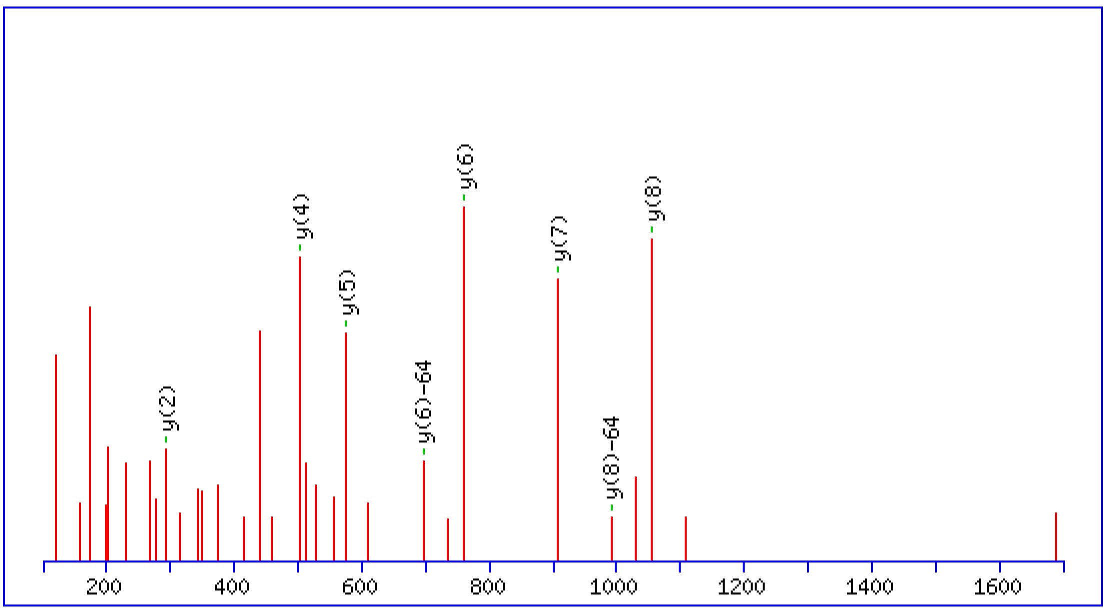
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TVFFWAPIMK**
Found in **BR44_HUMAN**, Brain protein 44 OS=Homo sapiens GN=BRP44 PE=1 SV=1

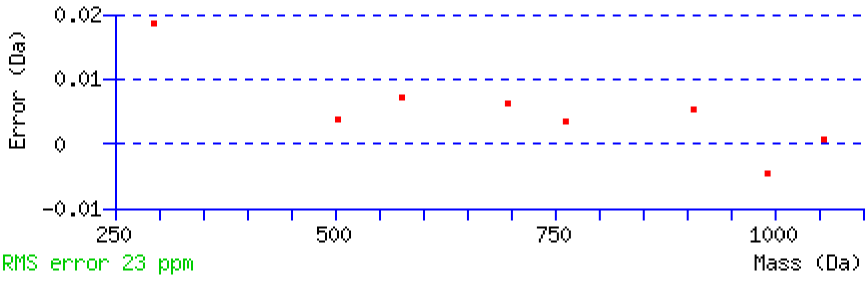
Match to Query 28912: 1254.651668 from(628.333110,2+) rtinseconds(3532) index(38051)
Title: Locus:1.1.1.2798.12
Data file 2011-11-13 - TFD - EP 7-7.mgf

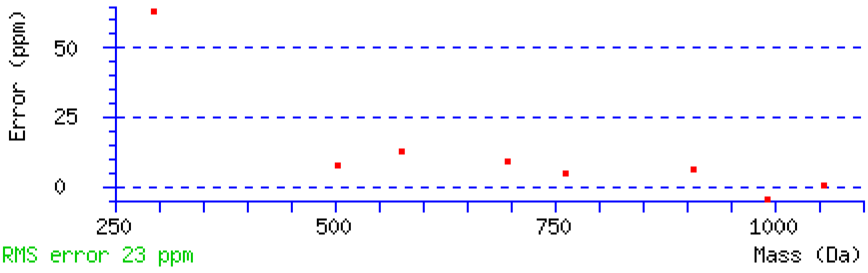
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1254.647110
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M9 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 50 **Expect:** 5.3e-005
Matches : 8/108 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	102.054955	51.531116	84.044390	42.525833	T					10
2	201.123369	101.065322	183.112804	92.060040	V	1154.606701	577.806988	1137.580152	569.293714	9
3	348.191783	174.599529	330.181218	165.594247	F	***1055.538287***	528.272781	1038.511738	519.759507	8
4	495.260197	248.133737	477.249632	239.128454	F	***908.469873***	454.738575	891.443324	446.225300	7
5	681.339510	341.173393	663.328945	332.168111	W	***761.401459***	381.204367	744.374910	372.691093	6
6	752.376624	376.691950	734.366059	367.686668	A	***575.322146***	288.164711	558.295597	279.651436	5
7	849.429388	425.218332	831.418823	416.213050	P	***504.285032***	252.646154	487.258483	244.132879	4
8	962.513452	481.760364	944.502887	472.755082	I	407.232268	204.119772	390.205719	195.606497	3
9	1109.548852	555.278064	1091.538287	546.272781	M	***294.148204***	147.577740	277.121655	139.064465	2
10					K	147.112804	74.060040	130.086255	65.546765	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
50.3	1254.647110	0.004558	TVFFWAPIMK
32.1	1254.647110	0.004558	TVFFWAPIMK
4.7	1254.650940	0.000728	LHPFDAGKWGK

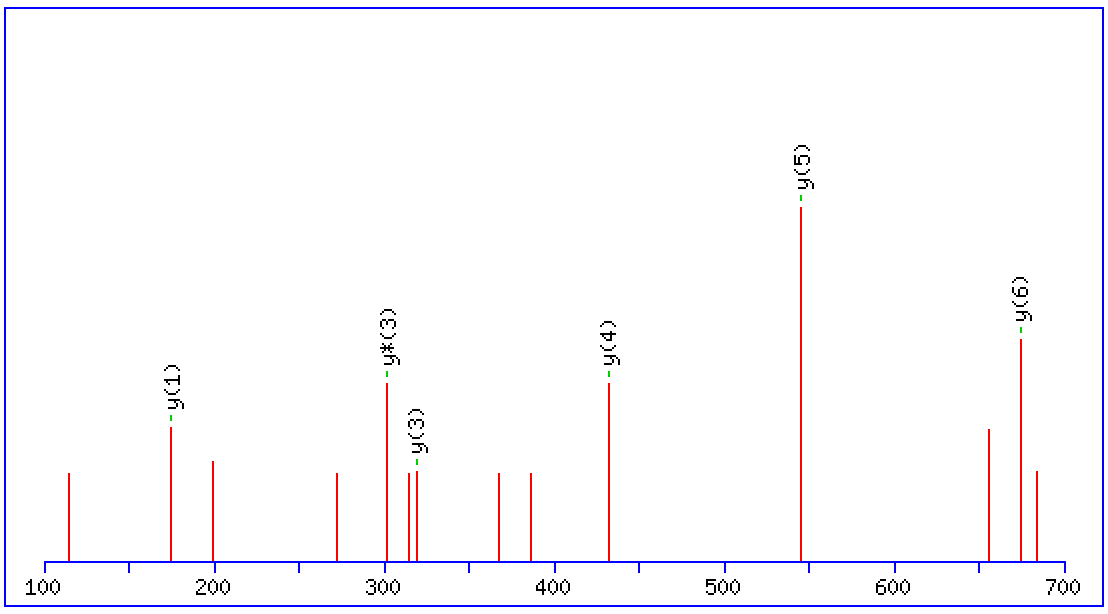
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SPEIISGR**
Found in **BR44L_HUMAN**, Brain protein 44-like protein OS=Homo sapiens GN=BRP44L PE=1 SV=1

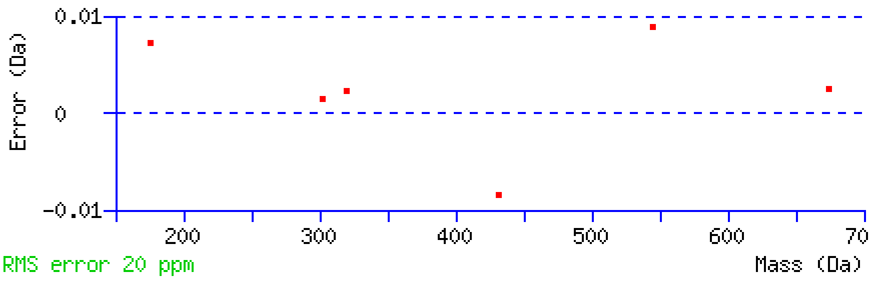
Match to Query 4874: 857.466408 from(429.740480,2+) rtinseconds(1360) index(5353)
Title: Locus:1.1.1.1924.10
Data file 2011-11-10 - TFD - EP 3-7.mgf

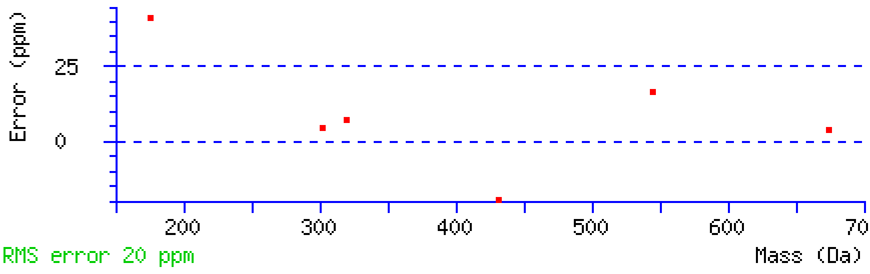
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 857.460663
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 54 **Expect:** 8.3e-005
Matches : 6/66 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	S							8
2	185.092068	93.049672	167.081503	84.044389	P	771.435929	386.221603	754.409380	377.708328	753.425364	377.216320	7
3	314.134661	157.570968	296.124096	148.565686	E	***674.383165***	337.695221	657.356616	329.181946	656.372600	328.689938	6
4	427.218725	214.113001	409.208160	205.107718	I	***545.340572***	273.173924	528.314023	264.660650	527.330007	264.168642	5
5	540.302789	270.655033	522.292224	261.649750	I	***432.256508***	216.631892	415.229959	208.118617	414.245943	207.626609	4
6	627.334817	314.171047	609.324252	305.165764	S	***319.172444***	160.089860	302.145895	151.576585	301.161879	151.084577	3
7	684.356281	342.681779	666.345716	333.676496	G	232.140416	116.573846	215.113867	108.060571			2
8					R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.0	857.460663	0.005745	SPEIISGR
18.1	857.471878	-0.005470	NAQLEKR
16.2	857.460648	0.005760	LAEEQLR
16.2	857.460648	0.005760	SPEELKR
16.2	857.460663	0.005745	SPEGLISR
15.9	857.460648	0.005760	AEIIQER
15.9	857.460663	0.005745	AELISGPR
15.9	857.460648	0.005760	AELLQER
15.9	857.471909	-0.005501	SLPPTRR
15.9	857.460663	0.005745	TDPLEKR

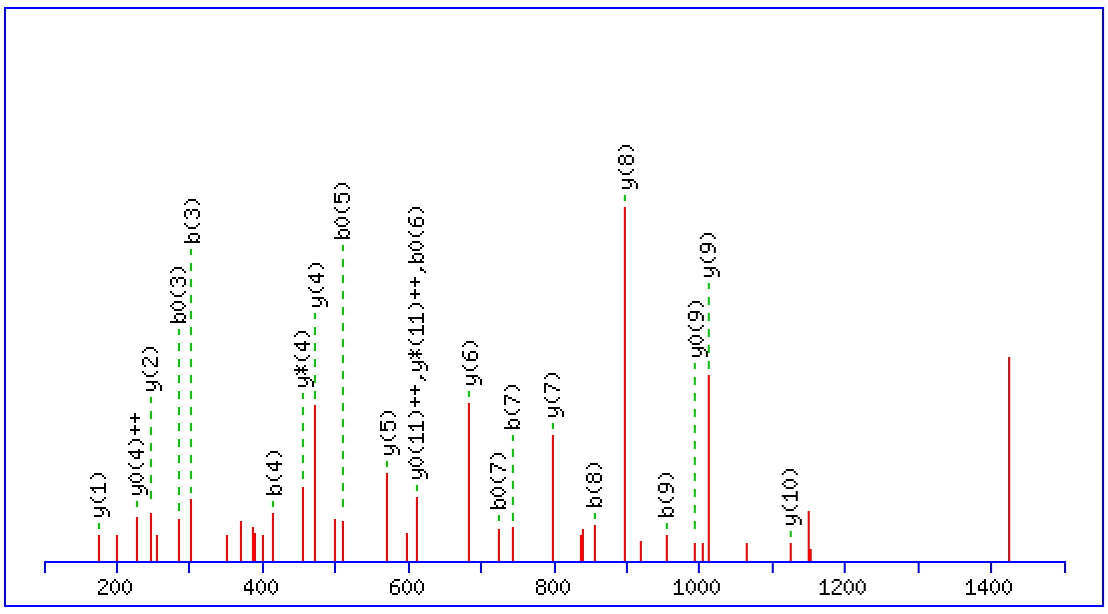
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EGDLITLLVPEAR**
Found in **BAIP2_HUMAN**, Brain-specific angiogenesis inhibitor 1-associated protein 2 OS=Homo sapiens GN=BAIAP2 PE=1 SV=1

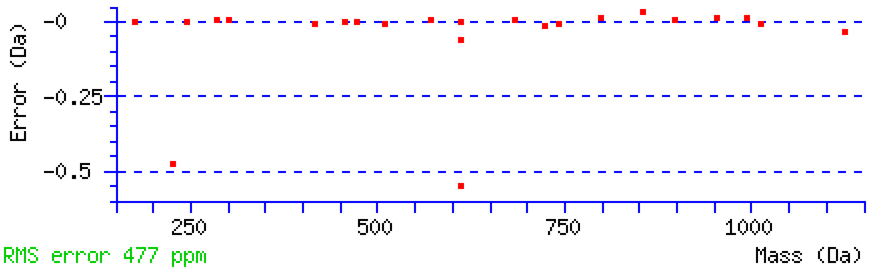
Match to Query 42348: 1424.790748 from(713.402650,2+) rtinseconds(3896) index(52026)
Title: Locus:1.1.1.2631.9
Data file 2011-11-12 - TFD - EP 6-6.mgf

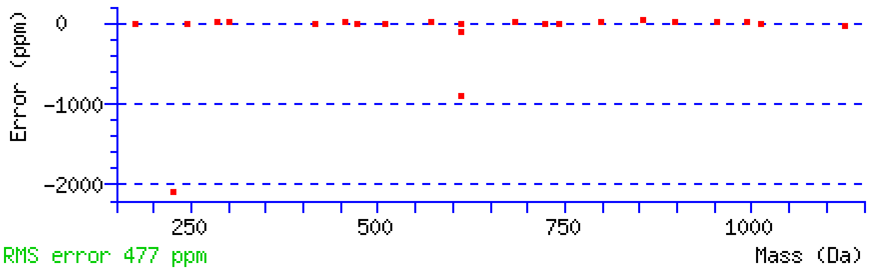
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1500] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1424.787476
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 74 **Expect:** 2.5e-007
Matches : 23/116 fragment ions using 29 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572	112.039304	56.523290	E							13
2	187.071333	94.039305	169.060768	85.034022	G	1296.752179	648.879728	1279.725630	640.366453	1278.741614	639.874445	12
3	**302.098276**	151.552776	284.087711	142.547494	D	1239.730715	620.368996	1222.704166	611.855721	1221.720150	611.363713	11
4	**415.182340**	208.094808	397.171775	199.089526	L	***1124.703772***	562.855524	1107.677223	554.342250	1106.693207	553.850242	10
5	528.266404	264.636840	510.255839	255.631558	I	***1011.619708***	506.313492	994.593159	497.800218	993.609143	497.308210	9
6	629.314083	315.160680	611.303518	306.155397	T	***898.535644***	449.771460	881.509095	441.258186	880.525079	440.766178	8
7	**742.398147**	371.702712	724.387582	362.697429	L	***797.487965***	399.247621	780.461416	390.734346	779.477400	390.242338	7
8	**855.482211**	428.244744	837.471646	419.239461	L	***684.403901***	342.705589	667.377352	334.192314	666.393336	333.700306	6
9	**954.550625**	477.778951	936.540060	468.773668	V	***571.319837***	286.163557	554.293288	277.650282	553.309272	277.158274	5
10	1051.603389	526.305333	1033.592824	517.300050	P	***472.251423***	236.629350	455.224874	228.116075	454.240858	227.624067	4
11	1180.645982	590.826629	1162.635417	581.821347	E	375.198659	188.102968	358.172110	179.589693	357.188094	179.097685	3
12	1251.683096	626.345186	1233.672531	617.339904	A	***246.156066***	123.581671	229.129517	115.068396			2
13					R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
74.2	1424.787476	0.003272	EGDLITLLVPEAR
13.9	1424.784973	0.005775	MIGLRLYDGLFK

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

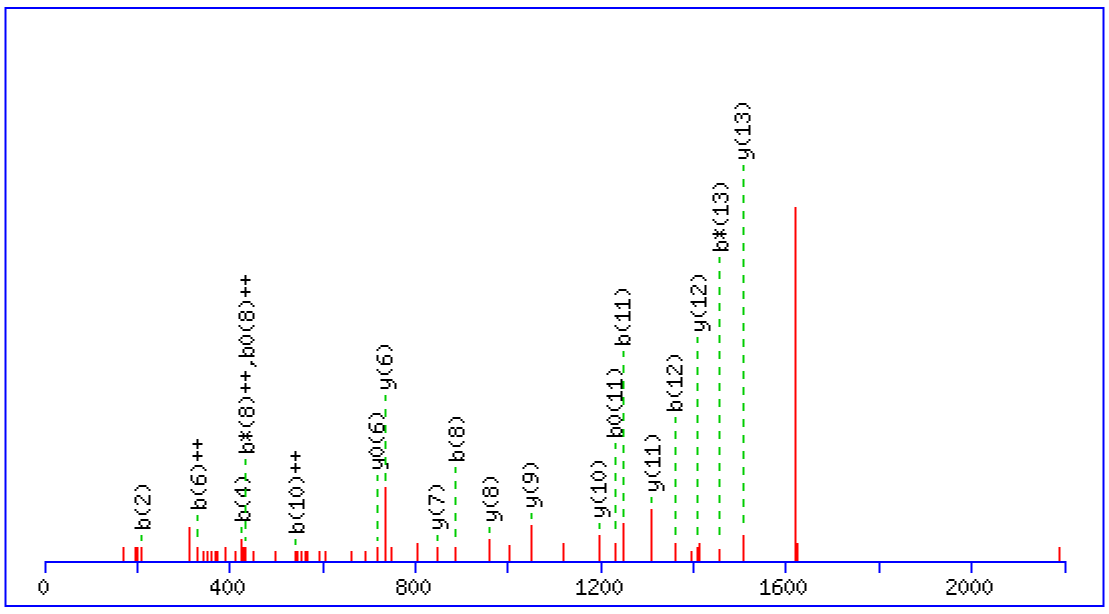
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LPVDFSNIPTYLLK**
Found in **BRE_HUMAN**, BRCA1-A complex subunit BRE OS=Homo sapiens GN=BRE PE=1 SV=2

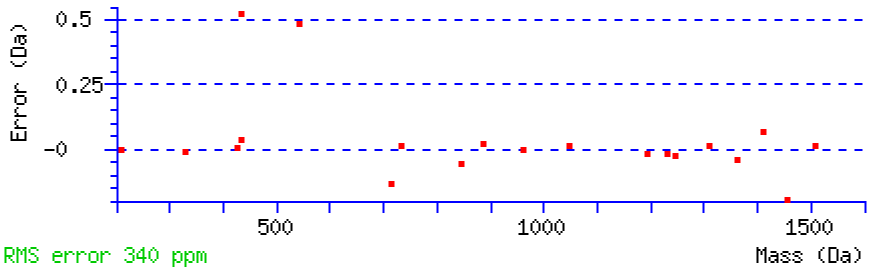
Match to Query 52808: 1618.903928 from(810.459240,2+) rtinseconds(3962) index(59453)
Title: Locus:1.1.1.2887.34
Data file 2011-11-14 - TFD - EP 8-4.mgf

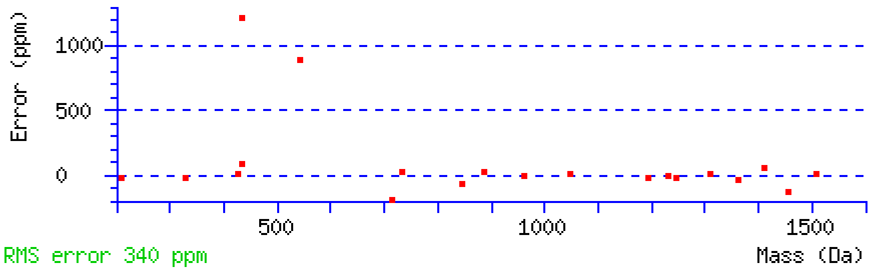
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1618.897034
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 46  Expect: 0.00011
Matches : 20/130 fragment ions using 34 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					L							14
2	***211.144104***	106.075690					P	***1506.820258***	753.913767	1489.793709	745.400493	1488.809693	744.908484	13
3	310.212518	155.609897					V	***1409.767494***	705.387385	1392.740945	696.874111	1391.756929	696.382102	12
4	***425.239461***	213.123369			407.228896	204.118086	D	***1310.699080***	655.853178	1293.672531	647.339903	1292.688515	646.847895	11
5	572.307875	286.657576			554.297310	277.652293	F	***1195.672137***	598.339706	1178.645588	589.826432	1177.661572	589.334424	10
6	659.339903	**330.173590**			641.329338	321.168307	S	***1048.603723***	524.805500	1031.577174	516.292225	1030.593158	515.800217	9
7	773.382830	387.195053	756.356281	378.681779	755.372265	378.189771	N	***961.571695***	481.289485	944.545146	472.776211	943.561130	472.284203	8
8	***886.466894***	443.737085	869.440345	435.223811	868.456329	434.731803	I	***847.528768***	424.268022	830.502219	415.754747	829.518203	415.262739	7
9	983.519658	492.263467	966.493109	483.750193	965.509093	483.258185	P	***734.444704***	367.725990	717.418155	359.212715	716.434139	358.720707	6
10	1084.567337	**542.787307**	1067.540788	534.274032	1066.556772	533.782024	T	637.391940	319.199608	620.365391	310.686333	619.381375	310.194325	5
11	***1247.630666***	624.318971	1230.604117	615.805697	1229.620101	615.313689	Y	536.344261	268.675769	519.317712	260.162494			4
12	***1360.714730***	680.861003	1343.688181	672.347729	1342.704165	671.855720	L	373.280932	187.144104	356.254383	178.630829			3
13	1473.798794	737.403035	1456.772245	728.889760	1455.788229	728.397752	L	260.196868	130.602072	243.170319	122.088797			2
14							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.4	1618.897034	0.006894	LPVDFSNIPTYLLK

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

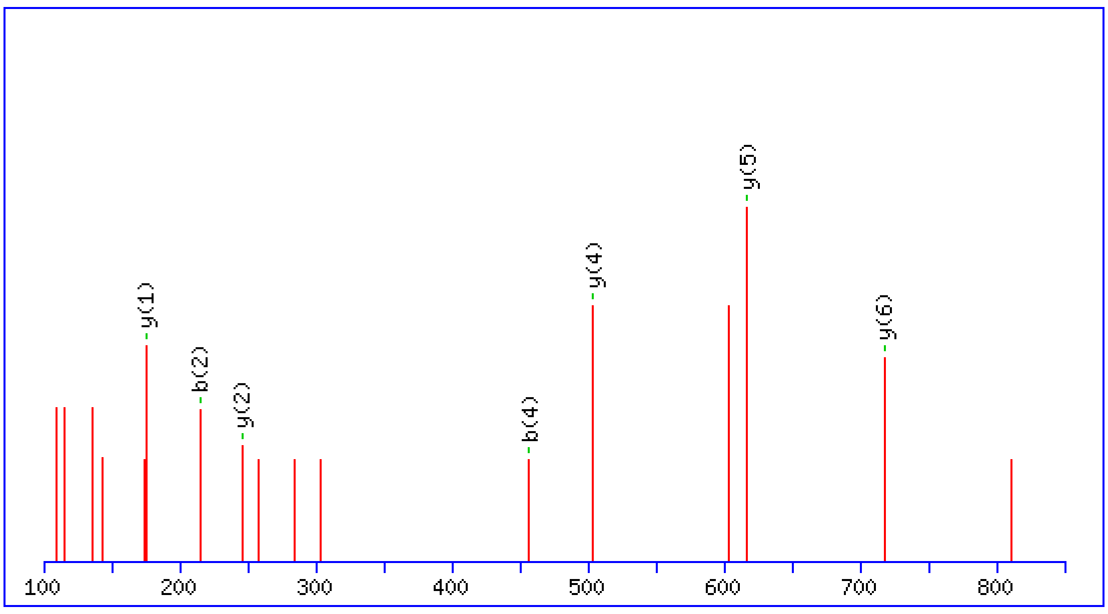
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LTLEEAR**
Found in **PGCB_HUMAN**, Brevican core protein OS=Homo sapiens GN=BCAN PE=1 SV=2

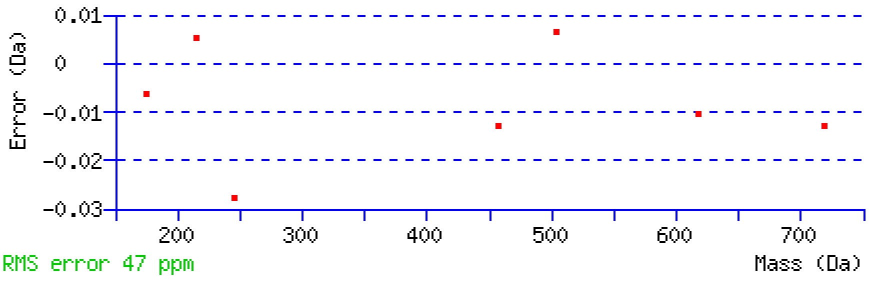
Match to Query 2540: 830.452128 from(416.233340,2+) rtinseconds(1442) index(10722)
Title: Locus:1.1.1.1841.6
Data file 2011-11-12 - TFD - EP 6-5.mgf

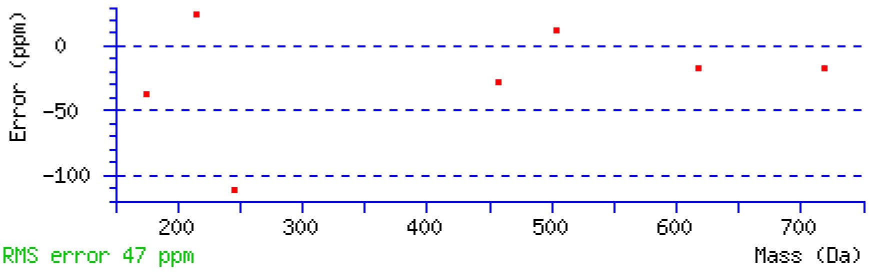
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 830.449753
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.0024
Matches : 7/54 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							7
2	**215.139019**	108.073147	197.128454	99.067865	T	***718.372995***	359.690136	701.346446	351.176861	700.362430	350.684853	6
3	328.223083	164.615179	310.212518	155.609897	L	***617.325316***	309.166296	600.298767	300.653022	599.314751	300.161014	5
4	**457.265676**	229.136476	439.255111	220.131193	E	***504.241252***	252.624264	487.214703	244.110989	486.230687	243.618981	4
5	586.308269	293.657773	568.297704	284.652490	E	375.198659	188.102967	358.172110	179.589693	357.188094	179.097685	3
6	657.345383	329.176330	639.334818	320.171047	A	***246.156066***	123.581671	229.129517	115.068396			2
7					R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.1	830.449753	0.002375	LTLEEAR
27.4	830.449753	0.002375	LTIAEER
15.7	830.449768	0.002360	TLPEISR
15.6	830.449753	0.002375	LTALEER
9.5	830.449753	0.002375	TIEELAR
7.5	830.454453	-0.002325	ICRAAAR
5.8	830.449768	0.002360	DVENKVK
5.1	830.449768	0.002360	LLSPTER
1.1	830.449753	0.002375	TLEEAIR
1.0	830.449768	0.002360	ITADGNLK

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

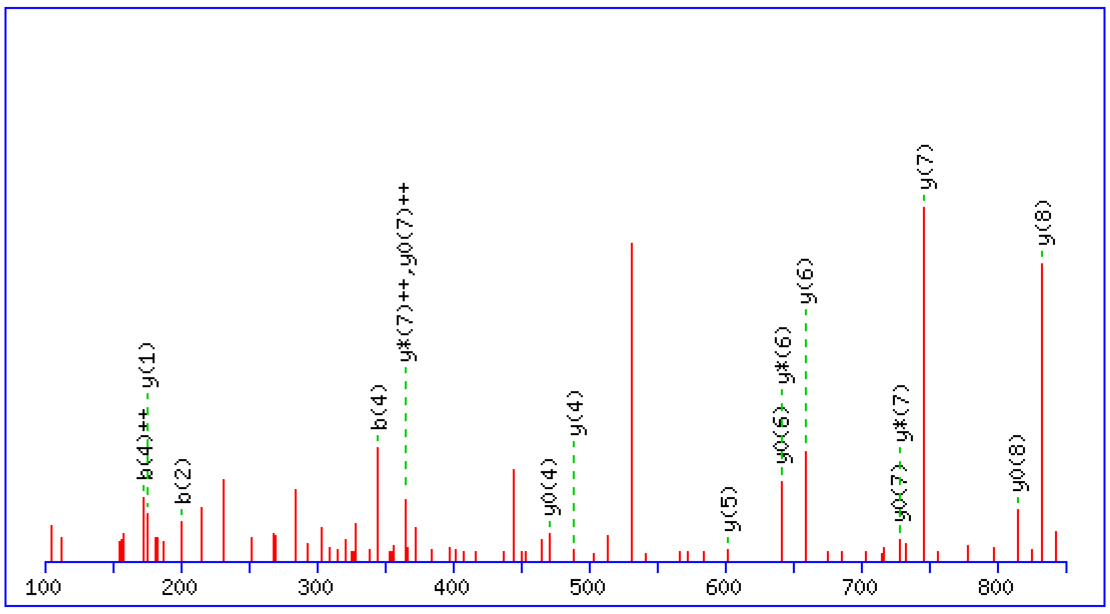
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSSGLTGRR**
Found in **BAHD1_HUMAN**, Bromo adjacent homology domain-containing 1 protein OS=Homo sapiens GN=BAHD1 PE=1 SV=2

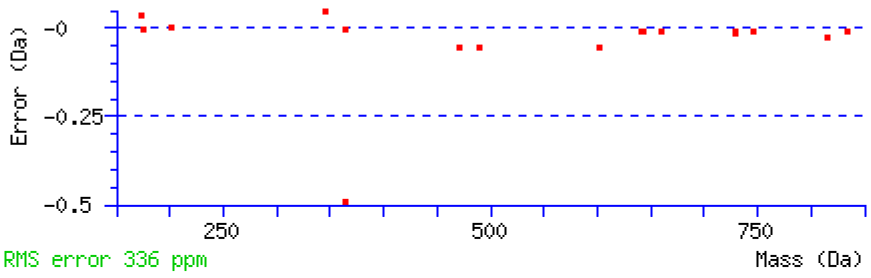
Match to Query 189107: 945.526388 from(473.770470,2+) rtinseconds(1467) index(419655)
Title: Locus:1.1.1.898.14
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

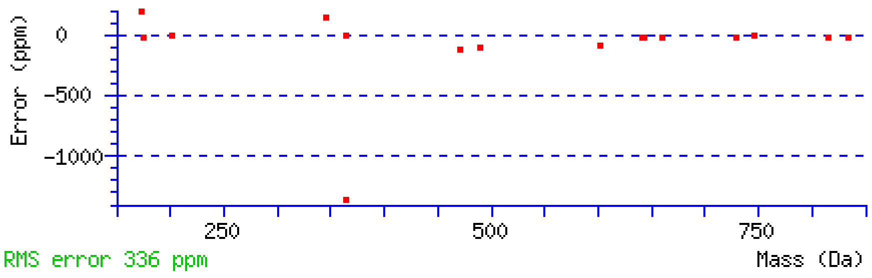
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 945.535568
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 34  Expect: 0.0047
Matches : 17/74 fragment ions using 32 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							9
2	**201.123368**	101.065322			183.112803	92.060039	S	***833.458790***	417.233033	816.432241	408.719759	815.448225	408.227751	8
3	288.155396	144.581336			270.144831	135.576053	S	***746.426762***	373.717019	729.400213	365.203745	728.416197	364.711737	7
4	**345.176860**	173.092068			327.166295	164.086785	G	***659.394734***	330.201005	642.368185	321.687731	641.384169	321.195723	6
5	458.260924	229.634100			440.250359	220.628817	L	***602.373270***	301.690273	585.346721	293.176999	584.362705	292.684991	5
6	559.308603	280.157940			541.298038	271.152657	T	***489.289206***	245.148241	472.262657	236.634966	471.278641	236.142958	4
7	616.330067	308.668672			598.319502	299.663389	G	388.241527	194.624402	371.214978	186.111127			3
8	772.431178	386.719227	755.404629	378.205953	754.420613	377.713945	R	331.220063	166.113669	314.193514	157.600395			2
9							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.9	945.535568	-0.009180	LSSGLTGRR
21.6	945.524323	0.002065	EQSVSKIR
20.1	945.524323	0.002065	ISQSTALAR
17.3	945.524338	0.002050	ISAQTLTGR
11.0	945.524323	0.002065	SEQSVKLR
9.7	945.521820	0.004568	CALWIRK
9.1	945.528366	-0.001978	LSFLPTPR
8.6	945.517807	0.008581	ICTRKPR
8.3	945.528366	-0.001978	LSFLPTPR
7.7	945.524307	0.002081	ESKLNSIR

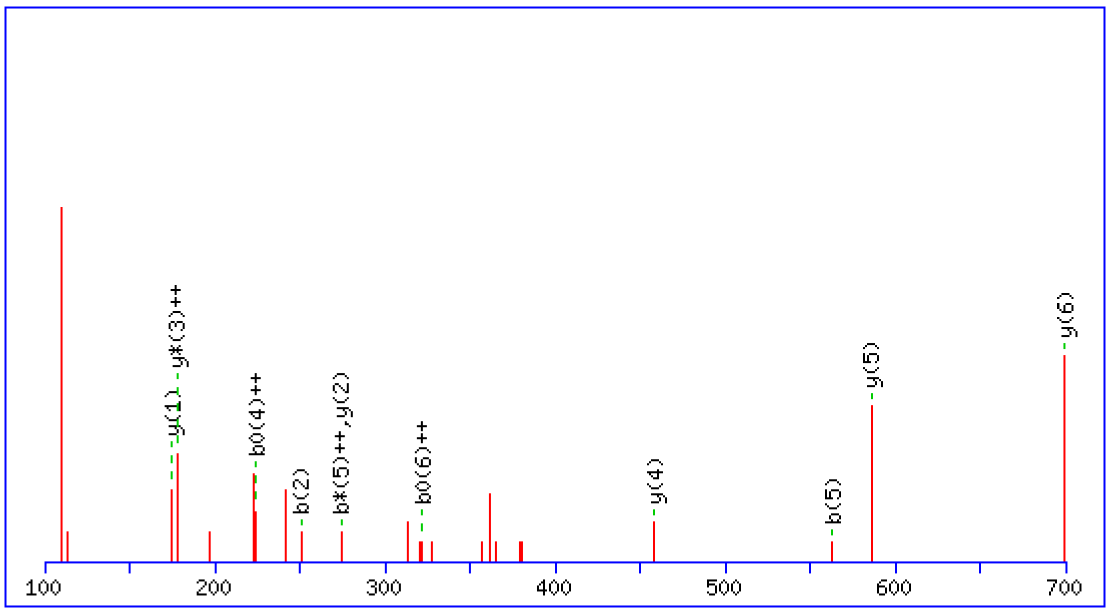
Mascot Search Results

Peptide View

MS/MS Fragmentation of **HLKSPVR**
Found in **BAZ2A_HUMAN**, Bromodomain adjacent to zinc finger domain protein 2A OS=Homo sapiens GN=BAZ2A PE=1 SV=4

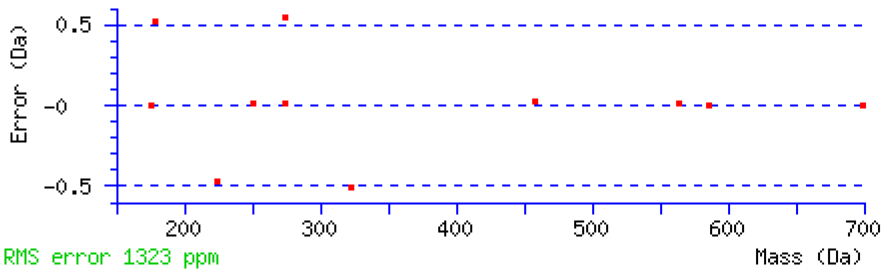
Match to Query 3274: 835.505208 from(418.759880,2+) rtinseconds(1402) index(6070)
Title: Locus:1.1.1.1940.6
Data file 2011-11-10 - TFD - EP 3-7.mgf

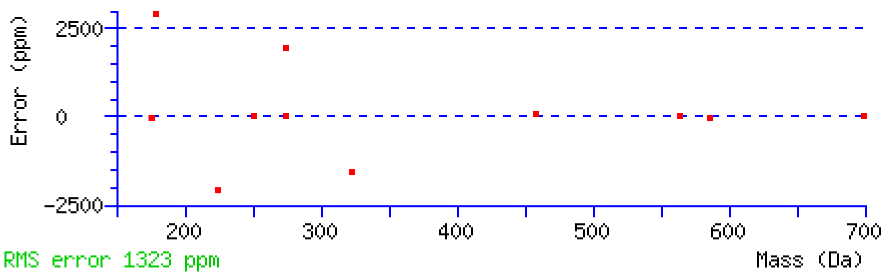
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 835.502808
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.00095
Matches : 11/56 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	138.066188	69.536732					**H**							7
2	**251.150252**	126.078764					**L**	***699.451185***	350.229231	682.424636	341.715956	681.440620	341.223948	6
3	379.245215	190.126245	362.218666	181.612971			**K**	***586.367121***	293.687199	569.340572	285.173924	568.356556	284.681916	5
4	466.277243	233.642259	449.250694	225.128985	448.266678	224.636977	**S**	***458.272158***	229.639717	441.245609	221.126443	440.261593	220.634435	4
5	**563.330007**	282.168642	546.303458	273.655367	545.319442	273.163359	**P**	371.240130	186.123703	354.213581	177.610429			3
6	662.398421	331.702849	645.371872	323.189574	644.387856	322.697566	**V**	***274.187366***	137.597321	257.160817	129.084047			2
7							**R**	***175.118952***	88.063114	158.092403	79.549840			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.8	835.502808	0.002400	HLKSPVR
28.8	835.502808	0.002400	HIKPVSR
26.1	835.502808	0.002400	HLQLAVR
6.6	835.502808	0.002400	HLPKLGR

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

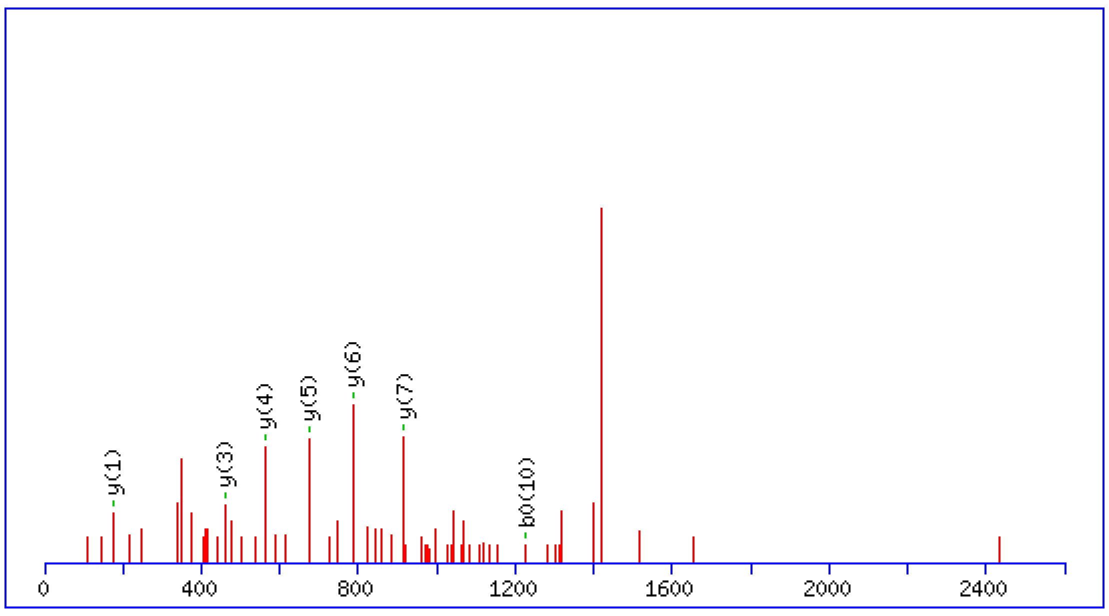
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GWYPKPLTVWR**
Found in **BT2A1_HUMAN**, Butyrophilin subfamily 2 member A1 OS=Homo sapiens GN=BTN2A1 PE=1 SV=3

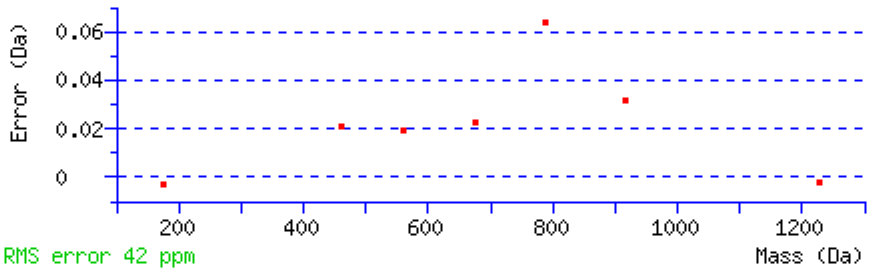
Match to Query 41830: 1417.763288 from(709.888920,2+) rtinseconds(3574) index(50480)
Title: Locus:1.1.1.2807.22
Data file 2011-11-14 - TFD - EP 7-2.mgf

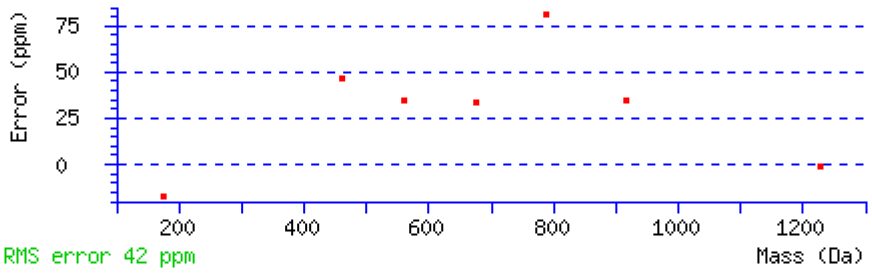
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1417.750656
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P6 : Oxidation (P)
Ions Score: 36 **Expect:** 0.0019
Matches : 7/92 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							11
2	244.108053	122.557665					W	1361.736470	681.371873	1344.709921	672.858599	1343.725905	672.366591	10
3	407.171382	204.089329					Y	1175.657157	588.332217	1158.630608	579.818942	1157.646592	579.326934	9
4	504.224146	252.615711					P	1012.593828	506.800552	995.567279	498.287278	994.583263	497.795270	8
5	632.319109	316.663193	615.292560	308.149918			K	***915.541064***	458.274170	898.514515	449.760896	897.530499	449.268888	7
6	745.366788	373.187032	728.340239	364.673758			P	***787.446101***	394.226689	770.419552	385.713414	769.435536	385.221406	6
7	858.450852	429.729064	841.424303	421.215790			L	***674.398422***	337.702849	657.371873	329.189575	656.387857	328.697567	5
8	959.498531	480.252904	942.471982	471.739629	941.487966	471.247621	T	***561.314358***	281.160817	544.287809	272.647543	543.303793	272.155535	4
9	1058.566945	529.787111	1041.540396	521.273836	1040.556380	520.781828	V	***460.266679***	230.636977	443.240130	222.123703			3
10	1244.646258	622.826767	1227.619709	614.313493	1226.635693	613.821485	W	361.198265	181.102770	344.171716	172.589496			2
11							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.9	1417.750656	0.012632	GWYPKPLTVWR
12.4	1417.750656	0.012632	GWYPKPLTVWR
4.7	1417.761215	0.002073	SLRLCPPHPTAR
4.7	1417.759872	0.003416	MAELQVRDLSLK
3.7	1417.767746	-0.004458	LYQRPGPGTAKAK
1.3	1417.767792	-0.004504	VAGATVGPGPVPAPGR
1.2	1417.756531	0.006757	WSETQNVVTKVK
0.1	1417.756516	0.006772	LVKYLDPNDLGR
0.1	1417.756531	0.006757	LPQKFDTLVGER

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

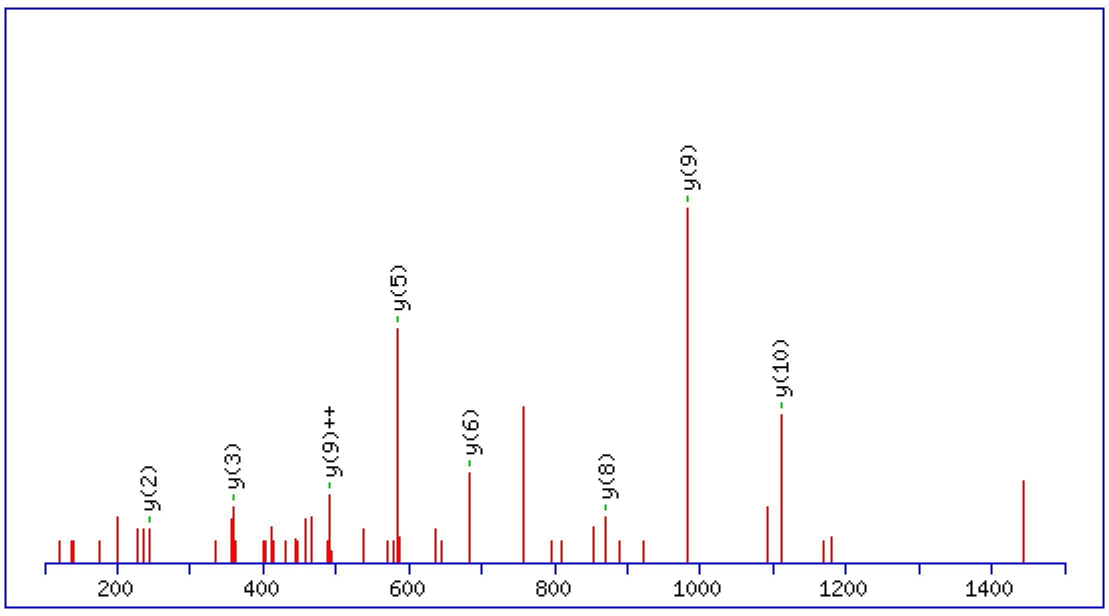
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALFKPADVILDPK**
Found in **BT3A1_HUMAN**, Butyrophilin subfamily 3 member A1 OS=Homo sapiens GN=BTN3A1 PE=2 SV=3

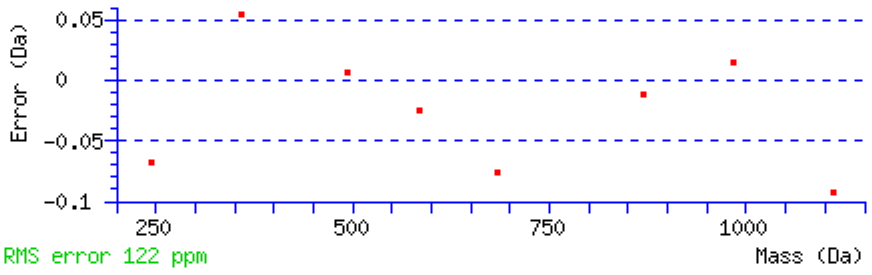
Match to Query 787091: 1441.819388 from(721.916970,2+) rtinseconds(2095) index(838085)
Title: Locus:1.1.1.1344.48
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

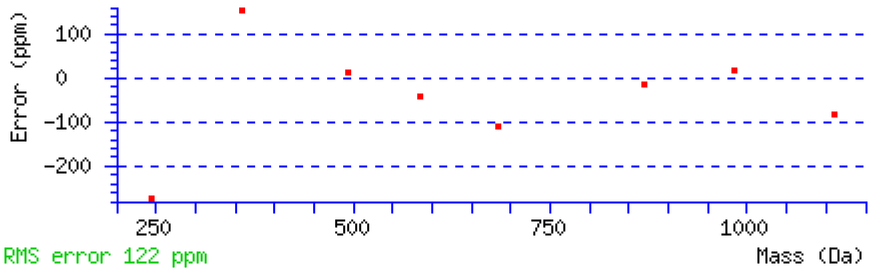
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1441.818054
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
P5 : Oxidation (P)
Ions Score: 53 **Expect:** 2.7e-005
Matches : 8/122 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					**A**							**13**
2	185.128454	93.067865					**L**	1371.788230	686.397753	1354.761681	677.884479	1353.777665	677.392471	**12**
3	332.196868	166.602072					**F**	1258.704166	629.855721	1241.677617	621.342447	1240.693601	620.850439	**11**
4	460.291831	230.649553	443.265282	222.136279			**K**	***1111.635752***	556.321514	1094.609203	547.808240	1093.625187	547.316232	**10**
5	573.339510	287.173393	556.312961	278.660119			**P**	***983.540789***	492.274033	966.514240	483.760758	965.530224	483.268750	**9**
6	644.376624	322.691950	627.350075	314.178676			**A**	***870.493110***	435.750193	853.466561	427.236919	852.482545	426.744911	**8**
7	759.403567	380.205422	742.377018	371.692147	741.393002	371.200139	**D**	799.455996	400.231636	782.429447	391.718362	781.445431	391.226354	**7**
8	858.471981	429.739628	841.445432	421.226354	840.461416	420.734346	**V**	***684.429053***	342.718165	667.402504	334.204890	666.418488	333.712882	**6**
9	971.556045	486.281660	954.529496	477.768386	953.545480	477.276378	**I**	***585.360639***	293.183958	568.334090	284.670683	567.350074	284.178675	**5**
10	1084.640109	542.823692	1067.613560	534.310418	1066.629544	533.818410	**L**	472.276575	236.641926	455.250026	228.128651	454.266010	227.636643	**4**
11	1199.667052	600.337164	1182.640503	591.823890	1181.656487	591.331882	**D**	***359.192511***	180.099894	342.165962	171.586619	341.181946	171.094611	**3**
12	1296.719816	648.863546	1279.693267	640.350272	1278.709251	639.858264	**P**	***244.165568***	122.586422	227.139019	114.073148			**2**
13							**K**	147.112804	74.060040	130.086255	65.546765			**1**





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
53.0	1441.818054	0.001334	ALFKPADVILDPK
10.8	1441.829285	-0.009897	PKPGVFDLINKAK
10.8	1441.829285	-0.009897	PKPGVFDLINKAK
8.1	1441.829285	-0.009897	NKHEFTILVTLK
4.9	1441.818054	0.001334	ALFKPADVILDPK
1.5	1441.819397	-0.000009	RLPTFWPSGLLR
0.1	1441.813995	0.005393	LKETLAQAQAELK

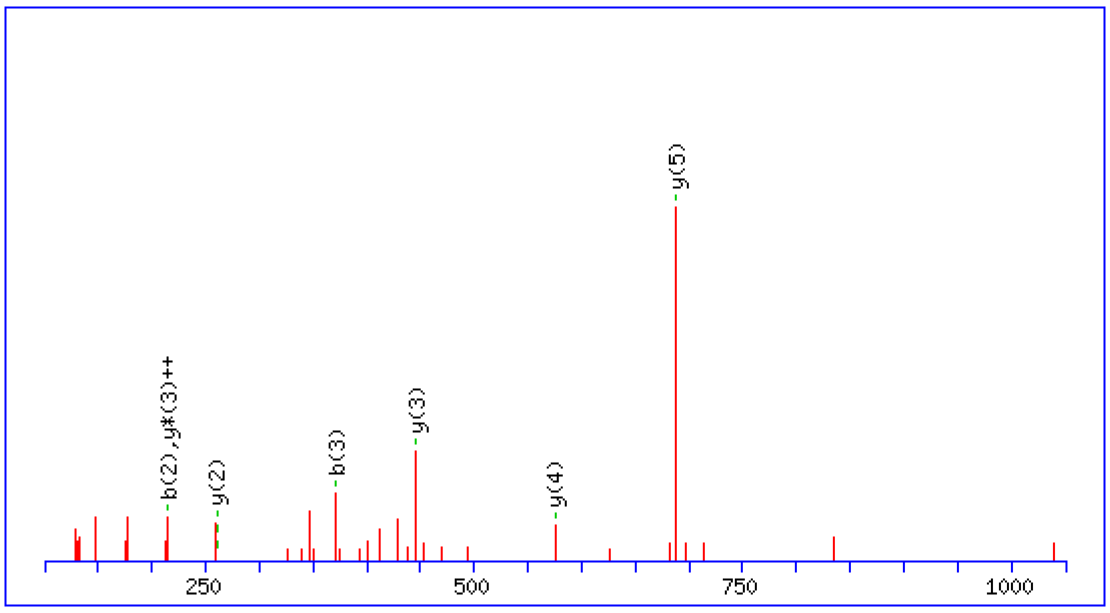
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TIRIEWLK**
Found in **CDHR1_HUMAN**, Cadherin-related family member 1 OS=Homo sapiens GN=CDHR1 PE=1 SV=2

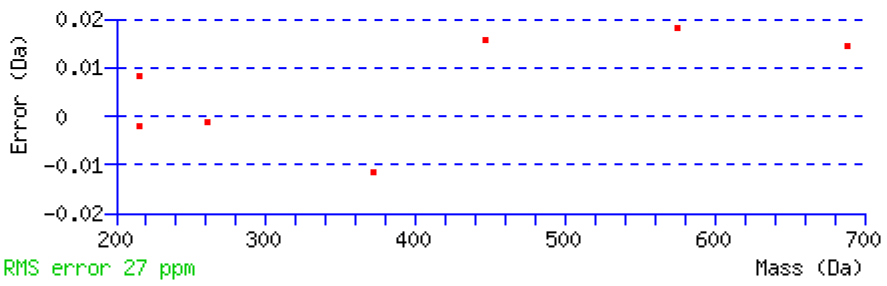
Match to Query 340333: 1057.636928 from(529.825740,2+) rtinseconds(1701) index(506215)
Title: Locus:1.1.1.978.28
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

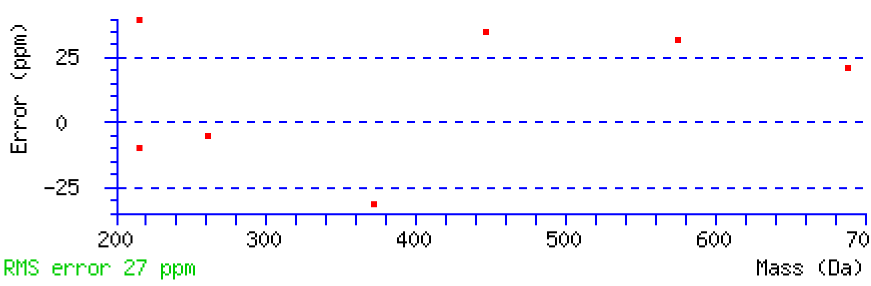
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1057.628387
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 34  Expect: 0.0012
Matches : 7/74 fragment ions using 8 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							8
2	**215.139019**	108.073147			197.128454	99.067865	I	957.588013	479.297645	940.561464	470.784370	939.577448	470.292362	7
3	**371.240130**	186.123703	354.213581	177.610428	353.229565	177.118420	R	844.503949	422.755613	827.477400	414.242338	826.493384	413.750330	6
4	484.324194	242.665735	467.297645	234.152460	466.313629	233.660452	I	***688.402838***	344.705057	671.376289	336.191783	670.392273	335.699775	5
5	613.366787	307.187032	596.340238	298.673757	595.356222	298.181749	E	***575.318774***	288.163025	558.292225	279.649751	557.308209	279.157743	4
6	799.446100	400.226688	782.419551	391.713414	781.435535	391.221406	W	***446.276181***	223.641728	429.249632	215.128454			3
7	912.530164	456.768720	895.503615	448.255446	894.519599	447.763438	L	***260.196868***	130.602072	243.170319	122.088797			2
8							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.7	1057.628387	0.008541	TIRIEWLK
7.0	1057.638290	-0.001362	EKITPLTLK
2.8	1057.628418	0.008510	VKSFLPVPR
2.0	1057.638275	-0.001347	LVKEIESLK
0.8	1057.638275	-0.001347	LKEVISLEK

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

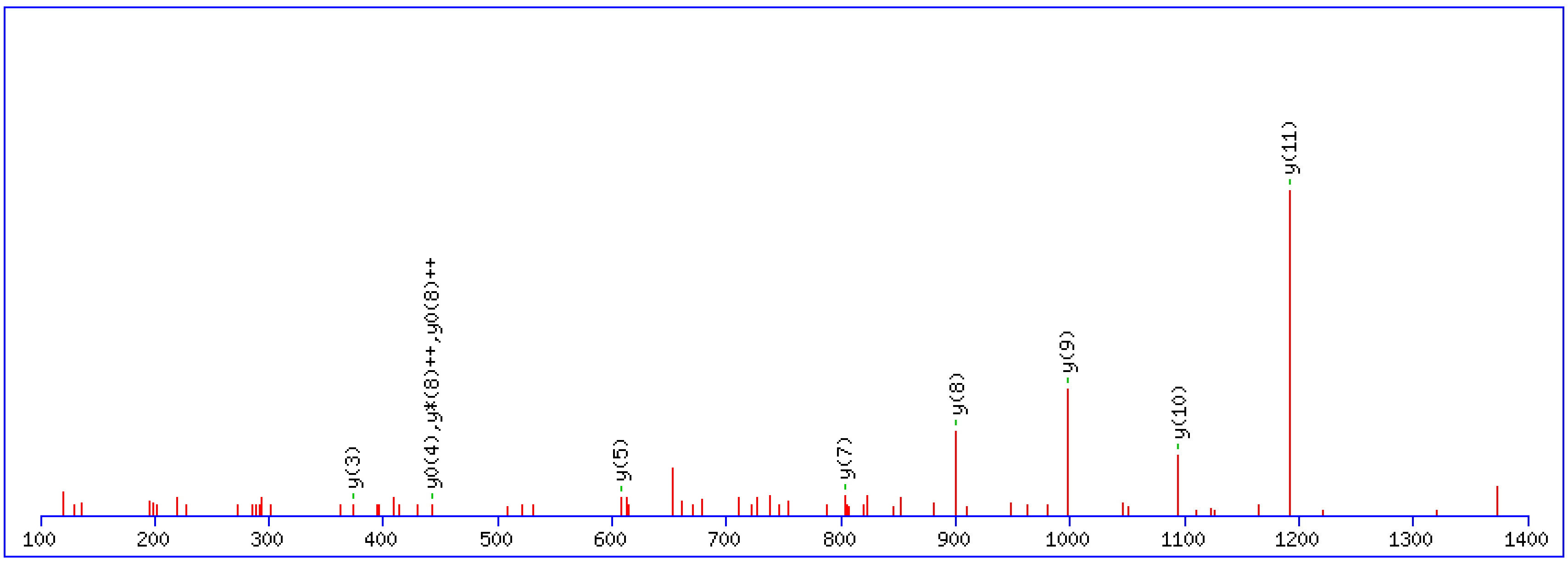
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VTPPPPPVFSLLK**
Found in **CLCA4_HUMAN**, Calcium-activated chloride channel regulator 4 OS=Homo sapiens GN=CLCA4 PE=1 SV=2

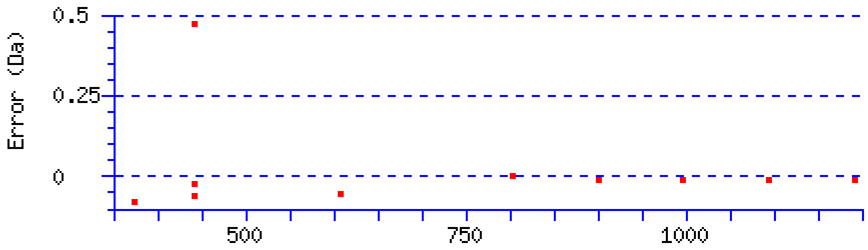
Match to Query 38141: 1390.809988 from(696.412270,2+) rtinseconds(3439) index(49639)
Title: Locus:1.1.1.1748.19
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 3.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●

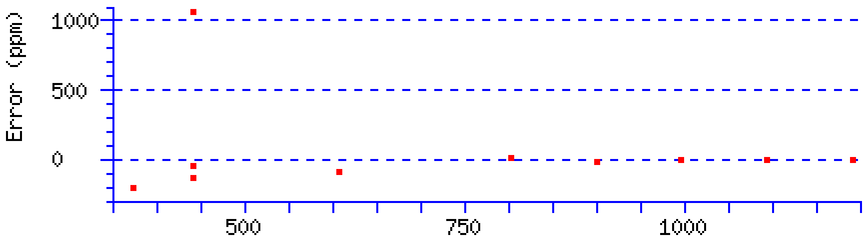


Monoisotopic mass of neutral peptide Mr(calc): 1390.822433
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.0014
Matches : 10/112 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483			V							13
2	201.123369	101.065322	183.112804	92.060040	T	1292.761287	646.884281	1275.734738	638.371007	1274.750722	637.878999	12
3	298.176133	149.591704	280.165568	140.586422	P	***1191.713608***	596.360442	1174.687059	587.847167	1173.703043	587.355159	11
4	395.228897	198.118087	377.218332	189.112804	P	***1094.660844***	547.834060	1077.634295	539.320785	1076.650279	538.828777	10
5	492.281661	246.644469	474.271096	237.639186	P	***997.608080***	499.307678	980.581531	490.794403	979.597515	490.302395	9
6	589.334425	295.170851	571.323860	286.165568	P	***900.555316***	450.781296	883.528767	442.268021	882.544751	441.776013	8
7	686.387189	343.697233	668.376624	334.691950	P	***803.502552***	402.254914	786.476003	393.741639	785.491987	393.249631	7
8	785.455603	393.231440	767.445038	384.226157	V	706.449788	353.728532	689.423239	345.215257	688.439223	344.723249	6
9	932.524017	466.765647	914.513452	457.760364	F	***607.381374***	304.194325	590.354825	295.681050	589.370809	295.189042	5
10	1019.556045	510.281661	1001.545480	501.276378	S	460.312960	230.660118	443.286411	222.146843	442.302395	221.654835	4
11	1132.640109	566.823692	1114.629544	557.818410	L	***373.280932***	187.144104	356.254383	178.630829			3
12	1245.724173	623.365724	1227.713608	614.360442	L	260.196868	130.602072	243.170319	122.088797			2
13					K	147.112804	74.060040	130.086255	65.546765			1



RMS error 346 ppm



RMS error 346 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.6	1390.822433	-0.012445	VTPPPPPVFSLLK
2.7	1390.815704	-0.005716	TRHLVLAGGSKPR

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

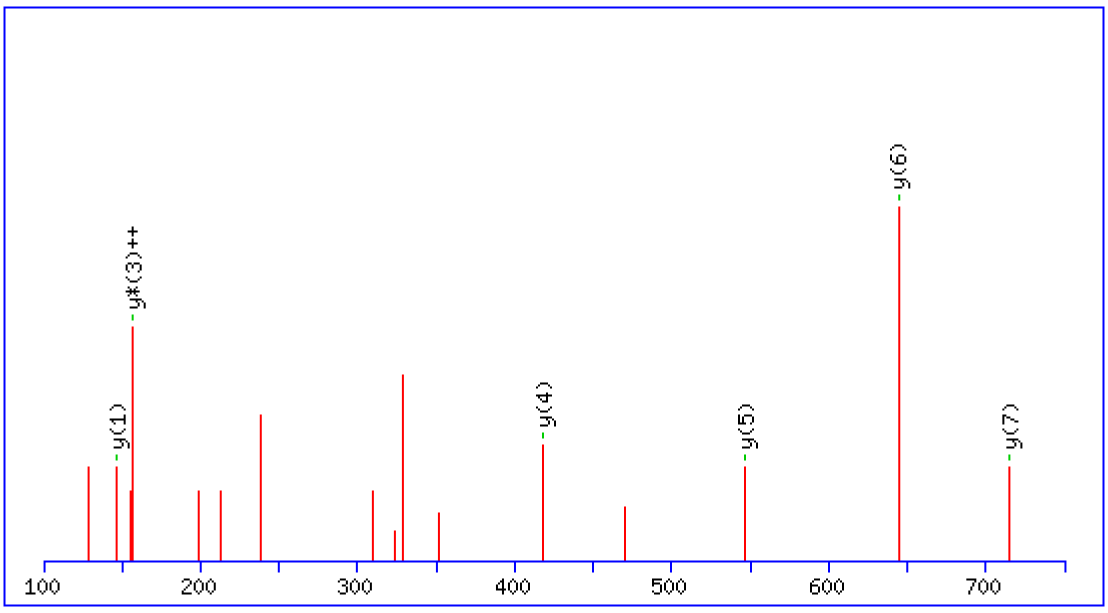
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IAPESAIK**
Found in **SCMC2_HUMAN**, Calcium-binding mitochondrial carrier protein SCaMC-2 OS=Homo sapiens GN=SLC25A25 PE=1 SV=1

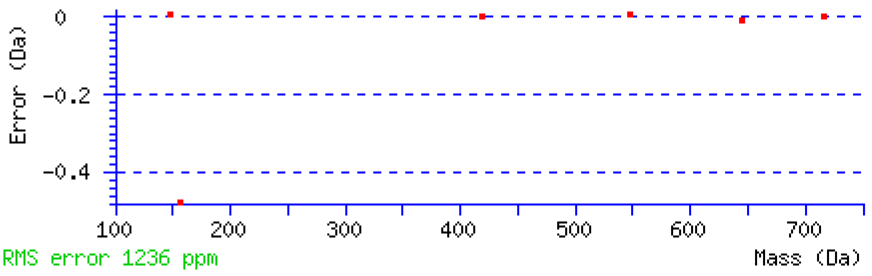
Match to Query 2457: 827.476948 from(414.745750,2+) rtinseconds(1064) index(4725)
Title: Locus:1.1.1.1748.6
Data file 2011-11-10 - TFD - EP 3-4.mgf

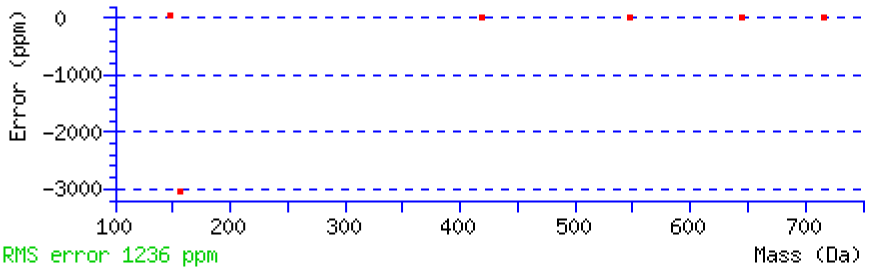
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 827.475235
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.0045
Matches : 6/58 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							8
2	185.128454	93.067865			A	***715.398481***	358.202879	698.371932	349.689604	697.387916	349.197596	7
3	282.181218	141.594247			P	***644.361367***	322.684322	627.334818	314.171047	626.350802	313.679039	6
4	411.223811	206.115544	393.213246	197.110261	E	***547.308603***	274.157940	530.282054	265.644665	529.298038	265.152657	5
5	498.255839	249.631557	480.245274	240.626275	S	***418.266010***	209.636643	401.239461	201.123368	400.255445	200.631360	4
6	569.292953	285.150115	551.282388	276.144832	A	331.233982	166.120629	314.207433	157.607354			3
7	682.377017	341.692147	664.366452	332.686864	I	260.196868	130.602072	243.170319	122.088798			2
8					K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.7	827.475235	0.001713	IAPESAIK
27.8	827.475250	0.001698	IAPETAVK
8.7	827.475266	0.001682	LPSGEVVK
6.7	827.475266	0.001682	IAIVPDGK
6.0	827.475266	0.001682	AIPGVVEK
5.2	827.475250	0.001698	LVPKDEK

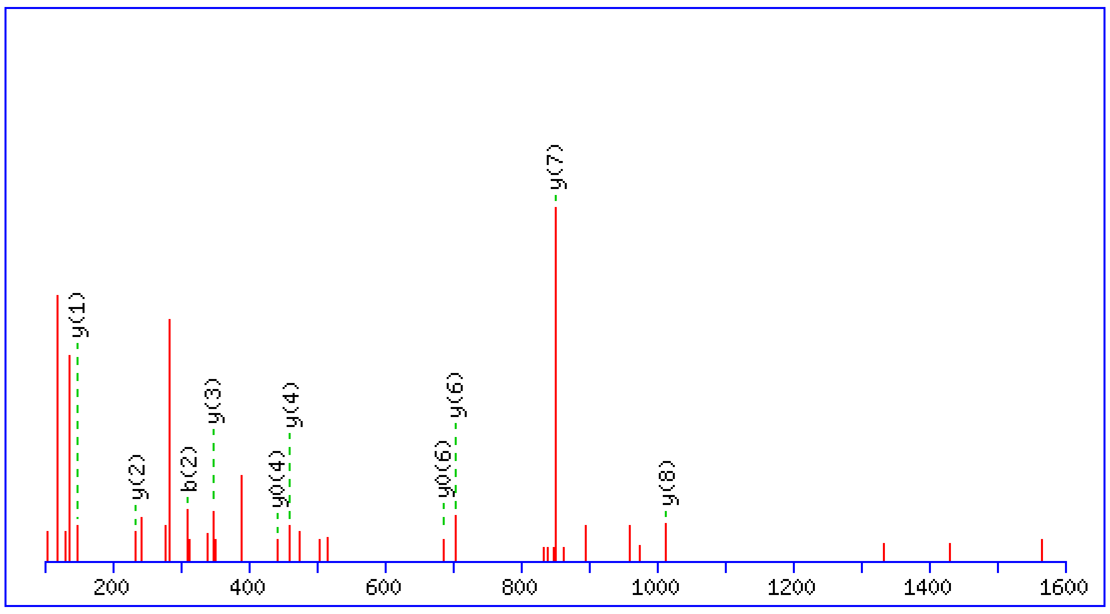
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FYFENLLSK**
Found in **KCC2G_HUMAN**, Calcium/calmodulin-dependent protein kinase type II subunit gamma OS=Homo sapiens GN=CAMK2G PE=1 SV=3

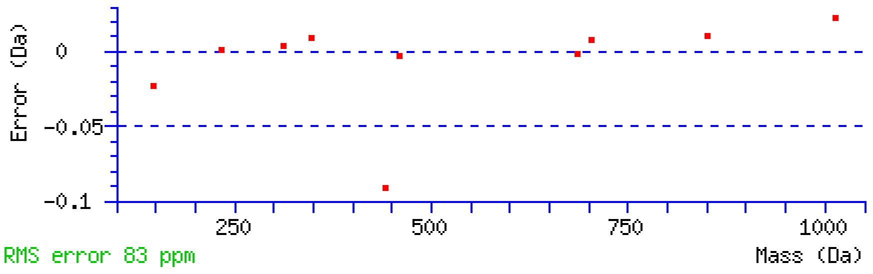
Match to Query 23789: 1159.600148 from(580.807350,2+) rtinseconds(3455) index(50951)
Title: Locus:1.1.1.2734.7
Data file 2011-11-10 - TFD - EP 3-3.mgf

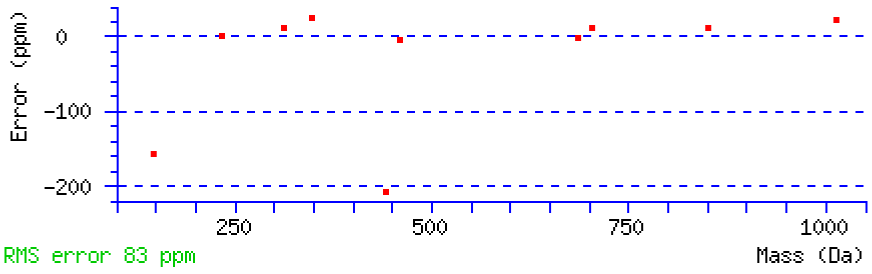
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1600] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1159.591339
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 31  Expect: 0.0068
Matches : 10/80 fragment ions using 28 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.075690	74.541483					**F**							9
2	311.139019	156.073148					**Y**	***1013.530223***	507.268750	996.503674	498.755475	995.519658	498.263467	8
3	458.207433	229.607354					**F**	***850.466894***	425.737085	833.440345	417.223811	832.456329	416.731803	7
4	587.250026	294.128651			569.239461	285.123369	**E**	***703.398480***	352.202878	686.371931	343.689604	685.387915	343.197596	6
5	701.292953	351.150115	684.266404	342.636840	683.282388	342.144832	**N**	574.355887	287.681582	557.329338	279.168307	556.345322	278.676299	5
6	814.377017	407.692147	797.350468	399.178872	796.366452	398.686864	**L**	***460.312960***	230.660118	443.286411	222.146843	442.302395	221.654835	4
7	927.461081	464.234179	910.434532	455.720904	909.450516	455.228896	**L**	***347.228896***	174.118086	330.202347	165.604811	329.218331	165.112803	3
8	1014.493109	507.750193	997.466560	499.236918	996.482544	498.744910	**S**	***234.144832***	117.576054	217.118283	109.062779	216.134267	108.570771	2
9							**K**	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.5	1159.591339	0.008809	FYFENLLSK
7.0	1159.598572	0.001576	KPNPPPPPPR
4.0	1159.598557	0.001591	WSSIPASKPR
1.3	1159.608429	-0.008281	NTEENLLSLK
1.3	1159.590714	0.009434	QKPSVTPPMK
0.6	1159.598557	0.001591	GPEATWRLSK

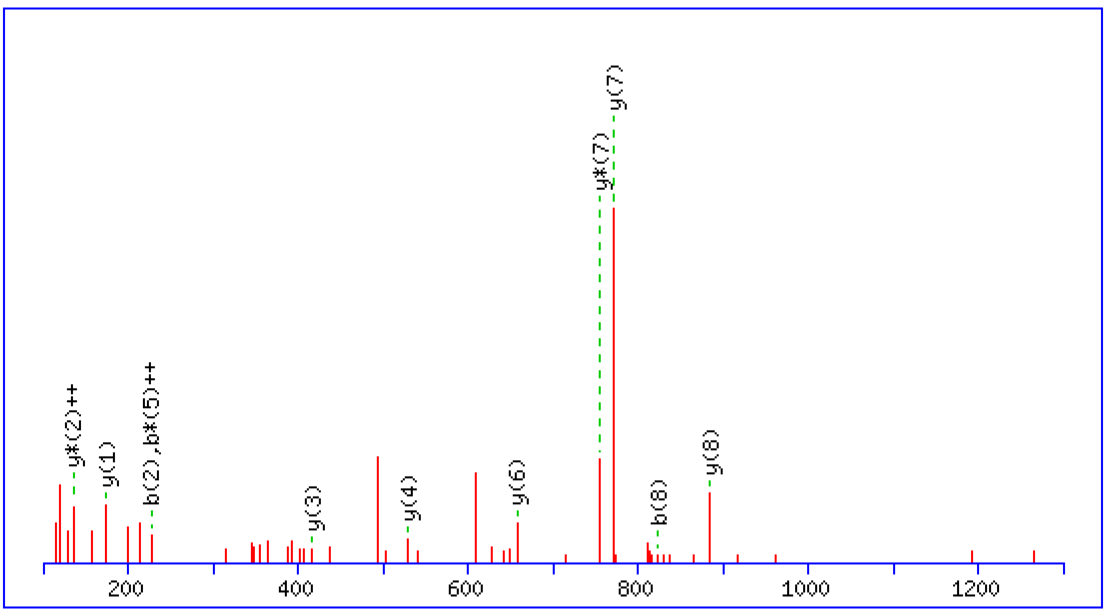
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LPNGALQNR**
Found in **CAMP2_HUMAN**, Calmodulin-regulated spectrin-associated protein 2 OS=Homo sapiens GN=CAMSAP2 PE=1 SV=3

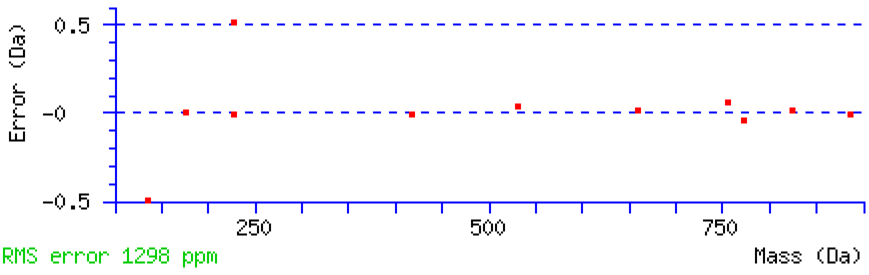
Match to Query 16135: 997.525368 from(499.769960,2+) rtinseconds(2480) index(31428)
Title: Locus:1.1.1.2384.11
Data file 2011-11-10 - TFD - EP 3-2.mgf

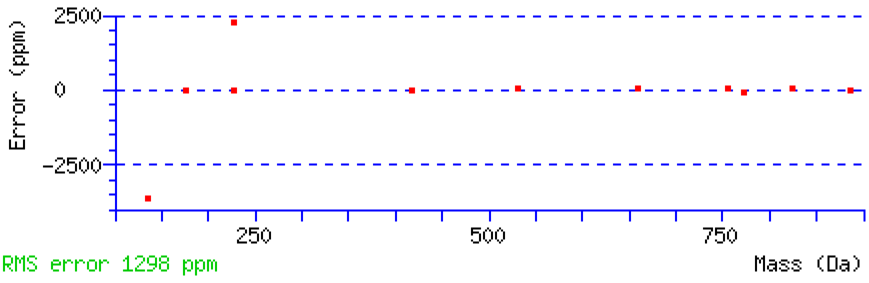
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 997.530472
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P2      : Oxidation (P)
Ions Score: 32  Expect: 0.007
Matches : 11/60 fragment ions using 26 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	114.091340	57.549308			L					9
2	**227.139019**	114.073147			P	***885.453705***	443.230491	868.427156	434.717216	8
3	341.181946	171.094611	324.155397	162.581336	N	***772.406026***	386.706651	755.379477	378.193377	7
4	398.203410	199.605343	381.176861	191.092068	G	***658.363099***	329.685188	641.336550	321.171913	6
5	469.240524	235.123900	452.213975	226.610626	A	601.341635	301.174456	584.315086	292.661181	5
6	582.324588	291.665932	565.298039	283.152658	L	***530.304521***	265.655899	513.277972	257.142624	4
7	710.383166	355.695221	693.356617	347.181947	Q	***417.220457***	209.113866	400.193908	200.600592	3
8	**824.426093**	412.716685	807.399544	404.203410	N	289.161879	145.084577	272.135330	136.571303	2
9					R	***175.118952***	88.063114	158.092403	79.549839	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.8	997.530472	-0.005104	LPNGALQNR
21.4	997.523270	0.002098	ILYDFTAR
13.8	997.519241	0.006127	LPENKPPR
13.2	997.530472	-0.005104	LPERNTPR
12.6	997.519257	0.006111	LLDQPSGPR
12.6	997.515396	0.009972	IYIDSLMK
12.6	997.534500	-0.009132	LPPANWLR
11.6	997.519257	0.006111	LLDQPSGPR
6.3	997.530487	-0.005119	LPPDTRQR
6.0	997.519241	0.006127	LTGPAAAEPR

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

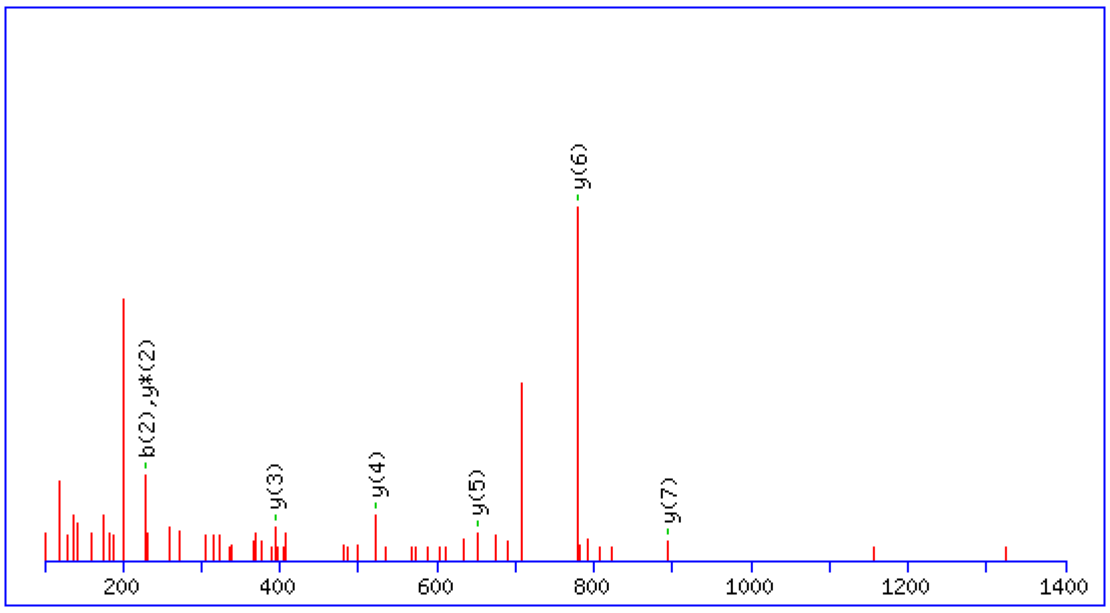
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LDQEEFAR**
Found in **CAN13_HUMAN**, Calpain-13 OS=Homo sapiens GN=CAPN13 PE=1 SV=2

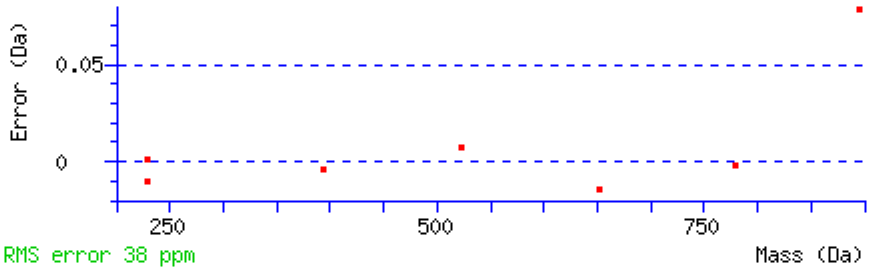
Match to Query 17079: 1006.474028 from(504.244290,2+) rtinseconds(2013) index(22690)
Title: Locus:1.1.1.2209.23
Data file 2011-11-10 - TFD - EP 3-2.mgf

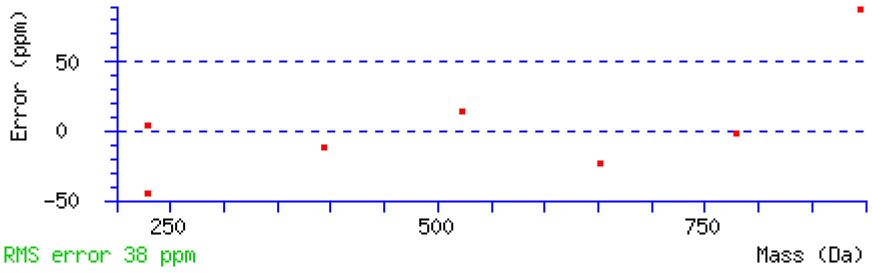
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1006.471954
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 39  Expect: 0.0014
Matches : 7/72 fragment ions using 8 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							8
2	229.118283	115.062779			211.107718	106.057497	D	***894.395187***	447.701232	877.368638	439.187957	876.384622	438.695949	7
3	357.176861	179.092068	340.150312	170.578794	339.166296	170.086786	Q	***779.368244***	390.187760	762.341695	381.674486	761.357679	381.182478	6
4	486.219454	243.613365	469.192905	235.100090	468.208889	234.608082	E	***651.309666***	326.158471	634.283117	317.645197	633.299101	317.153189	5
5	615.262047	308.134662	598.235498	299.621387	597.251482	299.129379	E	***522.267073***	261.637175	505.240524	253.123900	504.256508	252.631892	4
6	762.330461	381.668869	745.303912	373.155594	744.319896	372.663586	F	***393.224480***	197.115878	376.197931	188.602603			3
7	833.367575	417.187426	816.341026	408.674151	815.357010	408.182143	A	246.156066	123.581671	229.129517	115.068396			2
8							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.5	1006.471954	0.002074	LDQEEFAR
27.5	1006.471954	0.002074	DLAGEEAFR
2.2	1006.475311	-0.001283	EAATNNLMK
1.7	1006.475342	-0.001314	TGLQCETGK
1.2	1006.464096	0.009932	EVAEMDSVK
0.2	1006.471954	0.002074	IDPQYAER

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

{MATRIX SCIENCE}

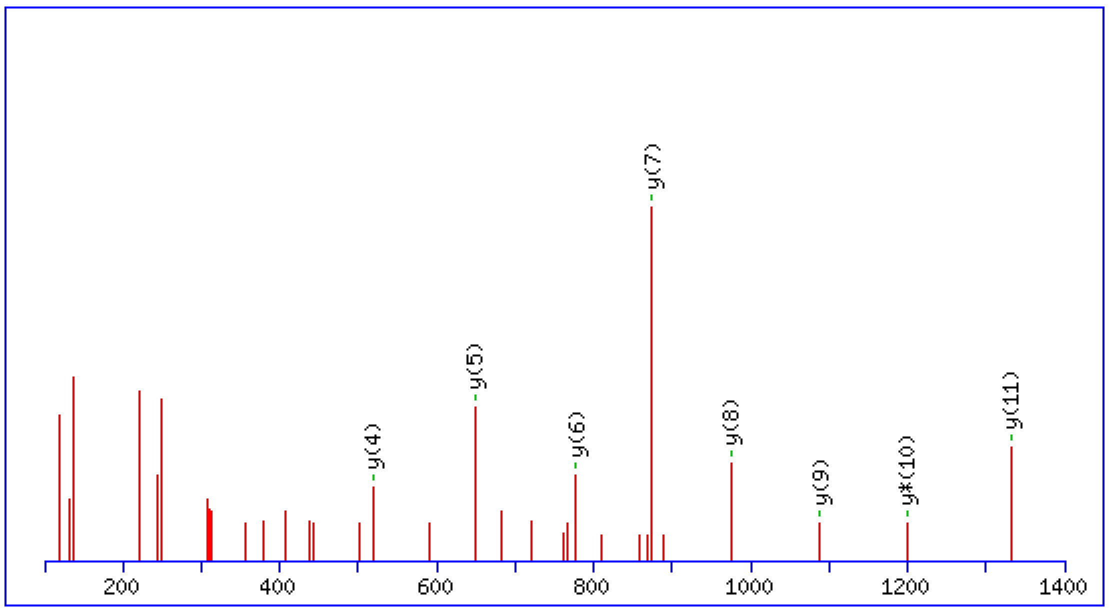
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TFDQLTPEESKER**
Found in **CALU_HUMAN**, Calumenin OS=Homo sapiens GN=CALU PE=1 SV=2

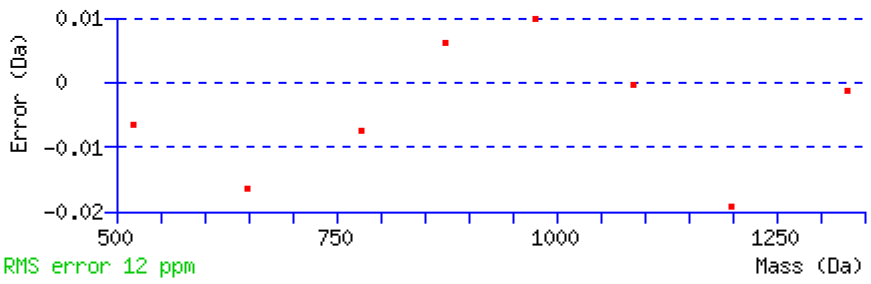
Match to Query 13397: 1578.757392 from(527.259740,3+) rtinseconds(1586) index(14845)
Title: Locus:1.1.1.2091.29
Data file 2011-11-10 - TFD - EP 4-3.mgf

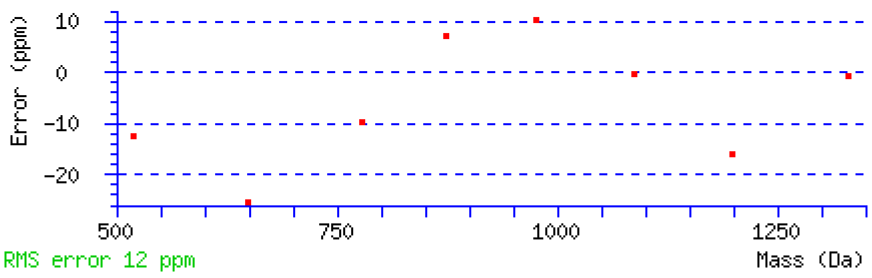
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1578.752548
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 50 **Expect:** 9.1e-005
Matches : 8/136 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							13
2	249.123369	125.065322			231.112804	116.060040	F	1478.712164	739.859720	1461.685615	731.346446	1460.701599	730.854438	12
3	364.150312	182.578794			346.139747	173.573512	D	***1331.643750***	666.325513	1314.617201	657.812239	1313.633185	657.320230	11
4	492.208890	246.608083	475.182341	238.094809	474.198325	237.602801	Q	1216.616807	608.812042	1199.590258	600.298767	1198.606242	599.806759	10
5	605.292954	303.150115	588.266405	294.636841	587.282389	294.144833	L	***1088.558229***	544.782753	1071.531680	536.269478	1070.547664	535.777470	9
6	706.340633	353.673955	689.314084	345.160680	688.330068	344.668672	T	***975.474165***	488.240721	958.447616	479.727446	957.463600	479.235438	8
7	803.393397	402.200337	786.366848	393.687062	785.382832	393.195054	P	***874.426486***	437.716881	857.399937	429.203607	856.415921	428.711599	7
8	932.435990	466.721633	915.409441	458.208359	914.425425	457.716351	E	***777.373722***	389.190499	760.347173	380.677225	759.363157	380.185217	6
9	1061.478583	531.242930	1044.452034	522.729655	1043.468018	522.237647	E	***648.331129***	324.669203	631.304580	316.155928	630.320564	315.663920	5
10	1148.510611	574.758944	1131.484062	566.245669	1130.500046	565.753661	S	***519.288536***	260.147906	502.261987	251.634632	501.277971	251.142624	4
11	1276.605574	638.806425	1259.579025	630.293151	1258.595009	629.801143	K	432.256508	216.631892	415.229959	208.118617	414.245943	207.626609	3
12	1405.648167	703.327722	1388.621618	694.814447	1387.637602	694.322439	E	304.161545	152.584410	287.134996	144.071136	286.150980	143.579128	2
13							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of TFDQLTPEESKER
(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	1578.752548	0.004844	TFDQLTPEESKER

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

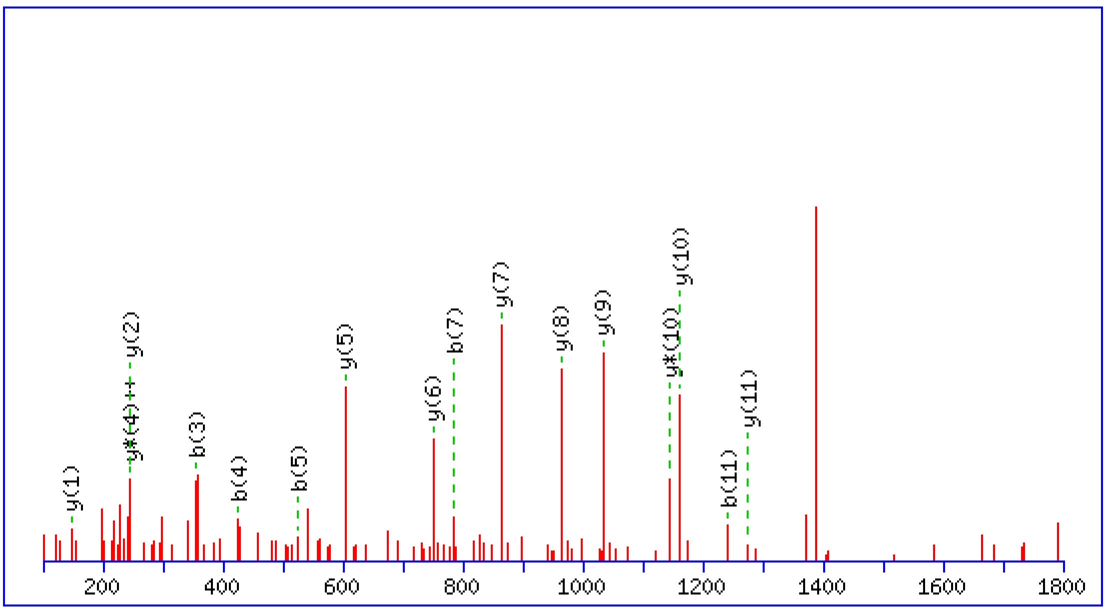
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILQAVNFPFLVK**
Found in **KAPCA_HUMAN**, cAMP-dependent protein kinase catalytic subunit alpha OS=Homo sapiens GN=PRKACA PE=1 SV=2

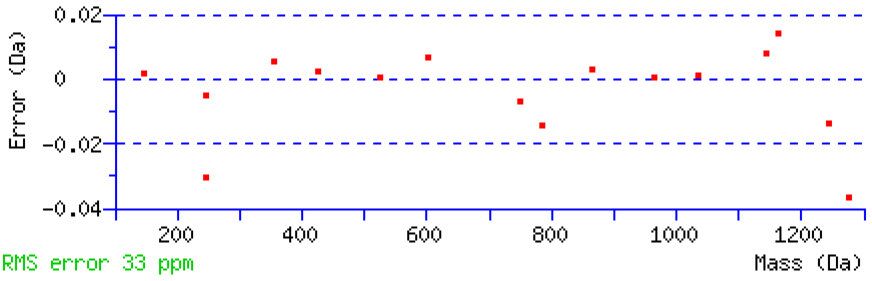
Match to Query 42388: 1387.825968 from(694.920260,2+) rtinseconds(3794) index(56417)
Title: Locus:1.1.1.2824.14
Data file 2011-11-14 - TFD - EP 8-4.mgf

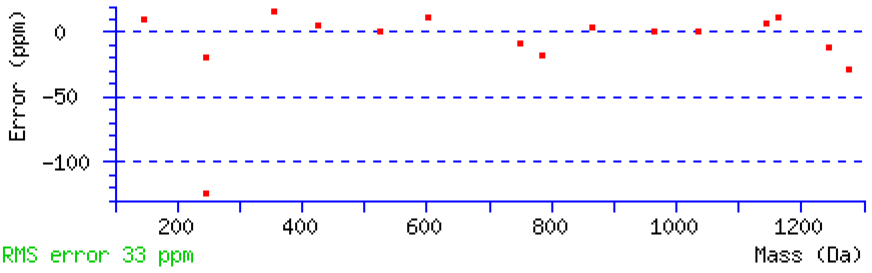
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1387.822754
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 71 **Expect:** 1.5e-007
Matches : 16/84 fragment ions using 25 most intense peaks (help)

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	114.091340	57.549308			I					12
2	227.175404	114.091340			L	*1275.745971*	638.376624	1258.719422	629.863349	11
3	**355.233982**	178.120629	338.207433	169.607355	Q	*1162.661907*	581.834591	1145.635358	573.321317	10
4	**426.271096**	213.639186	409.244547	205.125912	A	*1034.603329*	517.805303	1017.576780	509.292028	9
5	**525.339510**	263.173393	508.312961	254.660119	V	*963.566215*	482.286745	946.539666	473.773471	8
6	639.382437	320.194857	622.355888	311.681582	N	*864.497801*	432.752539	847.471252	424.239264	7
7	**786.450851**	393.729064	769.424302	385.215789	F	*750.454874*	375.731075	733.428325	367.217801	6
8	883.503615	442.255446	866.477066	433.742171	P	*603.386460*	302.196868	586.359911	293.683594	5
9	1030.572029	515.789652	1013.545480	507.276378	F	506.333696	253.670486	489.307147	245.157211	4
10	1143.656093	572.331684	1126.629544	563.818410	L	359.265282	180.136279	342.238733	171.623004	3
11	**1242.724507**	621.865891	1225.697958	613.352617	V	*246.181218*	123.594247	229.154669	115.080973	2
12					K	*147.112804*	74.060040	130.086255	65.546765	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
71.1	1387.822754	0.003214	ILQAVNFPFLVK
2.9	1387.818726	0.007242	KPSLLAHPGPLVK

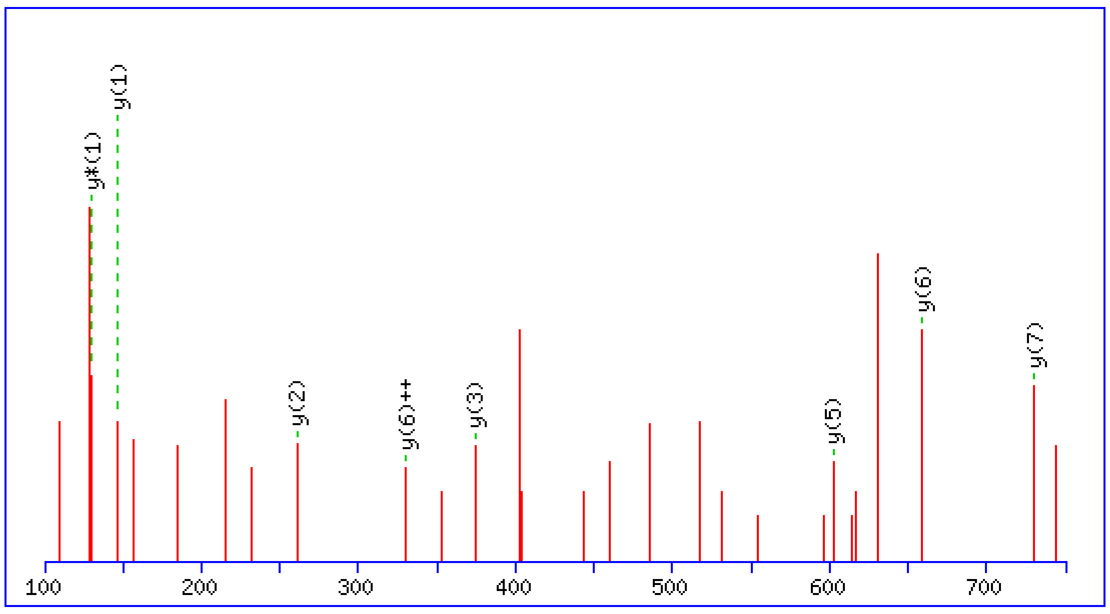
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LAGLDINK**
Found in **IPKA_HUMAN**, cAMP-dependent protein kinase inhibitor alpha OS=Homo sapiens GN=PKIA PE=1 SV=2

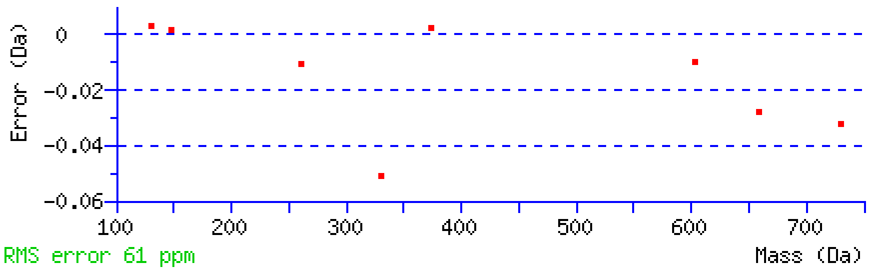
Match to Query 3098: 842.484808 from(422.249680,2+) rtinseconds(1177) index(7315)
Title: Locus:1.1.1.1861.10
Data file 2011-11-10 - TFD - EP 3-3.mgf

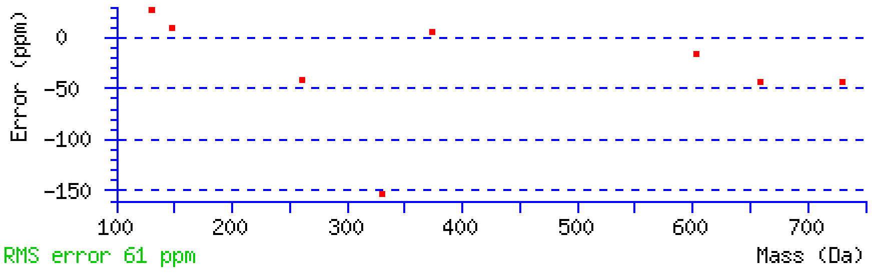
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 842.486145
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.0044
Matches : 8/58 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					L							8
2	185.128454	93.067865					A	***730.409380***	365.708328	713.382831	357.195054	712.398815	356.703046	7
3	242.149918	121.578597					G	***659.372266***	330.189771	642.345717	321.676497	641.361701	321.184489	6
4	355.233982	178.120629					L	***602.350802***	301.679039	585.324253	293.165765	584.340237	292.673757	5
5	470.260925	235.634100			452.250360	226.628818	D	489.266738	245.137007	472.240189	236.623732	471.256173	236.131724	4
6	583.344989	292.176133			565.334424	283.170850	I	***374.239795***	187.623535	357.213246	179.110261			3
7	697.387916	349.197596	680.361367	340.684322	679.377351	340.192314	N	***261.155731***	131.081503	244.129182	122.568229			2
8							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of LAGLDINK
(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	842.486145	-0.001337	LAGLDINK
22.1	842.486160	-0.001352	VIEQLGGK
22.1	842.486145	-0.001337	VLQELNK
10.6	842.486145	-0.001337	QLIDINK
10.0	842.486130	-0.001322	LAAIAQEK
10.0	842.486145	-0.001337	ALLDGLNK
9.7	842.486130	-0.001322	LKEAPAAK
9.7	842.486130	-0.001322	LQEALAAK
8.9	842.486130	-0.001322	LLLENNK
8.0	842.486145	-0.001337	LQTPKEK

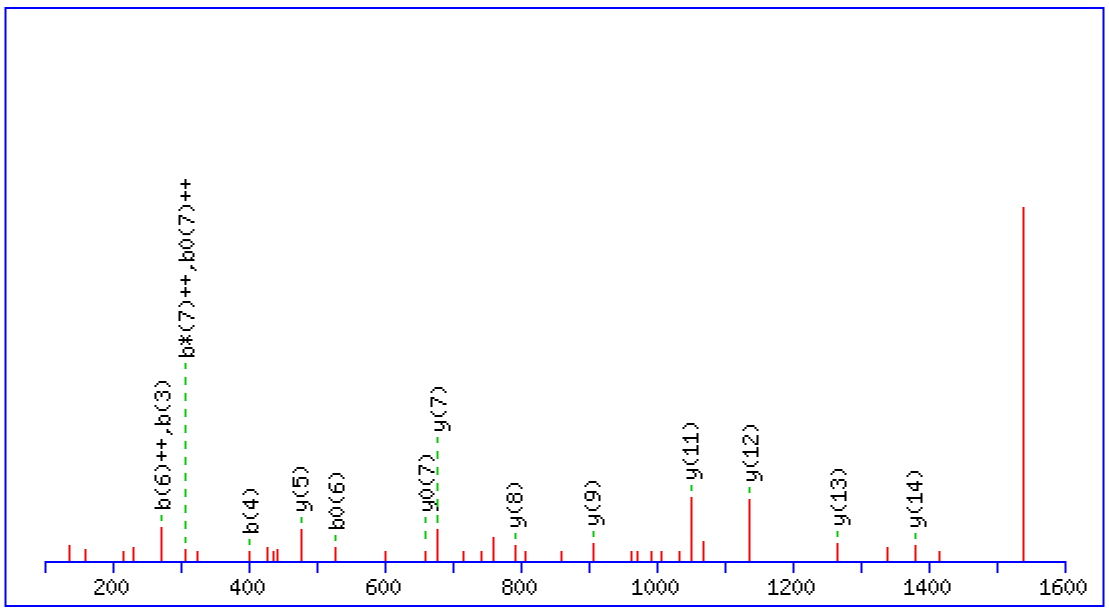
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TGNESGSNLSDSGSVK**
Found in **CLIP2_HUMAN**, CAP-Gly domain-containing linker protein 2 OS=Homo sapiens GN=CLIP2 PE=1 SV=1

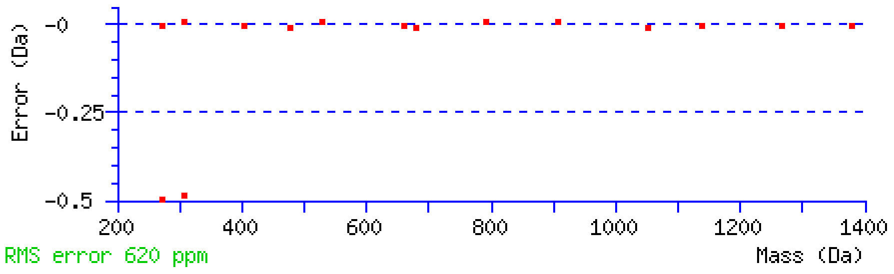
Match to Query 867072: 1537.693528 from(769.854040,2+) rtinseconds(1073) index(159290)
Title: Locus:1.1.1.1093.30
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

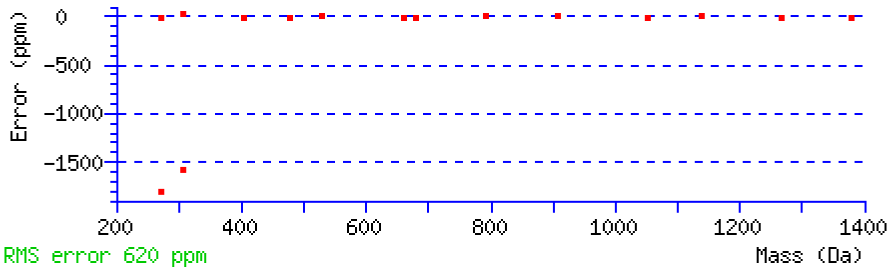
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1537.685608
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 54  Expect: 3.6e-005
Matches : 15/172 fragment ions using 22 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							16
2	159.076419	80.041847			141.065854	71.036565	G	1437.645204	719.326240	1420.618655	710.812966	1419.634639	710.320958	15
3	**273.119346**	137.063311	256.092797	128.550037	255.108781	128.058029	N	***1380.623740***	690.815508	1363.597191	682.302234	1362.613175	681.810226	14
4	**402.161939**	201.584608	385.135390	193.071333	384.151374	192.579325	E	***1266.580813***	633.794045	1249.554264	625.280770	1248.570248	624.788762	13
5	489.193967	245.100621	472.167418	236.587347	471.183402	236.095339	S	***1137.538220***	569.272748	1120.511671	560.759474	1119.527655	560.267466	12
6	546.215431	273.611354	529.188882	265.098079	528.204866	264.606071	G	***1050.506192***	525.756734	1033.479643	517.243460	1032.495627	516.751452	11
7	633.247459	317.127368	616.220910	308.614093	615.236894	308.122085	S	993.484728	497.246002	976.458179	488.732728	975.474163	488.240720	10
8	747.290386	374.148831	730.263837	365.635557	729.279821	365.143549	N	***906.452700***	453.729988	889.426151	445.216714	888.442135	444.724706	9
9	860.374450	430.690863	843.347901	422.177589	842.363885	421.685581	L	***792.409773***	396.708525	775.383224	388.195250	774.399208	387.703242	8
10	947.406478	474.206877	930.379929	465.693603	929.395913	465.201595	S	***679.325709***	340.166493	662.299160	331.653218	661.315144	331.161210	7
11	1062.433421	531.720349	1045.406872	523.207074	1044.422856	522.715066	D	592.293681	296.650479	575.267132	288.137204	574.283116	287.645196	6
12	1149.465449	575.236363	1132.438900	566.723088	1131.454884	566.231080	S	***477.266738***	239.137007	460.240189	230.623733	459.256173	230.131725	5
13	1206.486913	603.747095	1189.460364	595.233820	1188.476348	594.741812	G	390.234710	195.620993	373.208161	187.107719	372.224145	186.615711	4
14	1293.518941	647.263109	1276.492392	638.749834	1275.508376	638.257826	S	333.213246	167.110261	316.186697	158.596987	315.202681	158.104979	3
15	1392.587355	696.797316	1375.560806	688.284041	1374.576790	687.792033	V	246.181218	123.594247	229.154669	115.080973			2
16							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.2	1537.685608	0.007920	TGNESGSNLSDSGSVK

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

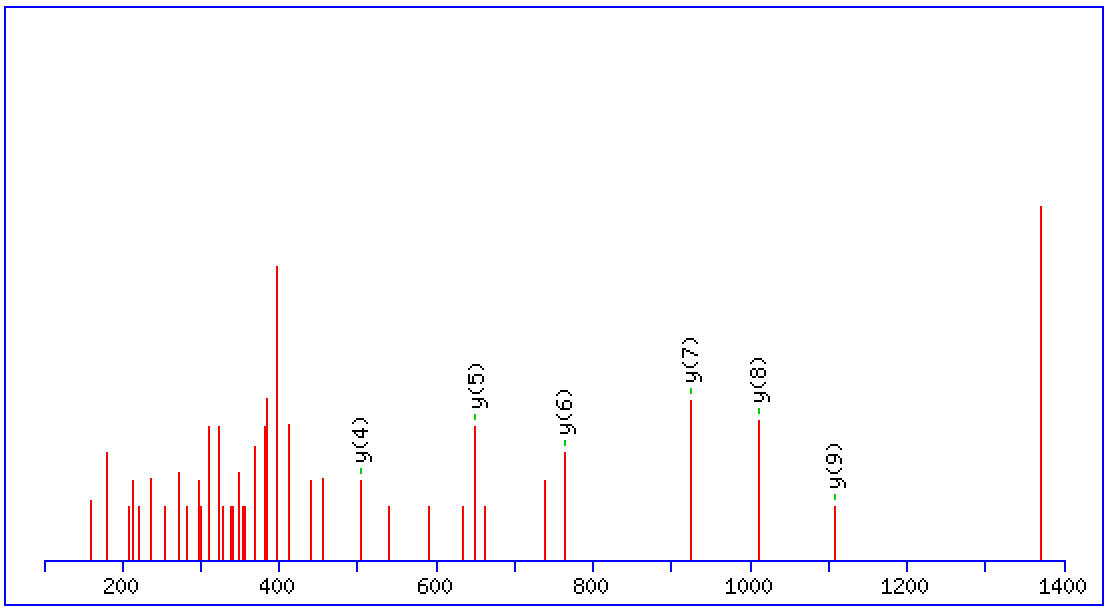
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FDPSCLFPACR**
Found in **CAH3_HUMAN**, Carbonic anhydrase 3 OS=Homo sapiens GN=CA3 PE=1 SV=3

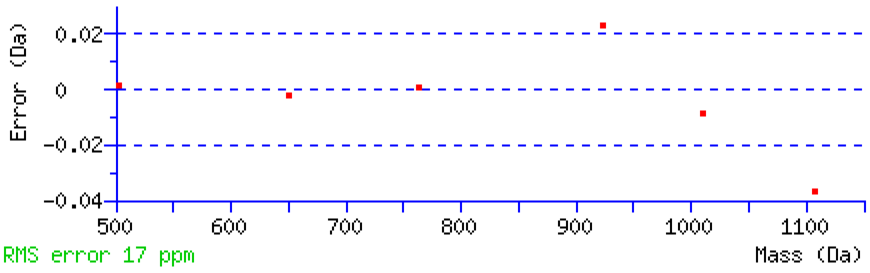
Match to Query 714854: 1368.592568 from(685.303560,2+) rtinseconds(3223) index(1013030)
Title: Locus:1.1.1.1722.32
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●

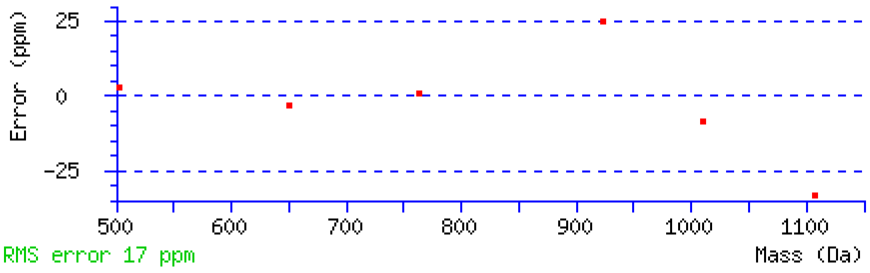


Monoisotopic mass of neutral peptide Mr(calc): 1368.595490
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 38 **Expect:** 0.00086
Matches : 6/84 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.075690	74.541483			**F**							**11**
2	263.102633	132.054954	245.092068	123.049672	**D**	1222.534341	611.770809	1205.507792	603.257534	1204.523776	602.765526	**10**
3	360.155397	180.581336	342.144832	171.576054	**P**	***1107.507398***	554.257337	1090.480849	545.744063	1089.496833	545.252055	**9**
4	447.187425	224.097350	429.176860	215.092068	**S**	***1010.454634***	505.730955	993.428085	497.217681	992.444069	496.725673	**8**
5	607.218074	304.112675	589.207509	295.107393	**C**	***923.422606***	462.214941	906.396057	453.701667			**7**
6	720.302138	360.654707	702.291573	351.649425	**L**	***763.391957***	382.199617	746.365408	373.686342			**6**
7	867.370552	434.188914	849.359987	425.183631	**F**	***650.307893***	325.657585	633.281344	317.144310			**5**
8	964.423316	482.715296	946.412751	473.710014	**P**	***503.239479***	252.123378	486.212930	243.610103			**4**
9	1035.460430	518.233853	1017.449865	509.228571	**A**	406.186715	203.596996	389.160166	195.083721			**3**
10	1195.491079	598.249178	1177.480514	589.243895	**C**	335.149601	168.078438	318.123052	159.565164			**2**
11					**R**	175.118952	88.063114	158.092403	79.549839			**1**



RMS error 17 ppm



RMS error 17 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.8	1368.595490	-0.002922	FDPSCLFPACR

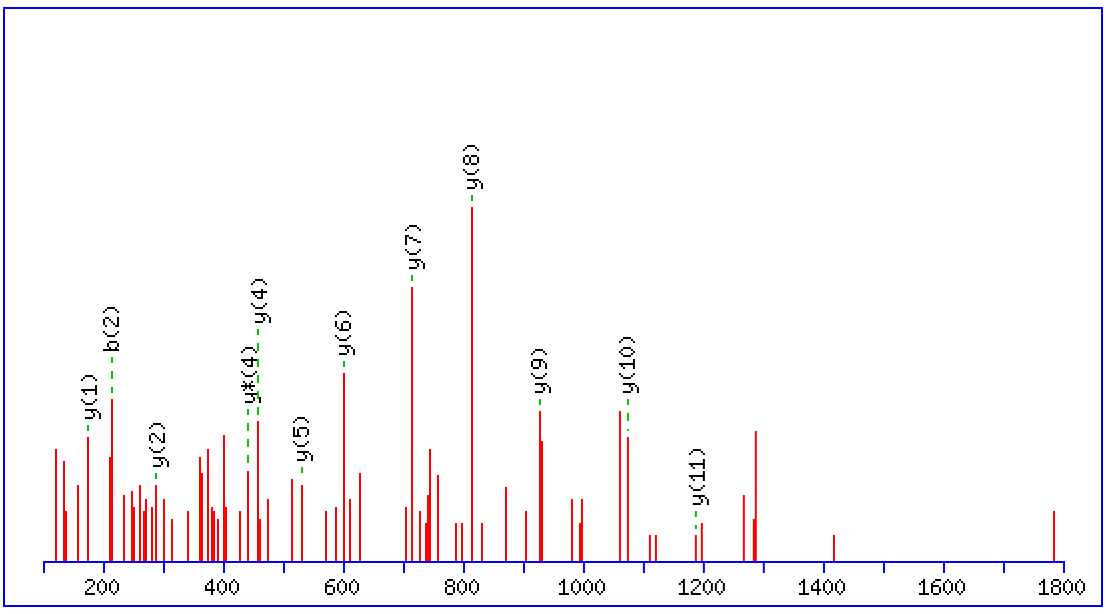
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VNFLVNAAGINR**
Found in **CBR4_HUMAN**, Carbonyl reductase family member 4 OS=Homo sapiens GN=CBR4 PE=1 SV=3

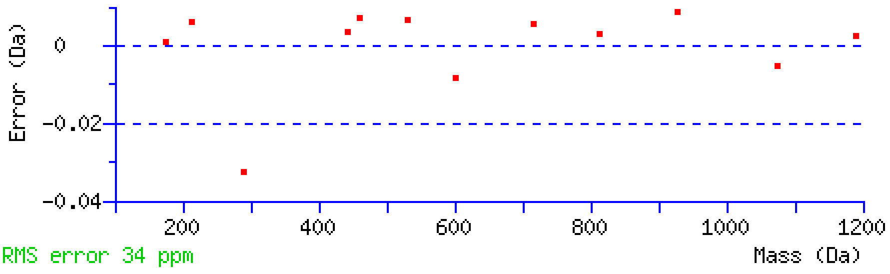
Match to Query 35990: 1286.713048 from(644.363800,2+) rtinseconds(2781) index(36066)
Title: Locus:1.1.1.2379.27
Data file 2011-11-14 - TFD - EP 8-5.mgf

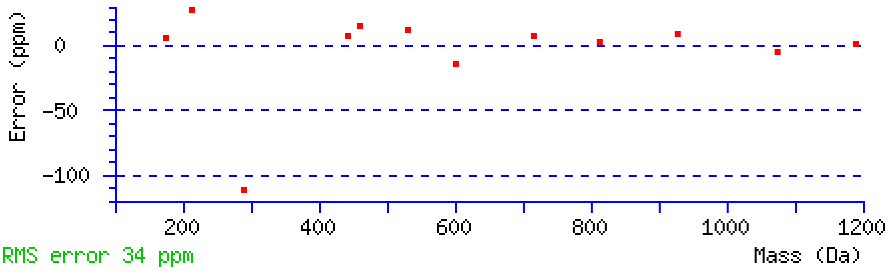
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1286.709503
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 70 **Expect:** 6.7e-007
Matches : 12/86 fragment ions using 24 most intense peaks (help)

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	100.075690	50.541483			V					12
2	214.118617	107.562947	197.092068	99.049672	N	***1188.648381***	594.827829	1171.621832	586.314554	11
3	361.187031	181.097153	344.160482	172.583879	F	***1074.605454***	537.806365	1057.578905	529.293091	10
4	474.271095	237.639186	457.244546	229.125911	L	***927.537040***	464.272158	910.510491	455.758884	9
5	573.339509	287.173393	556.312960	278.660118	V	***814.452976***	407.730126	797.426427	399.216852	8
6	687.382436	344.194856	670.355887	335.681581	N	***715.384562***	358.195919	698.358013	349.682645	7
7	758.419550	379.713413	741.393001	371.200138	A	***601.341635***	301.174456	584.315086	292.661181	6
8	829.456664	415.231970	812.430115	406.718695	A	***530.304521***	265.655899	513.277972	257.142624	5
9	886.478128	443.742702	869.451579	435.229427	G	***459.267407***	230.137342	442.240858	221.624067	4
10	999.562192	500.284734	982.535643	491.771459	I	402.245943	201.626610	385.219394	193.113335	3
11	1113.605119	557.306198	1096.578570	548.792923	N	***289.161879***	145.084577	272.135330	136.571303	2
12					R	***175.118952***	88.063114	158.092403	79.549839	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
70.1	1286.709503	0.003545	VNFLVNAAGINR
4.2	1286.709488	0.003560	VAAELWRSLSR
2.5	1286.723434	-0.010386	LPPVLTFELSR
2.3	1286.712875	0.000173	VGGDSMLARLLR

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

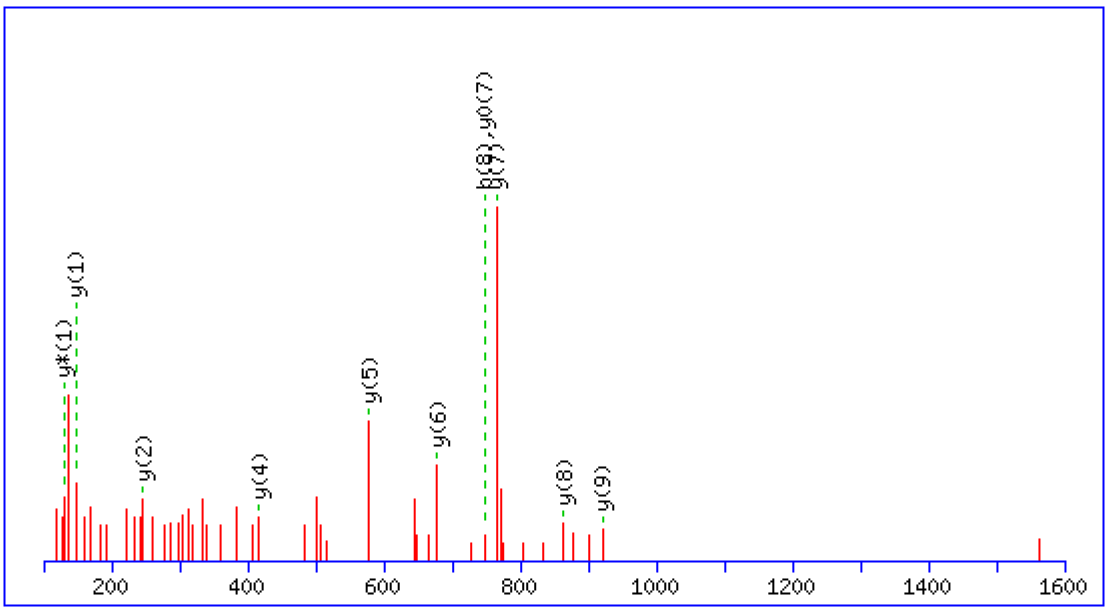
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AGVSVYGIVK**
Found in **CMBL_HUMAN**, Carboxymethylenebutenolidase homolog OS=Homo sapiens GN=CMBL PE=1 SV=1

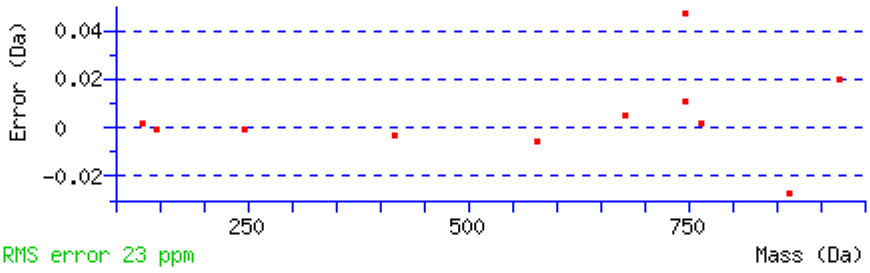
Match to Query 15195: 991.570148 from(496.792350,2+) rtinseconds(2304) index(27124)
Title: Locus:1.1.1.2169.12
Data file 2011-11-12 - TFD - EP 6-5.mgf

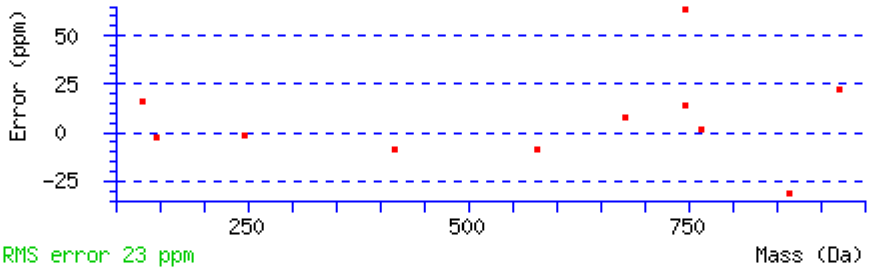
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 991.570236
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 50 **Expect:** 3.9e-005
Matches : 11/72 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			A							10
2	129.065854	65.036565			G	***921.540395***	461.273836	904.513846	452.760561	903.529830	452.268553	9
3	228.134268	114.570772			V	***864.518931***	432.763104	847.492382	424.249829	846.508366	423.757821	8
4	315.166296	158.086786	297.155731	149.081504	S	***765.450517***	383.228897	748.423968	374.715622	747.439952	374.223614	7
5	414.234710	207.620993	396.224145	198.615711	V	***678.418489***	339.712883	661.391940	331.199608			6
6	577.298039	289.152658	559.287474	280.147375	Y	***579.350075***	290.178676	562.323526	281.665401			5
7	634.319503	317.663390	616.308938	308.658107	G	***416.286746***	208.647011	399.260197	200.133737			4
8	747.403567	374.205422	729.393002	365.200139	I	359.265282	180.136279	342.238733	171.623004			3
9	846.471981	423.739629	828.461416	414.734346	V	***246.181218***	123.594247	229.154669	115.080972			2
10					K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
50.1	991.570236	-0.000088	AGVSVYGIVK
3.0	991.570221	-0.000073	APISFSKVK
2.9	991.570221	-0.000073	QSASFILVK
1.3	991.570206	-0.000058	KLINDYVK

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

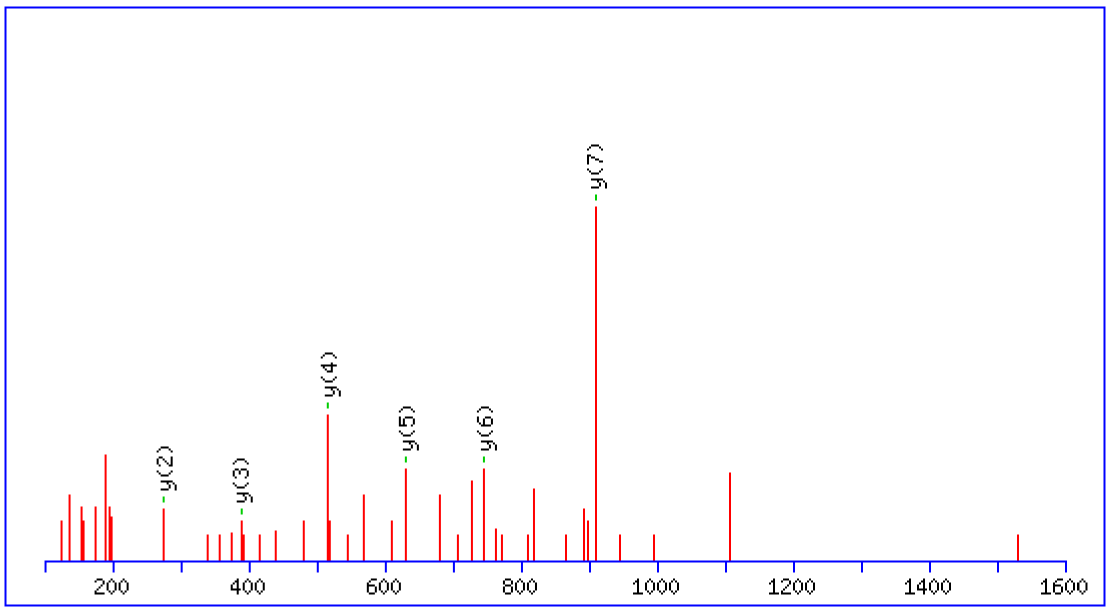
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SEYNDQLTR**
Found in **CPT2_HUMAN**, Carnitine O-palmitoyltransferase 2, mitochondrial OS=Homo sapiens GN=CPT2 PE=1 SV=2

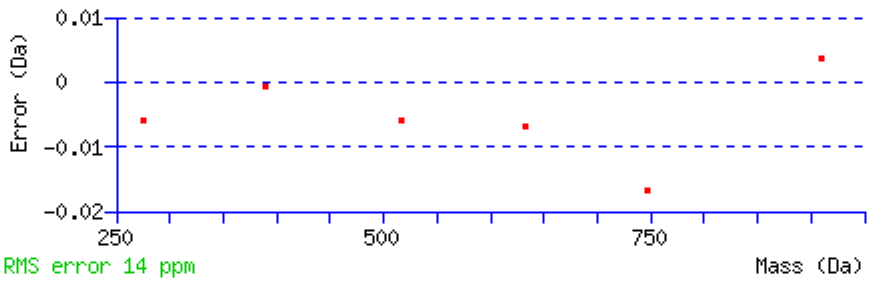
Match to Query 424975: 1124.510008 from(563.262280,2+) rtinseconds(1304) index(416830)
Title: Locus:1.1.1.834.32
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

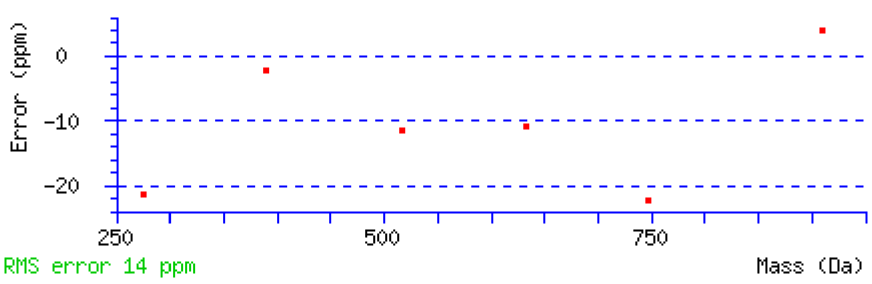
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1124.509796
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 47  Expect: 0.00014
Matches : 6/88 fragment ions using 10 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							9
2	217.081897	109.044586			199.071332	100.039304	E	1038.485065	519.746171	1021.458516	511.232896	1020.474500	510.740888	8
3	380.145226	190.576251			362.134661	181.570969	Y	***909.442472***	455.224874	892.415923	446.711600	891.431907	446.219592	7
4	494.188153	247.597715	477.161604	239.084440	476.177588	238.592432	N	***746.379143***	373.693210	729.352594	365.179935	728.368578	364.687927	6
5	609.215096	305.111186	592.188547	296.597912	591.204531	296.105904	D	***632.336216***	316.671746	615.309667	308.158472	614.325651	307.666464	5
6	737.273674	369.140475	720.247125	360.627201	719.263109	360.135193	Q	***517.309273***	259.158275	500.282724	250.645000	499.298708	250.152992	4
7	850.357738	425.682507	833.331189	417.169233	832.347173	416.677225	L	***389.250695***	195.128985	372.224146	186.615711	371.240130	186.123703	3
8	951.405417	476.206347	934.378868	467.693072	933.394852	467.201064	T	***276.166631***	138.586953	259.140082	130.073679	258.156066	129.581671	2
9							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.9	1124.509796	0.000212	SEYNDQLTR
5.6	1124.506653	0.003355	SCQISCKSR
2.9	1124.513168	-0.003160	RSPSASSLSSM

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

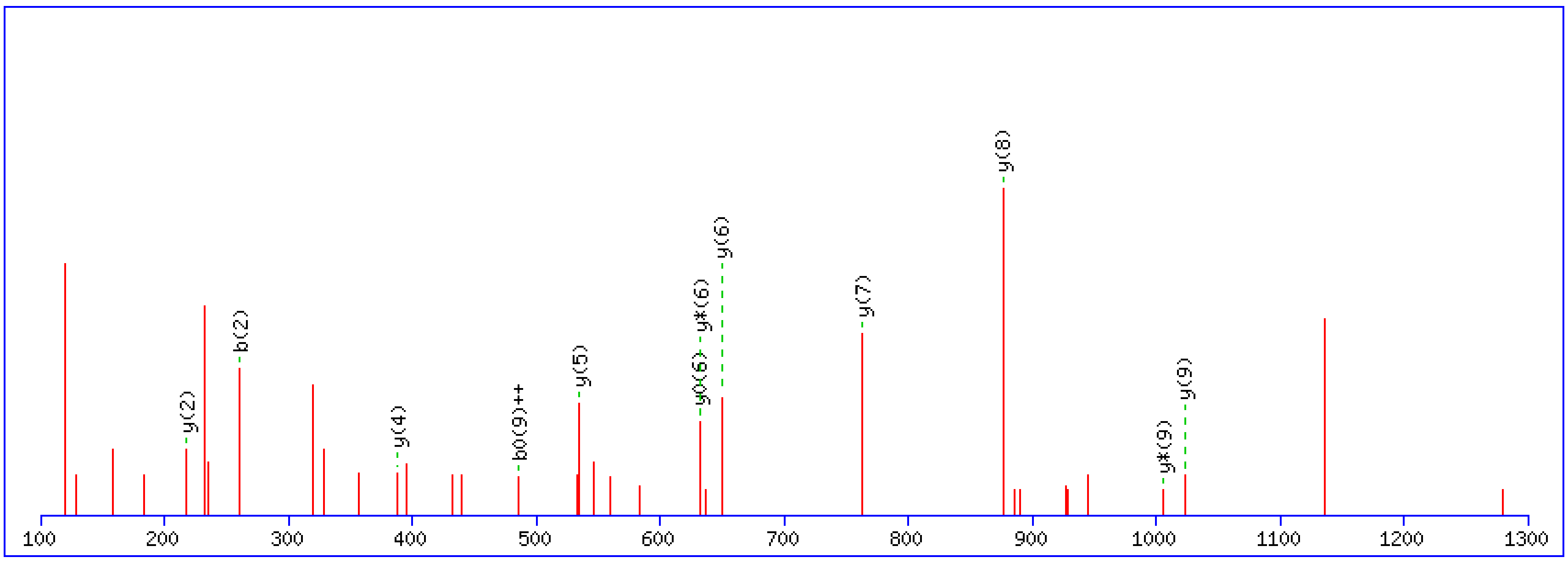
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LFLIDFGLAK**
Found in **KC1AL_HUMAN**, Casein kinase I isoform alpha-like OS=Homo sapiens GN=CSNK1A1L PE=2 SV=2

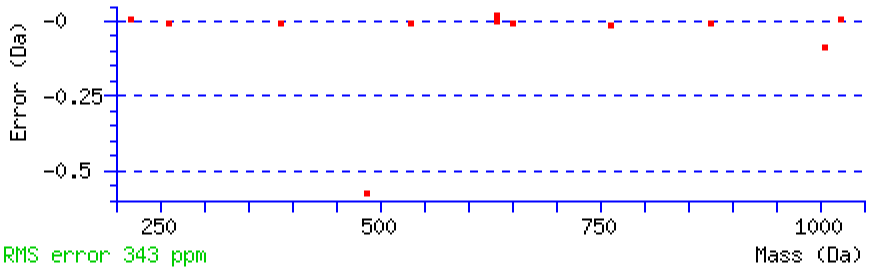
Match to Query 25273: 1135.661148 from(568.837850,2+) rtinseconds(4007) index(61097)
Title: Locus:1.1.1.1909.11
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 1.mgf

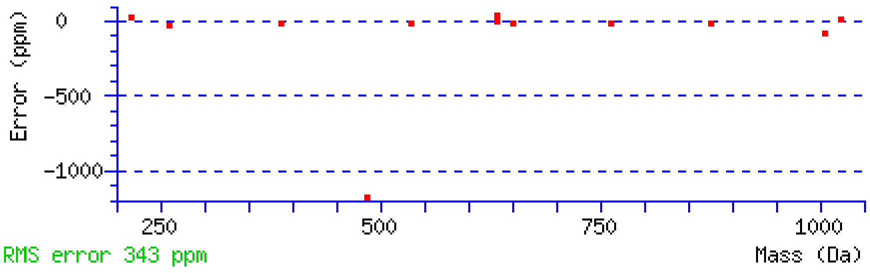
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 1300 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1135.664124
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.0028
Matches : 12/72 fragment ions using 32 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							10
2	261.159754	131.083515			F	***1023.587345***	512.297310	1006.560796	503.784036	1005.576780	503.292028	9
3	374.243818	187.625547			L	***876.518931***	438.763104	859.492382	430.249829	858.508366	429.757821	8
4	487.327882	244.167579			I	***763.434867***	382.221072	746.408318	373.707797	745.424302	373.215789	7
5	602.354825	301.681051	584.344260	292.675768	D	***650.350803***	325.679040	633.324254	317.165765	632.340238	316.673757	6
6	749.423239	375.215258	731.412674	366.209975	F	***535.323860***	268.165568	518.297311	259.652294			5
7	806.444703	403.725990	788.434138	394.720707	G	***388.255446***	194.631361	371.228897	186.118087			4
8	919.528767	460.268022	901.518202	451.262739	L	331.233982	166.120629	314.207433	157.607354			3
9	990.565881	495.786579	972.555316	486.781296	A	***218.149918***	109.578597	201.123369	101.065322			2
10					K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.4	1135.664124	-0.002976	LFLIDFGLAK

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

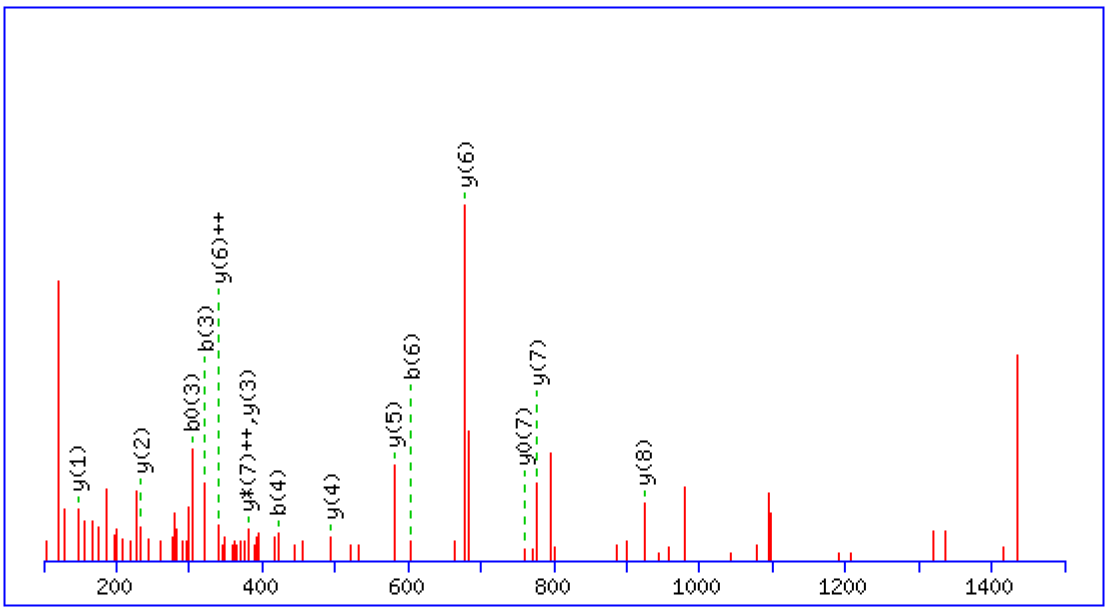
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SSFVPSLFSK**
Found in **CASP7_HUMAN**, Caspase-7 OS=Homo sapiens GN=CASP7 PE=1 SV=1

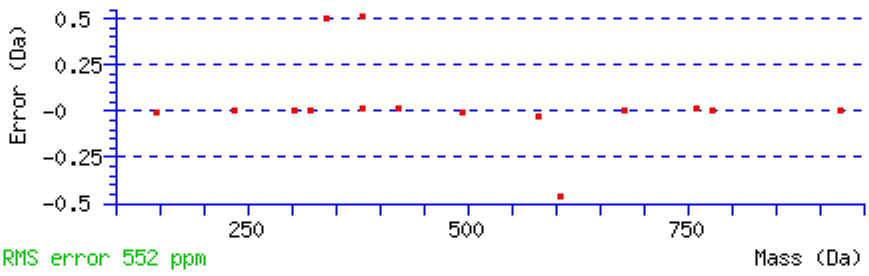
Match to Query 23146: 1097.584888 from(549.799720,2+) rtinseconds(3053) index(42476)
Title: Locus:1.1.1.2503.7
Data file 2011-11-10 - TFD - EP 3-4.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●

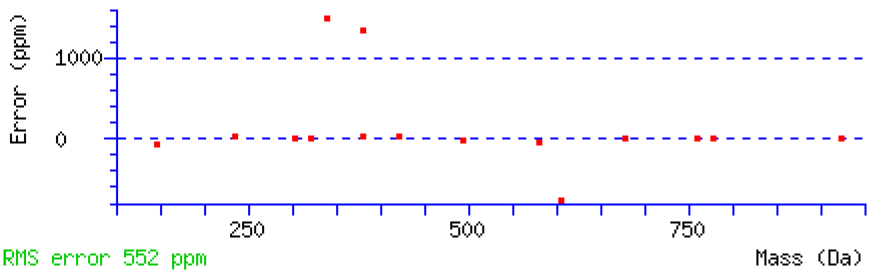


Monoisotopic mass of neutral peptide Mr(calc): 1097.575714
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 43 **Expect:** 0.00026
Matches : 15/88 fragment ions using 37 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	S							10
2	175.071332	88.039304	157.060767	79.034021	S	1011.550958	506.279117	994.524409	497.765843	993.540393	497.273835	9
3	**322.139746**	161.573511	304.129181	152.568229	F	***924.518930***	462.763103	907.492381	454.249829	906.508365	453.757821	8
4	**421.208160**	211.107718	403.197595	202.102436	V	***777.450516***	389.228896	760.423967	380.715622	759.439951	380.223614	7
5	518.260924	259.634100	500.250359	250.628818	P	***678.382102***	339.694689	661.355553	331.181415	660.371537	330.689407	6
6	**605.292952**	303.150114	587.282387	294.144832	S	***581.329338***	291.168307	564.302789	282.655033	563.318773	282.163025	5
7	718.377016	359.692146	700.366451	350.686864	L	***494.297310***	247.652293	477.270761	239.139019	476.286745	238.647011	4
8	865.445430	433.226353	847.434865	424.221071	F	***381.213246***	191.110261	364.186697	182.596987	363.202681	182.104979	3
9	952.477458	476.742367	934.466893	467.737084	S	***234.144832***	117.576054	217.118283	109.062780	216.134267	108.570772	2
10					K	***147.112804***	74.060040	130.086255	65.546766			1



RMS error 552 ppm



RMS error 552 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.8	1097.575714	0.009174	SSFVPSLFSK
4.3	1097.582901	0.001987	REIPPGIER
0.3	1097.590332	-0.005444	KFTVTVTMR

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

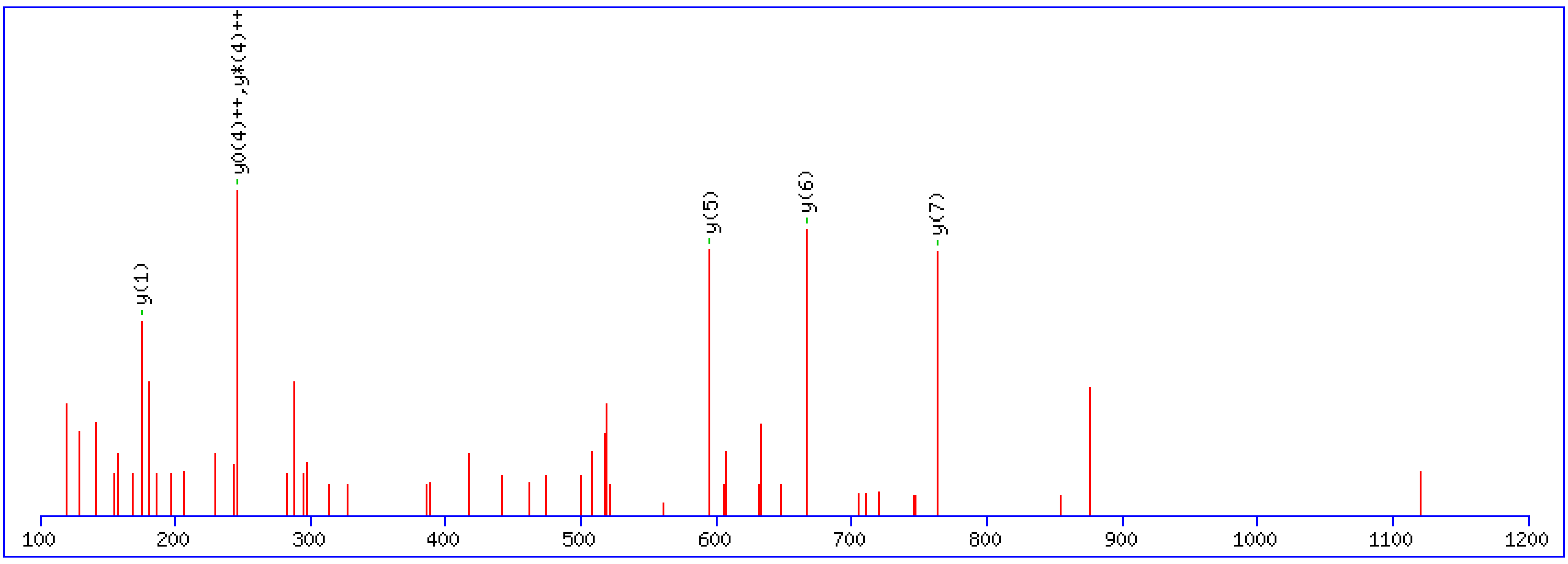
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LPASFDAR**
Found in **CATB_HUMAN**, Cathepsin B OS=Homo sapiens GN=CTSB PE=1 SV=3

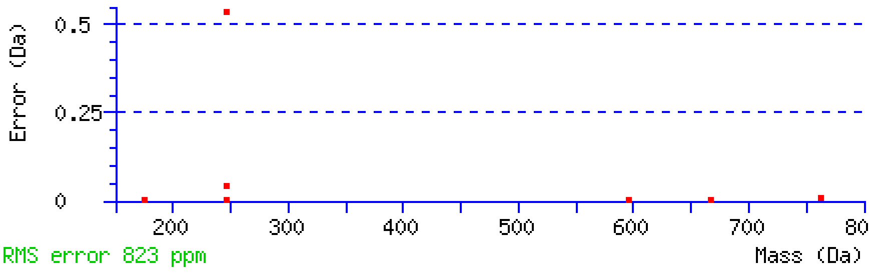
Match to Query 4766: 875.448848 from(438.731700,2+) rtinseconds(1610) index(15744)
Title: Locus:1.1.1.1002.7
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 1.mgf

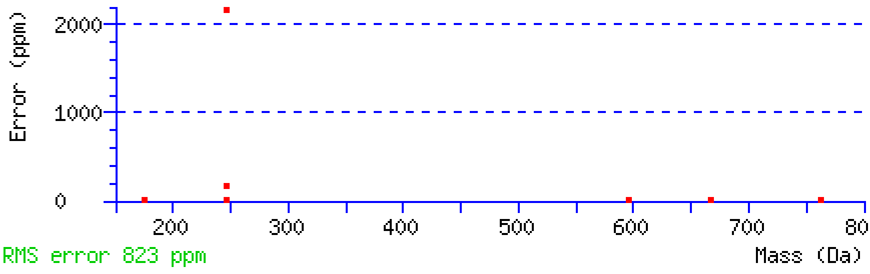
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 875.450104
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 39  Expect: 0.003
Matches : 7/60 fragment ions using 8 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							8
2	211.144104	106.075690			P	***763.373329***	382.190302	746.346780	373.677028	745.362764	373.185020	7
3	282.181218	141.594247			A	***666.320565***	333.663921	649.294016	325.150646	648.310000	324.658638	6
4	369.213246	185.110261	351.202681	176.104978	S	***595.283451***	298.145363	578.256902	289.632089	577.272886	289.140081	5
5	516.281660	258.644468	498.271095	249.639186	F	508.251423	254.629349	491.224874	246.116075	490.240858	245.624067	4
6	631.308603	316.157940	613.298038	307.152657	D	361.183009	181.095142	344.156460	172.581868	343.172444	172.089860	3
7	702.345717	351.676496	684.335152	342.671214	A	***246.156066***	123.581671	229.129517	115.068396			2
8					R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.8	875.450104	-0.001256	LPASFDAR
22.6	875.450119	-0.001271	IPFSPGSR
11.2	875.453461	-0.004613	LSMQELR
8.9	875.453461	-0.004613	IMAQIER
8.4	875.450119	-0.001271	IPNFDVR
7.0	875.453461	-0.004613	EIQMLAR
6.8	875.453476	-0.004628	EVMGALTR
6.5	875.457321	-0.008473	RAGTTGSAR
5.8	875.442261	0.006587	IPTGQLTM
5.8	875.442230	0.006618	LPSAETMK

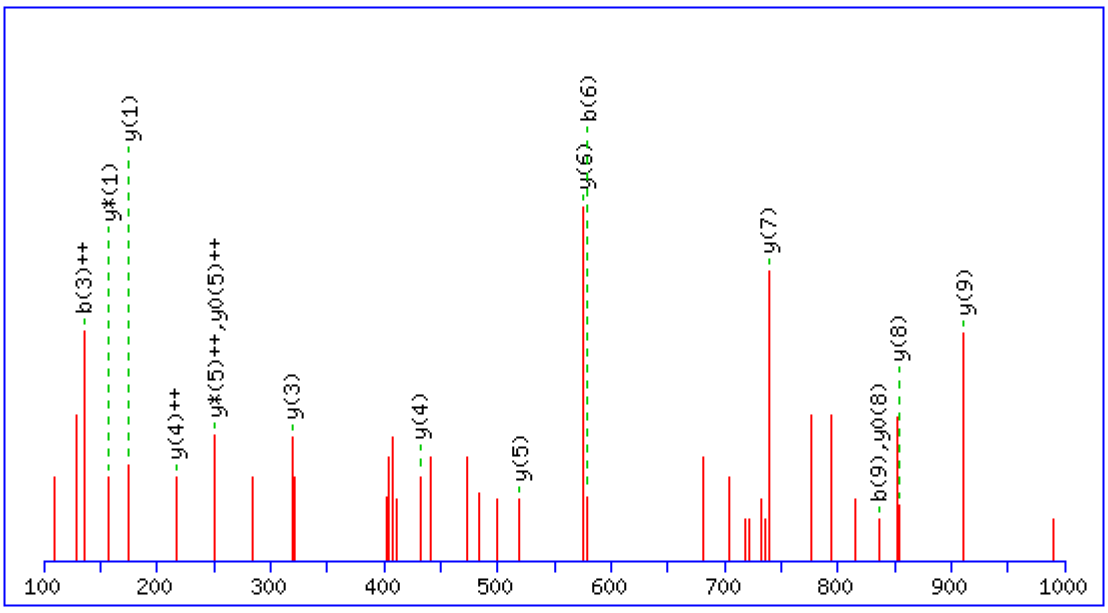
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VGDYGSLSGR**
Found in **CATZ_HUMAN**, Cathepsin Z OS=Homo sapiens GN=CTSZ PE=1 SV=1

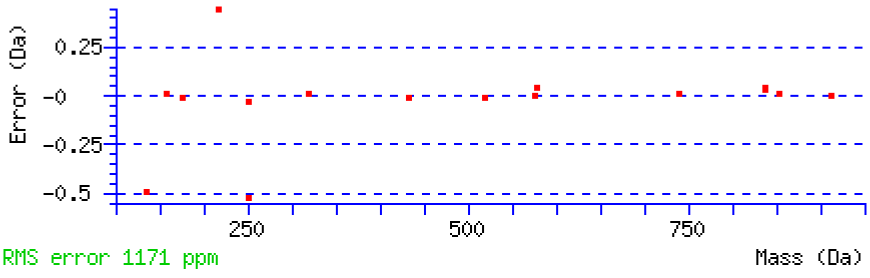
Match to Query 16715: 1009.474568 from(505.744560,2+) rtinseconds(1514) index(13814)
Title: Locus:1.1.1.1876.24
Data file 2011-11-12 - TFD - EP 6-4.mgf

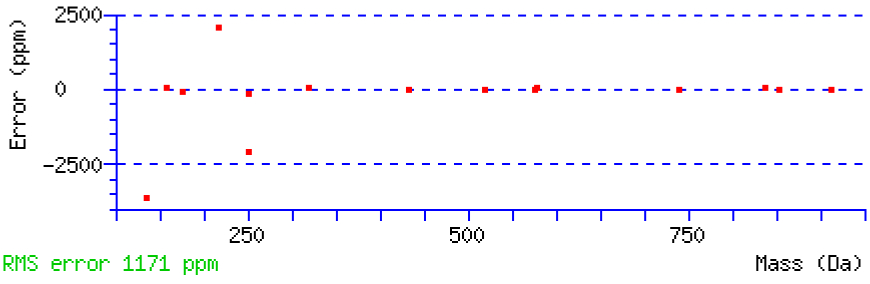
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1009.482880
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 48  Expect: 0.00013
Matches : 16/82 fragment ions using 30 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483			V							10
2	157.097154	79.052215			G	***911.421736***	456.214506	894.395187	447.701232	893.411171	447.209224	9
3	272.124097	136.565687	254.113532	127.560404	D	***854.400272***	427.703774	837.373723	419.190500	836.389707	418.698492	8
4	435.187426	218.097351	417.176861	209.092069	Y	***739.373329***	370.190303	722.346780	361.677028	721.362764	361.185020	7
5	492.208890	246.608083	474.198325	237.602801	G	***576.310000***	288.658638	559.283451	280.145364	558.299435	279.653356	6
6	**579.240918**	290.124097	561.230353	281.118815	S	***519.288536***	260.147906	502.261987	251.634632	501.277971	251.142624	5
7	692.324982	346.666129	674.314417	337.660847	L	***432.256508***	216.631892	415.229959	208.118617	414.245943	207.626609	4
8	779.357010	390.182143	761.346445	381.176861	S	***319.172444***	160.089860	302.145895	151.576585	301.161879	151.084577	3
9	**836.378474**	418.692875	818.367909	409.687593	G	232.140416	116.573846	215.113867	108.060571			2
10					R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.7	1009.482880	-0.008312	VGDYGSLSGR

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

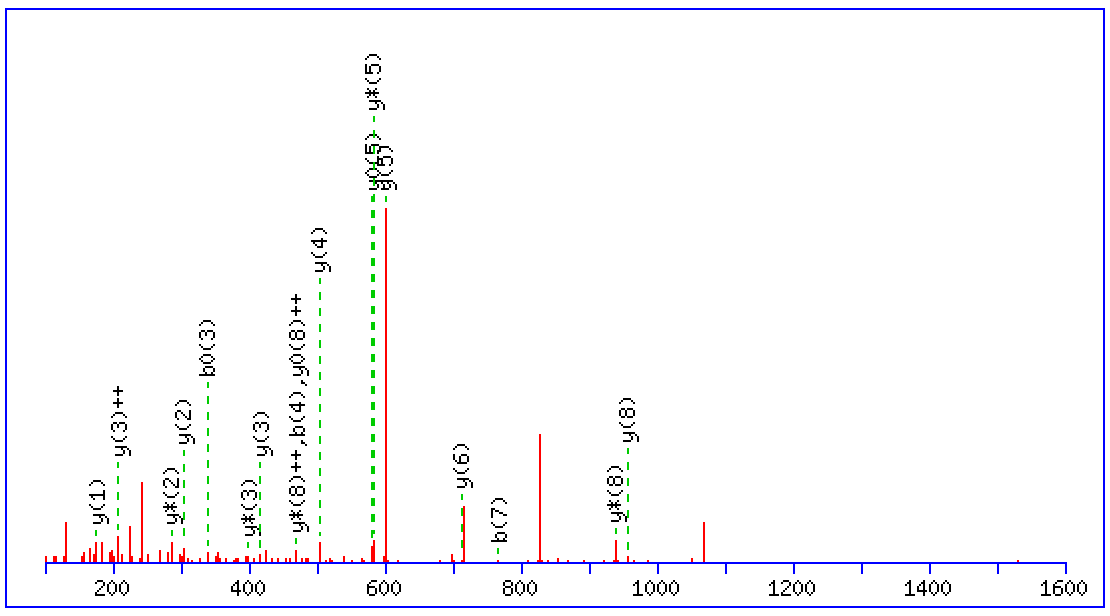
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LRSLPSPQR**
Found in **CTSRG_HUMAN**, Cation channel sperm-associated protein subunit gamma OS=Homo sapiens GN=CATSPERG PE=2 SV=3

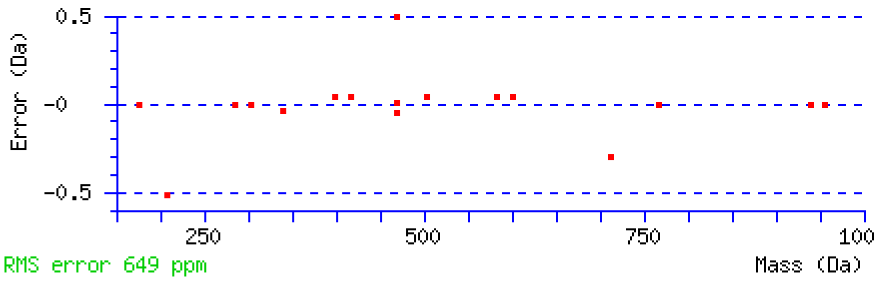
Match to Query 21031: 1068.597368 from(535.305960,2+) rtinseconds(1990) index(22393)
Title: Locus:1.1.1.2101.24
Data file 2011-11-10 - TFD - EP 3-4.mgf

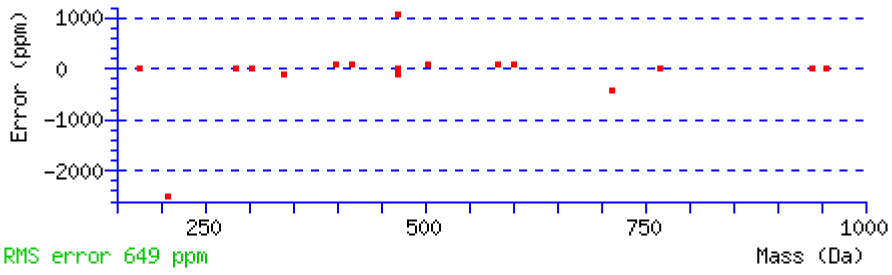
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1600] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1068.603973
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P7 : Oxidation (P)
Ions Score: 36 **Expect:** 0.0023
Matches : 18/84 fragment ions using 37 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.091340	57.549308					L							9
2	270.192451	135.599864	253.165902	127.086589			R	***956.527204***	478.767240	939.500655	470.253966	938.516639	469.761958	8
3	357.224479	179.115878	340.197930	170.602603	339.213914	170.110595	S	800.426093	400.716685	783.399544	392.203410	782.415528	391.711402	7
4	470.308543	235.657910	453.281994	227.144635	452.297978	226.652627	L	***713.394065***	357.200671	696.367516	348.687396	695.383500	348.195388	6
5	567.361307	284.184292	550.334758	275.671017	549.350742	275.179009	P	***600.310001***	300.658639	583.283452	292.145364	582.299436	291.653356	5
6	654.393335	327.700306	637.366786	319.187031	636.382770	318.695023	S	***503.257237***	252.132256	486.230688	243.618982	485.246672	243.126974	4
7	767.441014	384.224145	750.414465	375.710871	749.430449	375.218863	P	***416.225209***	208.616242	399.198660	200.102968			3
8	895.499592	448.253434	878.473043	439.740160	877.489027	439.248152	Q	***303.177530***	152.092403	286.150981	143.579128			2
9							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.6	1068.603973	-0.006605	LRSLPSPQR
19.9	1068.603973	-0.006605	LRSLPSPQR
14.1	1068.592743	0.004625	AATENIPVVR
13.6	1068.603973	-0.006605	SPGLPIRSAR
12.2	1068.592728	0.004640	LKPLGEQER
11.6	1068.603989	-0.006621	KPPPLTRGR
9.3	1068.603989	-0.006621	SPGPIVSRTR
9.2	1068.592743	0.004625	SVPADLSRPK
8.7	1068.608002	-0.010634	LISRIPSFH
8.0	1068.603958	-0.006590	IRISAPQER

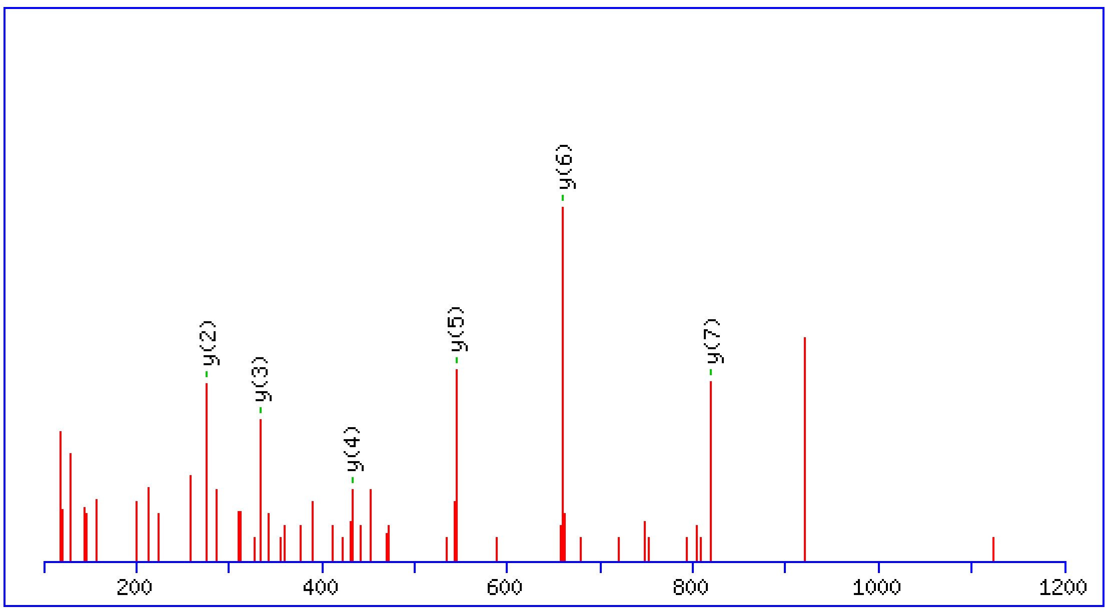
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TCDLVGEK**
Found in **MPRD_HUMAN**, Cation-dependent mannose-6-phosphate receptor OS=Homo sapiens GN=M6PR PE=1 SV=1

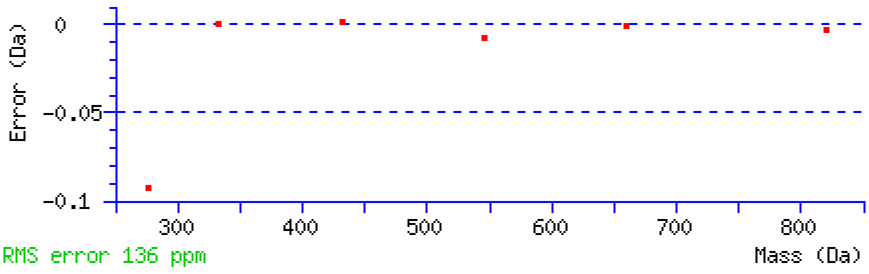
Match to Query 154718: 920.435668 from(461.225110,2+) rtinseconds(1092) index(330372)
Title: Locus:1.1.1.749.14
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

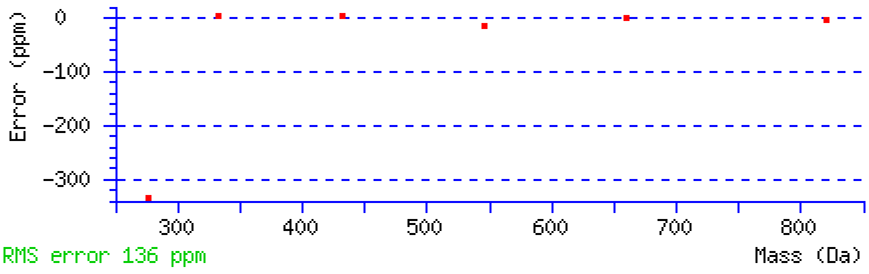
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 920.427338
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 53 **Expect:** 6.9e-005
Matches : 6/68 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116	84.044390	42.525833	T							8
2	262.085604	131.546440	244.075039	122.541158	C	*820.386931*	410.697104	803.360382	402.183829	802.376366	401.691821	7
3	377.112547	189.059912	359.101982	180.054629	D	*660.356282*	330.681779	643.329733	322.168505	642.345717	321.676497	6
4	490.196611	245.601944	472.186046	236.596661	L	*545.329339*	273.168308	528.302790	264.655033	527.318774	264.163025	5
5	589.265025	295.136151	571.254460	286.130868	V	*432.245275*	216.626275	415.218726	208.113001	414.234710	207.620993	4
6	646.286489	323.646883	628.275924	314.641600	G	*333.176861*	167.092069	316.150312	158.578794	315.166296	158.086786	3
7	775.329082	388.168179	757.318517	379.162897	E	*276.155397*	138.581336	259.128848	130.068062	258.144832	129.576054	2
8					K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
53.3	920.427338	0.008330	TCDLVGEK
8.4	920.438553	-0.002885	NGIMDISR
8.4	920.435196	0.000472	NPGFDLSR
8.3	920.427307	0.008361	QKIGEEAM
8.3	920.427322	0.008346	QQDLSIAM
7.0	920.438553	-0.002885	QELGTAMR
6.3	920.435181	0.000487	YPQSSPSR
6.1	920.438568	-0.002900	QVSTMPSR
5.5	920.438553	-0.002885	STSLNPMR
5.5	920.438553	-0.002885	STSLNPMR

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

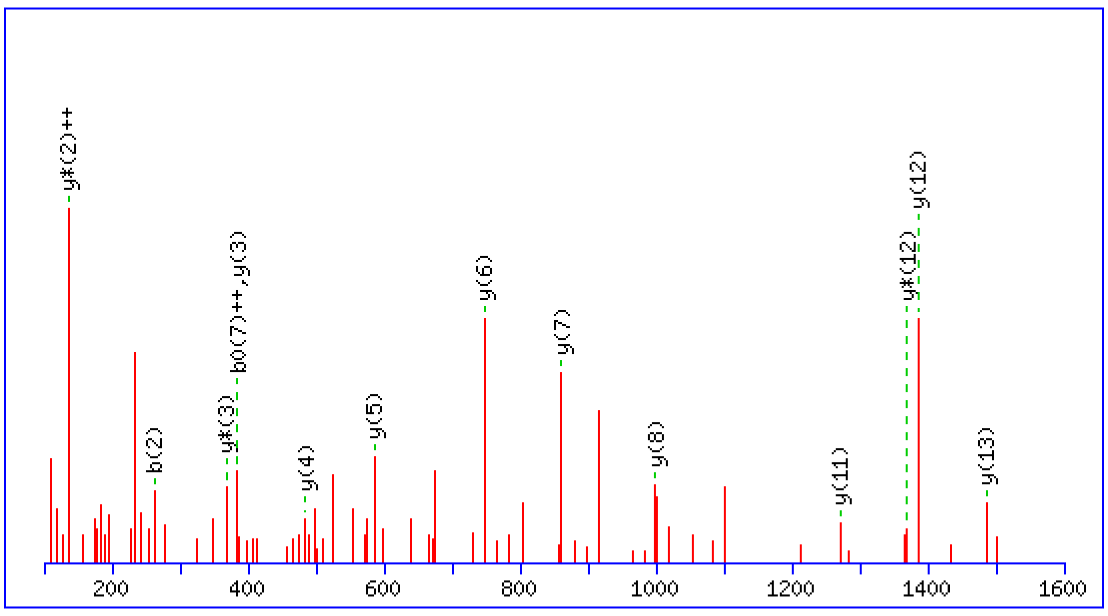
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YVDSEGHLYTVPIR**
Found in **CAV1_HUMAN**, Caveolin-1 OS=Homo sapiens GN=CAV1 PE=1 SV=4

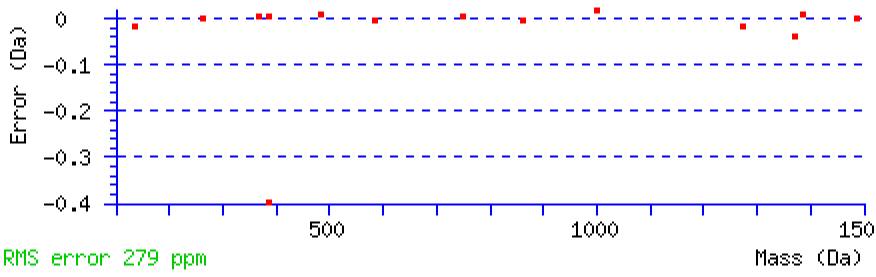
Match to Query 49308: 1647.823842 from(550.281890,3+) rtinseconds(2250) index(26094)
Title: Locus:1.1.1.2148.32
Data file 2011-11-12 - TFD - EP 6-5.mgf

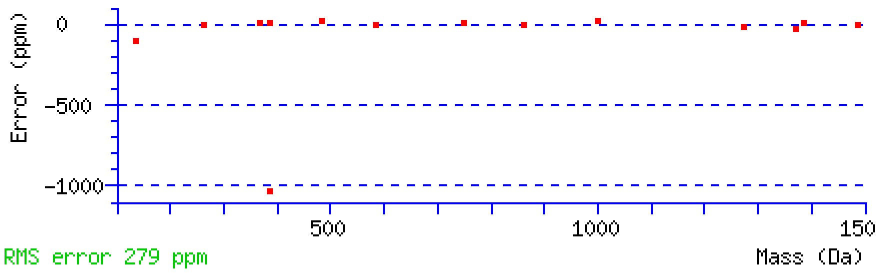
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1647.825668
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 52 **Expect:** 9.2e-005
Matches : 14/118 fragment ions using 26 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.070605	82.538940			Y							14
2	263.139019	132.073148			V	***1485.769620***	743.388448	1468.743071	734.875174	1467.759055	734.383166	13
3	378.165962	189.586619	360.155397	180.581337	D	***1386.701206***	693.854241	1369.674657	685.340967	1368.690641	684.848958	12
4	465.197990	233.102633	447.187425	224.097351	S	***1271.674263***	636.340770	1254.647714	627.827495	1253.663698	627.335487	11
5	594.240583	297.623930	576.230018	288.618647	E	1184.642235	592.824756	1167.615686	584.311481	1166.631670	583.819473	10
6	651.262047	326.134662	633.251482	317.129379	G	1055.599642	528.303459	1038.573093	519.790185	1037.589077	519.298176	9
7	788.320959	394.664118	770.310394	385.658835	H	***998.578178***	499.792727	981.551629	491.279452	980.567613	490.787444	8
8	901.405023	451.206150	883.394458	442.200867	L	***861.519266***	431.263271	844.492717	422.749997	843.508701	422.257989	7
9	1064.468352	532.737814	1046.457787	523.732532	Y	***748.435202***	374.721239	731.408653	366.207965	730.424637	365.715957	6
10	1165.516031	583.261654	1147.505466	574.256371	T	***585.371873***	293.189575	568.345324	284.676300	567.361308	284.184292	5
11	1264.584445	632.795861	1246.573880	623.790578	V	***484.324194***	242.665735	467.297645	234.152460			4
12	1361.637209	681.322243	1343.626644	672.316960	P	***385.255780***	193.131528	368.229231	184.618253			3
13	1474.721273	737.864275	1456.710708	728.858992	I	288.203016	144.605146	271.176467	136.091871			2
14					R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.3	1647.825668	-0.001826	YVDSEGHLYTVPIR
15.3	1647.832855	-0.009013	LEQEAGARQPPPAPR
11.3	1647.832855	-0.009013	LEQEAGARQPPPAPR
10.3	1647.832855	-0.009013	LEQEAGARQPPPAPR
8.2	1647.832855	-0.009013	LEQEAGARQPPPAPR
3.5	1647.829086	-0.005244	DGVVTIGCVGFPNVGK
2.8	1647.832855	-0.009013	LEQEAGARQPPPAPR
0.8	1647.821640	0.002202	APDPVAAETAAQGPTPR

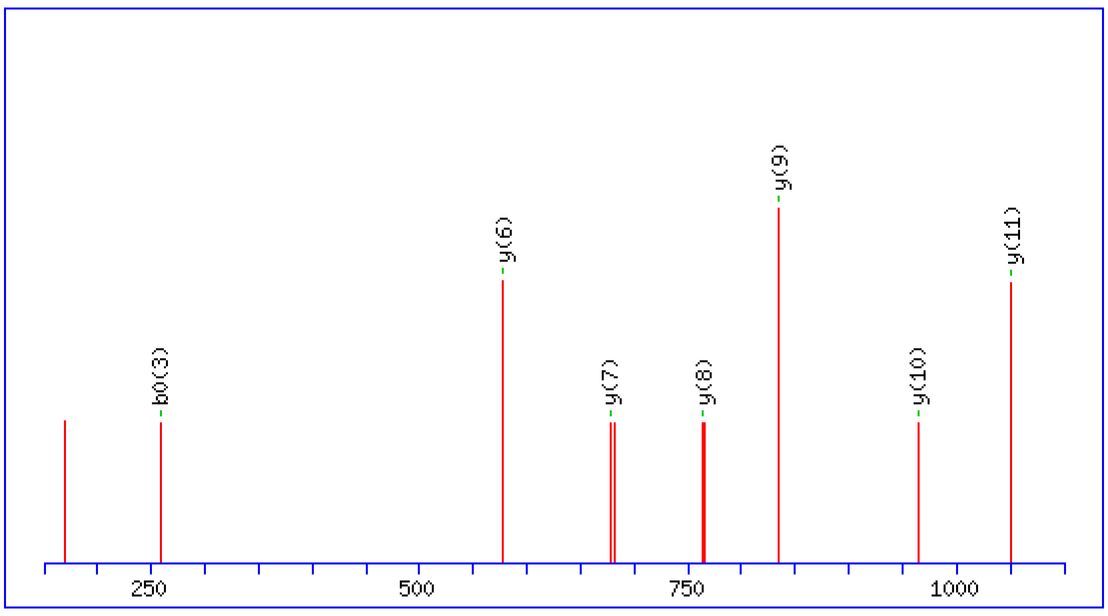
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TSSEASVSSSVAK**
Found in **CARF_HUMAN**, CDKN2A-interacting protein OS=Homo sapiens GN=CDKN2AIP PE=1 SV=3

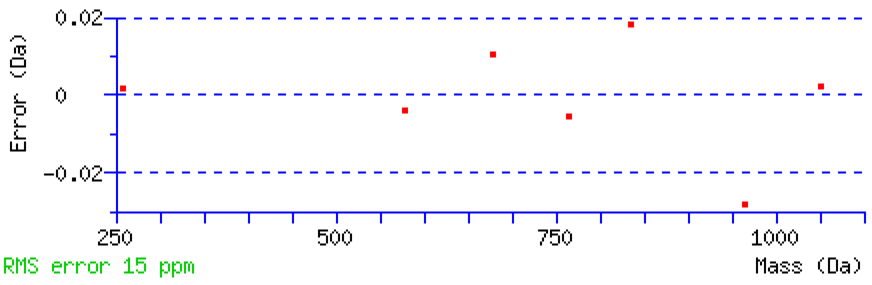
Match to Query 568086: 1238.598568 from(620.306560,2+) rtinseconds(1078) index(159353)
Title: Locus:1.1.1.1095.16
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

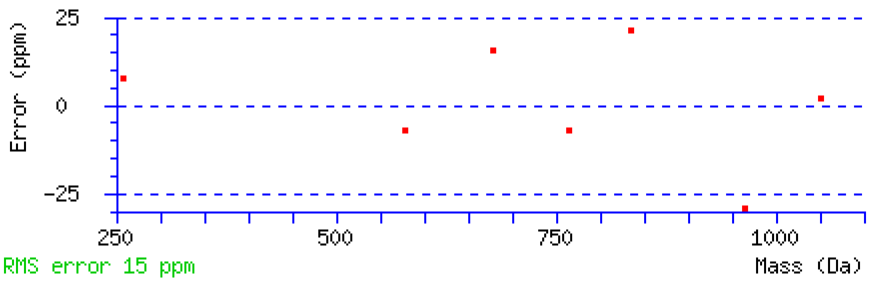
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1238.599014
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 46 **Expect:** 0.00027
Matches : 7/114 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116	84.044390	42.525833	**T**							**13**
2	189.086983	95.047129	171.076418	86.041847	**S**	1138.558621	569.782948	1121.532072	561.269674	1120.548056	560.777666	**12**
3	276.119011	138.563143	258.108446	129.557861	**S**	***1051.526593***	526.266934	1034.500044	517.753660	1033.516028	517.261652	**11**
4	405.161604	203.084440	387.151039	194.079157	**E**	***964.494565***	482.750921	947.468016	474.237646	946.484000	473.745638	**10**
5	476.198718	238.602997	458.188153	229.597714	**A**	***835.451972***	418.229624	818.425423	409.716349	817.441407	409.224341	**9**
6	563.230746	282.119011	545.220181	273.113728	**S**	***764.414858***	382.711067	747.388309	374.197792	746.404293	373.705784	**8**
7	662.299160	331.653218	644.288595	322.647935	**V**	***677.382830***	339.195053	660.356281	330.681779	659.372265	330.189771	**7**
8	749.331188	375.169232	731.320623	366.163949	**S**	***578.314416***	289.660846	561.287867	281.147572	560.303851	280.655564	**6**
9	836.363216	418.685246	818.352651	409.679963	**S**	491.282388	246.144832	474.255839	237.631557	473.271823	237.139549	**5**
10	923.395244	462.201260	905.384679	453.195977	**S**	404.250360	202.628818	387.223811	194.115544	386.239795	193.623536	**4**
11	1022.463658	511.735467	1004.453093	502.730184	**V**	317.218332	159.112804	300.191783	150.599530			**3**
12	1093.500772	547.254024	1075.490207	538.248741	**A**	218.149918	109.578597	201.123369	101.065323			**2**
13					**K**	147.112804	74.060040	130.086255	65.546765			**1**





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.4	1238.599014	-0.000446	TSSEASVSSSVAK
13.7	1238.603043	-0.004475	APDLPPVPEEK
9.4	1238.603012	-0.004444	EYLLGSTAEEK
1.6	1238.603043	-0.004475	APDLPPVPEEK
1.6	1238.603043	-0.004475	APDLPPVPEEK
1.6	1238.603043	-0.004475	APDLPPVPEEK
1.6	1238.604370	-0.005802	EKFYPDRPR
0.9	1238.610260	-0.011692	TSSTSSIGGISSR

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

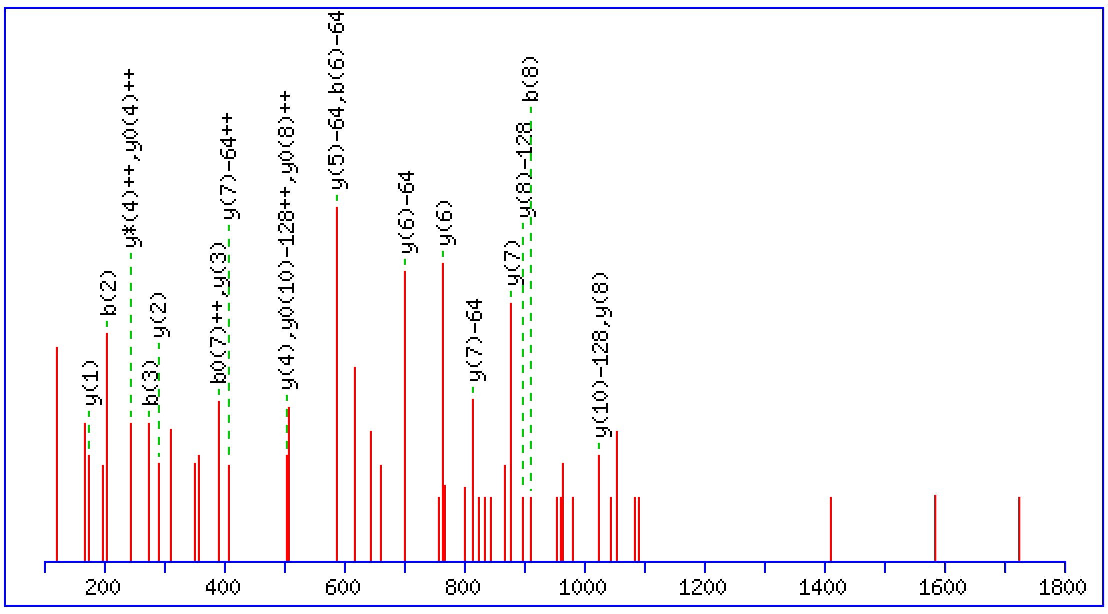
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FGAMLDMLTDR**
Found in **CDIPT_HUMAN**, CDP-diacylglycerol--inositol 3-phosphatidyltransferase OS=Homo sapiens GN=CDIPT PE=1 SV=1

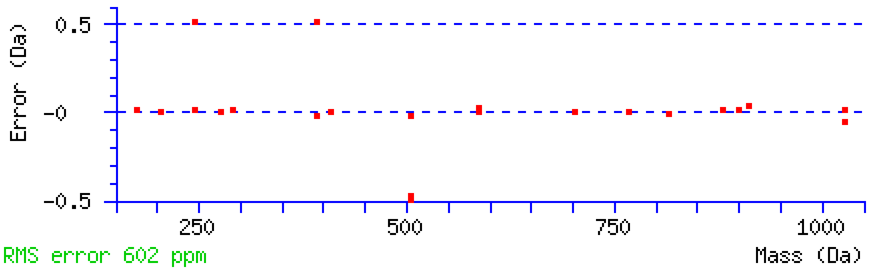
Match to Query 41731: 1300.578448 from(651.296500,2+) rtinseconds(2451) index(29438)
Title: Locus:1.1.1.2190.42
Data file 2011-11-10 - TFD - EP 4-6.mgf

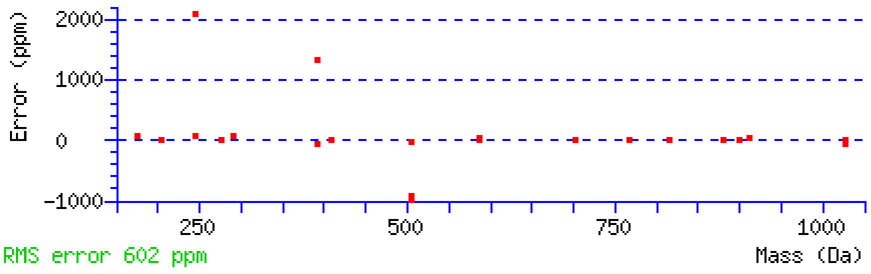
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1300.579163
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M4      : Oxidation (M), with neutral losses 63.998285(shown in table), 0.000000
M7      : Oxidation (M), with neutral losses 63.998285(shown in table), 0.000000
Ions Score: 40  Expect: 0.0004
Matches : 22/148 fragment ions using 43 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.075690	74.541483			F							11
2	**205.097154**	103.052215			G	***1026.521453***	513.764364	1009.494904	505.251090	1008.510888	504.759082	10
3	**276.134268**	138.570772			A	969.499989	485.253632	952.473440	476.740358	951.489424	476.248350	9
4	359.171383	180.089329			M	***898.462875***	449.735075	881.436326	441.221801	880.452310	440.729793	8
5	472.255447	236.631361			L	***815.425760***	408.216518	798.399211	399.703243	797.415195	399.211235	7
6	**587.282390**	294.144833	569.271825	285.139550	D	***702.341696***	351.674486	685.315147	343.161211	684.331131	342.669203	6
7	670.319505	335.663390	652.308940	326.658108	M	***587.314753***	294.161015	570.288204	285.647740	569.304188	285.155732	5
8	783.403569	392.205423	765.393004	383.200140	L	***504.277638***	252.642457	487.251089	244.129182	486.267073	243.637174	4
9	884.451248	442.729262	866.440683	433.723979	T	***391.193574***	196.100425	374.167025	187.587150	373.183009	187.095142	3
10	999.478191	500.242733	981.467626	491.237451	D	***290.145895***	145.576585	273.119346	137.063311	272.135330	136.571303	2
11					R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.9	1300.579163	-0.000715	FGAMLDMLTDR
2.7	1300.575760	0.002688	EEAYVMADAFR

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

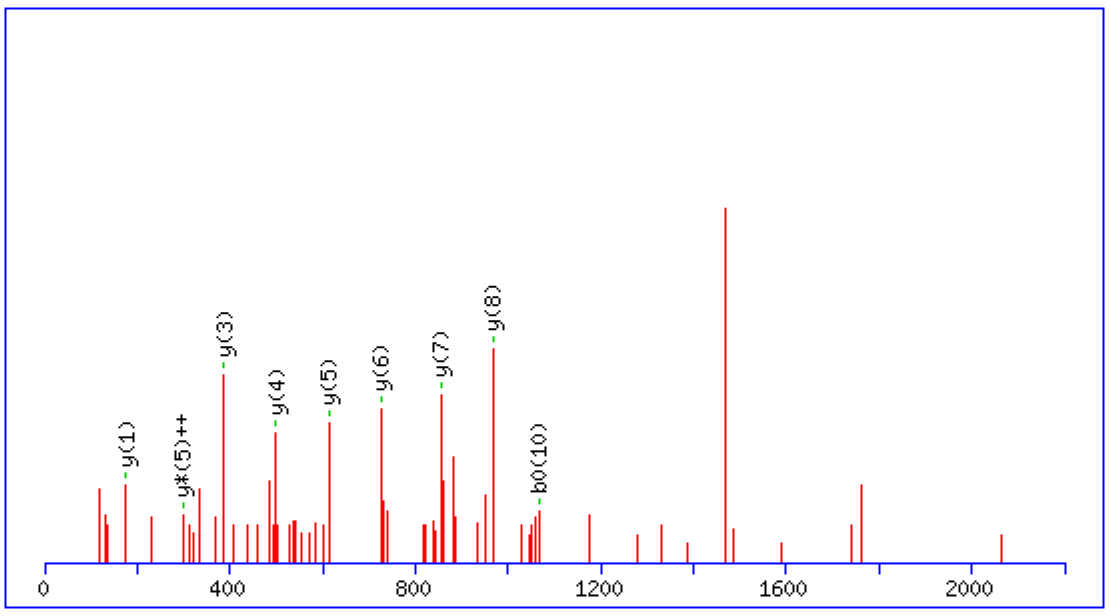
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SDDSVIQLLNPNR**
Found in **CADM1_HUMAN**, Cell adhesion molecule 1 OS=Homo sapiens GN=CADM1 PE=1 SV=2

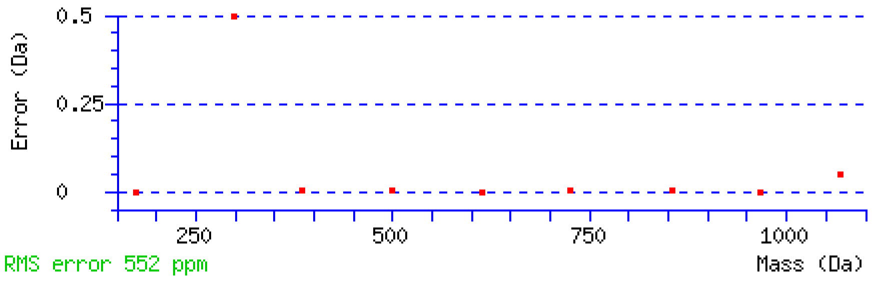
Match to Query 46225: 1469.753108 from(735.883830,2+) rtinseconds(3171) index(44354)
Title: Locus:1.1.1.2642.37
Data file 2011-11-10 - TFD - EP 3-2.mgf

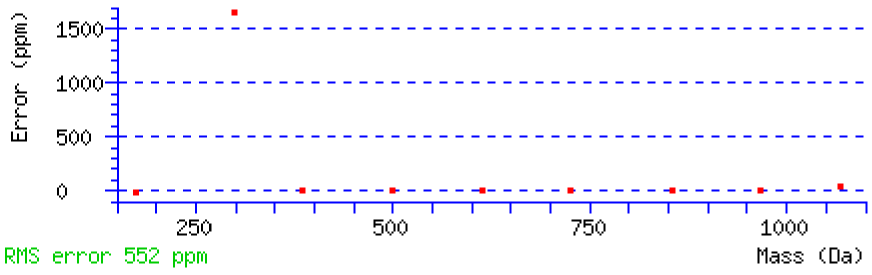
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1469.747406
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 51 **Expect:** 0.00012
Matches : 9/114 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							13
2	203.066247	102.036761			185.055682	93.031479	D	1383.722668	692.364972	1366.696119	683.851698	1365.712103	683.359689	12
3	318.093190	159.550233			300.082625	150.544951	D	1268.695725	634.851501	1251.669176	626.338226	1250.685160	625.846218	11
4	405.125218	203.066247			387.114653	194.060964	S	1153.668782	577.338029	1136.642233	568.824755	1135.658217	568.332746	10
5	504.193632	252.600454			486.183067	243.595171	V	1066.636754	533.822015	1049.610205	525.308741			9
6	617.277696	309.142486			599.267131	300.137204	I	***967.568340***	484.287808	950.541791	475.774534			8
7	745.336274	373.171775	728.309725	364.658501	727.325709	364.166493	Q	***854.484276***	427.745776	837.457727	419.232502			7
8	858.420338	429.713807	841.393789	421.200533	840.409773	420.708525	L	***726.425698***	363.716487	709.399149	355.203213			6
9	971.504402	486.255839	954.477853	477.742565	953.493837	477.250557	L	***613.341634***	307.174455	596.315085	298.661181			5
10	1085.547329	543.277303	1068.520780	534.764028	1067.536764	534.272020	N	***500.257570***	250.632423	483.231021	242.119148			4
11	1182.600093	591.803685	1165.573544	583.290410	1164.589528	582.798402	P	***386.214643***	193.610959	369.188094	185.097685			3
12	1296.643020	648.825148	1279.616471	640.311874	1278.632455	639.819865	N	289.161879	145.084577	272.135330	136.571303			2
13							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
50.9	1469.747406	0.005702	SDDSVIQLLNPNR
14.8	1469.766022	-0.012914	NVEIPQLNQLMR
14.2	1469.751404	0.001704	EAWLLPPEKEAR
11.8	1469.740860	0.012248	EMSPQRNLLPNR
8.5	1469.751434	0.001674	AIFQDPEGLPDLR
5.0	1469.747421	0.005687	TDVSTLVELSNHR
4.5	1469.740845	0.012263	ERVAAAMENPNLR
1.4	1469.762665	-0.009557	LAWAPLVDAQGSAR
0.1	1469.754837	-0.001729	ATVAPLPMTPVPGR

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

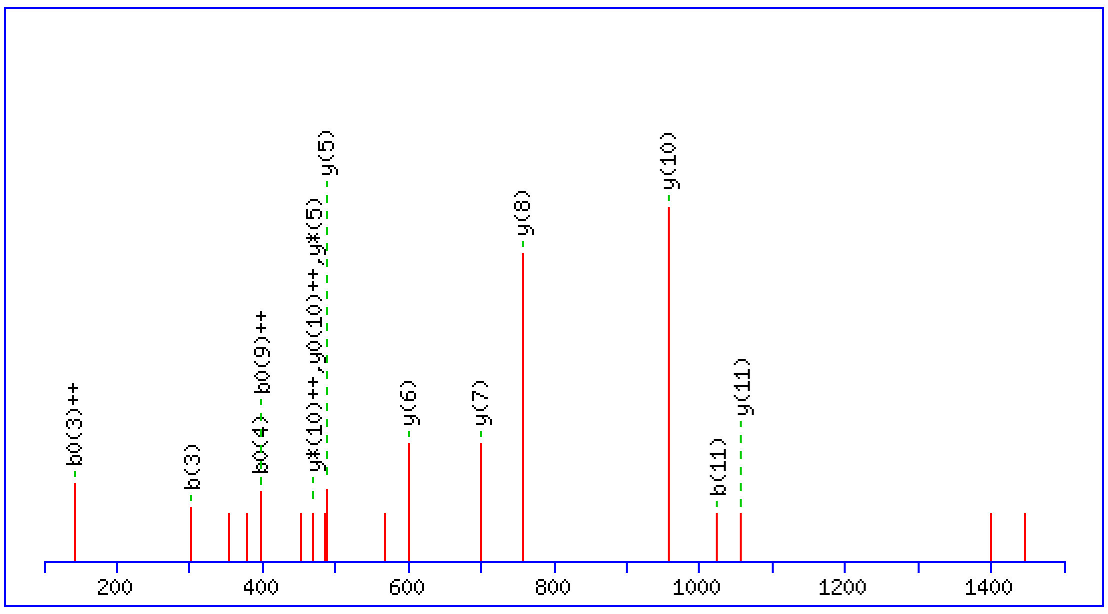
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LTSLGVIGALVK**
Found in **RCD1_HUMAN**, Cell differentiation protein RCD1 homolog OS=Homo sapiens GN=RQCD1 PE=1 SV=1

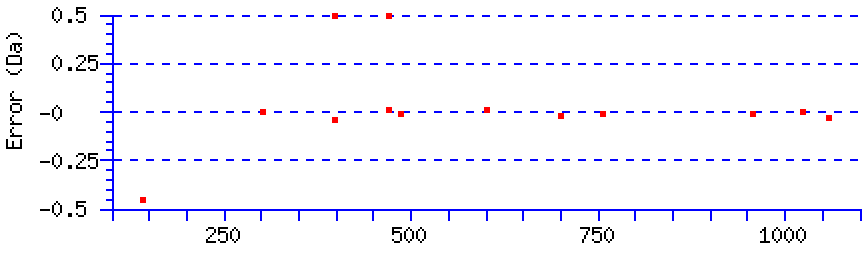
Match to Query 24345: 1169.740068 from(585.877310,2+) rtinseconds(3497) index(45636)
Title: Locus:1.1.1.2947.12
Data file 2011-11-10 - TFD - EP 3-5.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1500] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●

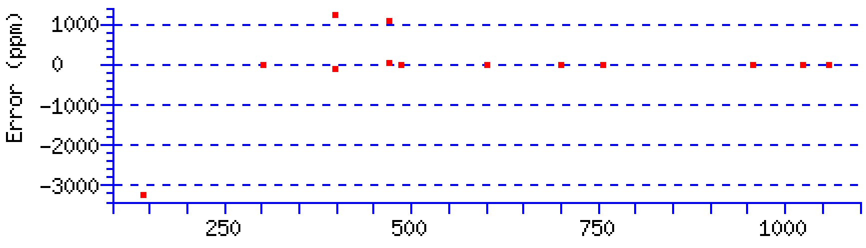


```
Monoisotopic mass of neutral peptide Mr(calc): 1169.738358
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 63  Expect: 6.4e-007
Matches : 14/90 fragment ions using 13 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							12
2	215.139019	108.073147	197.128454	99.067865	T	***1057.661573***	529.334425	1040.635024	520.821150	1039.651008	520.329142	11
3	**302.171047**	151.589161	284.160482	142.583879	S	***956.613894***	478.810585	939.587345	470.297311	938.603329	469.805303	10
4	415.255111	208.131193	397.244546	199.125911	L	869.581866	435.294571	852.555317	426.781297			9
5	472.276575	236.641925	454.266010	227.636643	G	***756.497802***	378.752539	739.471253	370.239265			8
6	571.344989	286.176133	553.334424	277.170850	V	***699.476338***	350.241807	682.449789	341.728533			7
7	684.429053	342.718165	666.418488	333.712882	I	***600.407924***	300.707600	583.381375	292.194326			6
8	741.450517	371.228897	723.439952	362.223614	G	***487.323860***	244.165568	470.297311	235.652294			5
9	812.487631	406.747454	794.477066	397.742171	A	430.302396	215.654836	413.275847	207.141562			4
10	925.571695	463.289486	907.561130	454.284203	L	359.265282	180.136279	342.238733	171.623005			3
11	**1024.640109**	512.823692	1006.629544	503.818410	V	246.181218	123.594247	229.154669	115.080973			2
12					K	147.112804	74.060040	130.086255	65.546766			1



RMS error 962 ppm



RMS error 962 ppm

NCBI **BLAST** search of LTSLGVIGALVK
(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	1169.738358	0.001710	LTSLGVIGALVK
6.1	1169.738342	0.001726	LITQDLVKLK
1.4	1169.738358	0.001710	VTITGLLPKTK

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

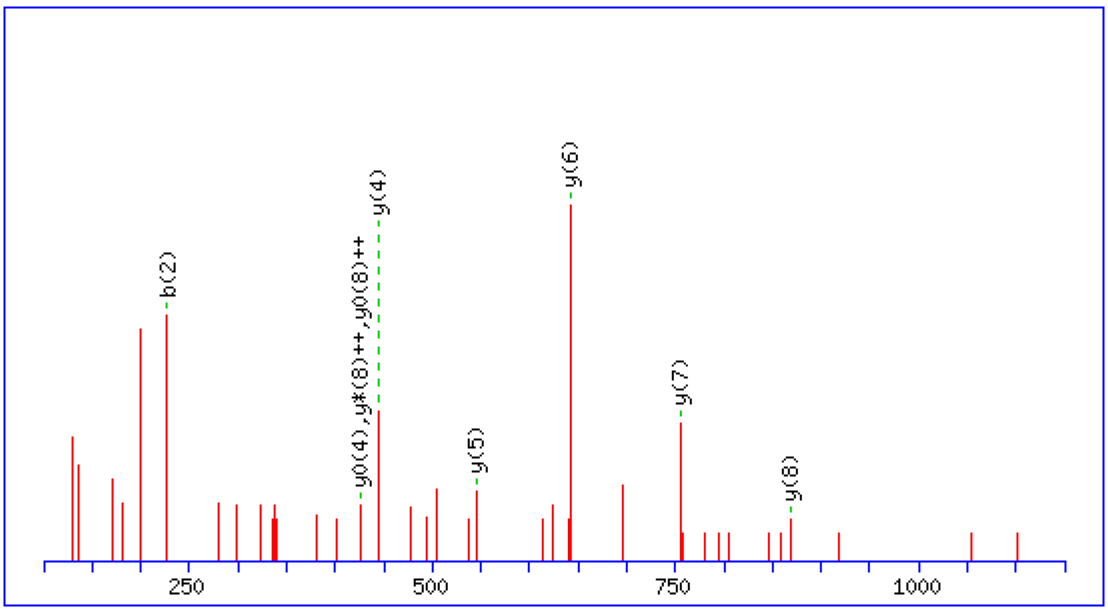
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLLPTPTVK**
Found in **CCAR1_HUMAN**, Cell division cycle and apoptosis regulator protein 1 OS=Homo sapiens GN=CCAR1 PE=1 SV=2

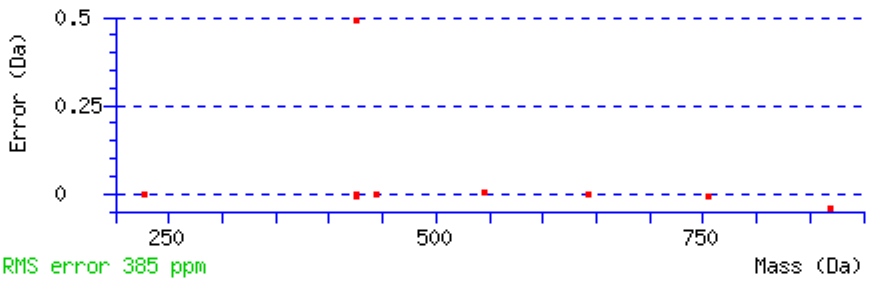
Match to Query 14410: 980.626788 from(491.320670,2+) rtinseconds(2482) index(31998)
Title: Locus:1.1.1.2260.9
Data file 2011-11-12 - TFD - EP 6-1.mgf

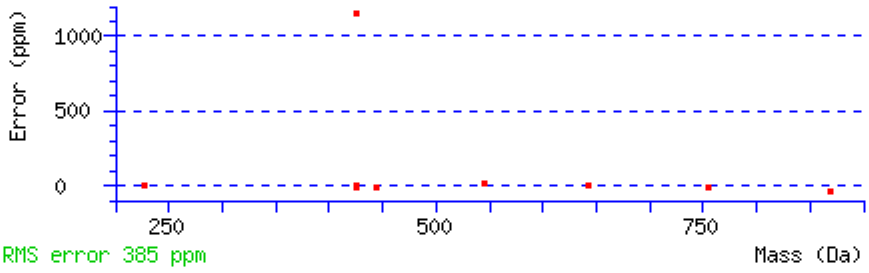
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 980.627014
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 41  Expect: 7.8e-005
Matches : 9/68 fragment ions using 8 most intense peaks   (help)
```

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308			L							9
2	227.175404	114.091340			L	***868.550232***	434.778754	851.523683	426.265480	850.539667	425.773472	8
3	340.259468	170.633372			L	***755.466168***	378.236722	738.439619	369.723448	737.455603	369.231440	7
4	437.312232	219.159754			P	***642.382104***	321.694690	625.355555	313.181416	624.371539	312.689408	6
5	538.359911	269.683594	520.349346	260.678311	T	***545.329340***	273.168308	528.302791	264.655034	527.318775	264.163026	5
6	635.412675	318.209976	617.402110	309.204693	P	***444.281661***	222.644468	427.255112	214.131194	426.271096	213.639186	4
7	736.460354	368.733815	718.449789	359.728533	T	347.228897	174.118086	330.202348	165.604812	329.218332	165.112804	3
8	835.528768	418.268022	817.518203	409.262740	V	246.181218	123.594247	229.154669	115.080972			2
9					K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.1	980.627014	-0.000226	LLLPTPTVK
12.4	980.626999	-0.000211	LLTPIIPSK
1.0	980.626999	-0.000211	LEPLGIIVK

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

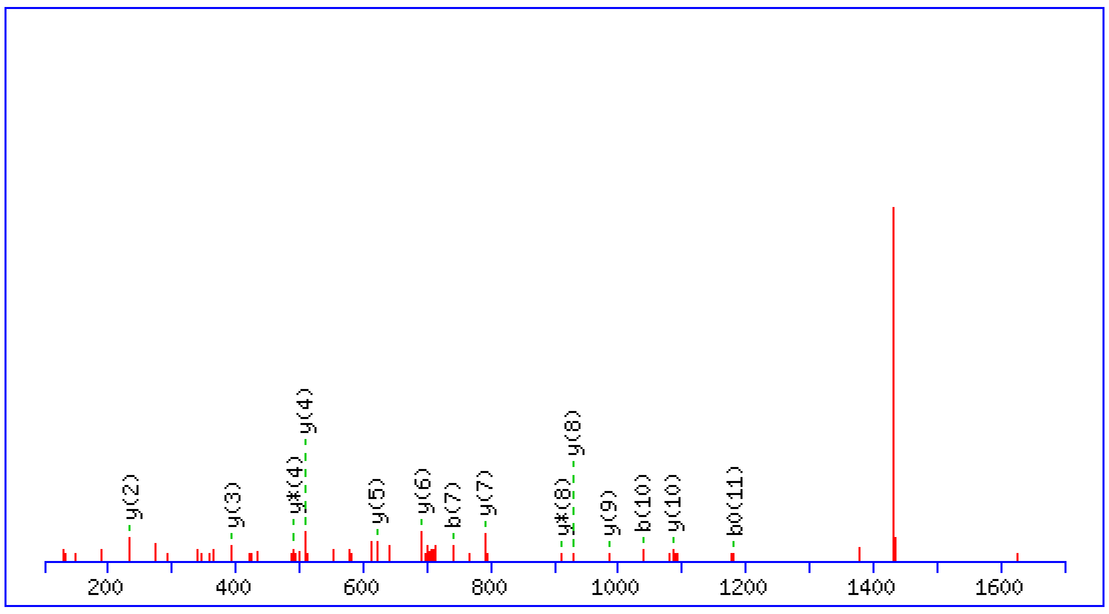
Mascot Search Results

Peptide View

MS/MS Fragmentation of **CGETGHVAINCSK**
Found in **CNBP_HUMAN**, Cellular nucleic acid-binding protein OS=Homo sapiens GN=CNBP PE=1 SV=1

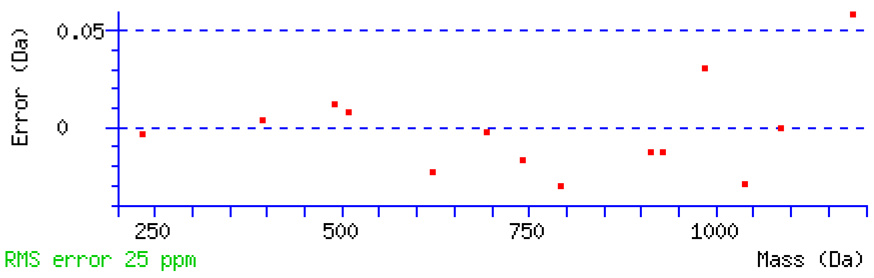
Match to Query 777755: 1431.632308 from(716.823430,2+) rtinseconds(1002) index(411943)
Title: Locus:1.1.1.716.17
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

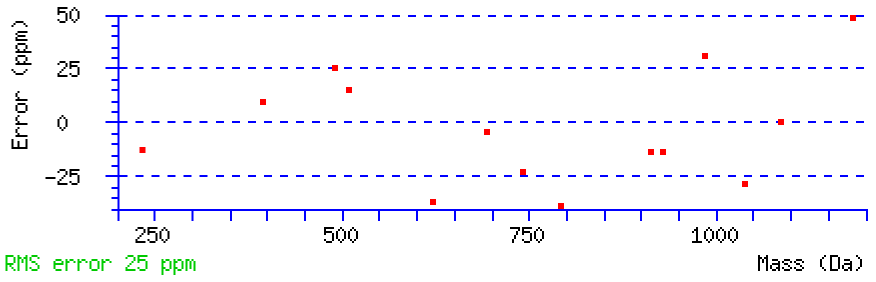
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1431.623489
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 72 **Expect:** 6.6e-007
Matches : 14/120 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	161.037925	81.022600					C							13
2	218.059389	109.533333					G	1272.600112	636.803694	1255.573563	628.290420	1254.589547	627.798412	12
3	347.101982	174.054629			329.091417	165.049347	E	1215.578648	608.292962	1198.552099	599.779688	1197.568083	599.287680	11
4	448.149661	224.578469			430.139096	215.573186	T	***1086.536055***	543.771666	1069.509506	535.258391	1068.525490	534.766383	10
5	505.171125	253.089201			487.160560	244.083918	G	***985.488376***	493.247826	968.461827	484.734552	967.477811	484.242544	9
6	642.230037	321.618657			624.219472	312.613374	H	***928.466912***	464.737094	911.440363	456.223820	910.456347	455.731812	8
7	**741.298451**	371.152864			723.287886	362.147581	V	***791.408000***	396.207638	774.381451	387.694364	773.397435	387.202356	7
8	812.335565	406.671421			794.325000	397.666138	A	***692.339586***	346.673431	675.313037	338.160157	674.329021	337.668149	6
9	925.419629	463.213453			907.409064	454.208170	I	***621.302472***	311.154874	604.275923	302.641600	603.291907	302.149592	5
10	**1039.462556**	520.234916	1022.436007	511.721641	1021.451991	511.229633	N	***508.218408***	254.612842	491.191859	246.099568	490.207843	245.607560	4
11	1199.493205	600.250241	1182.466656	591.736966	1181.482640	591.244958	C	***394.175481***	197.591379	377.148932	189.078104	376.164916	188.586096	3
12	1286.525233	643.766255	1269.498684	635.252980	1268.514668	634.760972	S	***234.144832***	117.576054	217.118283	109.062780	216.134267	108.570772	2
13							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
71.8	1431.623489	0.008819	CGETGHVAINCSK
3.5	1431.640518	-0.008210	EYEGYEVESSLK

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

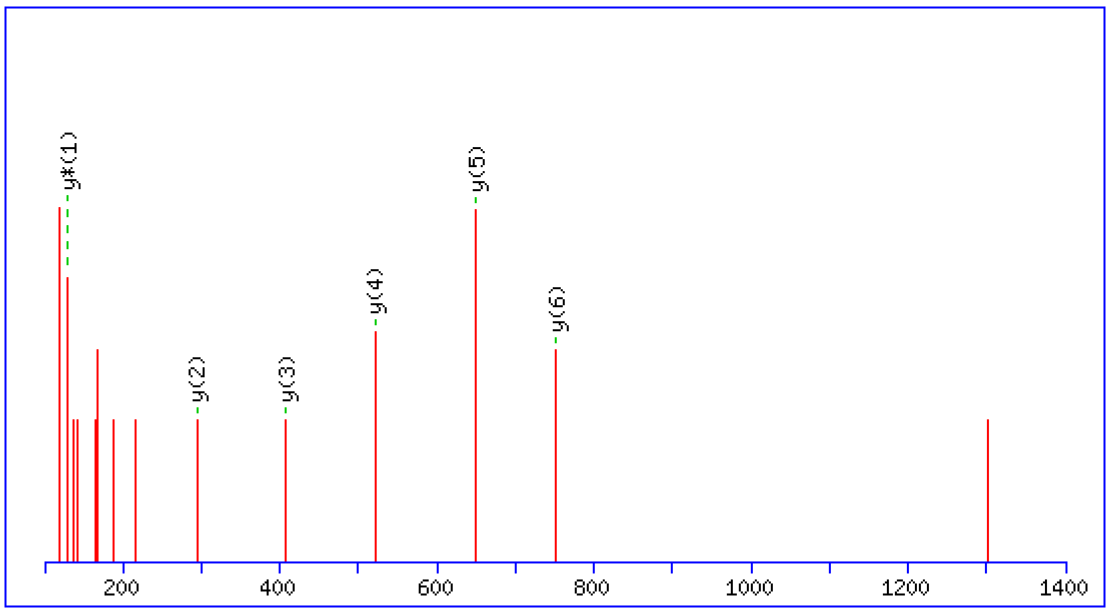
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TTEINFK**
Found in **RABP1_HUMAN**, Cellular retinoic acid-binding protein 1 OS=Homo sapiens GN=CRABP1 PE=1 SV=2

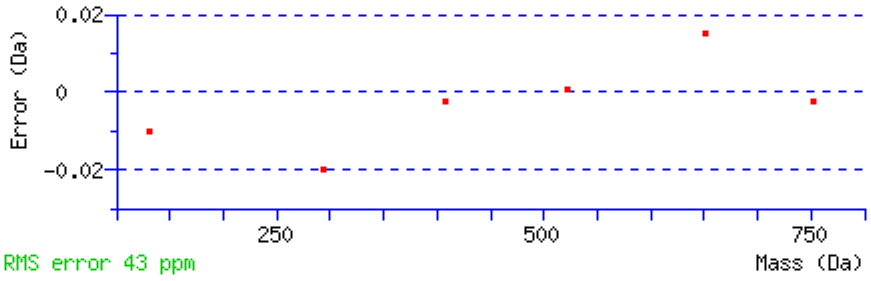
Match to Query 4462: 851.435008 from(426.724780,2+) rtinseconds(1625) index(9455)
Title: Locus:1.1.1.1946.6
Data file 2011-11-12 - TFD - EP 5-7.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●

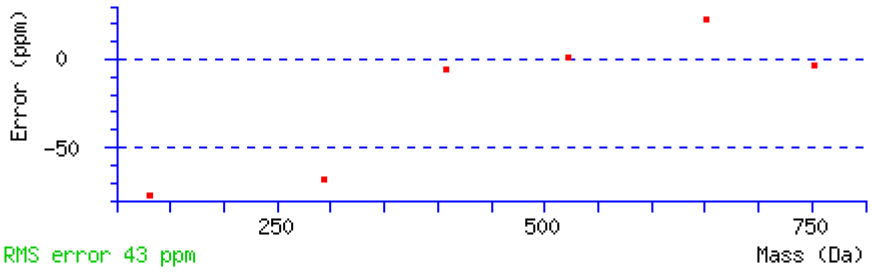


Monoisotopic mass of neutral peptide Mr(calc): 851.438873
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 48 **Expect:** 0.00014
Matches : 6/56 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	**T**							7
2	203.102634	102.054955			185.092069	93.049672	**T**	***751.398481***	376.202879	734.371932	367.689604	733.387916	367.197596	6
3	332.145227	166.576252			314.134662	157.570969	**E**	***650.350802***	325.679039	633.324253	317.165765	632.340237	316.673757	5
4	445.229291	223.118284			427.218726	214.113001	**I**	***521.308209***	261.157743	504.281660	252.644468			4
5	559.272218	280.139747	542.245669	271.626473	541.261653	271.134465	**N**	***408.224145***	204.615710	391.197596	196.102436			3
6	706.340632	353.673954	689.314083	345.160680	688.330067	344.668672	**F**	***294.181218***	147.594247	277.154669	139.080972			2
7							**K**	147.112804	74.060040	130.086255	65.546765			1



RMS error 43 ppm



RMS error 43 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.7	851.438873	-0.003865	TTEINFK
16.7	851.438873	-0.003865	TTLNEFK
6.2	851.438889	-0.003881	TTFDPKK

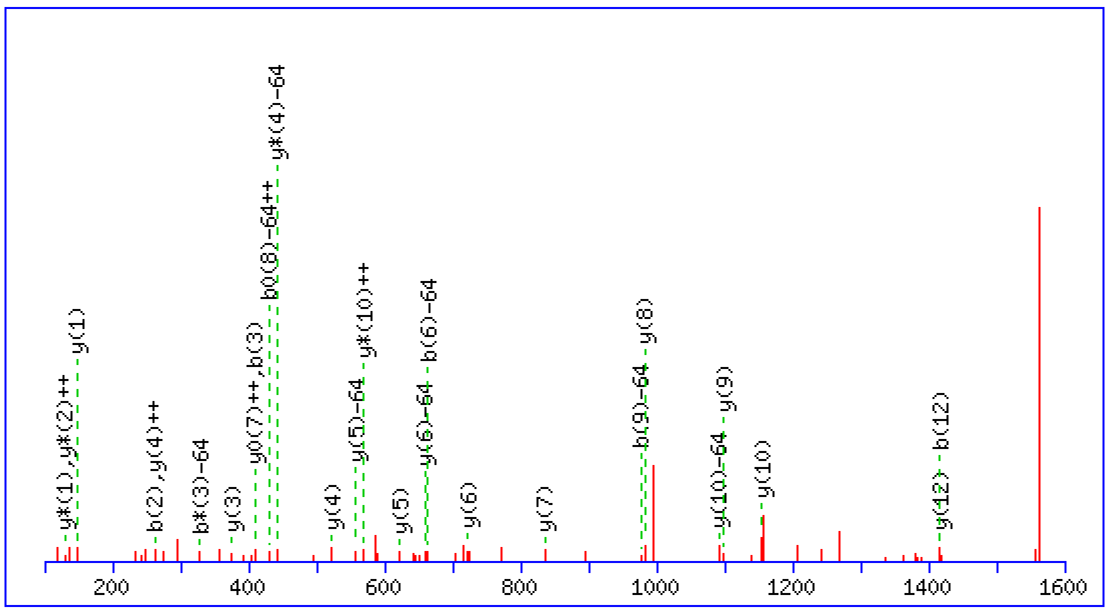
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MNFGDFLTVMTQK**
Found in **CETN2_HUMAN**, Centrin-2 OS=Homo sapiens GN=CETN2 PE=1 SV=1

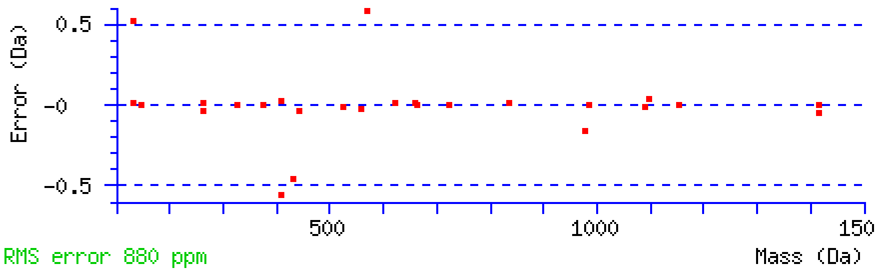
Match to Query 43285: 1562.700868 from(782.357710,2+) rtinseconds(3036) index(37439)
Title: Locus:1.1.1.2423.15
Data file 2011-11-10 - TFD - EP 3-6.mgf

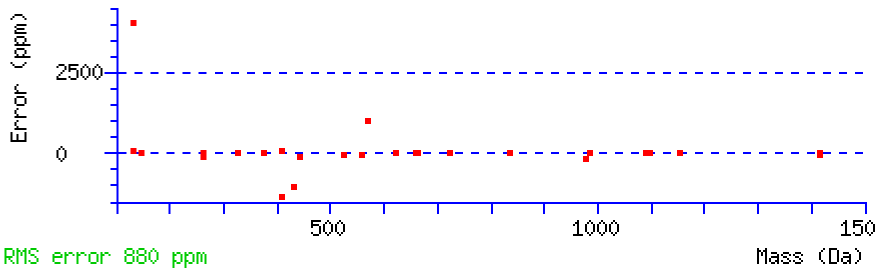
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1562.710922
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M1     : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
M10    : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 55  Expect: 1.9e-005
Matches : 26/246 fragment ions using 44 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.042676	74.524976					**M**							**13**
2	**262.085603**	131.546439	245.059054	123.033165			**N**	***1416.682780***	708.845028	1399.656231	700.331754	1398.672215	699.839746	**12**
3	**409.154017**	205.080647	392.127468	196.567372			**F**	1302.639853	651.823565	1285.613304	643.310290	1284.629288	642.818282	**11**
4	466.175481	233.591378	449.148932	225.078104			**G**	***1155.571439***	578.289358	1138.544890	569.776083	1137.560874	569.284075	**10**
5	581.202424	291.104850	564.175875	282.591576	563.191859	282.099568	**D**	***1098.549975***	549.778626	1081.523426	541.265351	1080.539410	540.773343	**9**
6	728.270838	364.639057	711.244289	356.125783	710.260273	355.633775	**F**	***983.523032***	492.265154	966.496483	483.751880	965.512467	483.259872	**8**
7	841.354902	421.181089	824.328353	412.667815	823.344337	412.175807	**L**	***836.454618***	418.730947	819.428069	410.217673	818.444053	409.725665	**7**
8	942.402581	471.704929	925.376032	463.191654	924.392016	462.699646	**T**	***723.370554***	362.188915	706.344005	353.675641	705.359989	353.183633	**6**
9	1041.470995	521.239136	1024.444446	512.725861	1023.460430	512.233853	**V**	***622.322875***	311.665076	605.296326	303.151801	604.312310	302.659793	**5**
10	1188.506395	594.756836	1171.479846	586.243561	1170.495830	585.751553	**M**	***523.254461***	262.130869	506.227912	253.617594	505.243896	253.125586	**4**
11	1289.554074	645.280675	1272.527525	636.767401	1271.543509	636.275393	**T**	***376.219061***	188.613168	359.192512	180.099894	358.208496	179.607886	**3**
12	**1417.612652**	709.309964	1400.586103	700.796690	1399.602087	700.304682	**Q**	275.171382	138.089329	258.144833	129.576054			**2**
13							**K**	***147.112804***	74.060040	130.086255	65.546765			**1**





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.8	1562.710922	-0.010054	MNFGDFLTVMTQK
5.7	1562.707336	-0.006468	KLDDDANHHQDQK
0.2	1562.689743	0.011125	YFASYMEQHLMK

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

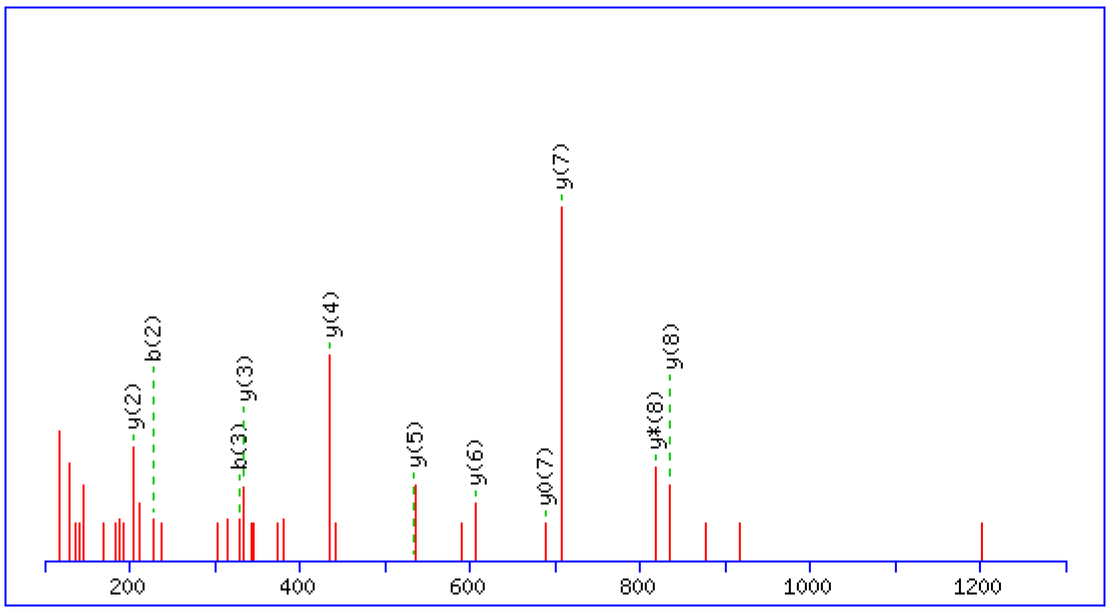
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VQTAVTMGK**
Found in **CHM1B_HUMAN**, Charged multivesicular body protein 1b OS=Homo sapiens GN=CHMP1B PE=1 SV=1

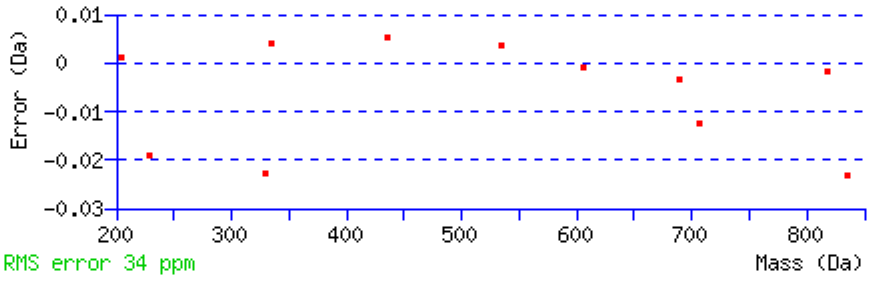
Match to Query 11131: 933.496468 from(467.755510,2+) rtinseconds(1163) index(5315)
Title: Locus:1.1.1.1763.19
Data file 2011-11-14 - TFD - EP 8-5.mgf

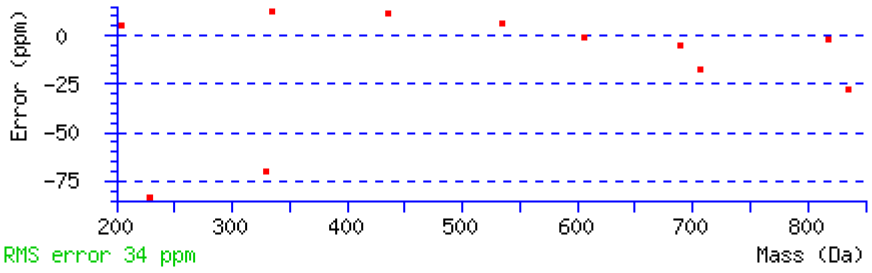
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 933.495361
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 67 **Expect:** 1.6e-006
Matches : 11/84 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							9
2	**228.134268**	114.570772	211.107719	106.057498			Q	***835.434217***	418.220747	818.407668	409.707472	817.423652	409.215464	8
3	**329.181947**	165.094612	312.155398	156.581337	311.171382	156.089329	T	***707.375639***	354.191458	690.349090	345.678183	689.365074	345.186175	7
4	400.219061	200.613169	383.192512	192.099894	382.208496	191.607886	A	***606.327960***	303.667618	589.301411	295.154344	588.317395	294.662336	6
5	499.287475	250.147376	482.260926	241.634101	481.276910	241.142093	V	***535.290846***	268.149061	518.264297	259.635787	517.280281	259.143779	5
6	600.335154	300.671215	583.308605	292.157941	582.324589	291.665933	T	***436.222432***	218.614854	419.195883	210.101579	418.211867	209.609571	4
7	731.375639	366.191458	714.349090	357.678183	713.365074	357.186175	M	***335.174753***	168.091015	318.148204	159.577740			3
8	788.397103	394.702190	771.370554	386.188915	770.386538	385.696907	G	***204.134268***	102.570772	187.107719	94.057498			2
9							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
66.5	933.495361	0.001107	VQTAVTMGK
4.4	933.503220	-0.006752	VFSKQPGR
0.8	933.503220	-0.006752	VTNFVAQR
0.6	933.503220	-0.006752	GLGFSIAGGR

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

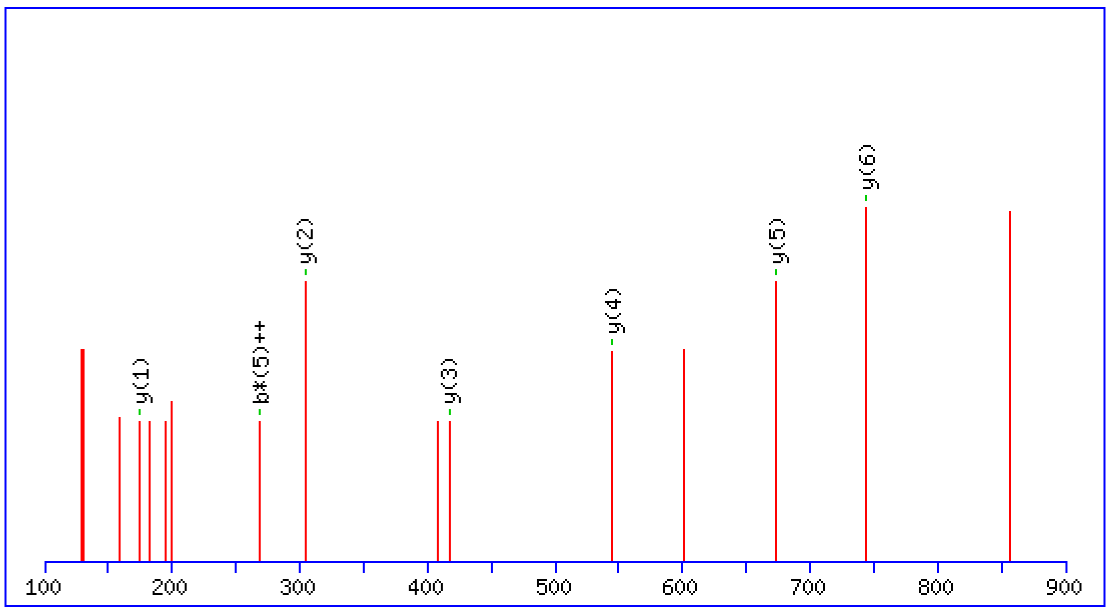
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IAQQLER**
Found in **CHMP6_HUMAN**, Charged multivesicular body protein 6 OS=Homo sapiens GN=CHMP6 PE=1 SV=3

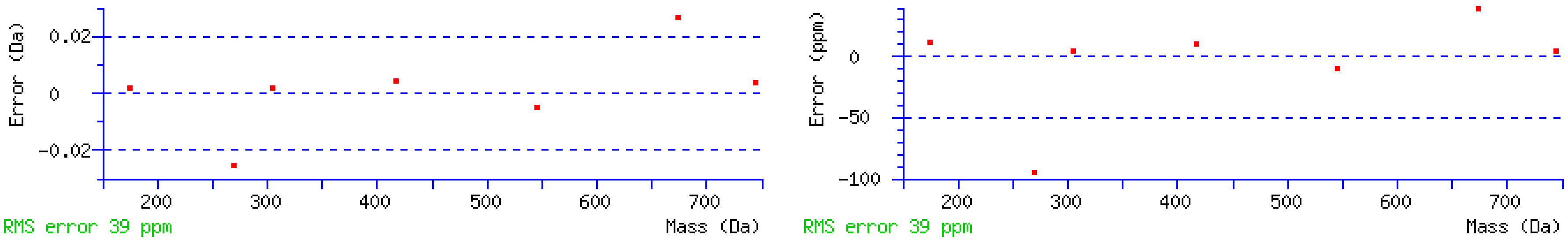
Match to Query 4695: 856.471588 from(429.243070,2+) rtinseconds(1034) index(3697)
Title: Locus:1.1.1.1812.11
Data file 2011-11-12 - TFD - EP 5-4.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 856.476639
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 42 **Expect:** 0.00083
Matches : 7/56 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					I							7
2	185.128454	93.067865					A	*744.399879*	372.703578	727.373330	364.190303	726.389314	363.698295	6
3	313.187032	157.097154	296.160483	148.583879			Q	*673.362765*	337.185021	656.336216	328.671746	655.352200	328.179738	5
4	441.245610	221.126443	424.219061	212.613169			Q	*545.304187*	273.155732	528.277638	264.642457	527.293622	264.150449	4
5	554.329674	277.668475	537.303125	269.155201			L	*417.245609*	209.126443	400.219060	200.613168	399.235044	200.121160	3
6	683.372267	342.189772	666.345718	333.676497	665.361702	333.184489	E	*304.161545*	152.584411	287.134996	144.071136	286.150980	143.579128	2
7							R	*175.118952*	88.063114	158.092403	79.549840			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.1	856.476639	-0.005051	IAQQLER
27.6	856.476639	-0.005051	LQAQLER
15.8	856.476639	-0.005051	KAPKPER
13.4	856.465408	0.006180	LAKEGDPK
6.3	856.476639	-0.005051	IAELQQR
6.3	856.476639	-0.005051	LAELQQR
6.3	856.476639	-0.005051	LAGQLEAR
6.3	856.476639	-0.005051	LASPNLSR
6.3	856.476639	-0.005051	KASPGLER
5.9	856.476639	-0.005051	QAIQELR

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

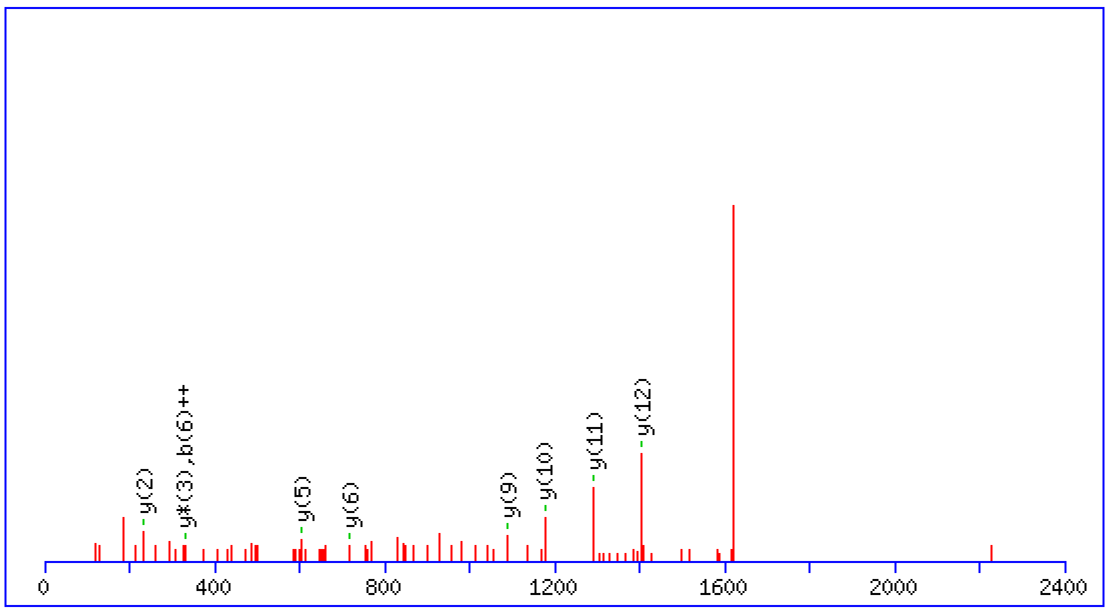
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NVLDSEDEIEELSK**
Found in **CHID1_HUMAN**, Chitinase domain-containing protein 1 OS=Homo sapiens GN=CHID1 PE=1 SV=1

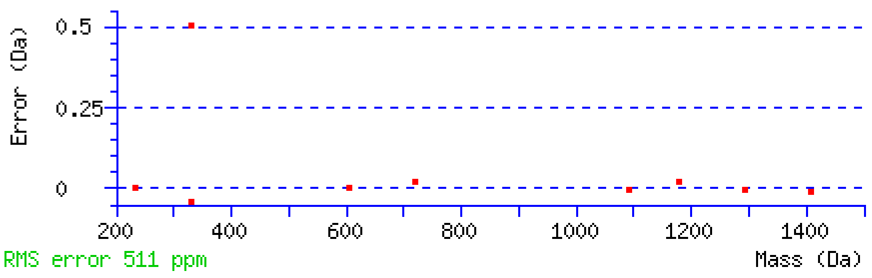
Match to Query 51273: 1618.760308 from(810.387430,2+) rtinseconds(2889) index(39822)
Title: Locus:1.1.1.2425.43
Data file 2011-11-10 - TFD - EP 4-4.mgf

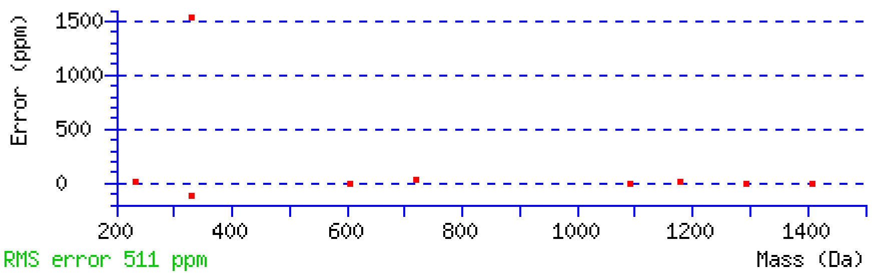
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1618.757339
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.00051
Matches : 9/148 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			N							14
2	214.118617	107.562947	197.092068	99.049672			V	1505.721724	753.364500	1488.695175	744.851226	1487.711159	744.359218	13
3	327.202681	164.104978	310.176132	155.591704			L	***1406.653310***	703.830293	1389.626761	695.317019	1388.642745	694.825010	12
4	442.229624	221.618450	425.203075	213.105176	424.219059	212.613168	D	***1293.569246***	647.288261	1276.542697	638.774987	1275.558681	638.282979	11
5	529.261652	265.134464	512.235103	256.621190	511.251087	256.129182	S	***1178.542303***	589.774790	1161.515754	581.261515	1160.531738	580.769507	10
6	658.304245	329.655761	641.277696	321.142486	640.293680	320.650478	E	***1091.510275***	546.258775	1074.483726	537.745501	1073.499710	537.253493	9
7	773.331188	387.169232	756.304639	378.655958	755.320623	378.163950	D	962.467682	481.737479	945.441133	473.224204	944.457117	472.732196	8
8	902.373781	451.690529	885.347232	443.177254	884.363216	442.685246	E	847.440739	424.224008	830.414190	415.710733	829.430174	415.218725	7
9	1015.457845	508.232561	998.431296	499.719286	997.447280	499.227278	I	***718.398146***	359.702711	701.371597	351.189437	700.387581	350.697429	6
10	1144.500438	572.753857	1127.473889	564.240583	1126.489873	563.748575	E	***605.314082***	303.160679	588.287533	294.647404	587.303517	294.155396	5
11	1273.543031	637.275153	1256.516482	628.761879	1255.532466	628.269871	E	476.271489	238.639382	459.244940	230.126108	458.260924	229.634100	4
12	1386.627095	693.817185	1369.600546	685.303911	1368.616530	684.811903	L	347.228896	174.118086	330.202347	165.604811	329.218331	165.112803	3
13	1473.659123	737.333199	1456.632574	728.819925	1455.648558	728.327917	S	***234.144832***	117.576054	217.118283	109.062780	216.134267	108.570772	2
14							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.1	1618.757339	0.002969	NVLDSEDEIEELSK

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

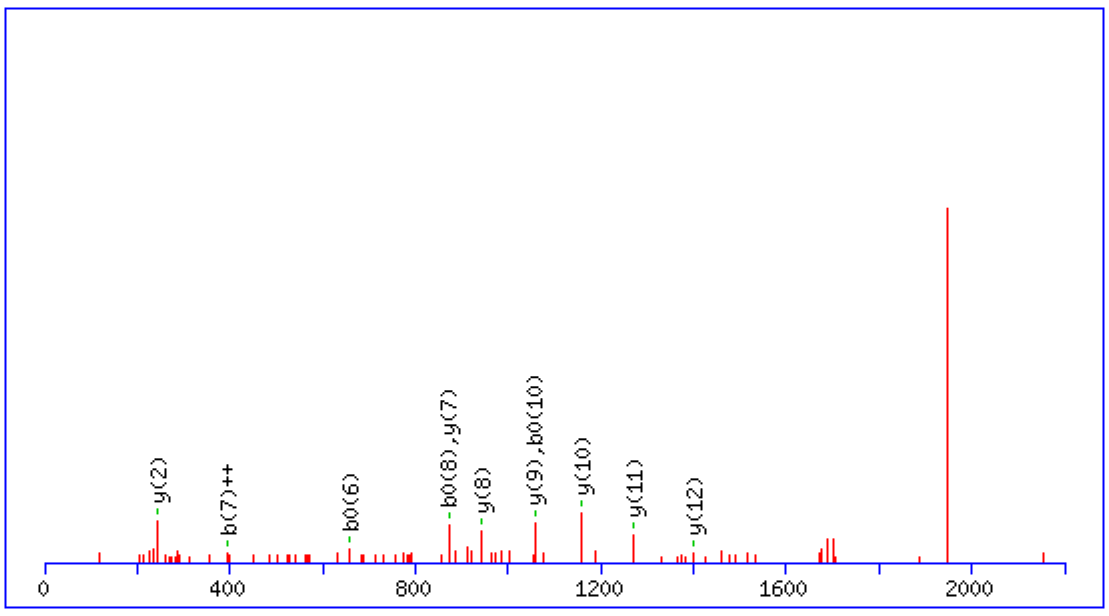
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FLDGDELTLADCNLLPK**
Found in **CLIC5_HUMAN**, Chloride intracellular channel protein 5 OS=Homo sapiens GN=CLIC5 PE=1 SV=3

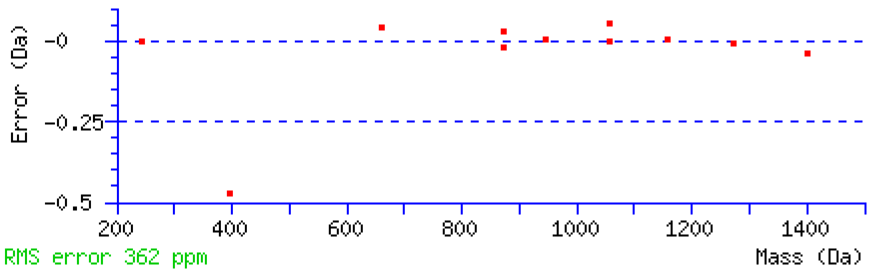
Match to Query 64741: 1946.966708 from(974.490630,2+) rtinseconds(3609) index(52384)
Title: Locus:1.1.1.2785.48
Data file 2011-11-12 - TFD - EP 5-4.mgf

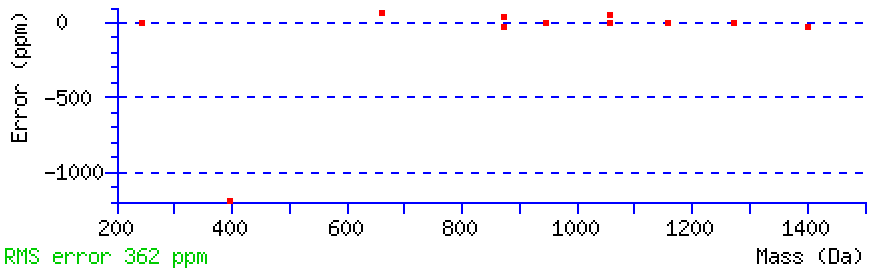
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1946.965912
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 32  Expect: 0.0047
Matches : 11/152 fragment ions using 17 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	148.075690	74.541483					F							17
2	261.159754	131.083515					L	1800.904793	900.956034	1783.878244	892.442760	1782.894228	891.950752	16
3	376.186697	188.596986			358.176132	179.591704	D	1687.820729	844.414003	1670.794180	835.900728	1669.810164	835.408720	15
4	433.208161	217.107718			415.197596	208.102436	G	1572.793786	786.900531	1555.767237	778.387257	1554.783221	777.895248	14
5	548.235104	274.621190			530.224539	265.615907	D	1515.772322	758.389799	1498.745773	749.876525	1497.761757	749.384517	13
6	677.277697	339.142487			659.267132	330.137204	E	***1400.745379***	700.876328	1383.718830	692.363053	1382.734814	691.871045	12
7	790.361761	395.684519			772.351196	386.679236	L	***1271.702786***	636.355031	1254.676237	627.841757	1253.692221	627.349749	11
8	891.409440	446.208358			873.398875	437.203076	T	***1158.618722***	579.812999	1141.592173	571.299725	1140.608157	570.807716	10
9	1004.493504	502.750390			986.482939	493.745108	L	***1057.571043***	529.289160	1040.544494	520.775885	1039.560478	520.283877	9
10	1075.530618	538.268947			1057.520053	529.263665	A	***944.486979***	472.747128	927.460430	464.233853	926.476414	463.741845	8
11	1190.557561	595.782419			1172.546996	586.777136	D	***873.449865***	437.228571	856.423316	428.715296	855.439300	428.223288	7
12	1364.603860	682.805568			1346.593295	673.800286	C	758.422922	379.715099	741.396373	371.201824			6
13	1478.646787	739.827032	1461.620238	731.313757	1460.636222	730.821749	N	584.376623	292.691949	567.350074	284.178675			5
14	1591.730851	796.369064	1574.704302	787.855789	1573.720286	787.363781	L	470.333696	235.670486	453.307147	227.157211			4
15	1704.814915	852.911095	1687.788366	844.397821	1686.804350	843.905813	L	357.249632	179.128454	340.223083	170.615179			3
16	1801.867679	901.437478	1784.841130	892.924203	1783.857114	892.432195	P	***244.165568***	122.586422	227.139019	114.073148			2
17							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.2	1946.965912	0.000796	FLDGDELTLADCNLLPK
7.1	1946.985886	-0.019178	VLWLFGMDLNKMTHSR
2.1	1946.969330	-0.002622	DPKTLLPMPGVMVGDIGK

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

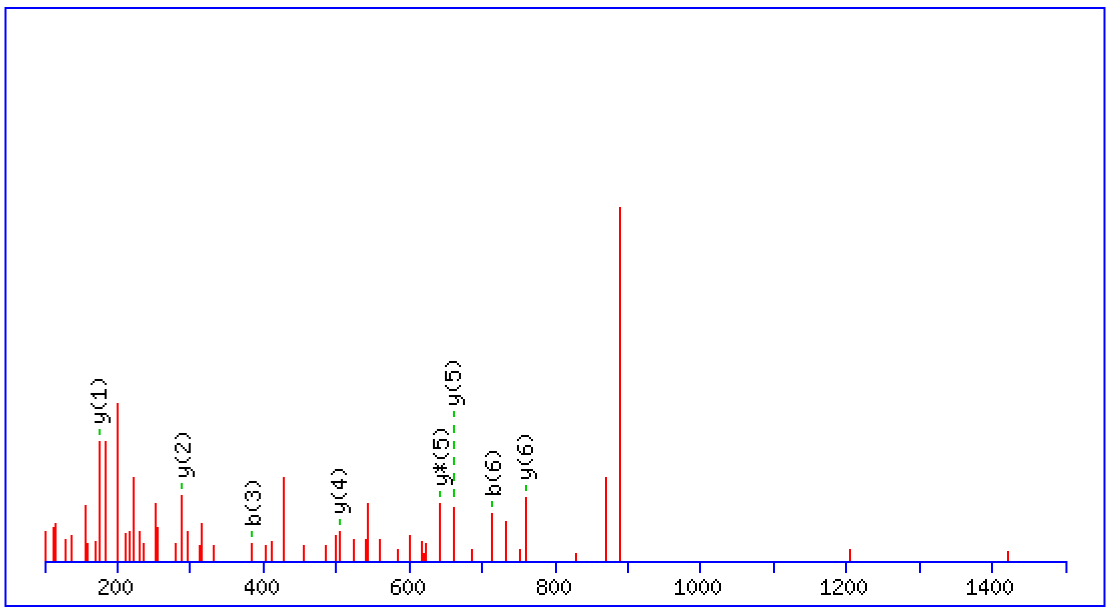
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EVRESIR**
Found in **CP46A_HUMAN**, Cholesterol 24-hydroxylase OS=Homo sapiens GN=CYP46A1 PE=1 SV=1

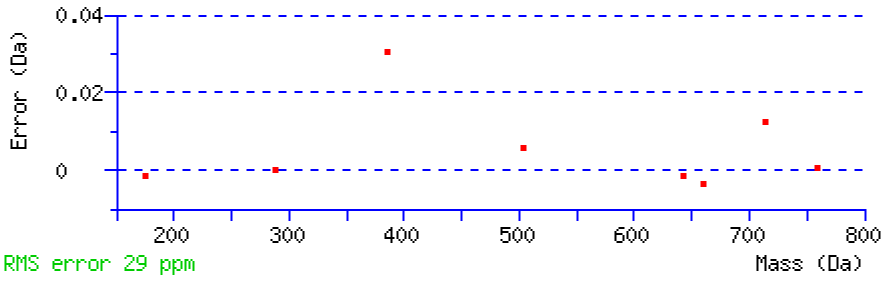
Match to Query 5918: 887.485488 from(444.750020,2+) rtinseconds(1004) index(3998)
Title: Locus:1.1.1.1794.17
Data file 2011-11-10 - TFD - EP 3-3.mgf

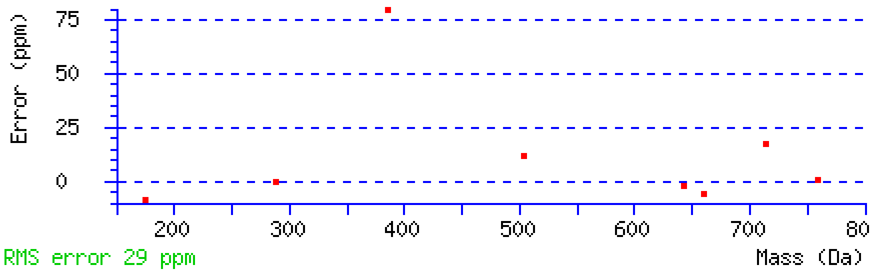
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 887.482452
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 34  Expect: 0.0062
Matches : 8/64 fragment ions using 16 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	E							7
2	229.118283	115.062780			211.107718	106.057497	V	*759.447162*	380.227219	742.420613	371.713945	741.436597	371.221937	6
3	**385.219394**	193.113335	368.192845	184.600061	367.208829	184.108053	R	*660.378748*	330.693012	643.352199	322.179738	642.368183	321.687730	5
4	514.261987	257.634632	497.235438	249.121357	496.251422	248.629349	E	*504.277637*	252.642456	487.251088	244.129182	486.267072	243.637174	4
5	601.294015	301.150646	584.267466	292.637371	583.283450	292.145363	S	375.235044	188.121160	358.208495	179.607885	357.224479	179.115877	3
6	**714.378079**	357.692678	697.351530	349.179403	696.367514	348.687395	I	*288.203016*	144.605146	271.176467	136.091871			2
7							R	*175.118952*	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.7	887.482452	0.003036	EVRESIR
21.1	887.489853	-0.004365	DIKMPLR
20.1	887.493683	-0.008195	SSSKPRAR
18.6	887.486481	-0.000993	IEFNPIR
15.1	887.493683	-0.008195	RASATINR
15.0	887.489838	-0.004350	CIELIAR
14.3	887.482452	0.003036	RDLESLR
12.9	887.482452	0.003036	RVEESLR
12.7	887.482452	0.003036	SLSLQANR
11.4	887.482452	0.003036	DRISELR

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

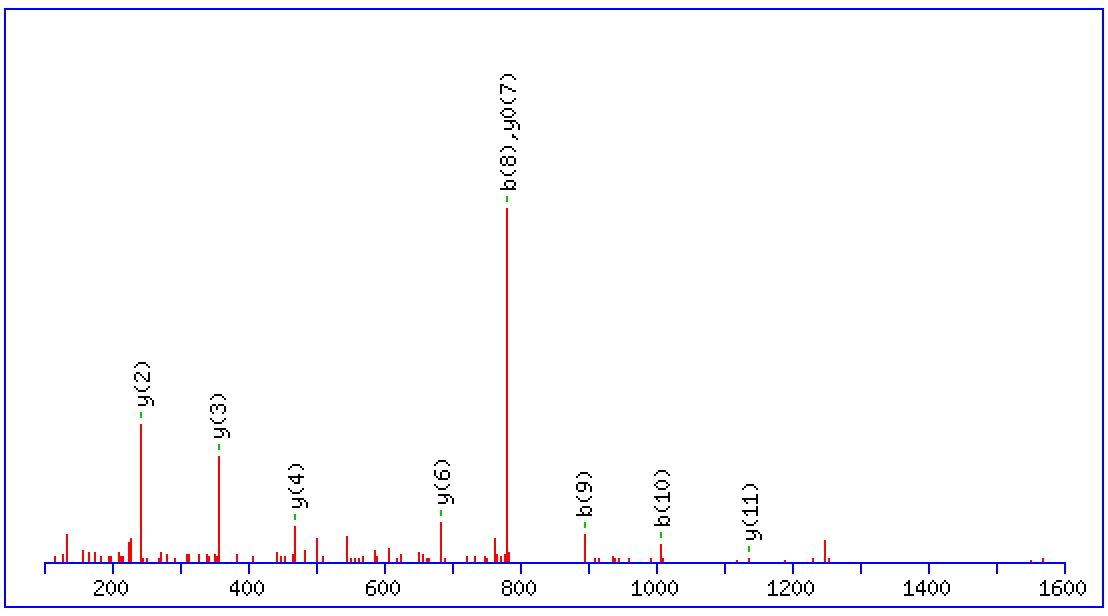
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **LPGPSDTPILPQ**
Found in **CGB2_HUMAN**, Choriogonadotropin subunit beta variant 2 OS=Homo sapiens GN=CGB2 PE=2 SV=4

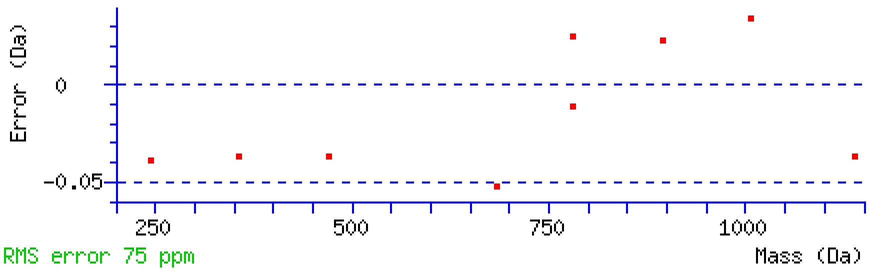
Match to Query 32717: 1249.643668 from(625.829110,2+) rtinseconds(1747) index(18287)
Title: Locus:1.1.1.1985.48
Data file 2011-11-12 - TFD - EP 6-1.mgf

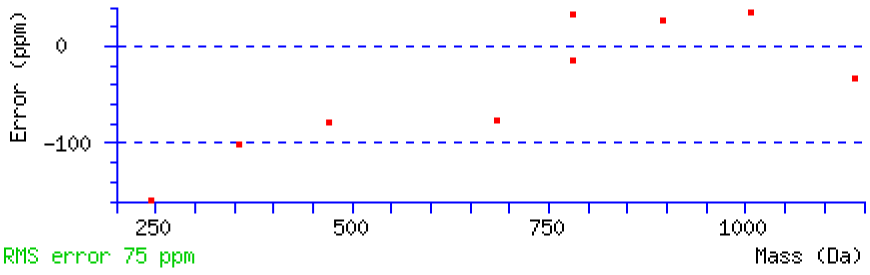
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1249.655426
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P8 : Oxidation (P)
Ions Score: 37 **Expect:** 0.0023
Matches : 9/92 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308			L							12
2	211.144104	106.075690			P	***1137.578632***	569.292954	1120.552083	560.779680	1119.568067	560.287672	11
3	268.165568	134.586422			G	1040.525868	520.766572	1023.499319	512.253298	1022.515303	511.761290	10
4	365.218332	183.112804			P	983.504404	492.255840	966.477855	483.742566	965.493839	483.250558	9
5	452.250360	226.628818	434.239795	217.623535	S	886.451640	443.729458	869.425091	435.216184	868.441075	434.724176	8
6	567.277303	284.142290	549.266738	275.137007	D	799.419612	400.213444	782.393063	391.700170	781.409047	391.208162	7
7	668.324982	334.666129	650.314417	325.660846	T	***684.392669***	342.699973	667.366120	334.186698	666.382104	333.694690	6
8	**781.372661**	391.189969	763.362096	382.184686	P	583.344990	292.176133	566.318441	283.662859			5
9	**894.456725**	447.732001	876.446160	438.726718	I	***470.297311***	235.652294	453.270762	227.139019			4
10	**1007.540789**	504.274033	989.530224	495.268750	L	***357.213247***	179.110262	340.186698	170.596987			3
11	1104.593553	552.800414	1086.582988	543.795132	P	***244.129183***	122.568230	227.102634	114.054955			2
12					Q	147.076419	74.041848	130.049870	65.528573			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.9	1249.655426	-0.011758	LPGPSDTPILPQ
33.7	1249.641479	0.002189	DQLLPPSPNNR
32.5	1249.655426	-0.011758	LPGPSDTPILPQ
32.5	1249.655426	-0.011758	LPGPSDTPILPQ
12.5	1249.652756	-0.009088	KGPGPGGPGGAGVAR
7.3	1249.652756	-0.009088	KGPGPGGPGGAGVAR
6.3	1249.652710	-0.009042	LPRSEKPHDR
3.1	1249.652710	-0.009042	LSRGHEELPGR
1.9	1249.655426	-0.011758	LPGPSDTPILPQ
1.6	1249.645508	-0.001840	LENSTFFHKK

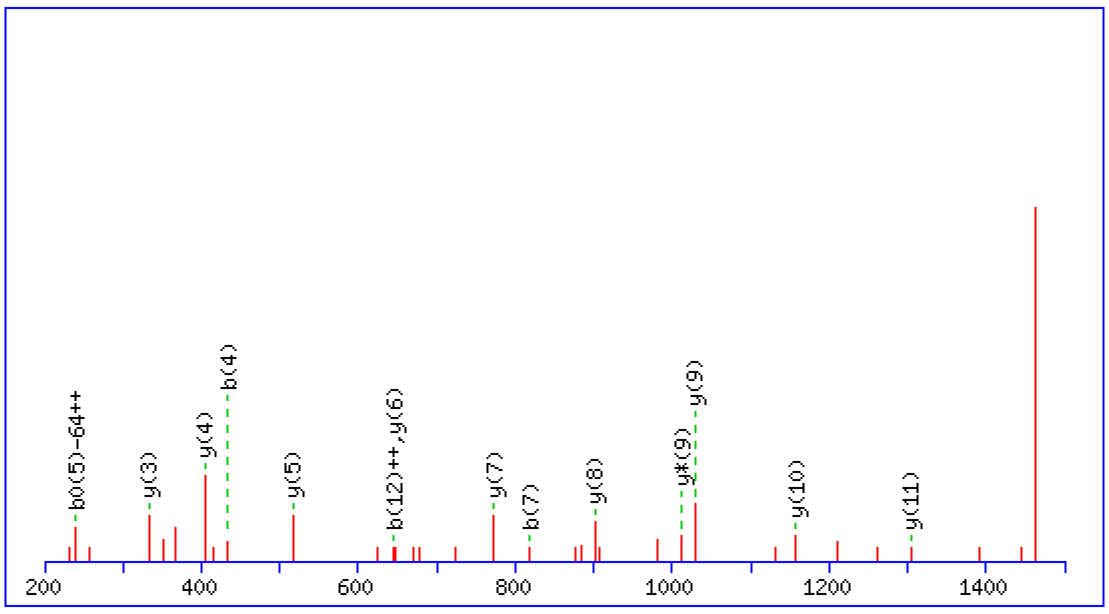
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ASMQQQQQLASAR**
Found in **CHTOP_HUMAN**, Chromatin target of PRMT1 protein OS=Homo sapiens GN=CHTOP PE=1 SV=2

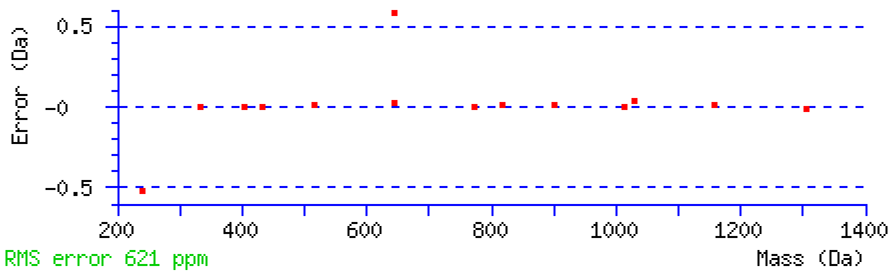
Match to Query 43529: 1461.693908 from(731.854230,2+) rtinseconds(1014) index(2783)
Title: Locus:1.1.1.1700.37
Data file 2011-11-10 - TFD - EP 4-5.mgf

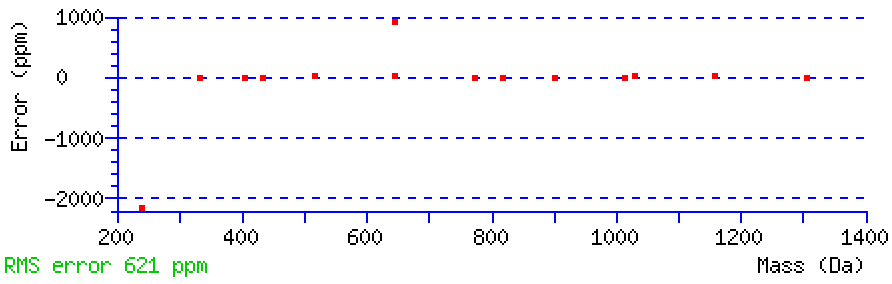
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1461.699402
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M3 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 68 **Expect:** 1.6e-006
Matches : 14/202 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	72.044390	36.525833					A							13
2	159.076418	80.041847			141.065853	71.036564	S	1391.669590	696.338433	1374.643041	687.825159	1373.659025	687.333151	12
3	306.111818	153.559547			288.101253	144.554264	M	***1304.637562***	652.822419	1287.611013	644.309145	1286.626997	643.817137	11
4	**434.170396**	217.588836	417.143847	209.075561	416.159831	208.583553	Q	***1157.602162***	579.304719	1140.575613	570.791445	1139.591597	570.299437	10
5	562.228974	281.618125	545.202425	273.104851	544.218409	272.612843	Q	***1029.543584***	515.275430	1012.517035	506.762156	1011.533019	506.270148	9
6	690.287552	345.647414	673.261003	337.134140	672.276987	336.642132	Q	***901.485006***	451.246141	884.458457	442.732867	883.474441	442.240859	8
7	**818.346130**	409.676703	801.319581	401.163429	800.335565	400.671421	Q	***773.426428***	387.216852	756.399879	378.703578	755.415863	378.211570	7
8	946.404708	473.705992	929.378159	465.192718	928.394143	464.700710	Q	***645.367850***	323.187563	628.341301	314.674289	627.357285	314.182281	6
9	1059.488772	530.248024	1042.462223	521.734750	1041.478207	521.242742	L	***517.309272***	259.158274	500.282723	250.645000	499.298707	250.152992	5
10	1130.525886	565.766581	1113.499337	557.253307	1112.515321	556.761299	A	***404.225208***	202.616242	387.198659	194.102967	386.214643	193.610959	4
11	1217.557914	609.282595	1200.531365	600.769321	1199.547349	600.277313	S	***333.188094***	167.097685	316.161545	158.584410	315.177529	158.092402	3
12	1288.595028	644.801152	1271.568479	636.287878	1270.584463	635.795870	A	246.156066	123.581671	229.129517	115.068396			2
13							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
67.7	1461.699402	-0.005494	ASMQQQQQLASAR
5.9	1461.696045	-0.002137	AFSQSSSLTNHQR

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

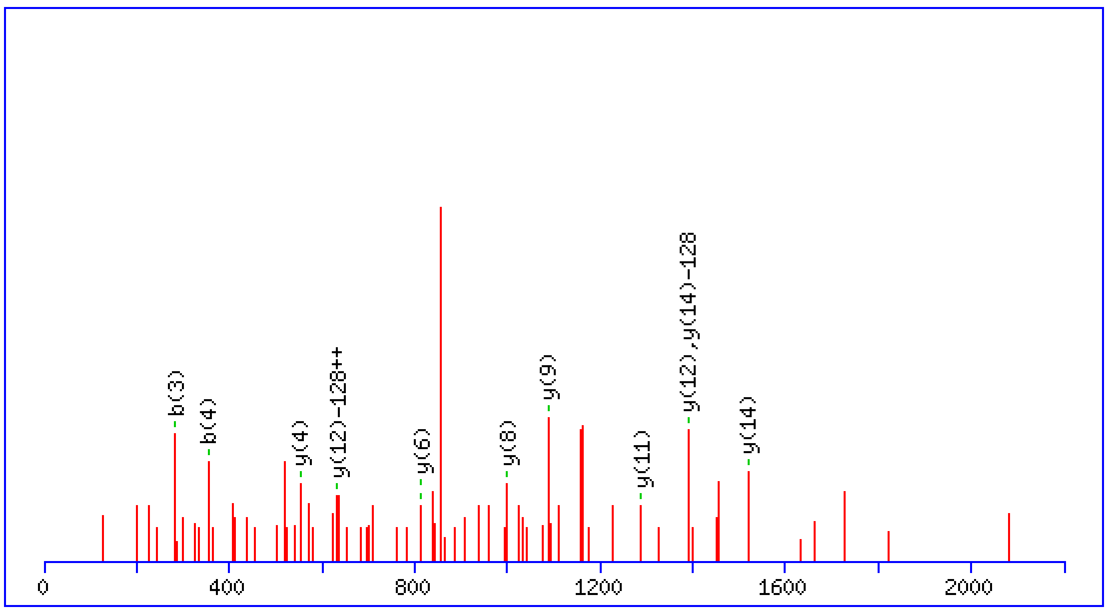
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IIGATDSSGELMFLMK**
Found in **CBX1_HUMAN**, Chromobox protein homolog 1 OS=Homo sapiens GN=CBX1 PE=1 SV=1

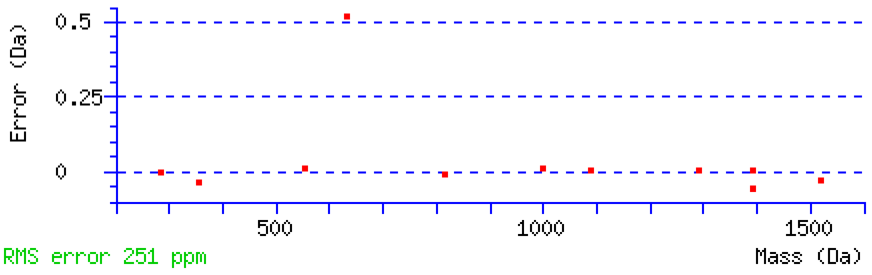
Match to Query 51983: 1743.831608 from(872.923080,2+) rtinseconds(2925) index(38849)
Title: Locus:1.1.1.2403.50
Data file 2011-11-12 - TFD - EP 6-5.mgf

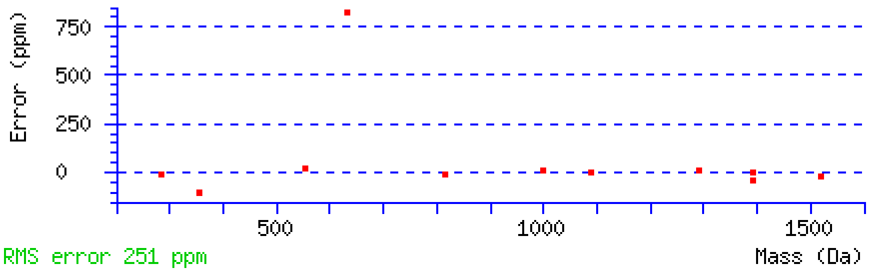
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1743.842300
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M12    : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
M15    : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 48  Expect: 0.00017
Matches : 11/220 fragment ions using 15 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							16
2	227.175404	114.091340			I	1631.765523	816.386400	1614.738974	807.873125	1613.754958	807.381117	15
3	**284.196868**	142.602072			G	***1518.681459***	759.844367	1501.654910	751.331093	1500.670894	750.839085	14
4	**355.233982**	178.120629			A	1461.659995	731.333636	1444.633446	722.820361	1443.649430	722.328353	13
5	456.281661	228.644469	438.271096	219.639186	T	***1390.622881***	695.815079	1373.596332	687.301804	1372.612316	686.809796	12
6	571.308604	286.157940	553.298039	277.152658	D	***1289.575202***	645.291239	1272.548653	636.777964	1271.564637	636.285956	11
7	658.340632	329.673954	640.330067	320.668672	S	1174.548259	587.777767	1157.521710	579.264493	1156.537694	578.772485	10
8	745.372660	373.189968	727.362095	364.184686	S	***1087.516231***	544.261753	1070.489682	535.748479	1069.505666	535.256471	9
9	802.394124	401.700700	784.383559	392.695418	G	***1000.484203***	500.745740	983.457654	492.232465	982.473638	491.740457	8
10	931.436717	466.221997	913.426152	457.216714	E	943.462739	472.235007	926.436190	463.721733	925.452174	463.229725	7
11	1044.520781	522.764028	1026.510216	513.758746	L	***814.420146***	407.713711	797.393597	399.200436			6
12	1191.556181	596.281728	1173.545616	587.276446	M	701.336082	351.171679	684.309533	342.658405			5
13	1338.624595	669.815936	1320.614030	660.810653	F	***554.300682***	277.653979	537.274133	269.140705			4
14	1451.708659	726.357967	1433.698094	717.352685	L	407.232268	204.119772	390.205719	195.606497			3
15	1598.744059	799.875667	1580.733494	790.870385	M	294.148204	147.577740	277.121655	139.064465			2
16					K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.2	1743.842300	-0.010692	IIGATDSSGELMFLMK

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

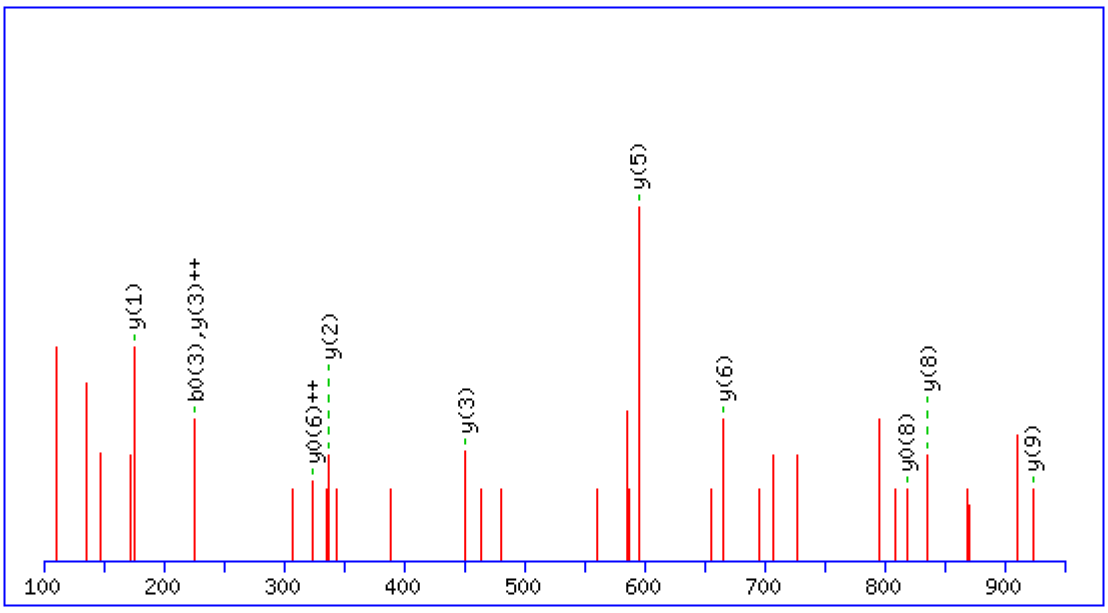
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VSGLAGSIYR**
Found in **JIP3_HUMAN**, C-Jun-amino-terminal kinase-interacting protein 3 OS=Homo sapiens GN=MAPK8IP3 PE=1 SV=3

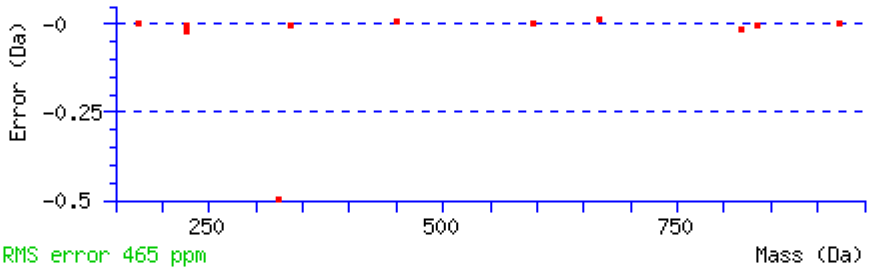
Match to Query 290591: 1021.553968 from(511.784260,2+) rtinseconds(2026) index(916344)
Title: Locus:1.1.1.1172.20
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

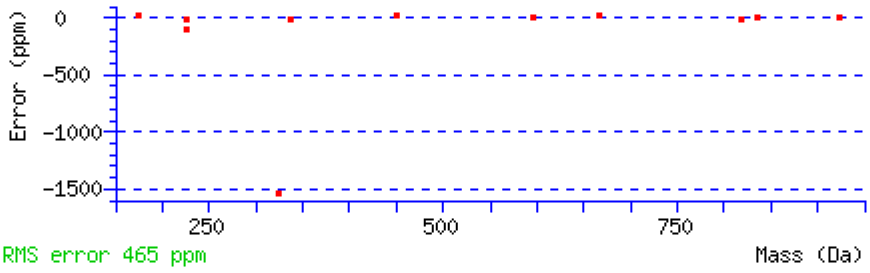
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1021.555634
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 47 **Expect:** 0.0002
Matches : 11/82 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483			**V**							**10**
2	187.107718	94.057497	169.097153	85.052214	**S**	***923.494507***	462.250892	906.467958	453.737617	905.483942	453.245609	**9**
3	244.129182	122.568229	226.118617	113.562946	**G**	***836.462479***	418.734878	819.435930	410.221603	818.451914	409.729595	**8**
4	357.213246	179.110261	339.202681	170.104978	**L**	779.441015	390.224146	762.414466	381.710871	761.430450	381.218863	**7**
5	428.250360	214.628818	410.239795	205.623535	**A**	***666.356951***	333.682114	649.330402	325.168839	648.346386	324.676831	**6**
6	485.271824	243.139550	467.261259	234.134267	**G**	***595.319837***	298.163557	578.293288	289.650282	577.309272	289.158274	**5**
7	572.303852	286.655564	554.293287	277.650282	**S**	538.298373	269.652825	521.271824	261.139550	520.287808	260.647542	**4**
8	685.387916	343.197596	667.377351	334.192314	**I**	***451.266345***	226.136810	434.239796	217.623536			**3**
9	848.451245	424.729261	830.440680	415.723978	**Y**	***338.182281***	169.594778	321.155732	161.081504			**2**
10					**R**	***175.118952***	88.063114	158.092403	79.549839			**1**





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.8	1021.555634	-0.001666	VSGLAGSIYR

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

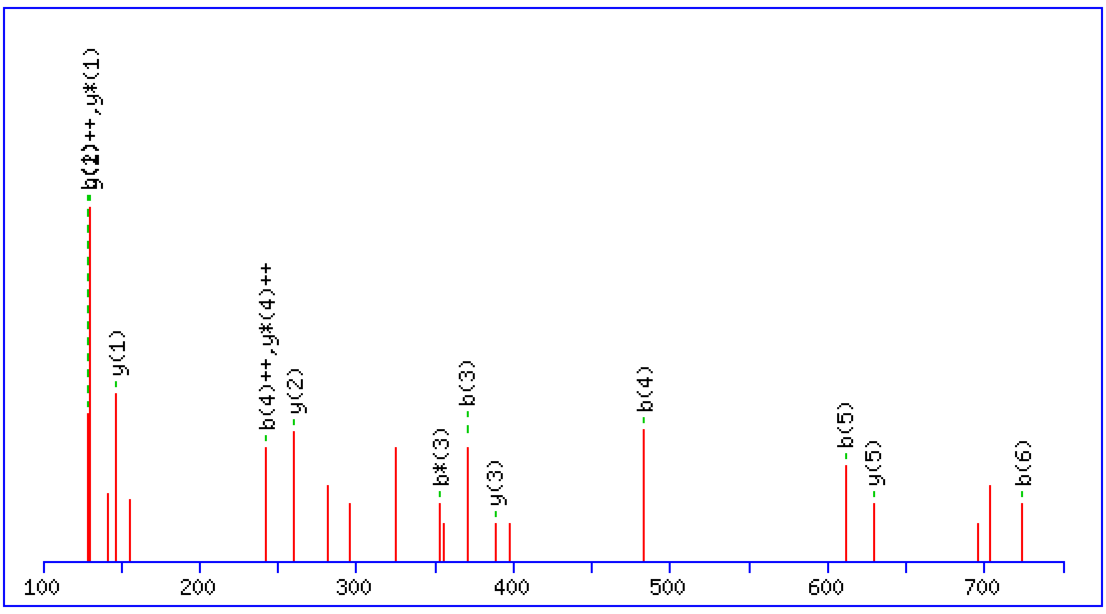
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KPKPKPK**
Found in **CLD23_HUMAN**, Claudin-23 OS=Homo sapiens GN=CLDN23 PE=1 SV=2

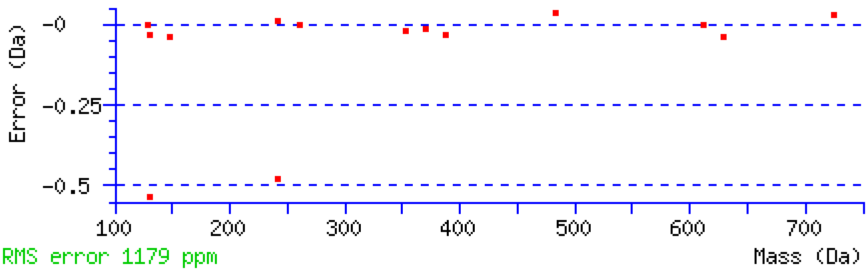
Match to Query 4564: 869.534968 from(435.774760,2+) rtinseconds(1662) index(4301)
Title: Locus:1.1.1.2245.6
Data file 2011-11-10 - TFD - EP 4-8.mgf

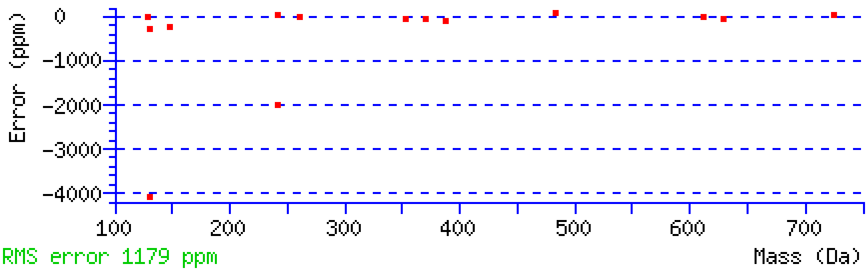
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 869.533432
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P2      : Oxidation (P)
P4      : Oxidation (P)
P6      : Oxidation (P)
Ions Score: 60  Expect: 4e-006
Matches : 15/48 fragment ions using 14 most intense peaks   (help)
```

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	129.102239	65.054757	112.075690	56.541483	K					7
2	242.149918	121.578597	225.123369	113.065322	P	742.445767	371.726522	725.419218	363.213247	6
3	370.244881	185.626079	353.218332	177.112804	K	629.398088	315.202682	612.371539	306.689408	5
4	483.292560	242.149918	466.266011	233.636644	P	501.303125	251.155201	484.276576	242.641926	4
5	611.387523	306.197400	594.360974	297.684125	K	388.255446	194.631361	371.228897	186.118087	3
6	724.435202	362.721239	707.408653	354.207965	P	260.160483	130.583879	243.133934	122.070605	2
7					K	147.112804	74.060040	130.086255	65.546765	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
60.1	869.533432	0.001536	KPKPKPK
60.1	869.533432	0.001536	QPQLKLK
43.6	869.533432	0.001536	KAAVPQIK
43.4	869.533432	0.001536	LKQIGALQ
42.0	869.533432	0.001536	KPLKQPK
40.6	869.533432	0.001536	QLQQLLK
40.5	869.533432	0.001536	KLQPIQK
27.2	869.533432	0.001536	QIPQLKK
27.2	869.533432	0.001536	QQLQLLK
27.0	869.533432	0.001536	QKLLGPSK

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

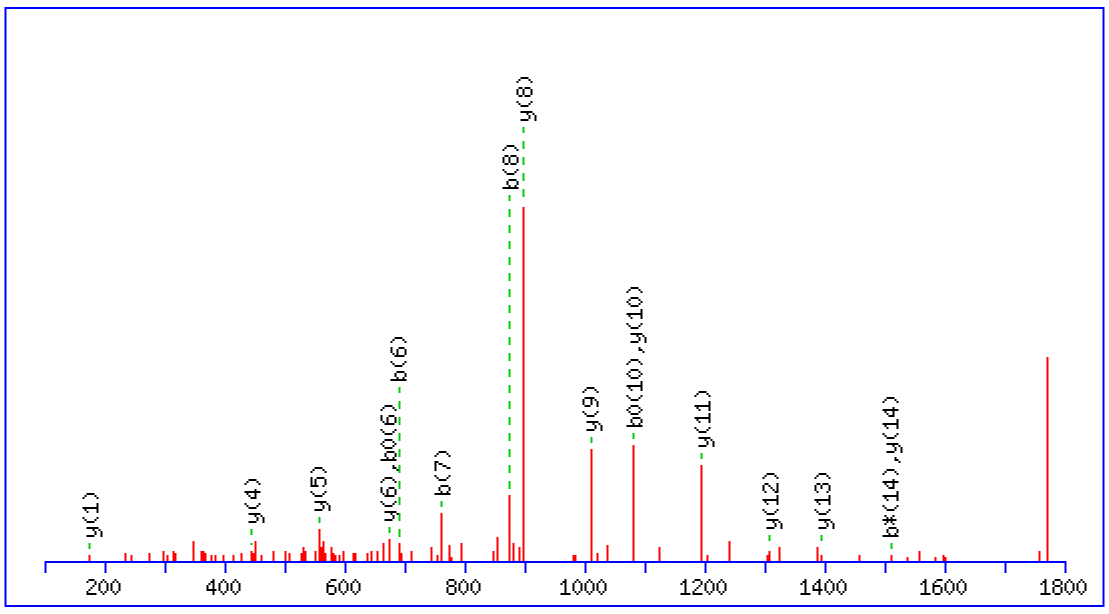
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VYDSLLALPQDLQAAR**
Found in **CLD3_HUMAN**, Claudin-3 OS=Homo sapiens GN=CLDN3 PE=1 SV=1

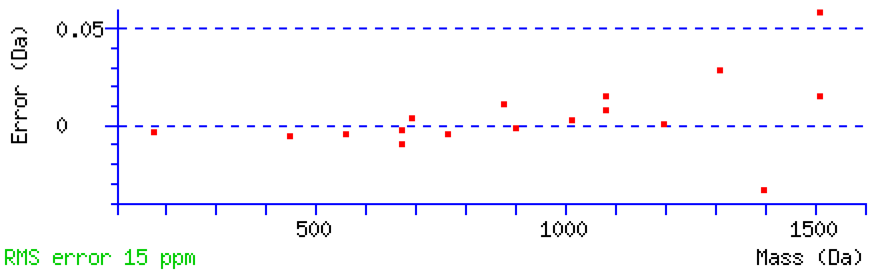
Match to Query 53267: 1771.950348 from(886.982450,2+) rtinseconds(3569) index(50066)
Title: Locus:1.1.1.2509.32
Data file 2011-11-12 - TFD - EP 6-6.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●

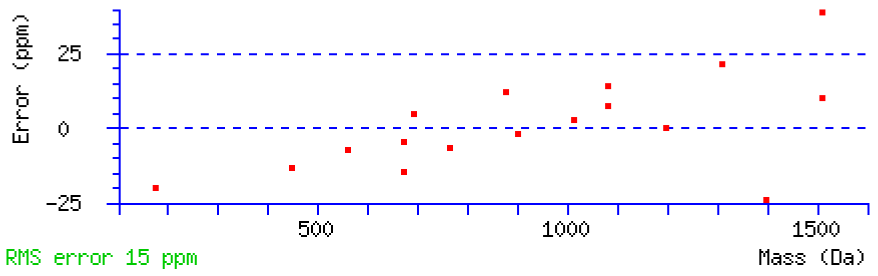


Monoisotopic mass of neutral peptide Mr(calc): 1771.946823
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 69 **Expect:** 5.3e-007
Matches : 17/148 fragment ions using 31 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	100.075690	50.541483					V							16
2	263.139019	132.073148					Y	1673.885713	837.446495	1656.859164	828.933220	1655.875148	828.441212	15
3	378.165962	189.586619			360.155397	180.581337	D	***1510.822384***	755.914830	1493.795835	747.401556	1492.811819	746.909548	14
4	465.197990	233.102633			447.187425	224.097351	S	***1395.795441***	698.401359	1378.768892	689.888084	1377.784876	689.396076	13
5	578.282054	289.644665			560.271489	280.639383	L	***1308.763413***	654.885345	1291.736864	646.372070	1290.752848	645.880062	12
6	**691.366118**	346.186697			673.355553	337.181415	L	***1195.679349***	598.343313	1178.652800	589.830038	1177.668784	589.338030	11
7	**762.403232**	381.705254			744.392667	372.699972	A	***1082.595285***	541.801281	1065.568736	533.288006	1064.584720	532.795998	10
8	**875.487296**	438.247286			857.476731	429.242004	L	***1011.558171***	506.282724	994.531622	497.769449	993.547606	497.277441	9
9	972.540060	486.773668			954.529495	477.768386	P	***898.474107***	449.740692	881.447558	441.227417	880.463542	440.735409	8
10	1100.598638	550.802957	1083.572089	542.289683	1082.588073	541.797675	Q	801.421343	401.214310	784.394794	392.701035	783.410778	392.209027	7
11	1215.625581	608.316429	1198.599032	599.803154	1197.615016	599.311146	D	***673.362765***	337.185021	656.336216	328.671746	655.352200	328.179738	6
12	1328.709645	664.858461	1311.683096	656.345186	1310.699080	655.853178	L	***558.335822***	279.671549	541.309273	271.158275			5
13	1456.768223	728.887750	1439.741674	720.374475	1438.757658	719.882467	Q	***445.251758***	223.129517	428.225209	214.616243			4
14	1527.805337	764.406307	1510.778788	755.893032	1509.794772	755.401024	A	317.193180	159.100228	300.166631	150.586953			3
15	1598.842451	799.924864	1581.815902	791.411589	1580.831886	790.919581	A	246.156066	123.581671	229.129517	115.068396			2
16							R	***175.118952***	88.063114	158.092403	79.549839			1



RMS error 15 ppm



RMS error 15 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
69.2	1771.946823	0.003525	VYDSLLALPQDLQAAR
2.2	1771.936935	0.013413	GPLDLIHLWLHESAR
1.0	1771.944321	0.006027	YPMIPPAQLFQLQAR

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

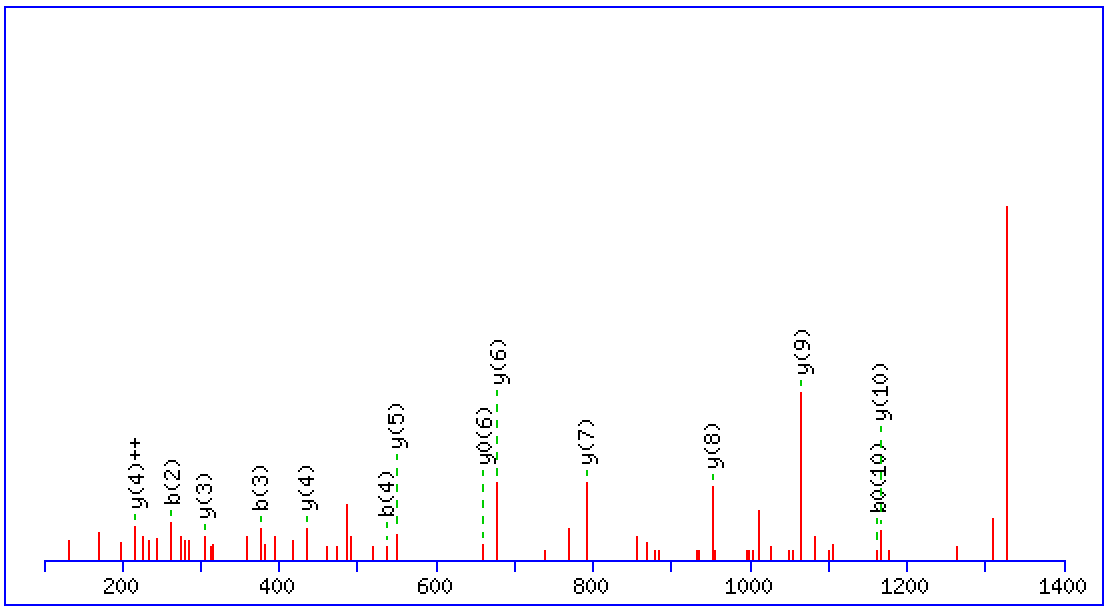
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **CTNCLEDESAK**
Found in **CLD4_HUMAN**, Claudin-4 OS=Homo sapiens GN=CLDN4 PE=1 SV=1

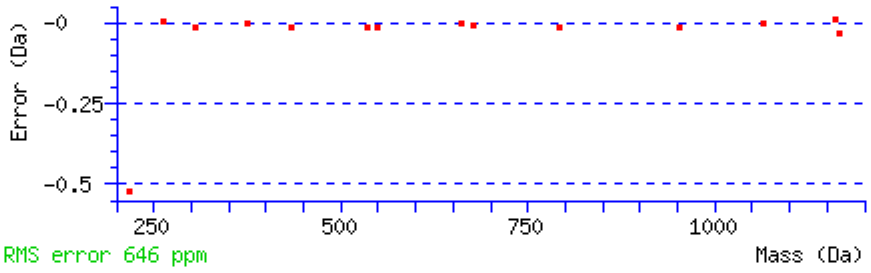
Match to Query 669135: 1325.524708 from(663.769630,2+) rtinseconds(1128) index(246155)
Title: Locus:1.1.1.871.37
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

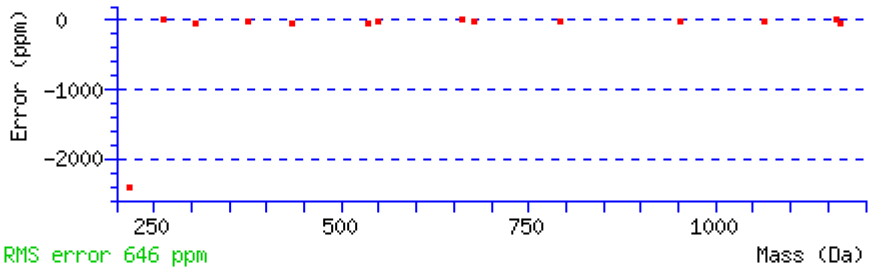
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1325.522751
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 56  Expect: 6.6e-006
Matches : 14/110 fragment ions using 24 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	161.037925	81.022600					C							11
2	**262.085604**	131.546440			244.075039	122.541158	T	***1166.499394***	583.753335	1149.472845	575.240061	1148.488829	574.748053	10
3	**376.128531**	188.567904	359.101982	180.054629	358.117966	179.562621	N	***1065.451715***	533.229496	1048.425166	524.716221	1047.441150	524.224213	9
4	**536.159180**	268.583228	519.132631	260.069954	518.148615	259.577946	C	***951.408788***	476.208032	934.382239	467.694758	933.398223	467.202750	8
5	649.243244	325.125260	632.216695	316.611986	631.232679	316.119978	L	***791.378139***	396.192708	774.351590	387.679433	773.367574	387.187425	7
6	778.285837	389.646557	761.259288	381.133282	760.275272	380.641274	E	***678.294075***	339.650676	661.267526	331.137401	660.283510	330.645393	6
7	893.312780	447.160028	876.286231	438.646754	875.302215	438.154746	D	***549.251482***	275.129379	532.224933	266.616105	531.240917	266.124097	5
8	1022.355373	511.681325	1005.328824	503.168050	1004.344808	502.676042	E	***434.224539***	217.615908	417.197990	209.102633	416.213974	208.610625	4
9	1109.387401	555.197339	1092.360852	546.684064	1091.376836	546.192056	S	***305.181946***	153.094611	288.155397	144.581337	287.171381	144.089329	3
10	1180.424515	590.715896	1163.397966	582.202621	1162.413950	581.710613	A	218.149918	109.578597	201.123369	101.065322			2
11							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.9	1325.522751	0.001957	CTNCLEDESAK

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

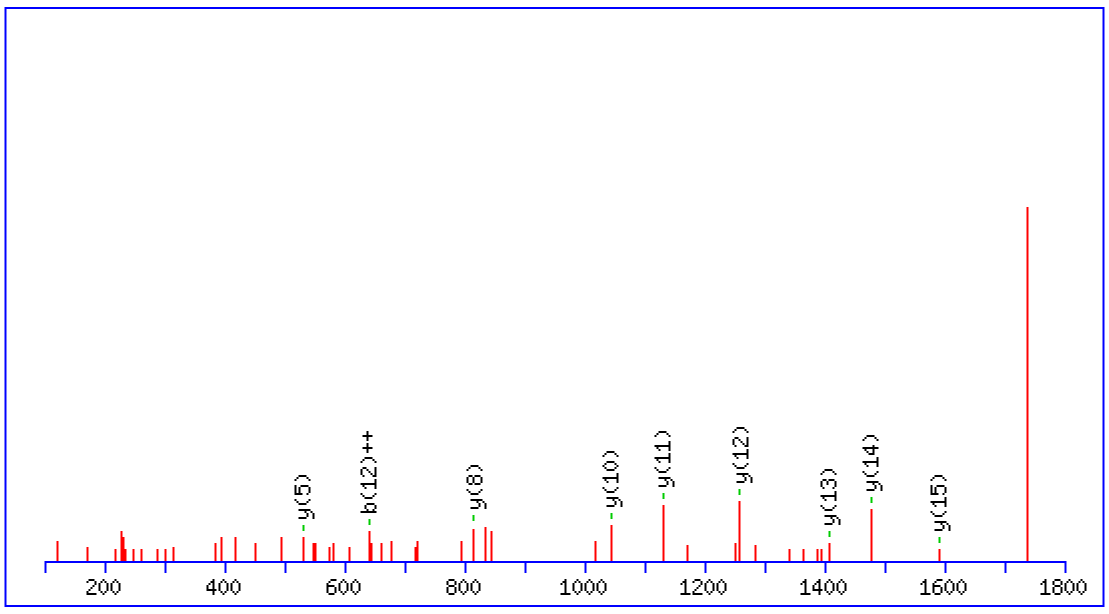
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FLAFESNIGDLASILK**
Found in **CSTF3_HUMAN**, Cleavage stimulation factor subunit 3 OS=Homo sapiens GN=CSTF3 PE=1 SV=1

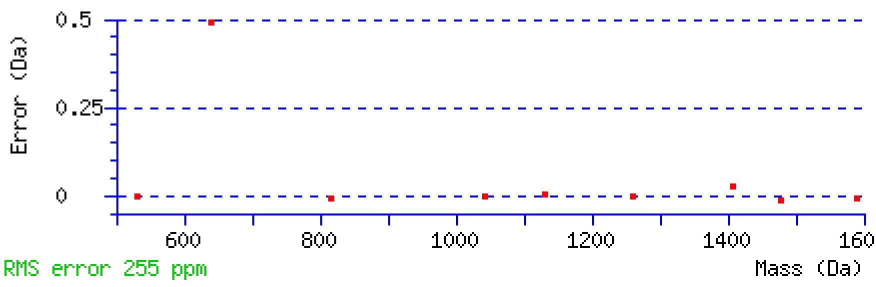
Match to Query 56378: 1736.942788 from(869.478670,2+) rtinseconds(4409) index(66404)
Title: Locus:1.1.1.3052.38
Data file 2011-11-12 - TFD - EP 6-2.mgf

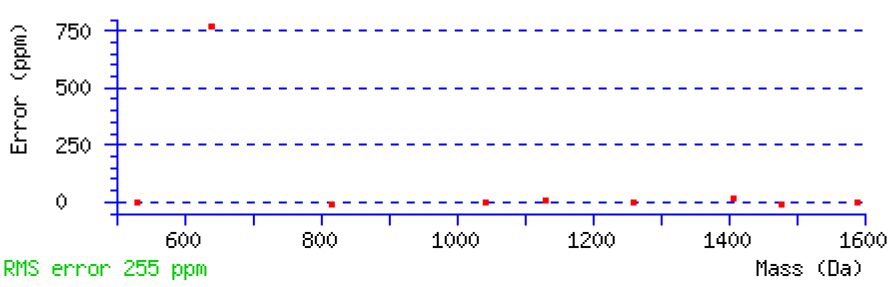
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1736.934860
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 50  Expect: 5.9e-005
Matches : 9/154 fragment ions using 15 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.075690	74.541483					F							16
2	261.159754	131.083515					L	***1590.873749***	795.940512	1573.847200	787.427238	1572.863184	786.935230	15
3	332.196868	166.602072					A	***1477.789685***	739.398480	1460.763136	730.885206	1459.779120	730.393198	14
4	479.265282	240.136279					F	***1406.752571***	703.879923	1389.726022	695.366649	1388.742006	694.874641	13
5	608.307875	304.657576			590.297310	295.652293	E	***1259.684157***	630.345716	1242.657608	621.832442	1241.673592	621.340434	12
6	695.339903	348.173589			677.329338	339.168307	S	***1130.641564***	565.824420	1113.615015	557.311145	1112.630999	556.819137	11
7	809.382830	405.195053	792.356281	396.681778	791.372265	396.189770	N	***1043.609536***	522.308406	1026.582987	513.795131	1025.598971	513.303123	10
8	922.466894	461.737085	905.440345	453.223810	904.456329	452.731802	I	929.566609	465.286942	912.540060	456.773668	911.556044	456.281660	9
9	979.488358	490.247817	962.461809	481.734542	961.477793	481.242534	G	***816.482545***	408.744910	799.455996	400.231636	798.471980	399.739628	8
10	1094.515301	547.761288	1077.488752	539.248014	1076.504736	538.756006	D	759.461081	380.234178	742.434532	371.720904	741.450516	371.228896	7
11	1207.599365	604.303320	1190.572816	595.790046	1189.588800	595.298038	L	644.434138	322.720707	627.407589	314.207432	626.423573	313.715424	6
12	1278.636479	639.821877	1261.609930	631.308603	1260.625914	630.816595	A	***531.350074***	266.178675	514.323525	257.665400	513.339509	257.173392	5
13	1365.668507	683.337891	1348.641958	674.824617	1347.657942	674.332609	S	460.312960	230.660118	443.286411	222.146843	442.302395	221.654835	4
14	1478.752571	739.879923	1461.726022	731.366649	1460.742006	730.874641	I	373.280932	187.144104	356.254383	178.630829			3
15	1591.836635	796.421955	1574.810086	787.908681	1573.826070	787.416673	L	260.196868	130.602072	243.170319	122.088797			2
16							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
50.4	1736.934860	0.007928	FLAFESNIGDLASILK

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

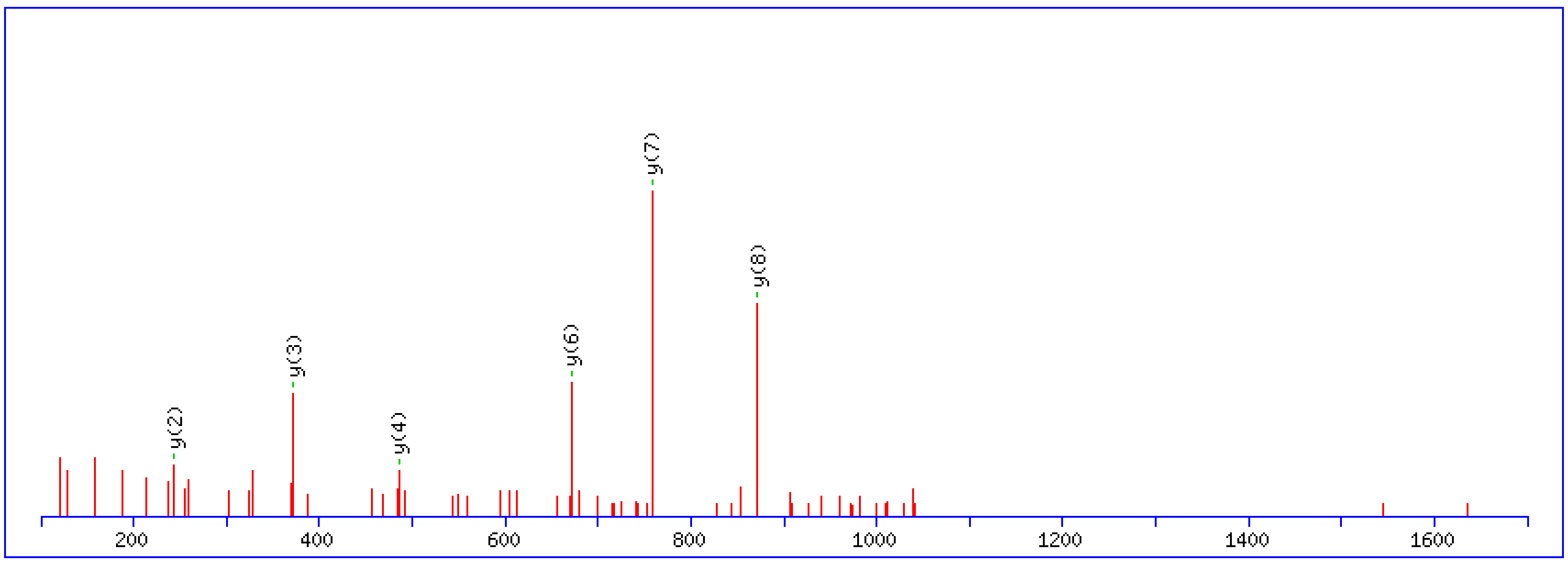
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QNKPSSVIQPK**
Found in **CDRT4_HUMAN**, CMT1A duplicated region transcript 4 protein OS=Homo sapiens GN=CDRT4 PE=2 SV=2

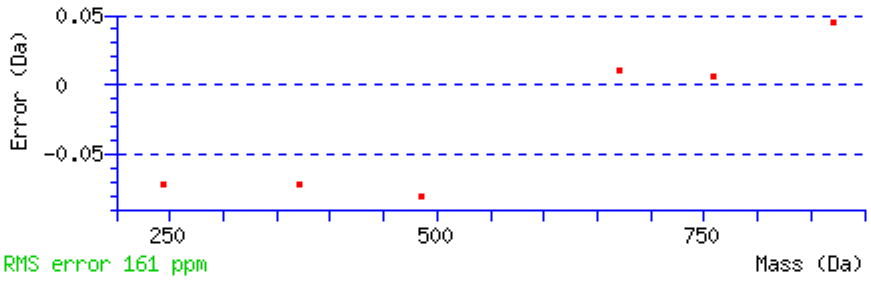
Match to Query 34581: 1240.676488 from(621.345520,2+) rtinseconds(2659) index(35759)
Title: Locus:1.1.1.1402.22
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 1.mgf

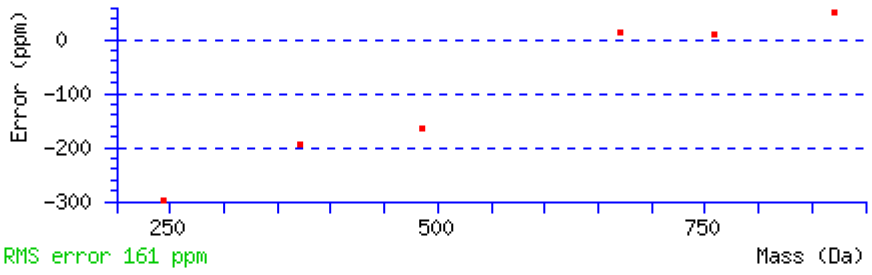
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1240.677536
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
P4 : Oxidation (P)
Ions Score: 42 **Expect:** 0.00074
Matches : 6/102 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	129.065854	65.036565	112.039305	56.523291			Q							11
2	243.108781	122.058029	226.082232	113.544754			N	1113.626249	557.316763	1096.599700	548.803488	1095.615684	548.311480	10
3	371.203744	186.105510	354.177195	177.592236			K	999.583322	500.295299	982.556773	491.782024	981.572757	491.290016	9
4	484.251423	242.629349	467.224874	234.116075			P	***871.488359***	436.247818	854.461810	427.734543	853.477794	427.242535	8
5	571.283451	286.145364	554.256902	277.632089	553.272886	277.140081	S	***758.440680***	379.723978	741.414131	371.210704	740.430115	370.718696	7
6	658.315479	329.661378	641.288930	321.148103	640.304914	320.656095	S	***671.408652***	336.207964	654.382103	327.694690	653.398087	327.202682	6
7	757.383893	379.195585	740.357344	370.682310	739.373328	370.190302	V	584.376624	292.691950	567.350075	284.178676			5
8	870.467957	435.737617	853.441408	427.224342	852.457392	426.732334	I	***485.308210***	243.157743	468.281661	234.644469			4
9	998.526535	499.766906	981.499986	491.253631	980.515970	490.761623	Q	***372.224146***	186.615711	355.197597	178.102437			3
10	1095.579299	548.293288	1078.552750	539.780013	1077.568734	539.288005	P	***244.165568***	122.586422	227.139019	114.073148			2
11							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.3	1240.677536	-0.001048	QNKPSSVIQPK
16.4	1240.677521	-0.001033	QEILEQVLNR
11.1	1240.666275	0.010213	KEEKPEPQIK
8.3	1240.684921	-0.008433	KPEPCKPILK
7.3	1240.677521	-0.001033	EQIIVEKNPR
4.6	1240.688736	-0.012248	EQLANLAARQK
4.5	1240.666275	0.010213	KEEKPEPQIK
1.1	1240.677521	-0.001033	AAEVLINQLDR
0.4	1240.688766	-0.012278	NQQPLGATIKR
0.3	1240.666321	0.010167	ASVPPVLPSSSGK

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

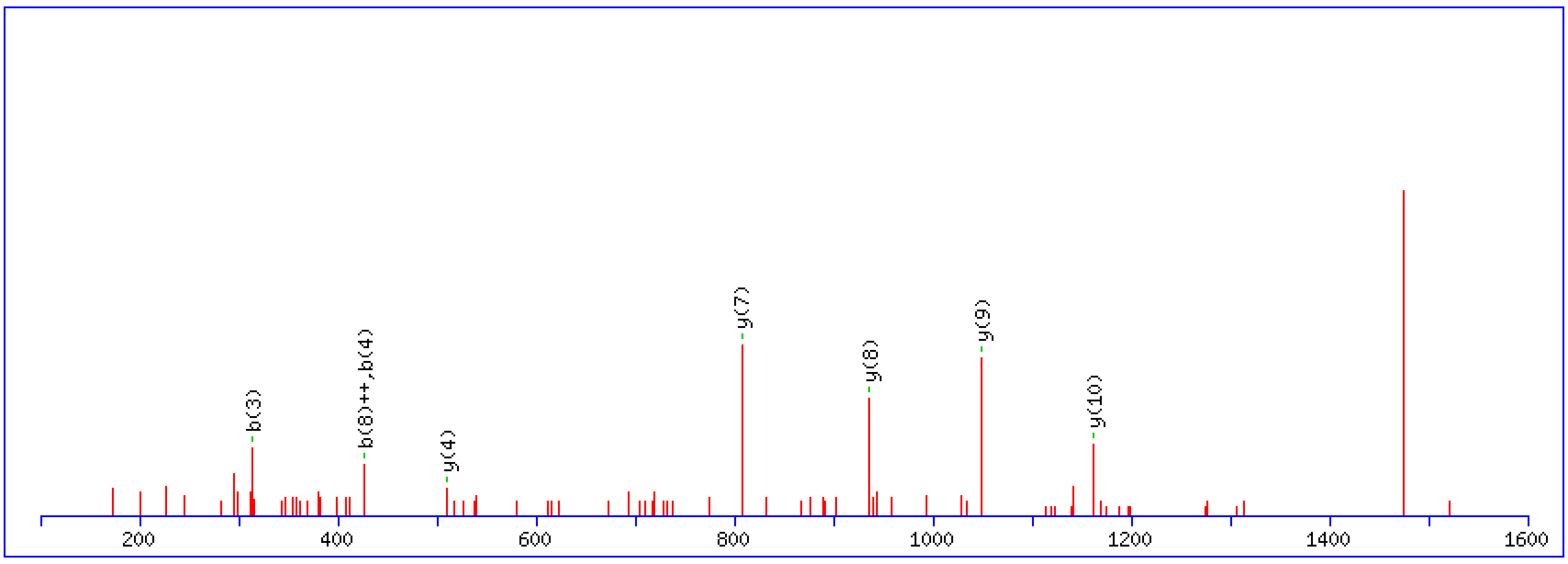
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EALILEPSLYTVK**
Found in **COPZ1_HUMAN**, Coatomer subunit zeta-1 OS=Homo sapiens GN=COPZ1 PE=1 SV=1

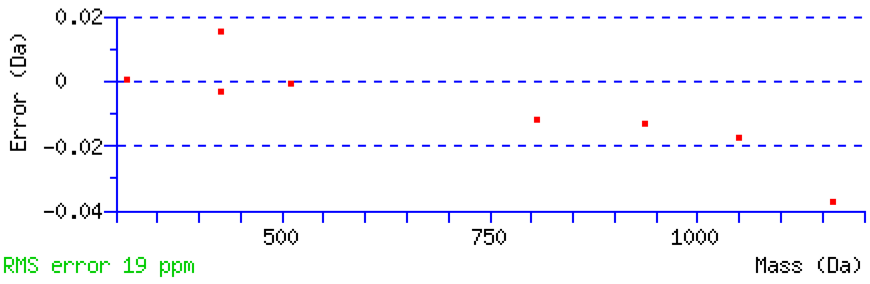
Match to Query 43861: 1474.815388 from(738.414970,2+) rtinseconds(3156) index(44355)
Title: Locus:1.1.1.1642.35
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 3.mgf

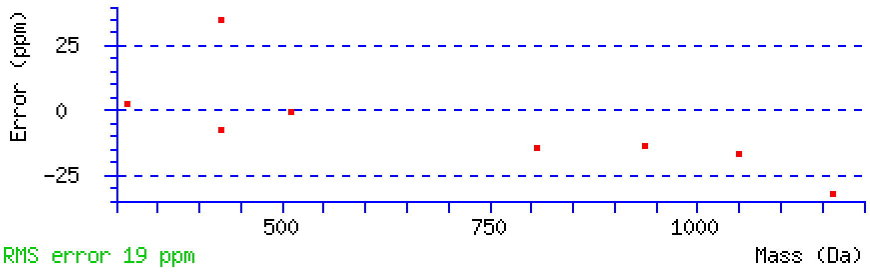
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1600] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1474.828262
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.0061
Matches : 8/116 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	130.049869	65.528572	112.039304	56.523290	E							13
2	201.086983	101.047130	183.076418	92.041847	A	1346.792981	673.900129	1329.766432	665.386854	1328.782416	664.894846	12
3	**314.171047**	157.589161	296.160482	148.583879	L	1275.755867	638.381572	1258.729318	629.868297	1257.745302	629.376289	11
4	**427.255111**	214.131193	409.244546	205.125911	I	***1162.671803***	581.839540	1145.645254	573.326265	1144.661238	572.834257	10
5	540.339175	270.673226	522.328610	261.667943	L	***1049.587739***	525.297508	1032.561190	516.784233	1031.577174	516.292225	9
6	669.381768	335.194522	651.371203	326.189240	E	***936.503675***	468.755476	919.477126	460.242201	918.493110	459.750193	8
7	766.434532	383.720904	748.423967	374.715622	P	***807.461082***	404.234179	790.434533	395.720905	789.450517	395.228897	7
8	853.466560	427.236918	835.455995	418.231636	S	710.408318	355.707797	693.381769	347.194523	692.397753	346.702515	6
9	966.550624	483.778950	948.540059	474.773668	L	623.376290	312.191783	606.349741	303.678509	605.365725	303.186501	5
10	1129.613953	565.310615	1111.603388	556.305332	Y	***510.292226***	255.649751	493.265677	247.136477	492.281661	246.644469	4
11	1230.661632	615.834454	1212.651067	606.829172	T	347.228897	174.118087	330.202348	165.604812	329.218332	165.112804	3
12	1329.730046	665.368661	1311.719481	656.363379	V	246.181218	123.594247	229.154669	115.080973			2
13					K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.3	1474.828262	-0.012874	EALILEPSLYTVK
8.8	1474.828278	-0.012890	IISLDLPVAEVYK
2.5	1474.814377	0.001011	VLVEVLADPLDHR

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

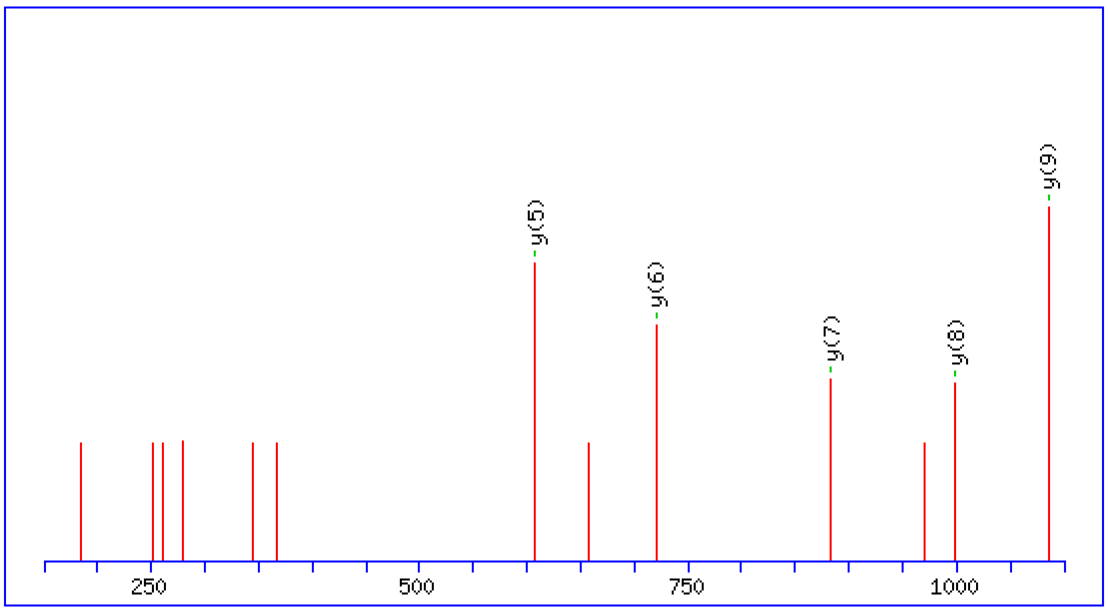
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSDYLFTLAR**
Found in **MMAB_HUMAN**, Cob(I)yrinic acid a,c-diamide adenosyltransferase, mitochondrial OS=Homo sapiens GN=MMAB PE=1 SV=1

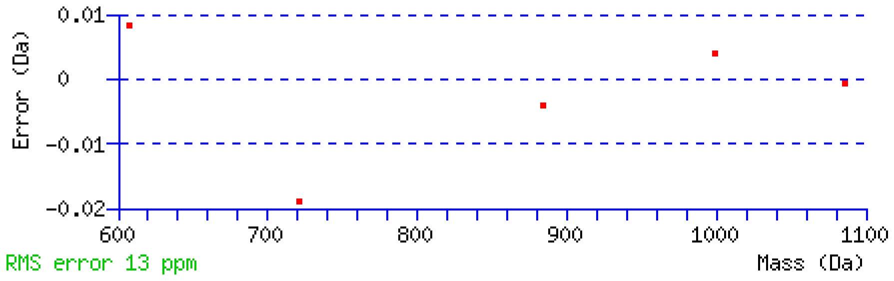
Match to Query 30107: 1197.635028 from(599.824790,2+) rtinseconds(3365) index(46479)
Title: Locus:1.1.1.2595.19
Data file 2011-11-10 - TFD - EP 4-5.mgf

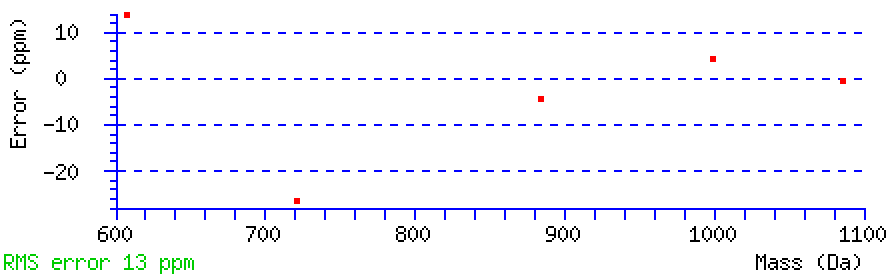
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1197.639359
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 36  Expect: 0.0027
Matches : 5/82 fragment ions using 8 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							10
2	201.123368	101.065322	183.112803	92.060039	S	***1085.562587***	543.284932	1068.536038	534.771657	1067.552022	534.279649	9
3	316.150311	158.578793	298.139746	149.573511	D	***998.530559***	499.768918	981.504010	491.255643	980.519994	490.763635	8
4	479.213640	240.110458	461.203075	231.105176	Y	***883.503616***	442.255446	866.477067	433.742171	865.493051	433.250163	7
5	592.297704	296.652490	574.287139	287.647208	L	***720.440287***	360.723782	703.413738	352.210507	702.429722	351.718499	6
6	739.366118	370.186697	721.355553	361.181415	F	***607.356223***	304.181750	590.329674	295.668475	589.345658	295.176467	5
7	840.413797	420.710537	822.403232	411.705254	T	460.287809	230.647542	443.261260	222.134268	442.277244	221.642260	4
8	953.497861	477.252569	935.487296	468.247286	L	359.240130	180.123703	342.213581	171.610428			3
9	1024.534975	512.771125	1006.524410	503.765843	A	246.156066	123.581671	229.129517	115.068396			2
10					R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.4	1197.639359	-0.004331	LSDYLFTLAR
11.4	1197.635330	-0.000302	LSDLQPQIER
0.7	1197.635330	-0.000302	INPETDLPRK
0.4	1197.639359	-0.004331	EVHLPEIFAK

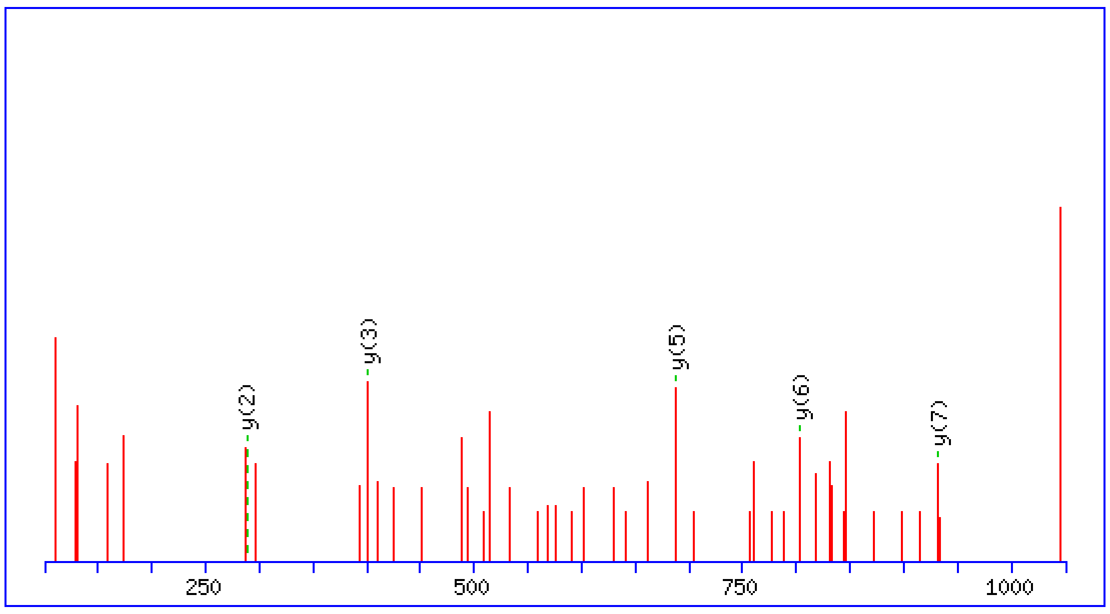
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LEDMRILR**
Found in **CC147_HUMAN**, Coiled-coil domain-containing protein 147 OS=Homo sapiens GN=CCDC147 PE=2 SV=1

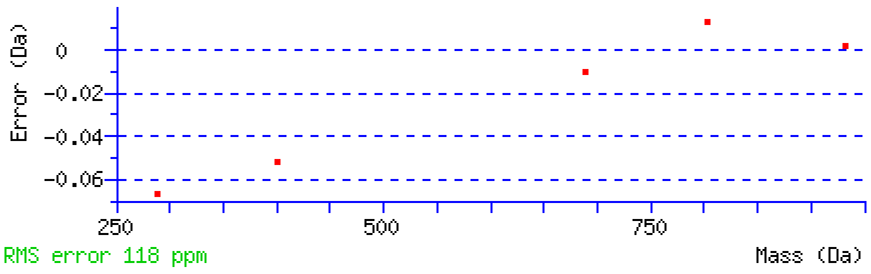
Match to Query 20132: 1044.578968 from(523.296760,2+) rtinseconds(2371) index(29387)
Title: Locus:1.1.1.2343.20
Data file 2011-11-10 - TFD - EP 3-2.mgf

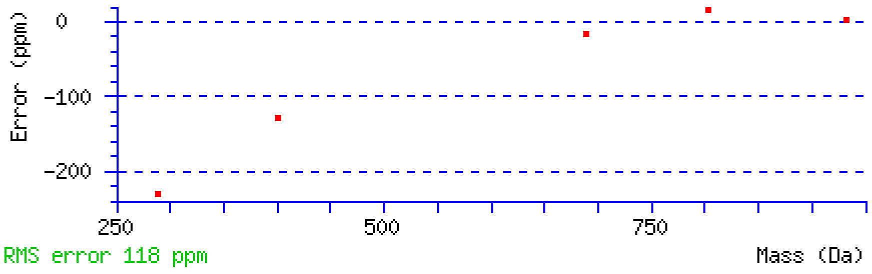
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1044.574966
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 34 **Expect:** 0.0041
Matches : 5/64 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							8
2	243.133933	122.070605			225.123368	113.065322	E	*932.498212*	466.752744	915.471663	458.239470	914.487647	457.747462	7
3	358.160876	179.584076			340.150311	170.578794	D	*803.455619*	402.231448	786.429070	393.718173	785.445054	393.226165	6
4	489.201361	245.104319			471.190796	236.099036	M	*688.428676*	344.717976	671.402127	336.204702			5
5	645.302472	323.154874	628.275923	314.641600	627.291907	314.149592	R	557.388191	279.197734	540.361642	270.684459			4
6	758.386536	379.696906	741.359987	371.183632	740.375971	370.691624	I	*401.287080*	201.147178	384.260531	192.633903			3
7	871.470600	436.238938	854.444051	427.725664	853.460035	427.233656	L	*288.203016*	144.605146	271.176467	136.091871			2
8							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LEDMRILR
(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	1044.574966	0.004002	LEDMRILR
23.0	1044.581512	-0.002544	LDTDISLIR
16.6	1044.574966	0.004002	QSAALCLLR
8.4	1044.570282	0.008686	ELDTVEVLK
8.2	1044.574966	0.004002	IKAAMNIPR
8.1	1044.570267	0.008701	LSEDIDLLK
8.0	1044.571609	0.007359	LSSAHVYLR
8.0	1044.581512	-0.002544	LSVEIDTLR
7.5	1044.570267	0.008701	EEVSIEVLK
5.4	1044.571625	0.007343	FPDRILPR

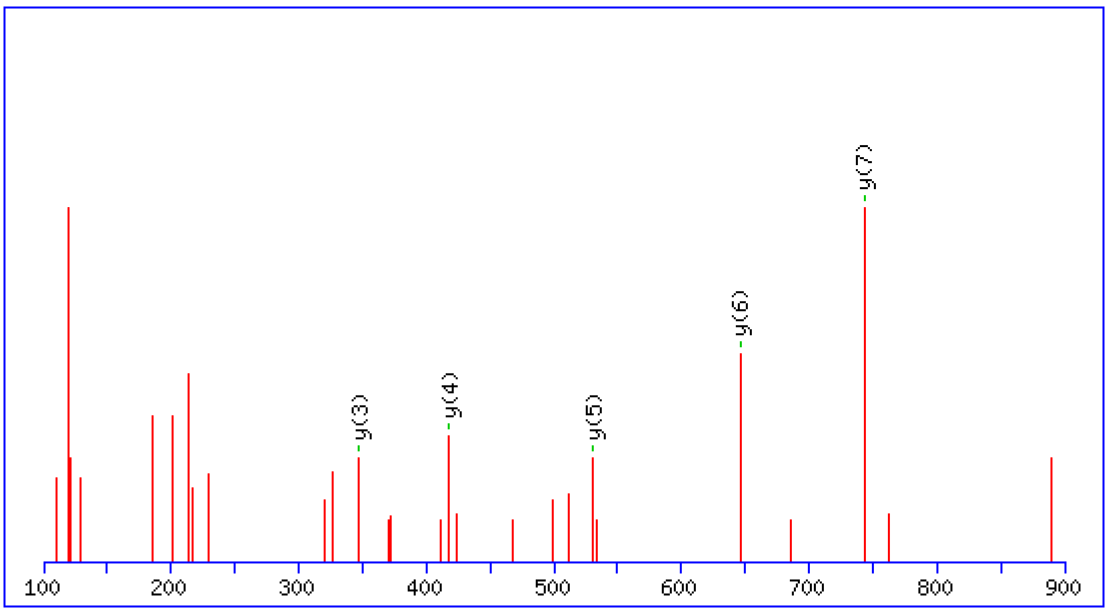
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FPDLAAEK**
Found in **CCD25_HUMAN**, Coiled-coil domain-containing protein 25 OS=Homo sapiens GN=CCDC25 PE=1 SV=2

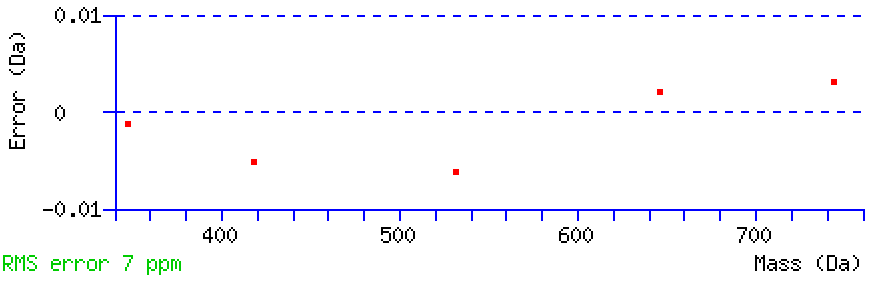
Match to Query 7473: 889.453188 from(445.733870,2+) rtinseconds(2076) index(22450)
Title: Locus:1.1.1.2106.6
Data file 2011-11-10 - TFD - EP 4-5.mgf

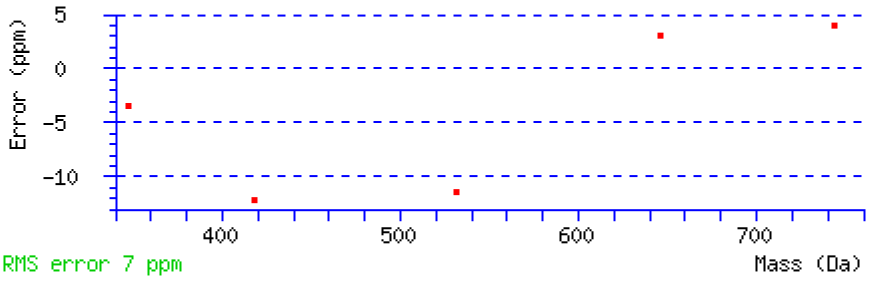
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 889.454514
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 40 **Expect:** 0.0016
Matches : 5/64 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.075690	74.541483			F							8
2	245.128454	123.067865			P	*743.393396*	372.200336	726.366847	363.687062	725.382831	363.195054	7
3	360.155397	180.581336	342.144832	171.576054	D	*646.340632*	323.673954	629.314083	315.160680	628.330067	314.668672	6
4	473.239461	237.123369	455.228896	228.118086	L	*531.313689*	266.160483	514.287140	257.647208	513.303124	257.155200	5
5	544.276575	272.641926	526.266010	263.636643	A	*418.229625*	209.618450	401.203076	201.105176	400.219060	200.613168	4
6	615.313689	308.160483	597.303124	299.155200	A	*347.192511*	174.099893	330.165962	165.586619	329.181946	165.094611	3
7	744.356282	372.681779	726.345717	363.676497	E	276.155397	138.581336	259.128848	130.068062	258.144832	129.576054	2
8					K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.7	889.454514	-0.001326	FPDLAAEK
18.5	889.450500	0.002688	KQPSDTAK

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

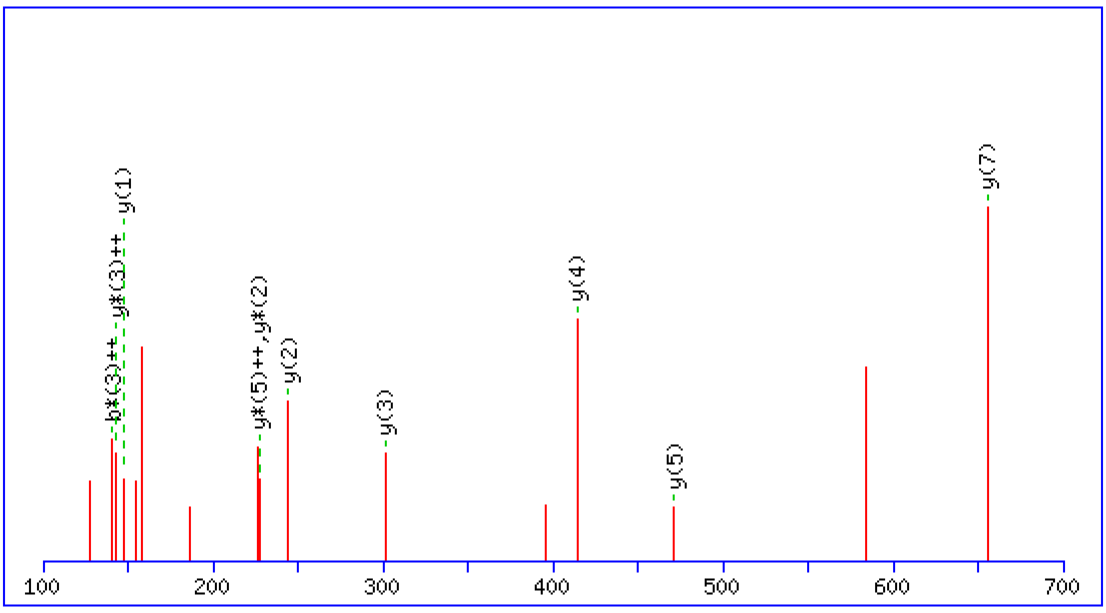
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QGPAGLGPK**
Found in **CC88B_HUMAN**, Coiled-coil domain-containing protein 88B OS=Homo sapiens GN=CCDC88B PE=1 SV=1

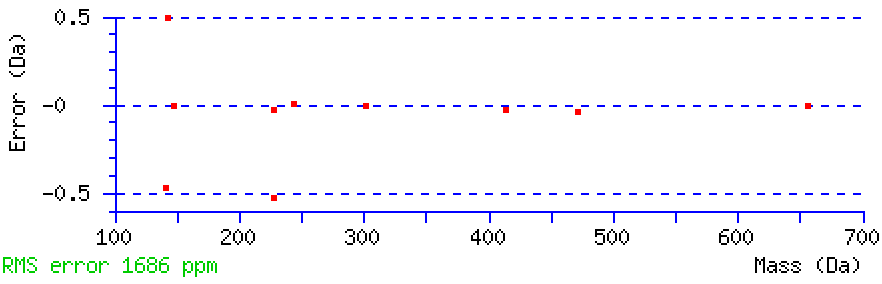
Match to Query 49924: 839.450788 from(420.732670,2+) rtinseconds(1047) index(244650)
Title: Locus:1.1.1.840.3
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

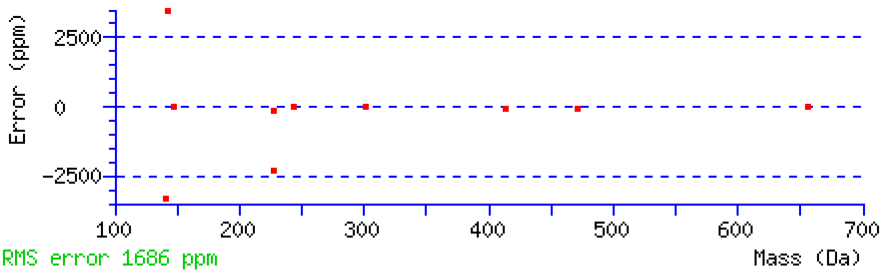
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [700] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 839.450119
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
P3      : Oxidation (P)
Ions Score: 47  Expect: 0.00015
Matches : 10/64 fragment ions using 13 most intense peaks   (help)
```

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	129.065854	65.036565	112.039305	56.523291	Q					9
2	186.087318	93.547297	169.060769	85.034023	G	712.398817	356.703047	695.372268	348.189772	8
3	299.134997	150.071136	282.108448	141.557862	P	***655.377353***	328.192315	638.350804	319.679040	7
4	370.172111	185.589694	353.145562	177.076419	A	542.329674	271.668475	525.303125	263.155201	6
5	427.193575	214.100426	410.167026	205.587151	G	***471.292560***	236.149918	454.266011	227.636643	5
6	540.277639	270.642458	523.251090	262.129183	L	***414.271096***	207.639186	397.244547	199.125912	4
7	597.299103	299.153190	580.272554	290.639915	G	***301.187032***	151.097154	284.160483	142.583880	3
8	694.351867	347.679572	677.325318	339.166297	P	***244.165568***	122.586422	227.139019	114.073148	2
9					K	***147.112804***	74.060040	130.086255	65.546765	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.9	839.450119	0.000669	QGPAGLGPK
6.1	839.450089	0.000699	SNAPNIPK

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

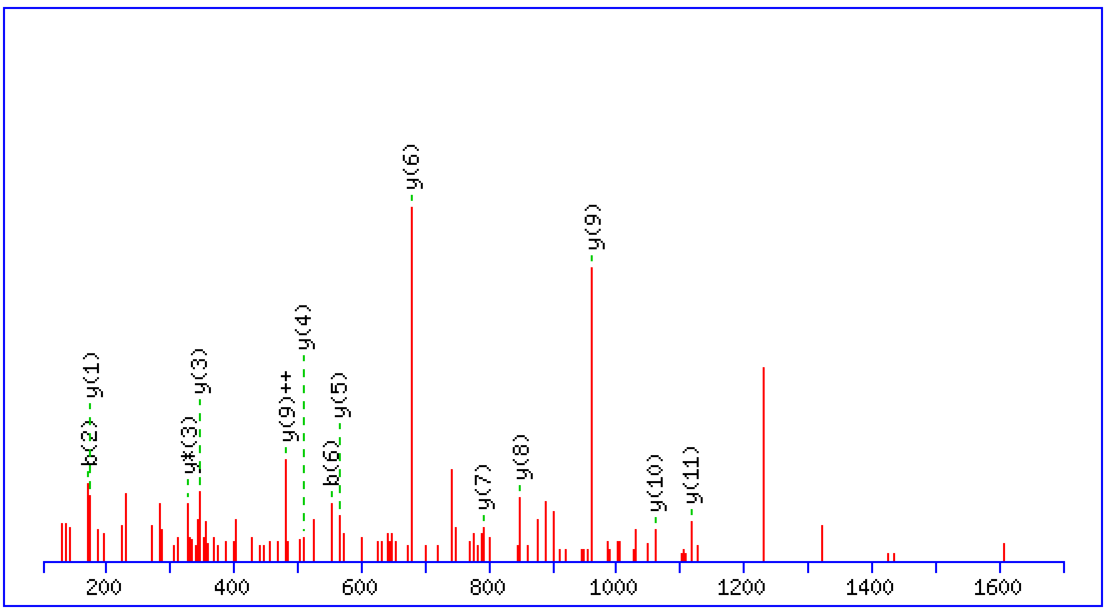
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGVPGLPGYPGR**
Found in **CO5A1_HUMAN**, Collagen alpha-1(V) chain OS=Homo sapiens GN=COL5A1 PE=1 SV=3

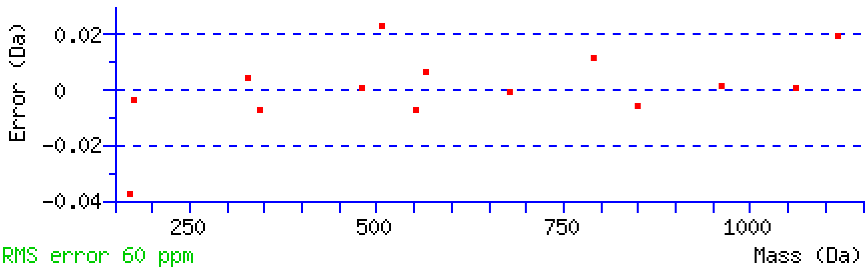
Match to Query 28102: 1229.643888 from(615.829220,2+) rtinseconds(2336) index(25761)
Title: Locus:1.1.1.2444.38
Data file 2011-11-12 - TFD - EP 5-1.mgf

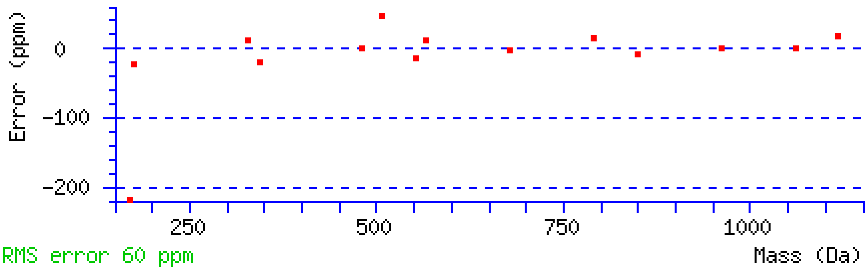
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1229.640457
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P4      : Oxidation (P)
P7      : Oxidation (P)
P10     : Oxidation (P)
Ions Score: 66  Expect: 6e-006
Matches : 14/66 fragment ions using 30 most intense peaks   (help)
```

#	b	b^{++}	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	114.091340	57.549308	L					12
2	**171.112804**	86.060040	G	***1117.563652***	559.285464	1100.537103	550.772190	11
3	270.181218	135.594247	V	***1060.542188***	530.774732	1043.515639	522.261458	10
4	383.228897	192.118087	P	***961.473774***	481.240525	944.447225	472.727250	9
5	440.250361	220.628818	G	***848.426095***	424.716685	831.399546	416.203411	8
6	**553.334425**	277.170851	L	***791.404631***	396.205953	774.378082	387.692679	7
7	666.382104	333.694690	P	***678.320567***	339.663922	661.294018	331.150647	6
8	723.403568	362.205422	G	***565.272888***	283.140082	548.246339	274.626807	5
9	886.466897	443.737087	Y	***508.251424***	254.629350	491.224875	246.116075	4
10	999.514576	500.260926	P	***345.188095***	173.097685	328.161546	164.584411	3
11	1056.536040	528.771658	G	232.140416	116.573846	215.113867	108.060571	2
12			R	***175.118952***	88.063114	158.092403	79.549839	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
65.9	1229.640457	0.003431	LGVPGLPGYPGR
8.9	1229.643768	0.000120	LLEEICNLGR
3.6	1229.651672	-0.007784	VPGEAFRPLGR
2.8	1229.655045	-0.011157	VAVVCVSNVNR

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

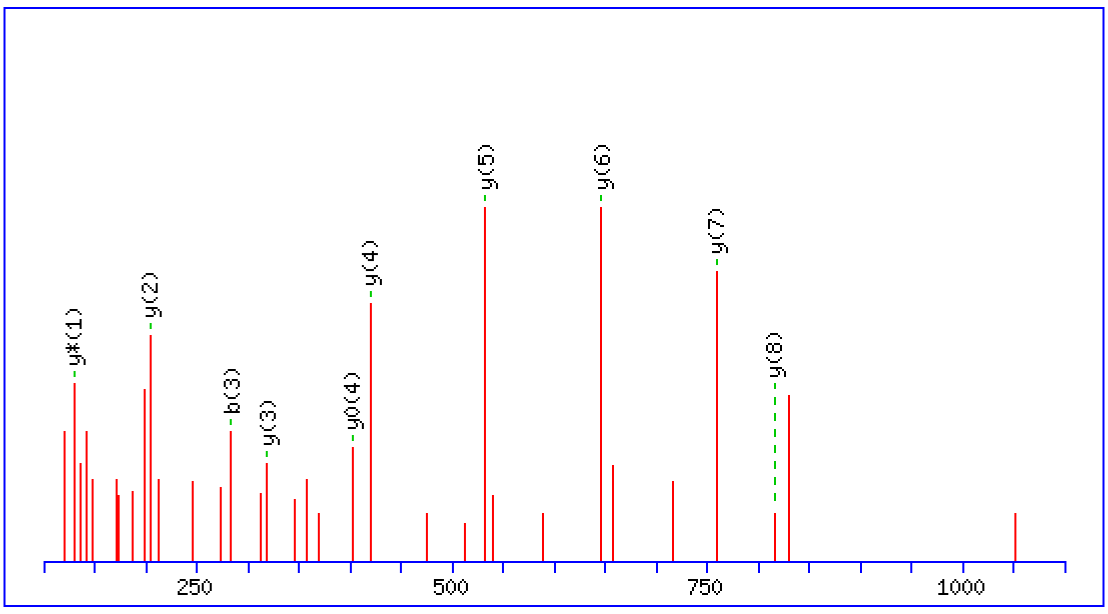
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IGILITDGK**
Found in **COEA1_HUMAN**, Collagen alpha-1(XIV) chain OS=Homo sapiens GN=COL14A1 PE=1 SV=3

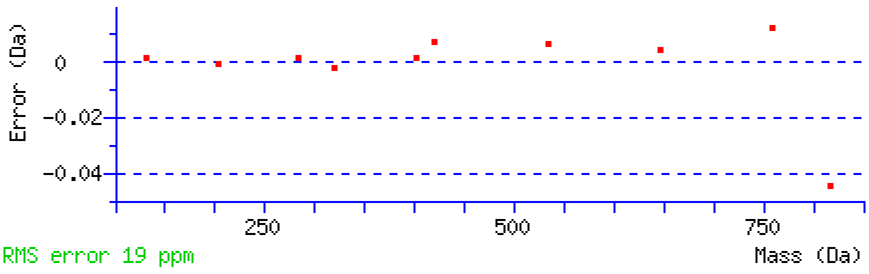
Match to Query 8672: 928.557648 from(465.286100,2+) rtinseconds(1914) index(17887)
Title: Locus:1.1.1.2287.14
Data file 2011-11-12 - TFD - EP 5-1.mgf

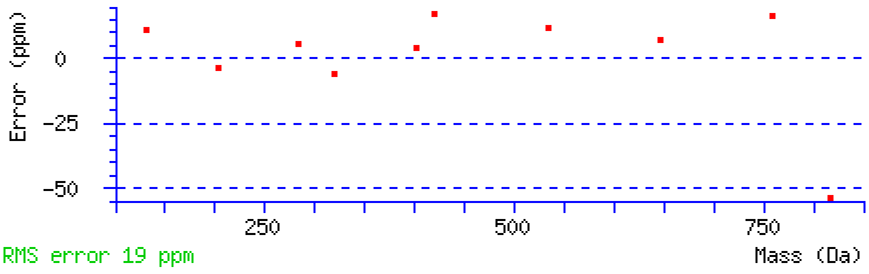
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 928.559326
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 57 **Expect:** 1.2e-005
Matches : 10/66 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308			I							9
2	171.112804	86.060040			G	***816.482546***	408.744911	799.455997	400.231637	798.471981	399.739629	8
3	284.196868	142.602072			I	***759.461082***	380.234179	742.434533	371.720905	741.450517	371.228897	7
4	397.280932	199.144104			L	***646.377018***	323.692147	629.350469	315.178873	628.366453	314.686865	6
5	510.364996	255.686136			I	***533.292954***	267.150115	516.266405	258.636841	515.282389	258.144833	5
6	611.412675	306.209976	593.402110	297.204693	T	***420.208890***	210.608083	403.182341	202.094808	402.198325	201.602800	4
7	726.439618	363.723447	708.429053	354.718165	D	***319.161211***	160.084243	302.134662	151.570969	301.150646	151.078961	3
8	783.461082	392.234179	765.450517	383.228897	G	***204.134268***	102.570772	187.107719	94.057498			2
9					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of IGILITDGK
(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	928.559326	-0.001678	VAIIITDGK
56.9	928.559326	-0.001678	IGILITDGK
12.2	928.564011	-0.006363	LVALARMR
7.5	928.549438	0.008210	GIPFRPVK
5.5	928.559311	-0.001663	IINILTDK
5.5	928.559311	-0.001663	LQVLIESK
4.7	928.549408	0.008240	KYQIHLK
2.0	928.559296	-0.001648	LVKELEAK
1.4	928.559341	-0.001693	APVLTVVSK
0.7	928.552780	0.004868	IGLACLLR

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

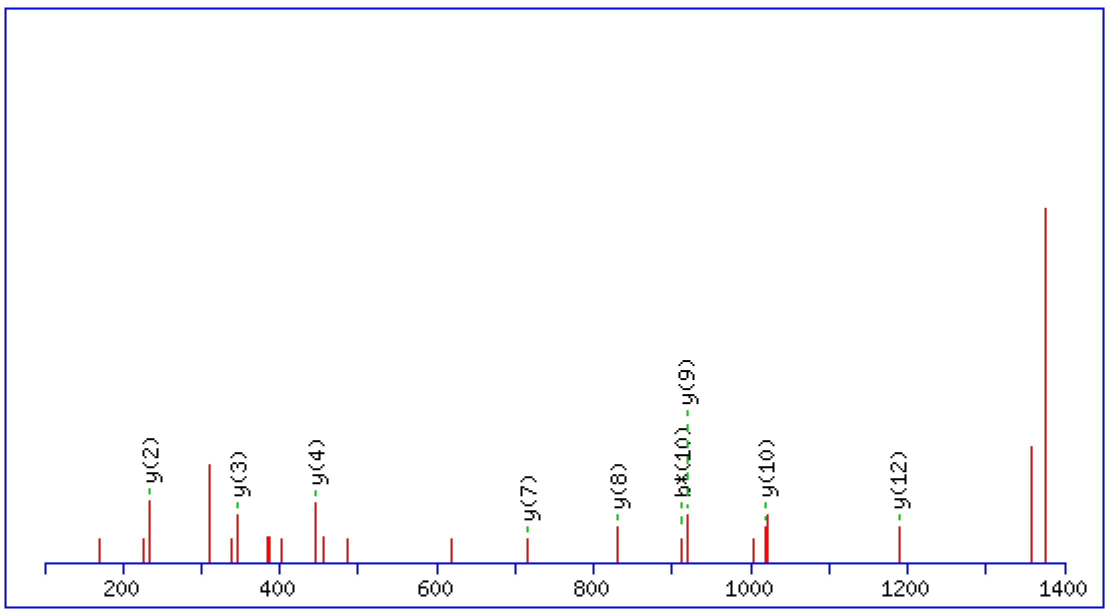
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QGGITSDQAAVISK**
Found in **COMD1_HUMAN**, COMM domain-containing protein 1 OS=Homo sapiens GN=COMMD1 PE=1 SV=1

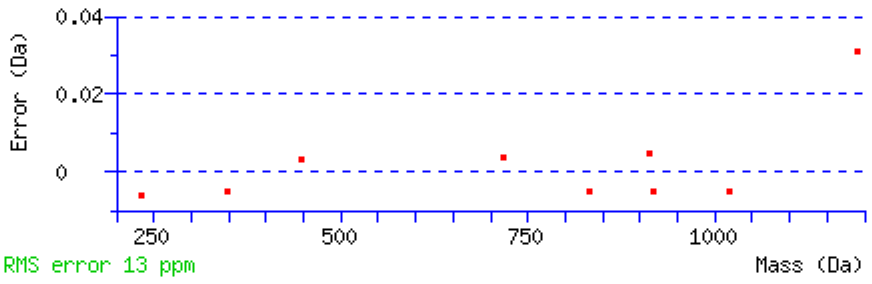
Match to Query 39615: 1373.724428 from(687.869490,2+) rtinseconds(1668) index(13215)
Title: Locus:1.1.1.1906.50
Data file 2011-11-14 - TFD - EP 8-6.mgf

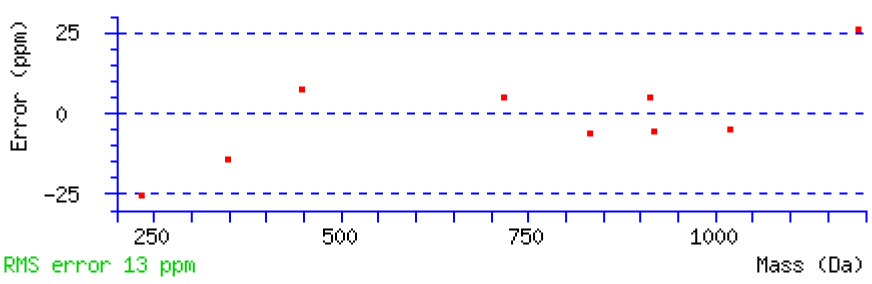
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1373.715057
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 56  Expect: 1.2e-005
Matches : 9/146 fragment ions using 16 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	129.065854	65.036565	112.039305	56.523291			Q							14
2	186.087318	93.547297	169.060769	85.034023			G	1246.663758	623.835517	1229.637209	615.322243	1228.653193	614.830234	13
3	243.108782	122.058029	226.082233	113.544755			G	***1189.642294***	595.324785	1172.615745	586.811511	1171.631729	586.319503	12
4	356.192846	178.600061	339.166297	170.086787			I	1132.620830	566.814053	1115.594281	558.300779	1114.610265	557.808771	11
5	457.240525	229.123901	440.213976	220.610626	439.229960	220.118618	T	***1019.536766***	510.272021	1002.510217	501.758746	1001.526201	501.266738	10
6	544.272553	272.639915	527.246004	264.126640	526.261988	263.634632	S	***918.489087***	459.748181	901.462538	451.234907	900.478522	450.742899	9
7	659.299496	330.153386	642.272947	321.640112	641.288931	321.148104	D	***831.457059***	416.232168	814.430510	407.718893	813.446494	407.226885	8
8	787.358074	394.182675	770.331525	385.669401	769.347509	385.177393	Q	***716.430116***	358.718696	699.403567	350.205422	698.419551	349.713414	7
9	858.395188	429.701232	841.368639	421.187958	840.384623	420.695950	A	588.371538	294.689407	571.344989	286.176132	570.360973	285.684125	6
10	929.432302	465.219789	912.405753	456.706515	911.421737	456.214507	A	517.334424	259.170850	500.307875	250.657576	499.323859	250.165568	5
11	1028.500716	514.753996	1011.474167	506.240722	1010.490151	505.748714	V	***446.297310***	223.652293	429.270761	215.139018	428.286745	214.647010	4
12	1141.584780	571.296028	1124.558231	562.782754	1123.574215	562.290745	I	***347.228896***	174.118086	330.202347	165.604811	329.218331	165.112803	3
13	1228.616808	614.812042	1211.590259	606.298768	1210.606243	605.806760	S	***234.144832***	117.576054	217.118283	109.062780	216.134267	108.570772	2
14							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.2	1373.715057	0.009371	QGGITSDQAAVISK
3.6	1373.715042	0.009386	KPATSSKPGSAPSK
1.2	1373.733658	-0.009230	GLNVAATAAVMAASK
1.1	1373.719757	0.004671	SVALGGCGQLSRR
0.5	1373.733673	-0.009245	AVLRSPGMTVAEK
0.5	1373.733673	-0.009245	AVLRSPGMTVAEK
0.0	1373.716385	0.008043	SFSQSSGLLRHR

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

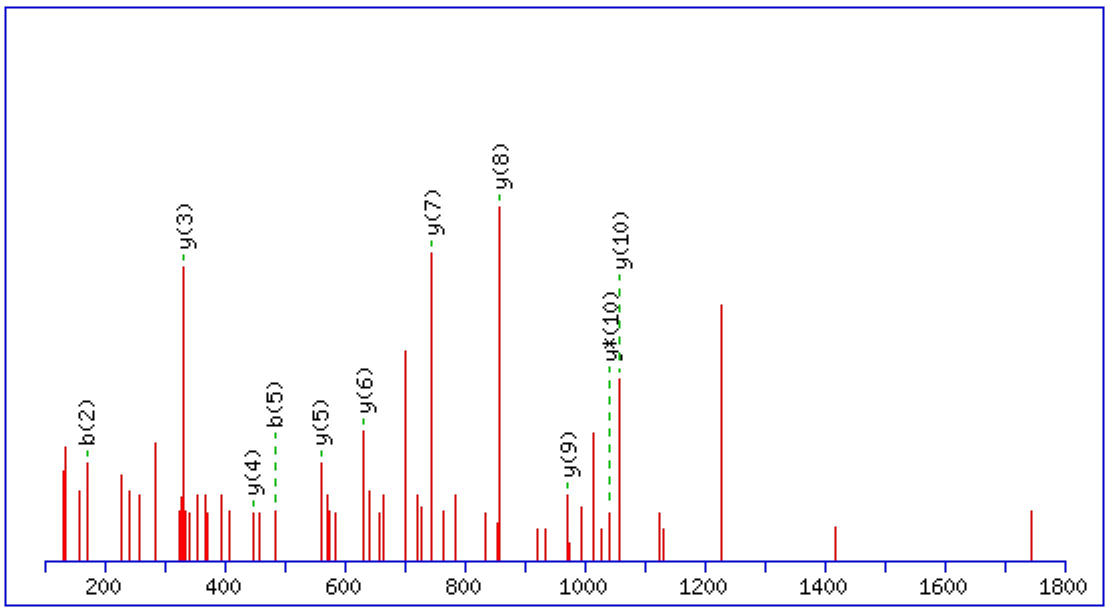
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AVSLINAIDTGR**
Found in **COMDA_HUMAN**, COMM domain-containing protein 10 OS=Homo sapiens GN=COMMD10 PE=1 SV=1

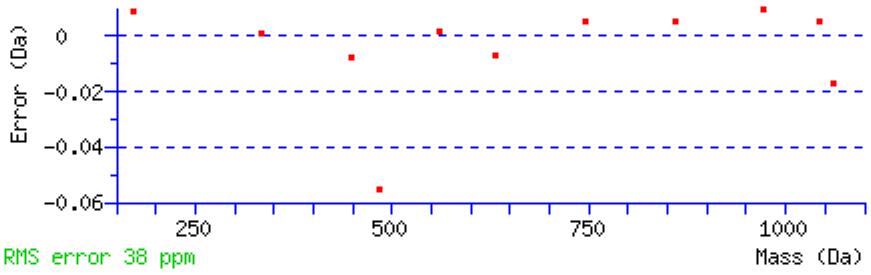
Match to Query 30729: 1228.675848 from(615.345200,2+) rtinseconds(2786) index(33315)
Title: Locus:1.1.1.2645.27
Data file 2011-11-12 - TFD - EP 5-5.mgf

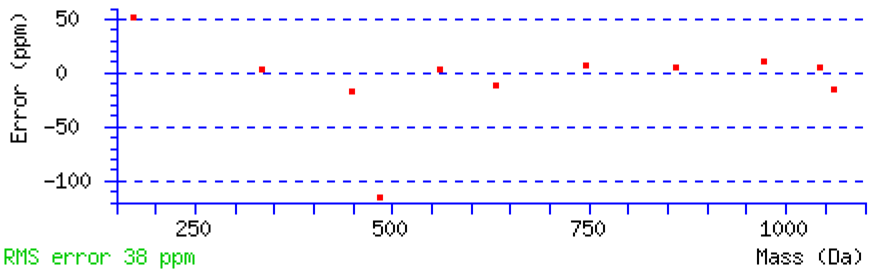
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1228.677536
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 53 **Expect:** 6.6e-005
Matches : 11/114 fragment ions using 21 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	72.044390	36.525833					A							12
2	**171.112804**	86.060040					V	1158.647713	579.827495	1141.621164	571.314220	1140.637148	570.822212	11
3	258.144832	129.576054			240.134267	120.570772	S	***1059.579299***	530.293288	1042.552750	521.780013	1041.568734	521.288005	10
4	371.228896	186.118086			353.218331	177.112804	L	***972.547271***	486.777274	955.520722	478.263999	954.536706	477.771991	9
5	**484.312960**	242.660118			466.302395	233.654836	I	***859.463207***	430.235242	842.436658	421.721967	841.452642	421.229959	8
6	598.355887	299.681582	581.329338	291.168307	580.345322	290.676299	N	***746.379143***	373.693210	729.352594	365.179935	728.368578	364.687927	7
7	669.393001	335.200139	652.366452	326.686864	651.382436	326.194856	A	***632.336216***	316.671746	615.309667	308.158472	614.325651	307.666464	6
8	782.477065	391.742171	765.450516	383.228896	764.466500	382.736888	I	***561.299102***	281.153189	544.272553	272.639915	543.288537	272.147907	5
9	897.504008	449.255642	880.477459	440.742368	879.493443	440.250360	D	***448.215038***	224.611157	431.188489	216.097882	430.204473	215.605874	4
10	998.551687	499.779482	981.525138	491.266207	980.541122	490.774199	T	***333.188095***	167.097685	316.161546	158.584411	315.177530	158.092403	3
11	1055.573151	528.290214	1038.546602	519.776939	1037.562586	519.284931	G	232.140416	116.573846	215.113867	108.060571			2
12							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
53.5	1228.677536	-0.001688	AVSLINAIDTGR

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

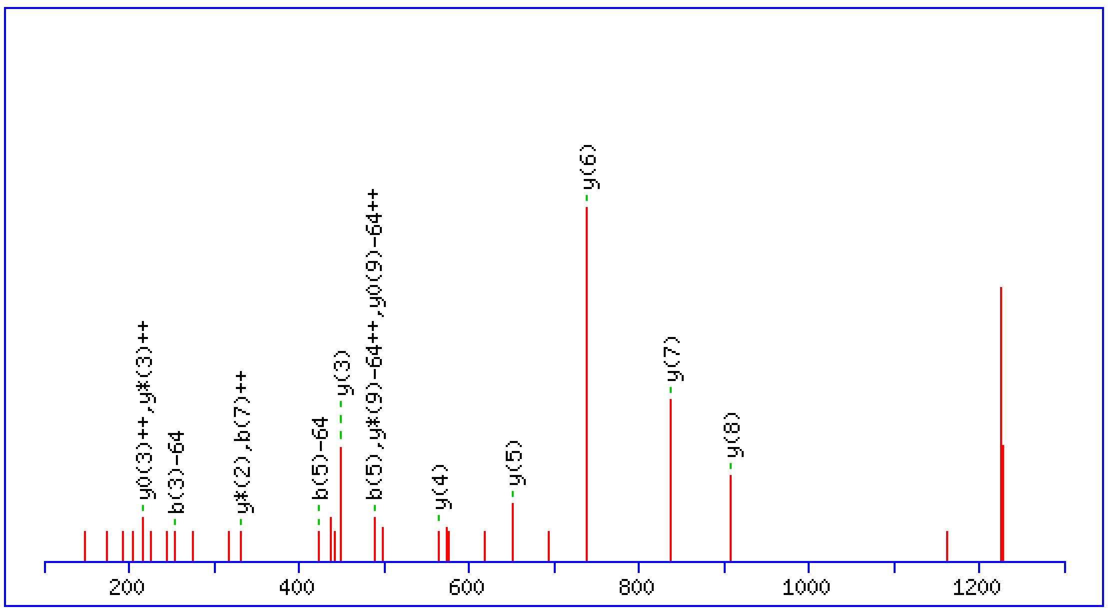
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGMAVSSDTCR**
Found in **COMD6_HUMAN**, COMM domain-containing protein 6 OS=Homo sapiens GN=COMMD6 PE=1 SV=1

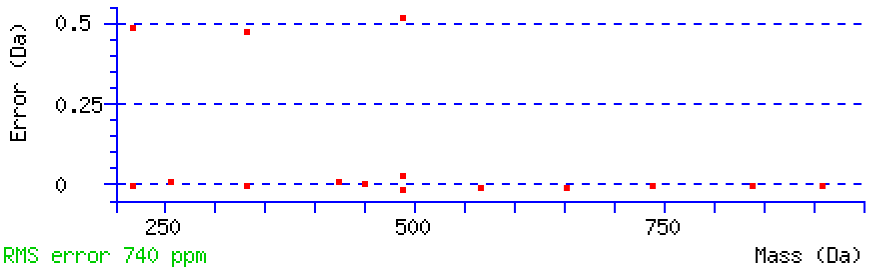
Match to Query 28204: 1225.543648 from(613.779100,2+) rtinseconds(1107) index(2357)
Title: Locus:1.1.1.1752.24
Data file 2011-11-12 - TFD - EP 6-7.mgf

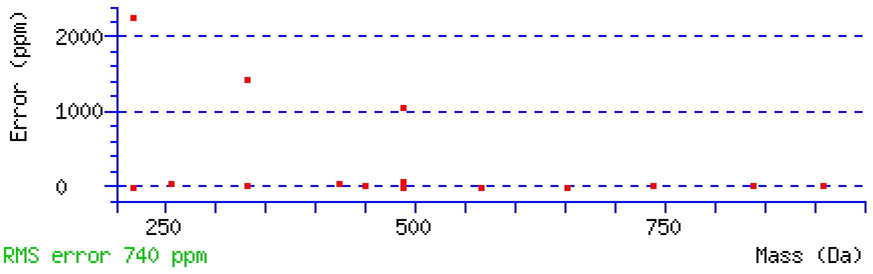
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1225.543106
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M3      : Oxidation (M), with neutral losses 63.998285(shown in table), 0.000000
Ions Score: 53  Expect: 2.1e-005
Matches : 15/124 fragment ions using 15 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							11
2	171.112804	86.060040			G	1049.468036	525.237656	1032.441487	516.724382	1031.457471	516.232374	10
3	**254.149919**	127.578597			M	992.446572	496.726924	975.420023	488.213649	974.436007	487.721641	9
4	325.187033	163.097154			A	***909.409457***	455.208367	892.382908	446.695092	891.398892	446.203084	8
5	**424.255447**	212.631362			V	***838.372343***	419.689810	821.345794	411.176535	820.361778	410.684527	7
6	511.287475	256.147376	493.276910	247.142093	S	***739.303929***	370.155602	722.277380	361.642328	721.293364	361.150320	6
7	598.319503	299.663390	580.308938	290.658107	S	***652.271901***	326.639589	635.245352	318.126314	634.261336	317.634306	5
8	713.346446	357.176861	695.335881	348.171579	D	***565.239873***	283.123575	548.213324	274.610300	547.229308	274.118292	4
9	814.394125	407.700701	796.383560	398.695418	T	***450.212930***	225.610103	433.186381	217.096828	432.202365	216.604820	3
10	988.440424	494.723850	970.429859	485.718567	C	349.165251	175.086263	332.138702	166.572989			2
11					R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
53.1	1225.543106	0.000542	LGMAVSSDTCR
7.7	1225.550980	-0.007332	MQPAPADGHVR
3.2	1225.543610	0.000038	GQSQSGGHGPGGGK
1.5	1225.531845	0.011803	LLMNSCSEDK
0.3	1225.547592	-0.003944	GDESGYRWTR

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

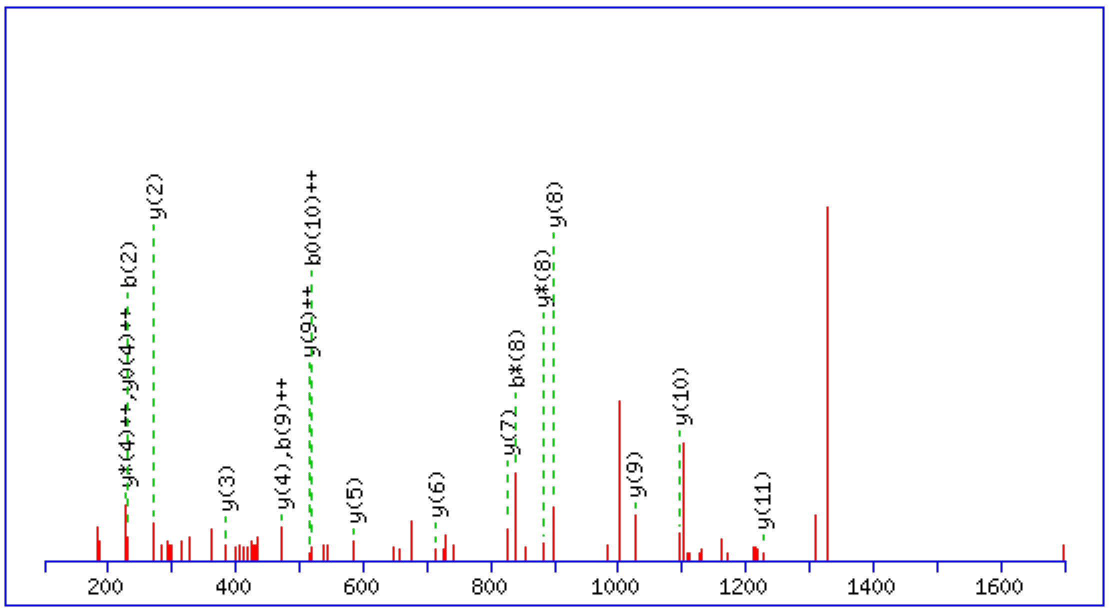
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TEAQANQISLPR**
Found in **COMD9_HUMAN**, COMM domain-containing protein 9 OS=Homo sapiens GN=COMMD9 PE=1 SV=2

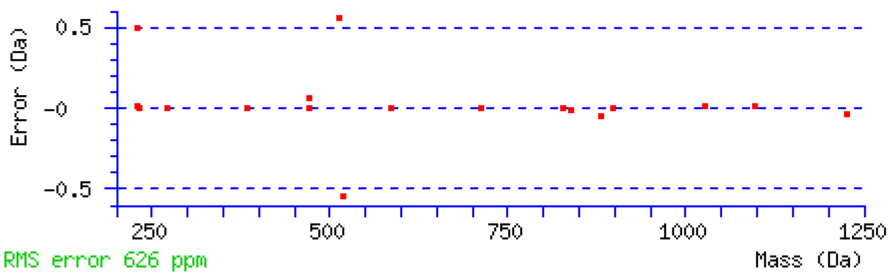
Match to Query 43147: 1326.677928 from(664.346240,2+) rtinseconds(1935) index(19604)
Title: Locus:1.1.1.1993.35
Data file 2011-11-10 - TFD - EP 4-6.mgf

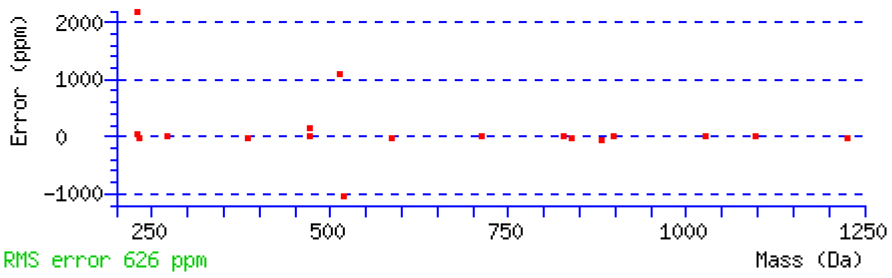
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1326.689148
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 51 **Expect:** 0.00022
Matches : 18/120 fragment ions using 41 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							12
2	231.097548	116.052412			213.086983	107.047130	E	*1226.648776*	613.828026	1209.622227	605.314752	1208.638211	604.822744	11
3	302.134662	151.570969			284.124097	142.565687	A	*1097.606183*	549.306730	1080.579634	540.793455	1079.595618	540.301447	10
4	430.193240	215.600258	413.166691	207.086984	412.182675	206.594976	Q	*1026.569069*	513.788173	1009.542520	505.274898	1008.558504	504.782890	9
5	501.230354	251.118815	484.203805	242.605540	483.219789	242.113532	A	*898.510491*	449.758884	881.483942	441.245609	880.499926	440.753601	8
6	615.273281	308.140279	598.246732	299.627004	597.262716	299.134996	N	*827.473377*	414.240327	810.446828	405.727052	809.462812	405.235044	7
7	743.331859	372.169568	726.305310	363.656293	725.321294	363.164285	Q	*713.430450*	357.218863	696.403901	348.705589	695.419885	348.213581	6
8	856.415923	428.711600	839.389374	420.198325	838.405358	419.706317	I	*585.371872*	293.189574	568.345323	284.676300	567.361307	284.184292	5
9	943.447951	472.227614	926.421402	463.714339	925.437386	463.222331	S	*472.287808*	236.647542	455.261259	228.134267	454.277243	227.642259	4
10	1056.532015	528.769646	1039.505466	520.256371	1038.521450	519.764363	L	*385.255780*	193.131528	368.229231	184.618253			3
11	1153.584779	577.296028	1136.558230	568.782753	1135.574214	568.290745	P	*272.171716*	136.589496	255.145167	128.076221			2
12							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of TEAQANQISLPR
(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	1326.689148	-0.011220	TEAQANQISLPR
1.4	1326.679260	-0.001332	NGAGNWLAQQIR

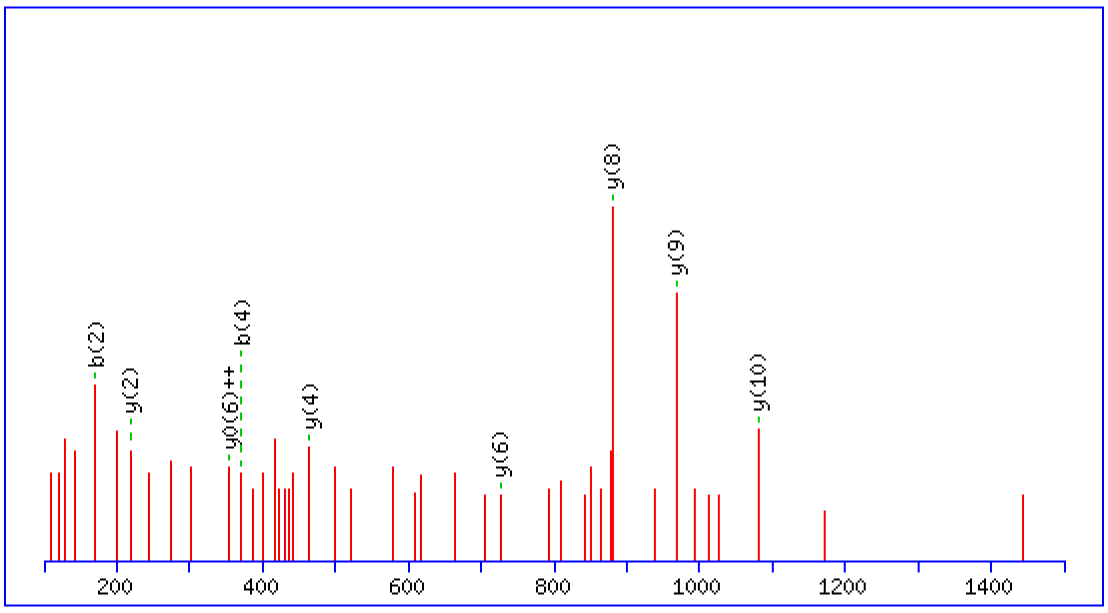
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AVISPGFDVFAK**
Found in **CO2_HUMAN**, Complement C2 OS=Homo sapiens GN=C2 PE=1 SV=2

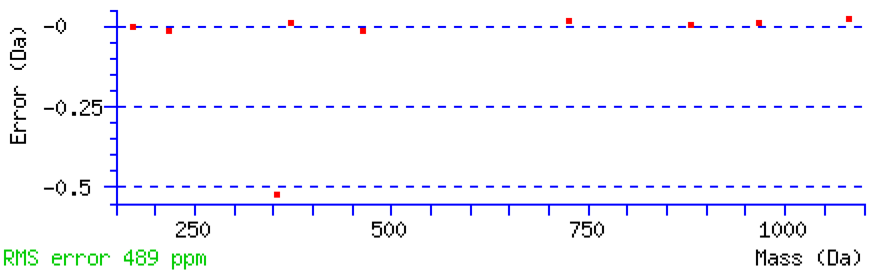
Match to Query 34578: 1249.666568 from(625.840560,2+) rtinseconds(3164) index(43918)
Title: Locus:1.1.1.2626.23
Data file 2011-11-14 - TFD - EP 8-2.mgf

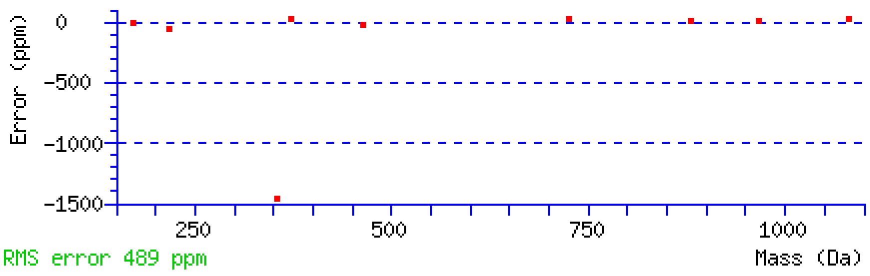
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1249.670685
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.008
Matches : 9/96 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			A							12
2	**171.112804**	86.060040			V	1179.640837	590.324057	1162.614288	581.810782	1161.630272	581.318774	11
3	284.196868	142.602072			I	***1080.572423***	540.789850	1063.545874	532.276575	1062.561858	531.784567	10
4	**371.228896**	186.118086	353.218331	177.112804	S	***967.488359***	484.247818	950.461810	475.734543	949.477794	475.242535	9
5	468.281660	234.644468	450.271095	225.639186	P	***880.456331***	440.731804	863.429782	432.218529	862.445766	431.726521	8
6	525.303124	263.155200	507.292559	254.149918	G	783.403567	392.205422	766.377018	383.692147	765.393002	383.200139	7
7	672.371538	336.689407	654.360973	327.684125	F	***726.382103***	363.694690	709.355554	355.181415	708.371538	354.689407	6
8	787.398481	394.202879	769.387916	385.197596	D	579.313689	290.160483	562.287140	281.647208	561.303124	281.155200	5
9	886.466895	443.737086	868.456330	434.731803	V	***464.286746***	232.647011	447.260197	224.133737			4
10	1033.535309	517.271293	1015.524744	508.266010	F	365.218332	183.112804	348.191783	174.599530			3
11	1104.572423	552.789850	1086.561858	543.784567	A	***218.149918***	109.578597	201.123369	101.065322			2
12					K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.6	1249.670685	-0.004117	AVISPGFDVFAK
8.2	1249.666611	-0.000043	KELSANTAAFAK

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

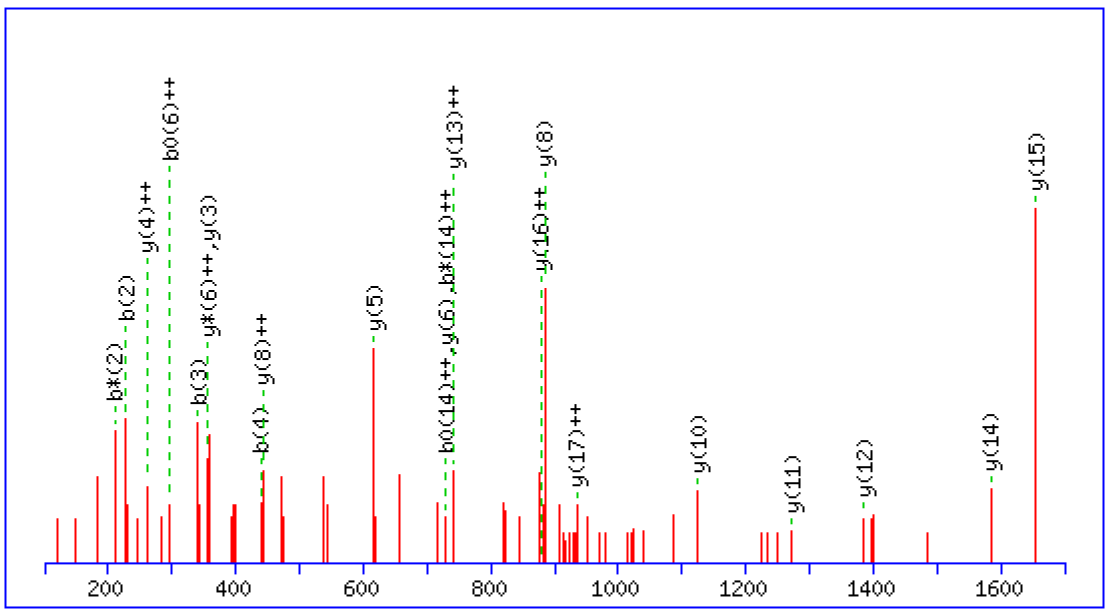
Mascot Search Results

Peptide View

MS/MS Fragmentation of LNLVATPLFLKPGIPYPIK
Found in CO5_HUMAN, Complement C5 OS=Homo sapiens GN=C5 PE=1 SV=4

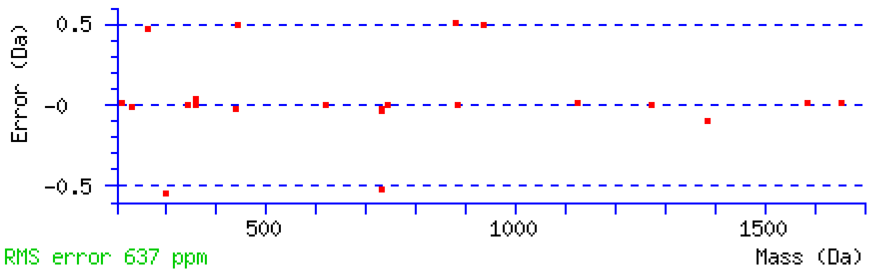
Match to Query 66113: 2093.263362 from(698.761730,3+) rtinseconds(3799) index(55427)
Title: Locus:1.1.1.2826.25
Data file 2011-11-12 - TFD - EP 6-2.mgf

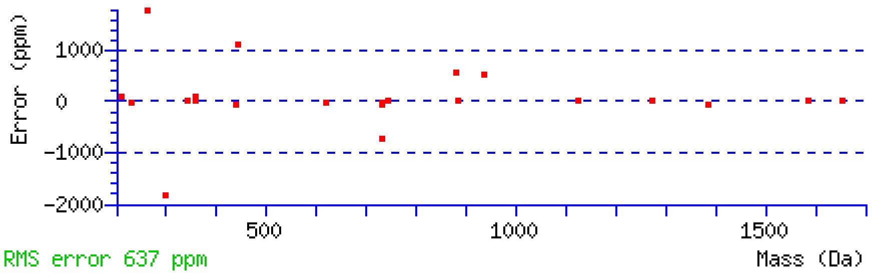
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2093.265244
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 53  Expect: 4.9e-006
Matches : 22/178 fragment ions using 39 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.091340	57.549308					L							19
2	**228.134267**	114.570771	211.107718	106.057497			N	1981.188484	991.097880	1964.161935	982.584606	1963.177919	982.092598	18
3	**341.218331**	171.112803	324.191782	162.599529			L	1867.145557	934.076417	1850.119008	925.563142	1849.134992	925.071134	17
4	**440.286745**	220.647010	423.260196	212.133736			V	1754.061493	877.534385	1737.034944	869.021110	1736.050928	868.529102	16
5	511.323859	256.165568	494.297310	247.652293			A	***1654.993079***	828.000178	1637.966530	819.486903	1636.982514	818.994895	15
6	612.371538	306.689407	595.344989	298.176133	594.360973	297.684125	T	***1583.955965***	792.481621	1566.929416	783.968346	1565.945400	783.476338	14
7	709.424302	355.215789	692.397753	346.702515	691.413737	346.210507	P	1482.908286	741.957781	1465.881737	733.444507			13
8	822.508366	411.757821	805.481817	403.244547	804.497801	402.752539	L	***1385.855522***	693.431399	1368.828973	684.918125			12
9	969.576780	485.292028	952.550231	476.778754	951.566215	476.286746	F	***1272.771458***	636.889367	1255.744909	628.376093			11
10	1082.660844	541.834060	1065.634295	533.320786	1064.650279	532.828778	L	***1125.703044***	563.355160	1108.676495	554.841886			10
11	1210.755807	605.881542	1193.729258	597.368267	1192.745242	596.876259	K	1012.618980	506.813128	995.592431	498.299854			9
12	1307.808571	654.407924	1290.782022	645.894649	1289.798006	645.402641	P	***884.524017***	442.765647	867.497468	434.252372			8
13	1364.830035	682.918656	1347.803486	674.405381	1346.819470	673.913373	G	787.471253	394.239265	770.444704	385.725990			7
14	1477.914099	739.460687	1460.887550	730.947413	1459.903534	730.455405	I	***730.449789***	365.728533	713.423240	357.215258			6
15	1574.966863	787.987069	1557.940314	779.473795	1556.956298	778.981787	P	***617.365725***	309.186501	600.339176	300.673226			5
16	1738.030192	869.518734	1721.003643	861.005460	1720.019627	860.513451	Y	520.312961	260.660119	503.286412	252.146844			4
17	1835.082956	918.045116	1818.056407	909.531842	1817.072391	909.039833	P	***357.249632***	179.128454	340.223083	170.615180			3
18	1948.167020	974.587148	1931.140471	966.073873	1930.156455	965.581865	I	260.196868	130.602072	243.170319	122.088798			2
19							K	147.112804	74.060040	130.086255	65.546766			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
53.1	2093.265244	-0.001882	LNLVATPLFLKPGIPYPIK

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

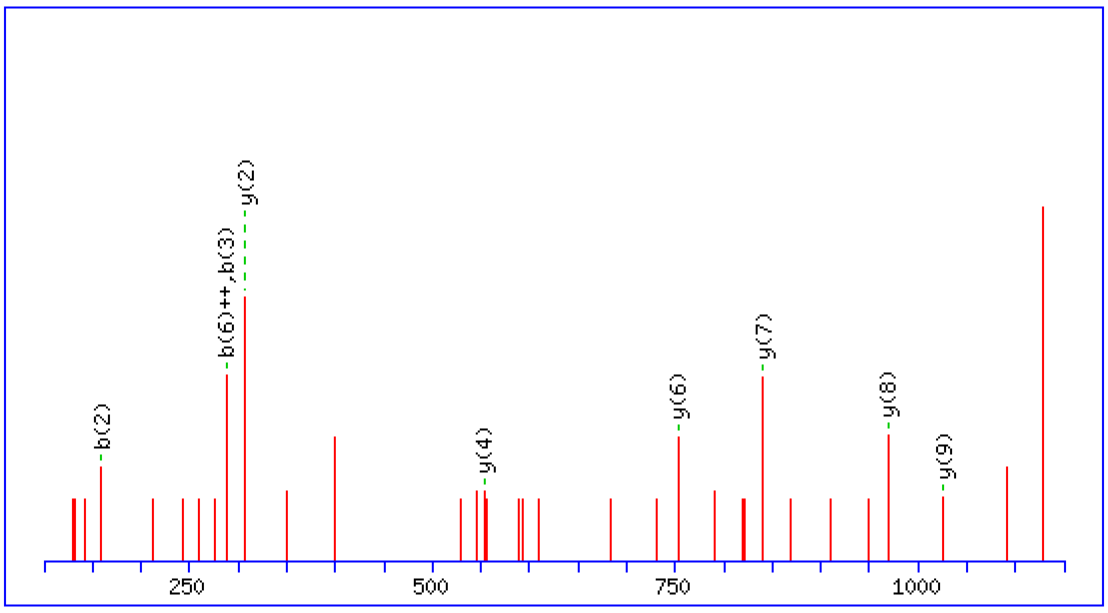
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TGESAEFVCK**
Found in **FHR1_HUMAN**, Complement factor H-related protein 1 OS=Homo sapiens GN=CFHR1 PE=1 SV=2

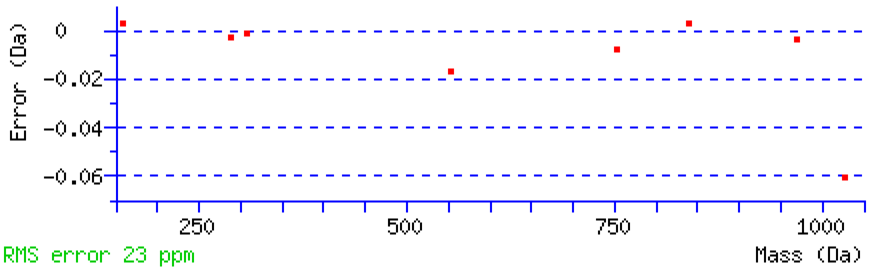
Match to Query 427298: 1126.502168 from(564.258360,2+) rtinseconds(1374) index(335559)
Title: Locus:1.1.1.859.31
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

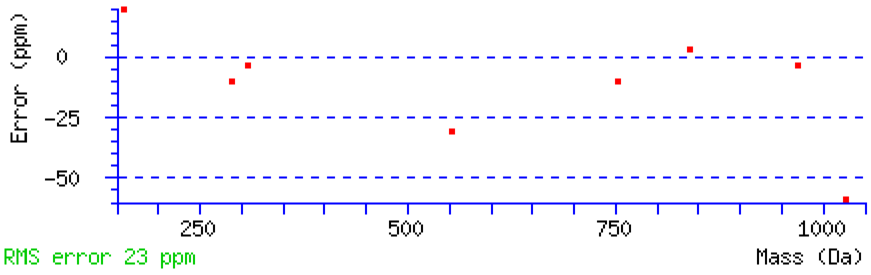
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1126.496475
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 37 **Expect:** 0.0015
Matches : 9/82 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116	84.044390	42.525833	T							10
2	**159.076419**	80.041847	141.065854	71.036565	G	***1026.456073***	513.731675	1009.429524	505.218400	1008.445508	504.726392	9
3	**288.119012**	144.563144	270.108447	135.557862	E	***969.434609***	485.220943	952.408060	476.707668	951.424044	476.215660	8
4	375.151040	188.079158	357.140475	179.073876	S	***840.392016***	420.699646	823.365467	412.186372	822.381451	411.694364	7
5	446.188154	223.597715	428.177589	214.592433	A	***753.359988***	377.183632	736.333439	368.670358	735.349423	368.178350	6
6	575.230747	288.119012	557.220182	279.113729	E	682.322874	341.665075	665.296325	333.151801	664.312309	332.659793	5
7	722.299161	361.653219	704.288596	352.647936	F	***553.280281***	277.143779	536.253732	268.630504			4
8	821.367575	411.187426	803.357010	402.182143	V	406.211867	203.609571	389.185318	195.096297			3
9	981.398224	491.202750	963.387659	482.197468	C	***307.143453***	154.075365	290.116904	145.562090			2
10					K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.0	1126.496475	0.005693	TGESAEFVCK

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

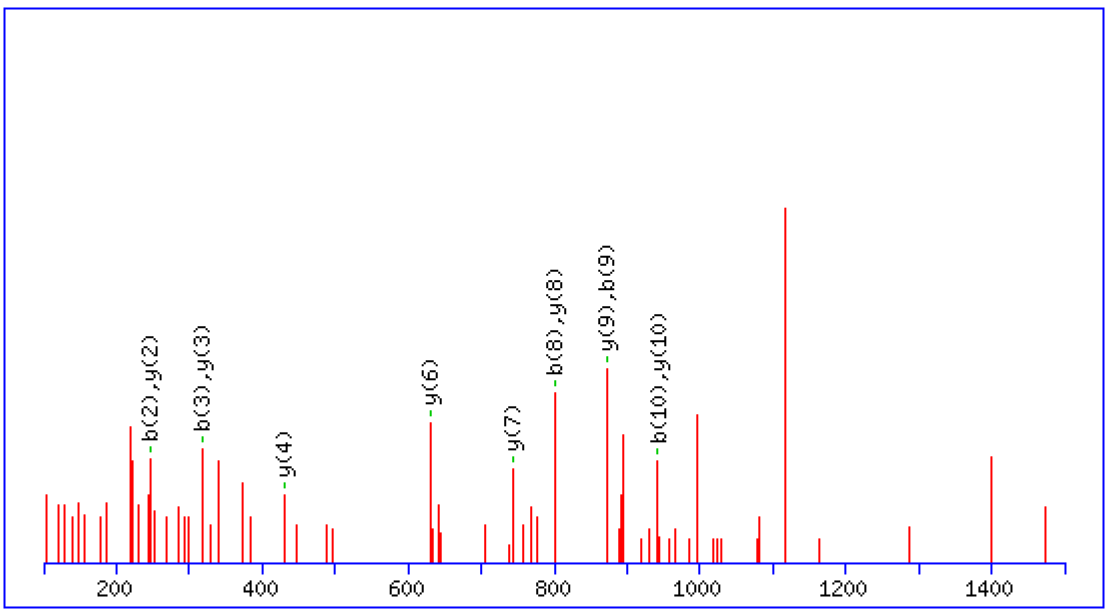
Mascot Search Results

Peptide View

MS/MS Fragmentation of **CAAGLAELAAR**
Found in **CSN1_HUMAN**, COP9 signalosome complex subunit 1 OS=Homo sapiens GN=GPS1 PE=1 SV=4

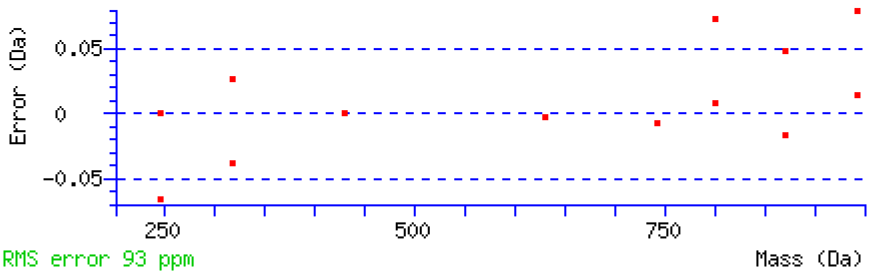
Match to Query 20894: 1115.575228 from(558.794890,2+) rtinseconds(2139) index(25525)
Title: Locus:1.1.1.2184.25
Data file 2011-11-12 - TFD - EP 6-3.mgf

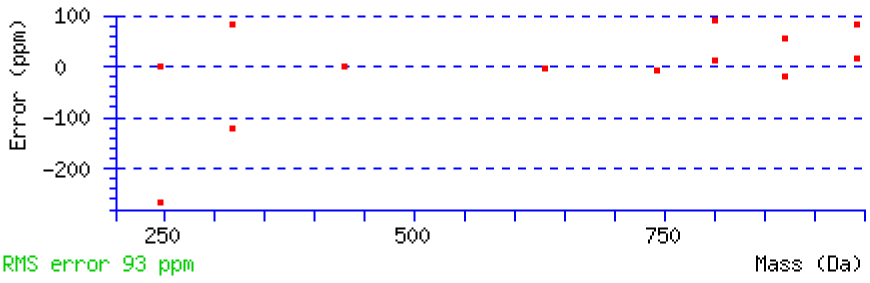
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1115.575684
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 55 **Expect:** 6.2e-005
Matches : 13/80 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	175.053575	88.030425			C							11
2	**246.090689**	123.548982			A	***942.536707***	471.771992	925.510158	463.258717	924.526142	462.766709	10
3	**317.127803**	159.067540			A	***871.499593***	436.253435	854.473044	427.740160	853.489028	427.248152	9
4	374.149267	187.578272			G	***800.462479***	400.734878	783.435930	392.221603	782.451914	391.729595	8
5	487.233331	244.120304			L	***743.441015***	372.224146	726.414466	363.710871	725.430450	363.218863	7
6	558.270445	279.638861			A	***630.356951***	315.682114	613.330402	307.168839	612.346386	306.676831	6
7	687.313038	344.160157	669.302473	335.154875	E	559.319837	280.163557	542.293288	271.650282	541.309272	271.158274	5
8	**800.397102**	400.702189	782.386537	391.696907	L	***430.277244***	215.642260	413.250695	207.128985			4
9	**871.434216**	436.220746	853.423651	427.215464	A	***317.193180***	159.100228	300.166631	150.586953			3
10	**942.471330**	471.739303	924.460765	462.734021	A	***246.156066***	123.581671	229.129517	115.068396			2
11					R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.5	1115.575684	-0.000456	CAAGLAELAAR
15.7	1115.575684	-0.000456	MNEIQAIAAR
14.2	1115.582260	-0.007032	SLGTAGPPSAVK
13.0	1115.564484	0.010744	ALNMAIPGGPK
7.0	1115.586288	-0.011060	LPFDTPPIGK
5.8	1115.575714	-0.000486	ACAAGTPAVIR
4.8	1115.572357	0.002871	EVQTWVQAR
4.5	1115.583572	-0.008344	TFPNAPRAAR
4.5	1115.583572	-0.008344	TFPNAPRAAR
4.3	1115.568298	0.006930	ESQELRQAR

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

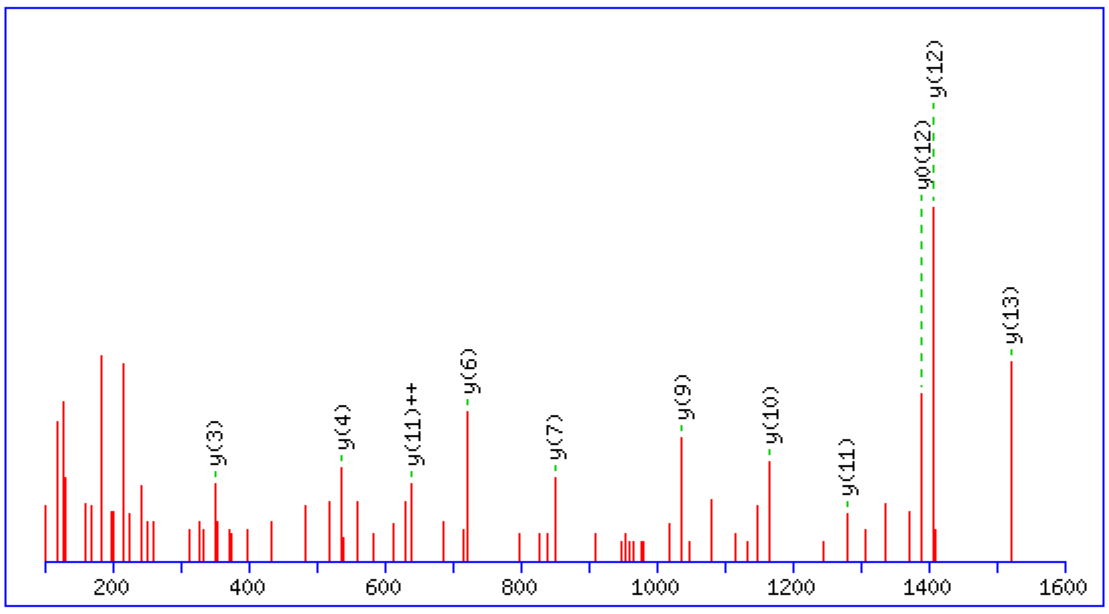
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLELEGEKGEWGFK**
Found in **CSN2_HUMAN**, COP9 signalosome complex subunit 2 OS=Homo sapiens GN=COPS2 PE=1 SV=1

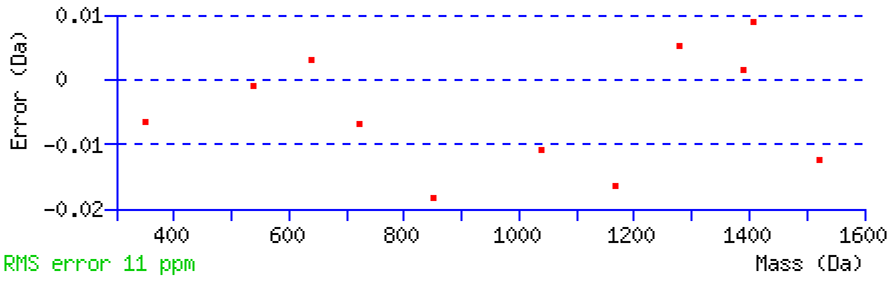
Match to Query 47153: 1619.816592 from(540.946140,3+) rtinseconds(2728) index(36629)
Title: Locus:1.1.1.2527.13
Data file 2011-11-10 - TFD - EP 4-3.mgf

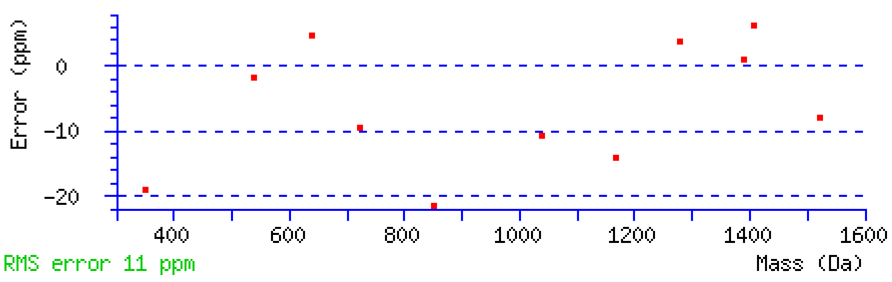
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1619.819504
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 70 **Expect:** 9.6e-007
Matches : 11/130 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							14
2	213.159754	107.083515					L	***1521.758386***	761.382831	1504.731837	752.869557	1503.747821	752.377548	13
3	342.202347	171.604811			324.191782	162.599529	E	***1408.674322***	704.840799	1391.647773	696.327525	1390.663757	695.835517	12
4	455.286411	228.146843			437.275846	219.141561	L	***1279.631729***	640.319503	1262.605180	631.806228	1261.621164	631.314220	11
5	584.329004	292.668140			566.318439	283.662858	E	***1166.547665***	583.777471	1149.521116	575.264196	1148.537100	574.772188	10
6	641.350468	321.178872			623.339903	312.173590	G	***1037.505072***	519.256174	1020.478523	510.742900	1019.494507	510.250892	9
7	770.393061	385.700169			752.382496	376.694886	E	980.483608	490.745442	963.457059	482.232168	962.473043	481.740160	8
8	898.488024	449.747650	881.461475	441.234376	880.477459	440.742368	K	***851.441015***	426.224146	834.414466	417.710871	833.430450	417.218863	7
9	955.509488	478.258382	938.482939	469.745108	937.498923	469.253100	G	***723.346052***	362.176664	706.319503	353.663389	705.335487	353.171382	6
10	1084.552081	542.779679	1067.525532	534.266404	1066.541516	533.774396	E	666.324588	333.665932	649.298039	325.152657	648.314023	324.660649	5
11	1270.631394	635.819335	1253.604845	627.306061	1252.620829	626.814053	W	***537.281995***	269.144636	520.255446	260.631361			4
12	1327.652858	664.330067	1310.626309	655.816793	1309.642293	655.324784	G	***351.202682***	176.104979	334.176133	167.591704			3
13	1474.721272	737.864274	1457.694723	729.351000	1456.710707	728.858992	F	294.181218	147.594247	277.154669	139.080973			2
14							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
70.4	1619.819504	-0.002912	VLELEGEKGEWGFK
6.2	1619.816345	0.000247	ALINPFAPSRMPMK
5.3	1619.816345	0.000247	ALINPFAPSRMPMK

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

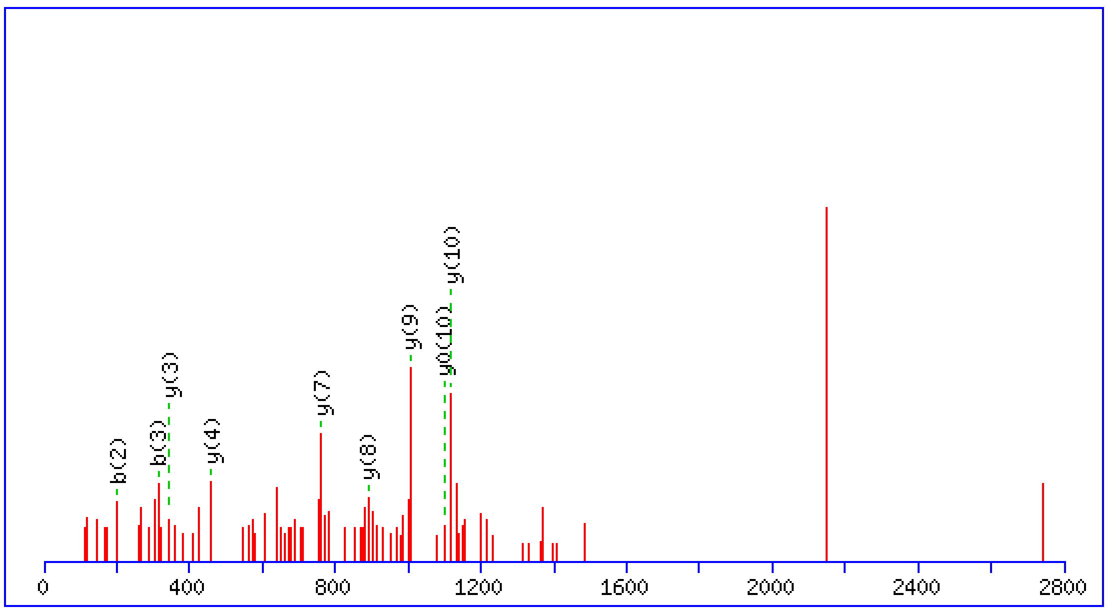
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SLIIDEGEDDLGR**
Found in **CCS_HUMAN**, Copper chaperone for superoxide dismutase OS=Homo sapiens GN=CCS PE=1 SV=1

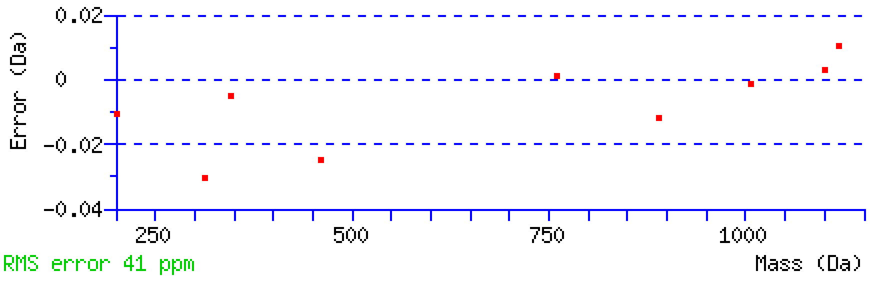
Match to Query 43452: 1430.694988 from(716.354770,2+) rtinseconds(2580) index(33025)
Title: Locus:1.1.1.2398.39
Data file 2011-11-12 - TFD - EP 5-4.mgf

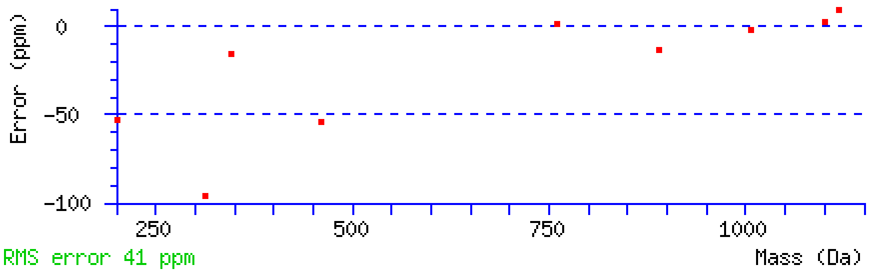
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1430.688889
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.00088
Matches : 9/114 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	S							13
2	**201.123368**	101.065322	183.112803	92.060039	L	1344.664151	672.835713	1327.637602	664.322439	1326.653586	663.830431	12
3	**314.207432**	157.607354	296.196867	148.602071	I	1231.580087	616.293681	1214.553538	607.780407	1213.569522	607.288399	11
4	427.291496	214.149386	409.280931	205.144104	I	***1118.496023***	559.751649	1101.469474	551.238375	1100.485458	550.746367	10
5	542.318439	271.662858	524.307874	262.657575	D	***1005.411959***	503.209617	988.385410	494.696343	987.401394	494.204335	9
6	671.361032	336.184154	653.350467	327.178872	E	***890.385016***	445.696146	873.358467	437.182871	872.374451	436.690863	8
7	728.382496	364.694886	710.371931	355.689604	G	***761.342423***	381.174849	744.315874	372.661575	743.331858	372.169567	7
8	857.425089	429.216183	839.414524	420.210900	E	704.320959	352.664117	687.294410	344.150843	686.310394	343.658835	6
9	972.452032	486.729654	954.441467	477.724372	D	575.278366	288.142821	558.251817	279.629546	557.267801	279.137538	5
10	1087.478975	544.243126	1069.468410	535.237843	D	***460.251423***	230.629349	443.224874	222.116075	442.240858	221.624067	4
11	1200.563039	600.785157	1182.552474	591.779875	L	***345.224480***	173.115878	328.197931	164.602603			3
12	1257.584503	629.295889	1239.573938	620.290607	G	232.140416	116.573846	215.113867	108.060571			2
13					R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.7	1430.688889	0.006099	SLIIDEGEDDLGR
4.1	1430.700104	-0.005116	AEPASVAAESLAGSR

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

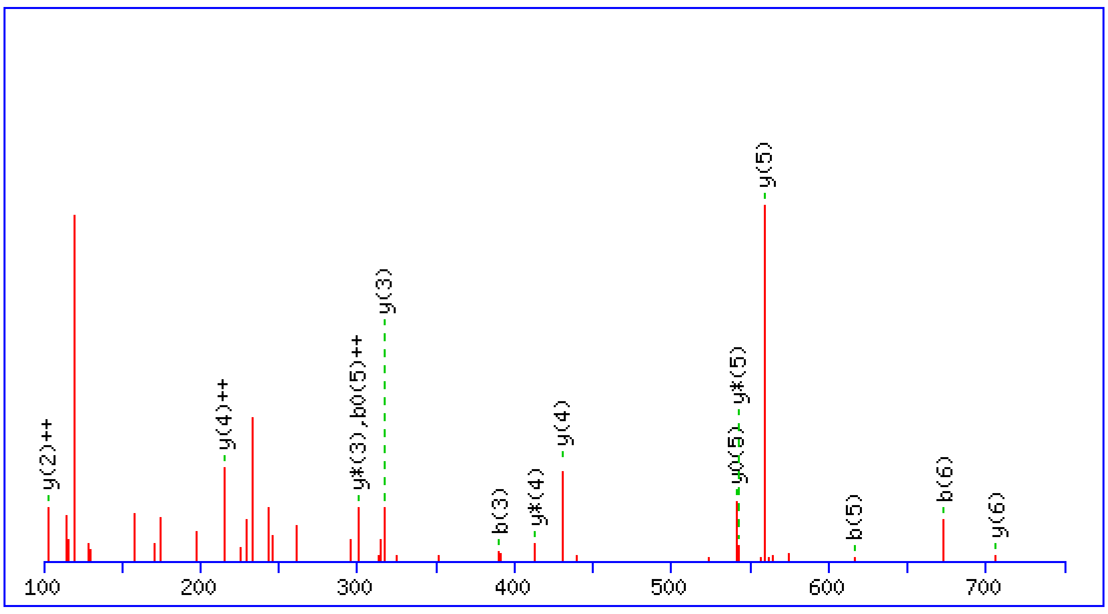
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LMEIIGK**
Found in **CRF_HUMAN**, Corticoliberin OS=Homo sapiens GN=CRH PE=1 SV=1

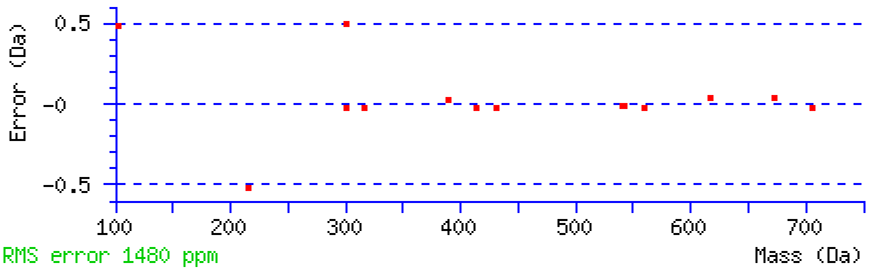
Match to Query 1277: 818.463328 from(410.238940,2+) rtinseconds(1924) index(18077)
Title: Locus:1.1.1.2291.4
Data file 2011-11-12 - TFD - EP 5-1.mgf

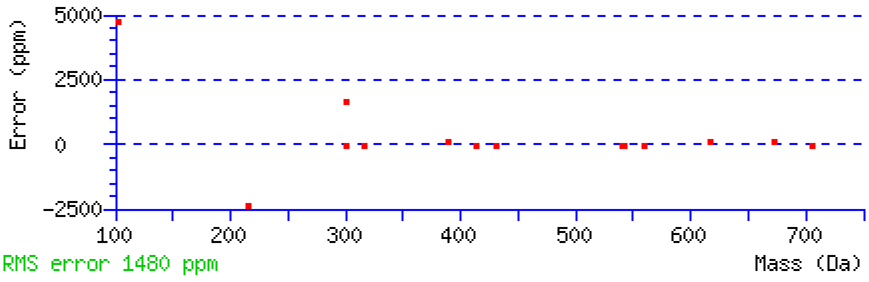
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 818.457153
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M2 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 31 **Expect:** 0.0046
Matches : 14/72 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							7
2	261.126740	131.067008			M	***706.380389***	353.693833	689.353840	345.180558	688.369824	344.688550	6
3	***390.169333***	195.588304	372.158768	186.583022	E	***559.344989***	280.176133	542.318440	271.662858	541.334424	271.170850	5
4	503.253397	252.130337	485.242832	243.125054	I	***430.302396***	215.654836	413.275847	207.141562			4
5	***616.337461***	308.672369	598.326896	299.667086	I	***317.218332***	159.112804	300.191783	150.599530			3
6	***673.358925***	337.183101	655.348360	328.177818	G	204.134268	102.570772	187.107719	94.057498			2
7					K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.2	818.457153	0.006175	LMEIIGK
30.9	818.465012	-0.001684	FIEIAAR
11.1	818.465027	-0.001699	FLPSLAR
9.0	818.457153	0.006175	EIMLGLK
4.9	818.457153	0.006175	IEAMVLK
4.8	818.465042	-0.001714	FLLVGDR
4.6	818.457169	0.006159	LMSPVLK
4.1	818.465027	-0.001699	YPVLTAR
3.8	818.465027	-0.001699	NGFAGLIK
3.5	818.468384	-0.005056	MLALISR

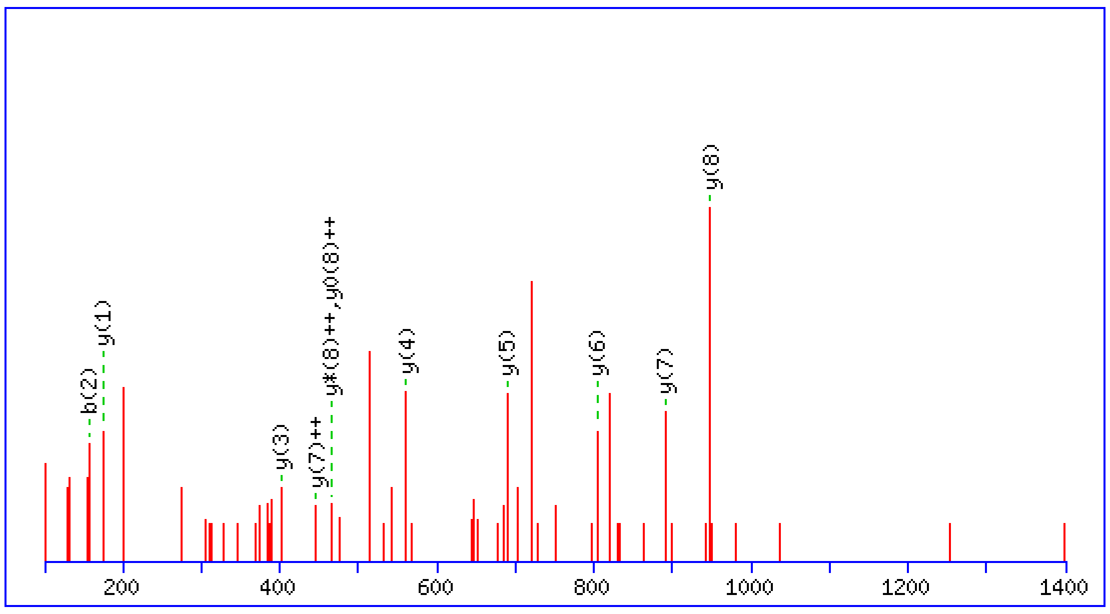
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VGSDQCLLR**
Found in **CXAR_HUMAN**, Coxsackievirus and adenovirus receptor OS=Homo sapiens GN=CXADR PE=1 SV=1

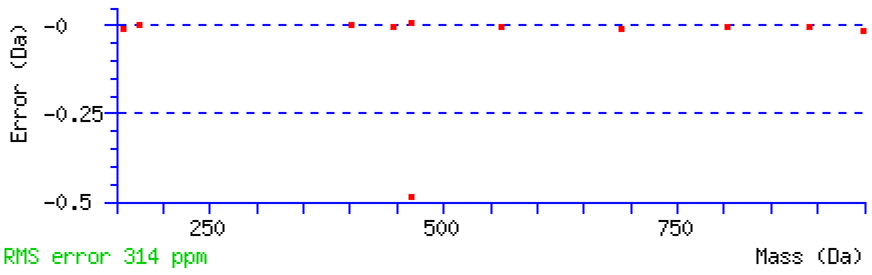
Match to Query 324606: 1046.522068 from(524.268310,2+) rtinseconds(1596) index(504186)
Title: Locus:1.1.1.937.24
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

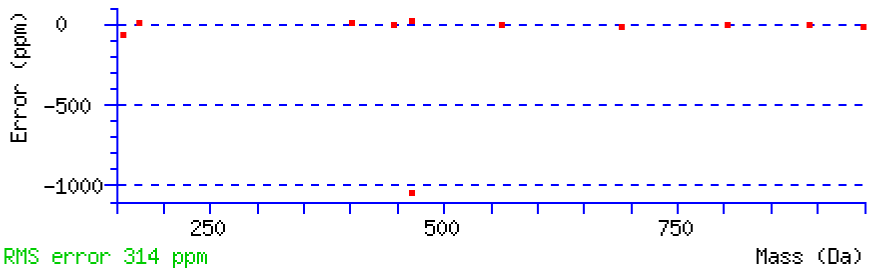
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1046.517883
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 35 **Expect:** 0.0053
Matches : 11/74 fragment ions using 26 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	100.075690	50.541483					V							9
2	157.097154	79.052215					G	*948.456742*	474.732009	931.430193	466.218735	930.446177	465.726727	8
3	244.129182	122.568229			226.118617	113.562946	S	*891.435278*	446.221277	874.408729	437.708003	873.424713	437.215995	7
4	359.156125	180.081700			341.145560	171.076418	D	*804.403250*	402.705263	787.376701	394.191989	786.392685	393.699981	6
5	487.214703	244.110989	470.188154	235.597715	469.204138	235.105707	Q	*689.376307*	345.191792	672.349758	336.678517			5
6	647.245352	324.126314	630.218803	315.613040	629.234787	315.121032	C	*561.317729*	281.162503	544.291180	272.649228			4
7	760.329416	380.668346	743.302867	372.155072	742.318851	371.663064	L	*401.287080*	201.147178	384.260531	192.633904			3
8	873.413480	437.210378	856.386931	428.697104	855.402915	428.205096	L	288.203016	144.605146	271.176467	136.091872			2
9							R	*175.118952*	88.063114	158.092403	79.549840			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.0	1046.517883	0.004185	VGSDQCLLR
11.7	1046.517883	0.004185	VNGDTCIIR
9.8	1046.531784	-0.009716	VGSDIAELLM
4.5	1046.529114	-0.007046	VATSPTCRR
4.1	1046.529083	-0.007015	RATAAECLR
3.7	1046.521912	0.000156	VMWTPPLR
3.1	1046.529755	-0.007687	YFSQHLPR

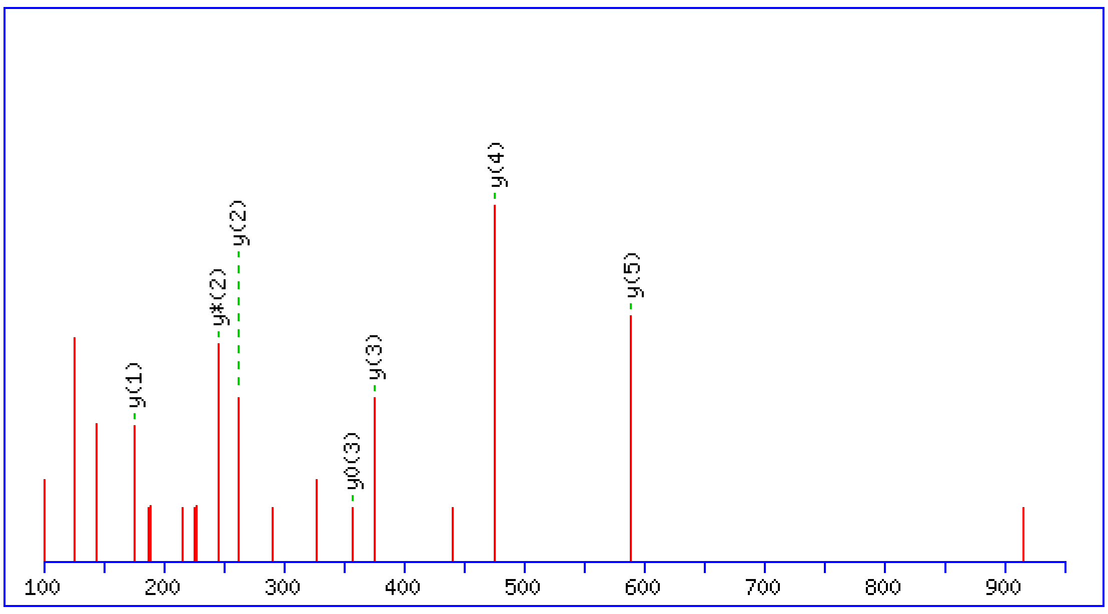
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TDLTLSR**
Found in **CRTC3_HUMAN**, CREB-regulated transcription coactivator 3 OS=Homo sapiens GN=CRTC3 PE=1 SV=2

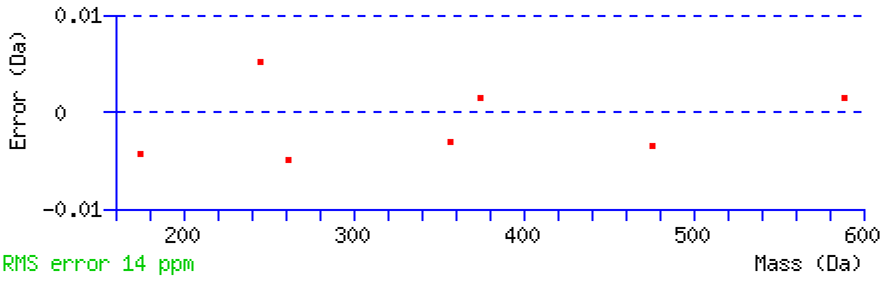
Match to Query 9228: 804.439928 from(403.227240,2+) rtinseconds(1370) index(335482)
Title: Locus:1.1.1.858.2
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

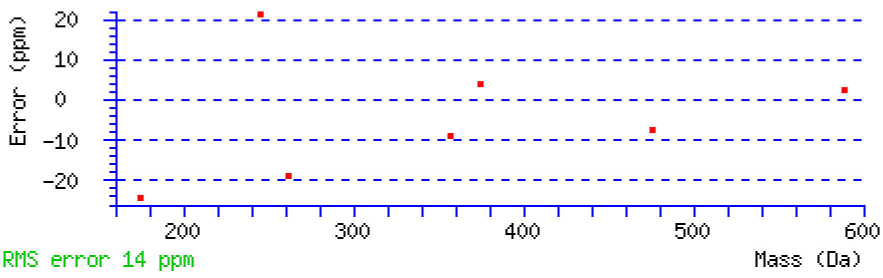
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 804.434128
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 37  Expect: 0.0021
Matches : 7/58 fragment ions using 12 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116	84.044390	42.525833	**T**							7
2	217.081898	109.044587	199.071333	100.039304	**D**	704.393730	352.700503	687.367181	344.187229	686.383165	343.695221	6
3	330.165962	165.586619	312.155397	156.581336	**L**	***589.366787***	295.187032	572.340238	286.673757	571.356222	286.181749	5
4	431.213641	216.110458	413.203076	207.105176	**T**	***476.282723***	238.644999	459.256174	230.131725	458.272158	229.639717	4
5	544.297705	272.652491	526.287140	263.647208	**L**	***375.235044***	188.121160	358.208495	179.607885	357.224479	179.115877	3
6	631.329733	316.168505	613.319168	307.163222	**S**	***262.150980***	131.579128	245.124431	123.065853	244.140415	122.573845	2
7					**R**	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.8	804.434128	0.005800	TDLTLSR
11.2	804.434113	0.005815	TESLISR
10.3	804.434113	0.005815	LSELTSR
8.0	804.434113	0.005815	SSSLGNLK
7.8	804.434113	0.005815	SELISTR
6.7	804.441528	-0.001600	GLGILTTM
5.8	804.434113	0.005815	SSSNILGK
2.4	804.434113	0.005815	DTISNKK
2.0	804.434128	0.005800	SLDLTTR
0.5	804.441513	-0.001585	GMLDLLK

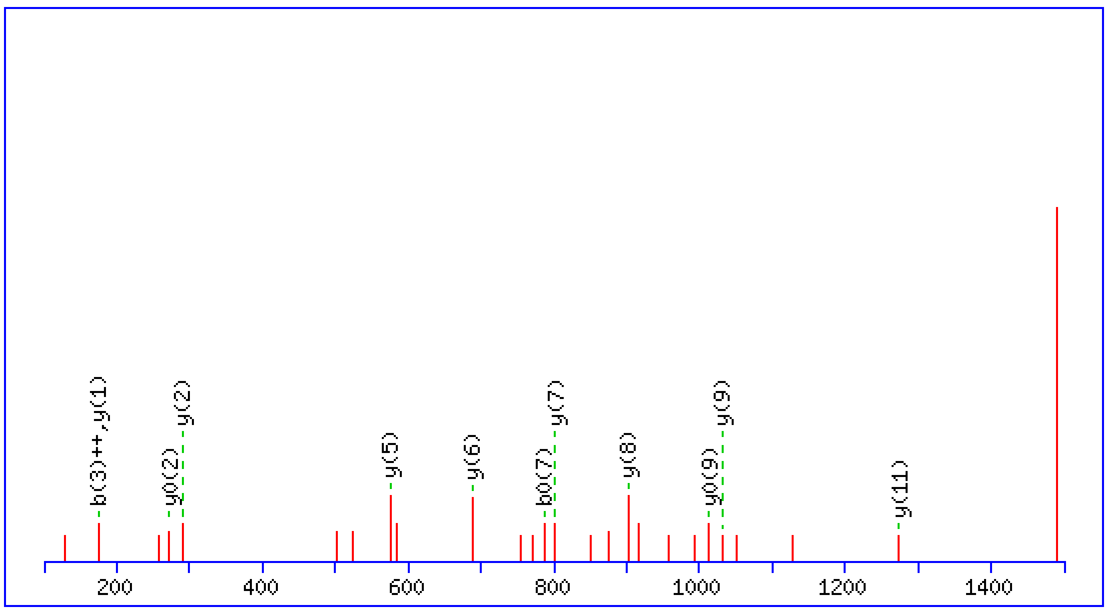
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FAELETILGDIDR**
Found in **CRNL1_HUMAN**, Crooked neck-like protein 1 OS=Homo sapiens GN=CRNKL1 PE=1 SV=4

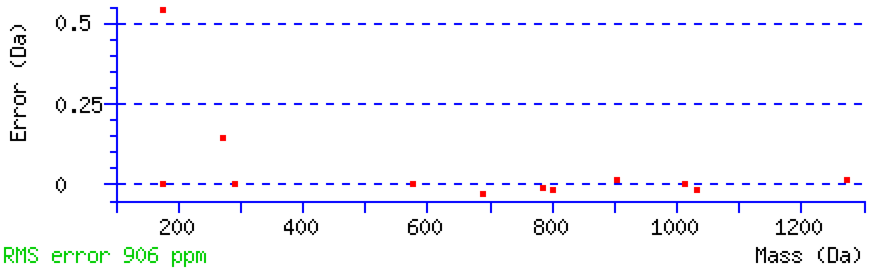
Match to Query 47278: 1490.754368 from(746.384460,2+) rtinseconds(4059) index(60765)
Title: Locus:1.1.1.2971.32
Data file 2011-11-10 - TFD - EP 3-2.mgf

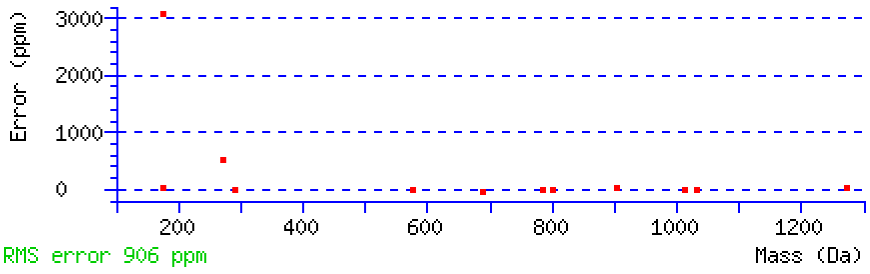
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1490.761658
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 54  Expect: 4.9e-005
Matches : 12/114 fragment ions using 18 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.075690	74.541483			**F**							**13**
2	219.112804	110.060040			**A**	1344.700537	672.853906	1327.673988	664.340632	1326.689972	663.848624	**12**
3	348.155397	174.581336	330.144832	165.576054	**E**	***1273.663423***	637.335350	1256.636874	628.822075	1255.652858	628.330067	**11**
4	461.239461	231.123369	443.228896	222.118086	**L**	1144.620830	572.814053	1127.594281	564.300779	1126.610265	563.808771	**10**
5	590.282054	295.644665	572.271489	286.639383	**E**	***1031.536766***	516.272021	1014.510217	507.758746	1013.526201	507.266738	**9**
6	691.329733	346.168505	673.319168	337.163222	**T**	***902.494173***	451.750725	885.467624	443.237450	884.483608	442.745442	**8**
7	804.413797	402.710537	786.403232	393.705254	**I**	***801.446494***	401.226885	784.419945	392.713611	783.435929	392.221603	**7**
8	917.497861	459.252569	899.487296	450.247286	**L**	***688.362430***	344.684853	671.335881	336.171579	670.351865	335.679571	**6**
9	974.519325	487.763301	956.508760	478.758018	**G**	***575.278366***	288.142821	558.251817	279.629547	557.267801	279.137539	**5**
10	1089.546268	545.276772	1071.535703	536.271490	**D**	518.256902	259.632089	501.230353	251.118814	500.246337	250.626806	**4**
11	1202.630332	601.818804	1184.619767	592.813521	**I**	403.229959	202.118617	386.203410	193.605343	385.219394	193.113335	**3**
12	1317.657275	659.332276	1299.646710	650.326993	**D**	***290.145895***	145.576585	273.119346	137.063311	272.135330	136.571303	**2**
13					**R**	***175.118952***	88.063114	158.092403	79.549839			**1**





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.1	1490.761658	-0.007290	FAELETILGDIDR
2.5	1490.767700	-0.013332	HCNIHAGLRPFR
0.4	1490.761673	-0.007305	SSDVNIDIKFPPK

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

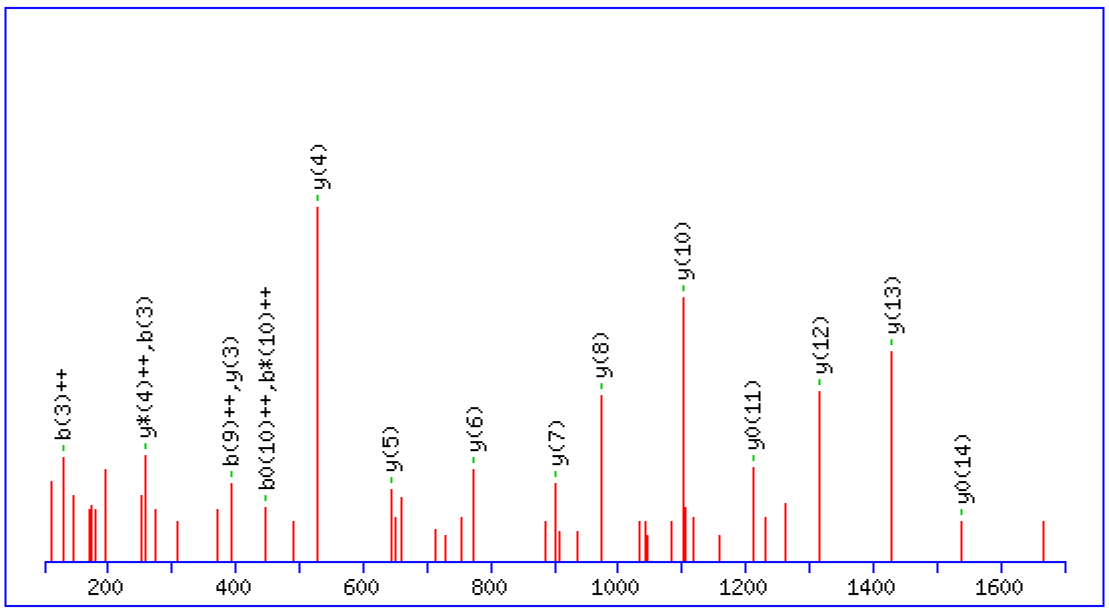
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AGQLSQGAAEEDHGCR**
Found in **MRC2_HUMAN**, C-type mannose receptor 2 OS=Homo sapiens GN=MRC2 PE=1 SV=2

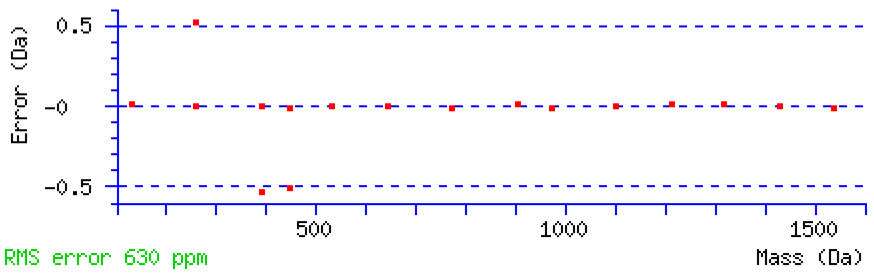
Match to Query 953211: 1684.726602 from(562.582810,3+) rtinseconds(999) index(411919)
Title: Locus:1.1.1.715.25
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

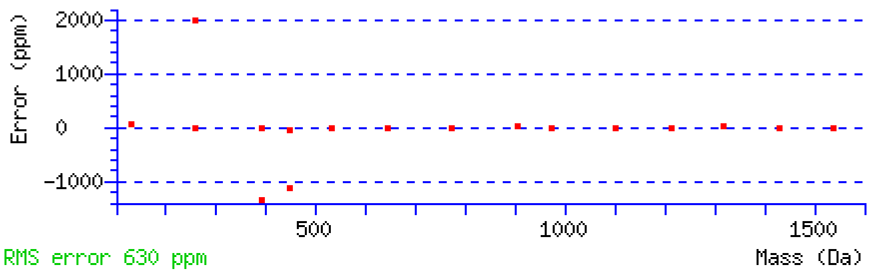
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1684.722336
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 88  Expect: 6.2e-009
Matches : 18/160 fragment ions using 16 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							16
2	**129.065854**	65.036565					G	1614.692510	807.849893	1597.665961	799.336619	1596.681945	798.844611	15
3	**257.124432**	**129.065854**	240.097883	120.552580			Q	1557.671046	779.339161	1540.644497	770.825887	1539.660481	770.333879	14
4	370.208496	185.607886	353.181947	177.094612			L	***1429.612468***	715.309872	1412.585919	706.796598	1411.601903	706.304590	13
5	457.240524	229.123900	440.213975	220.610626	439.229959	220.118618	S	***1316.528404***	658.767840	1299.501855	650.254566	1298.517839	649.762557	12
6	585.299102	293.153189	568.272553	284.639915	567.288537	284.147907	Q	1229.496376	615.251826	1212.469827	606.738552	1211.485811	606.246544	11
7	642.320566	321.663921	625.294017	313.150647	624.310001	312.658639	G	***1101.437798***	551.222537	1084.411249	542.709263	1083.427233	542.217255	10
8	713.357680	357.182478	696.331131	348.669204	695.347115	348.177196	A	1044.416334	522.711805	1027.389785	514.198531	1026.405769	513.706523	9
9	784.394794	**392.701035**	767.368245	384.187761	766.384229	383.695753	A	***973.379220***	487.193248	956.352671	478.679974	955.368655	478.187966	8
10	913.437387	457.222332	896.410838	448.709057	895.426822	448.217049	E	***902.342106***	451.674691	885.315557	443.161417	884.331541	442.669409	7
11	1042.479980	521.743628	1025.453431	513.230354	1024.469415	512.738346	E	***773.299513***	387.153395	756.272964	378.640120	755.288948	378.148112	6
12	1157.506923	579.257100	1140.480374	570.743825	1139.496358	570.251817	D	***644.256920***	322.632098	627.230371	314.118824	626.246355	313.626816	5
13	1294.565835	647.786556	1277.539286	639.273281	1276.555270	638.781273	H	***529.229977***	265.118627	512.203428	256.605352			4
14	1351.587299	676.297288	1334.560750	667.784013	1333.576734	667.292005	G	***392.171065***	196.589170	375.144516	188.075896			3
15	1511.617948	756.312612	1494.591399	747.799338	1493.607383	747.307330	C	335.149601	168.078438	318.123052	159.565164			2
16							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
88.2	1684.722336	0.004266	AGQLSQGAAEEDHGCR
0.7	1684.732407	-0.005805	MLYCEAESPPTVEK
0.7	1684.732407	-0.005805	MLYCEAESPPTVEK

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

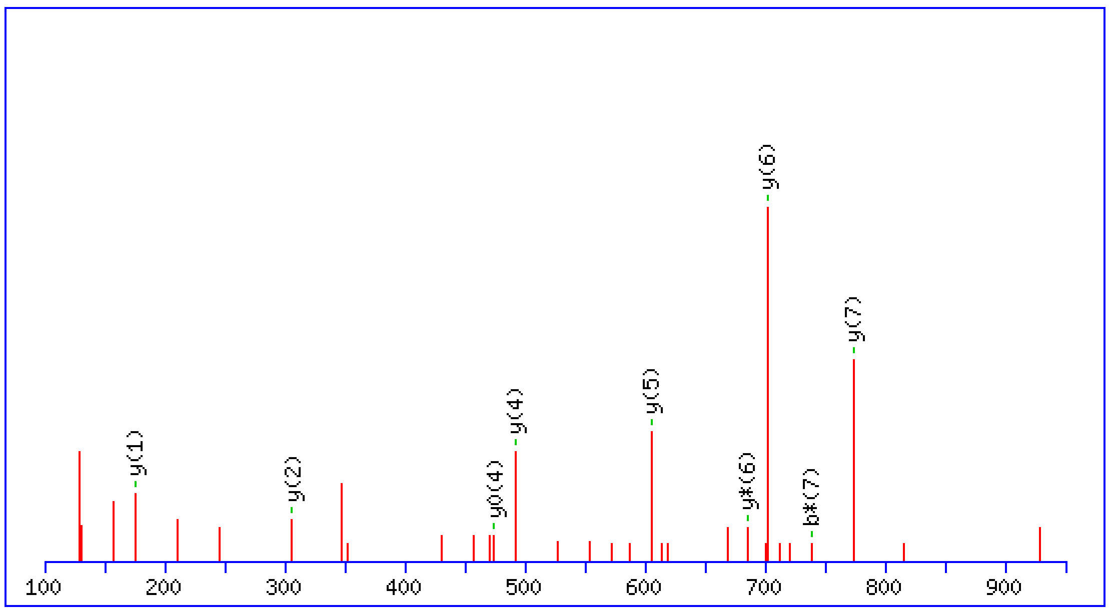
Mascot Search Results

Peptide View

MS/MS Fragmentation of RAPPVSMR
Found in CXL14_HUMAN, C-X-C motif chemokine 14 OS=Homo sapiens GN=CXCL14 PE=1 SV=2

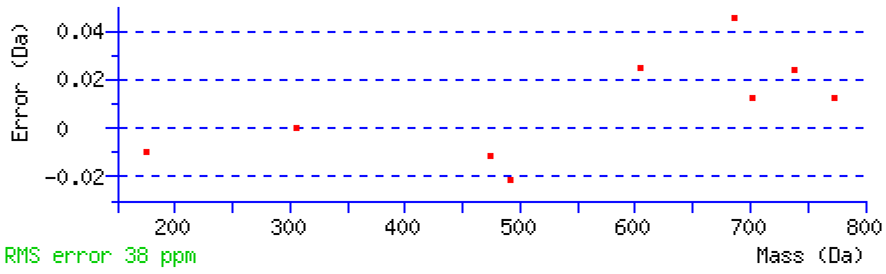
Match to Query 10554: 928.492848 from(465.253700,2+) rtinseconds(2700) index(34289)
Title: Locus:1.1.1.2343.8
Data file 2011-11-10 - TFD - EP 4-5.mgf

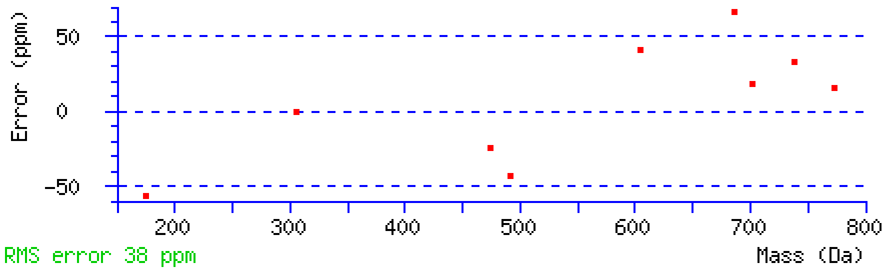
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 928.491257
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P4      : Oxidation (P)
Ions Score: 45  Expect: 0.00058
Matches : 9/70 fragment ions using 14 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	157.108387	79.057831	140.081838	70.544557			R							8
2	228.145501	114.576388	211.118952	106.063114			A	*773.397436*	387.202356	756.370887	378.689081	755.386871	378.197073	7
3	325.198265	163.102770	308.171716	154.589496			P	*702.360322*	351.683799	685.333773	343.170524	684.349757	342.678516	6
4	438.245944	219.626610	421.219395	211.113335			P	*605.307558*	303.157417	588.281009	294.644142	587.296993	294.152134	5
5	537.314358	269.160817	520.287809	260.647542			V	*492.259879*	246.633577	475.233330	238.120303	474.249314	237.628295	4
6	624.346386	312.676831	607.319837	304.163556	606.335821	303.671548	S	393.191465	197.099370	376.164916	188.586096	375.180900	188.094088	3
7	755.386871	378.197073	738.360322	369.683799	737.376306	369.191791	M	*306.159437*	153.583356	289.132888	145.070082			2
8							R	*175.118952*	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.5	928.491257	0.001591	RAPPVSMR
41.6	928.495285	-0.002437	GVAPLWMR
30.7	928.491257	0.001591	RAPPVSMR
21.9	928.491257	0.001591	RAPPVSMR
11.9	928.483856	0.008992	RAGSQSPAR
10.3	928.497787	-0.004939	EVIQGEVR
10.2	928.497787	-0.004939	KVEDVPSR
9.7	928.497772	-0.004924	INEVQQAK
6.3	928.483887	0.008961	LGGGRGGPSR
5.7	928.497787	-0.004939	LNSVEPVR

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

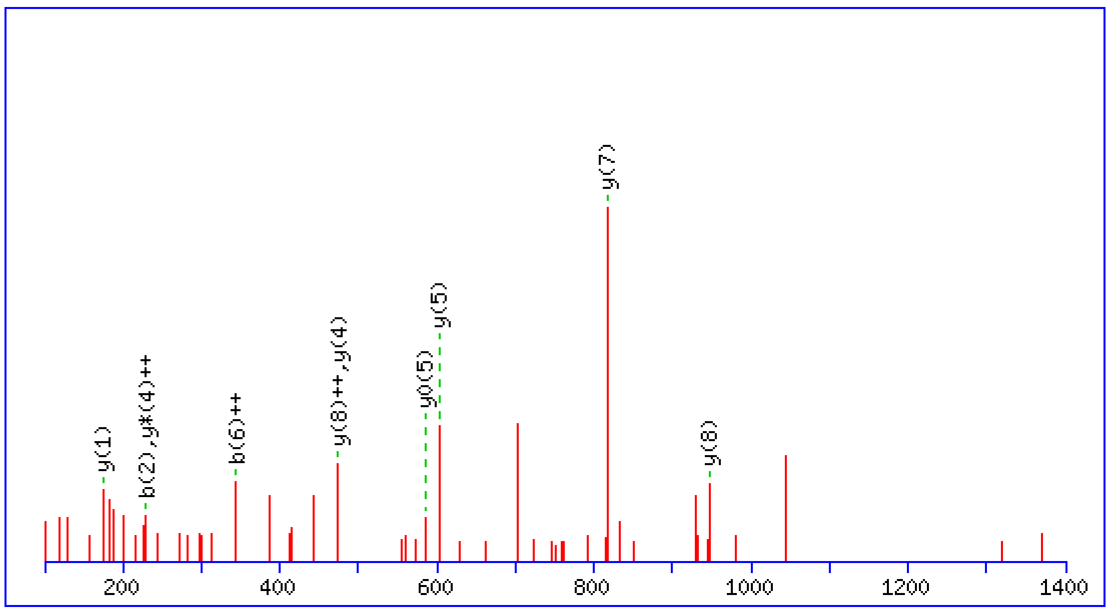
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VETLENANR**
Found in **CR3L1_HUMAN**, Cyclic AMP-responsive element-binding protein 3-like protein 1 OS=Homo sapiens GN=CREB3L1 PE=1 SV=1

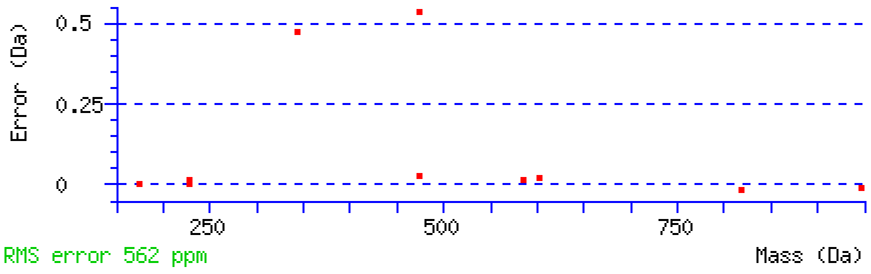
Match to Query 19509: 1044.513748 from(523.264150,2+) rtinseconds(1714) index(15746)
Title: Locus:1.1.1.2112.28
Data file 2011-11-14 - TFD - EP 7-2.mgf

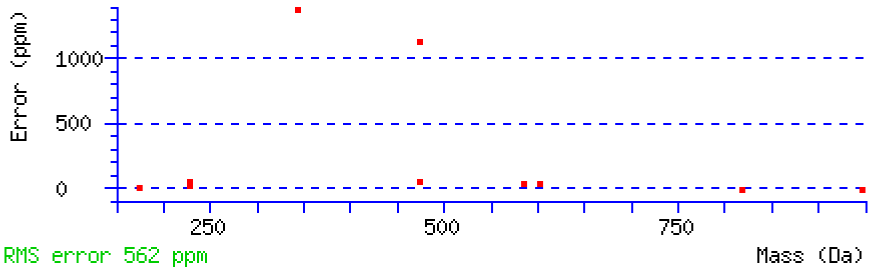
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1400] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1044.519958
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 40  Expect: 0.0013
Matches : 10/76 fragment ions using 9 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	100.075690	50.541483					**V**							9
2	229.118283	115.062780			211.107718	106.057497	**E**	***946.458849***	473.733063	929.432300	465.219788	928.448284	464.727780	8
3	330.165962	165.586619			312.155397	156.581337	**T**	***817.416256***	409.211766	800.389707	400.698491	799.405691	400.206483	7
4	443.250026	222.128651			425.239461	213.123369	**L**	716.368577	358.687927	699.342028	350.174652	698.358012	349.682644	6
5	572.292619	286.649948			554.282054	277.644665	**E**	***603.284513***	302.145894	586.257964	293.632620	585.273948	293.140612	5
6	686.335546	343.671411	669.308997	335.158137	668.324981	334.666129	**N**	***474.241920***	237.624598	457.215371	229.111323			4
7	757.372660	379.189968	740.346111	370.676694	739.362095	370.184686	**A**	360.198993	180.603134	343.172444	172.089860			3
8	871.415587	436.211432	854.389038	427.698157	853.405022	427.206149	**N**	289.161879	145.084577	272.135330	136.571303			2
9							**R**	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
62.9	1044.508743	0.005005	VEDVEALDR
40.2	1044.519958	-0.006210	VETLENANR
16.8	1044.524017	-0.010269	LDPVFDSPR
4.4	1044.519974	-0.006226	VSNGSPSLER
3.3	1044.508713	0.005035	LDAEEAEIR
2.5	1044.519989	-0.006241	ATGLQTSDPR
2.3	1044.519974	-0.006226	LSDQQEAVR
1.9	1044.519958	-0.006210	VLDREEER
1.1	1044.519974	-0.006226	NEETAQVVR
0.5	1044.510071	0.003677	EKQGQYHR

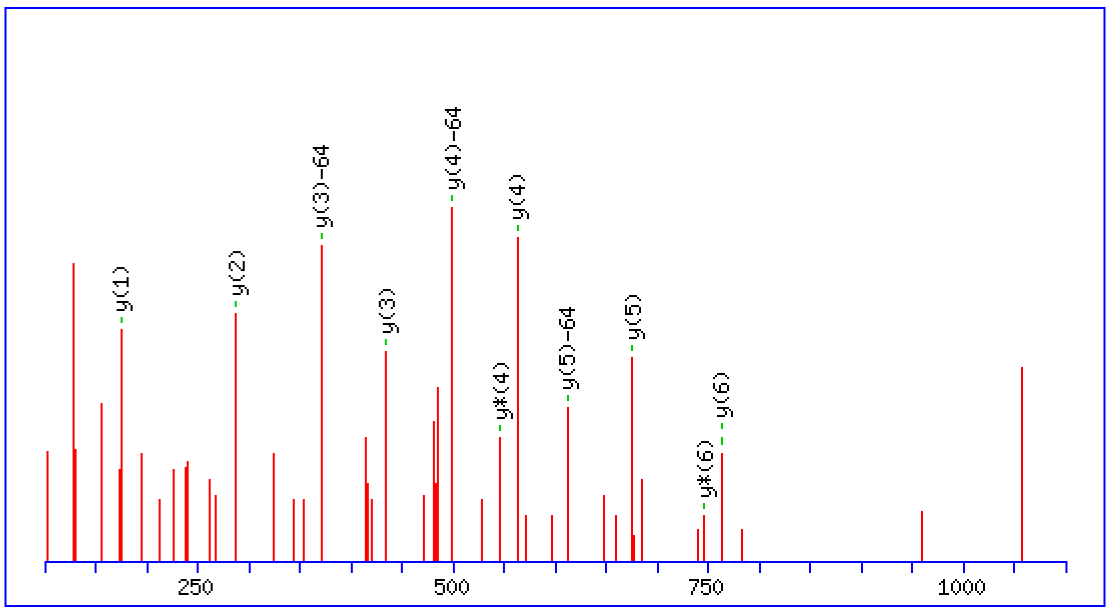
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSPQMLR**
Found in **CD5R2_HUMAN**, Cyclin-dependent kinase 5 activator 2 OS=Homo sapiens GN=CDK5R2 PE=1 SV=1

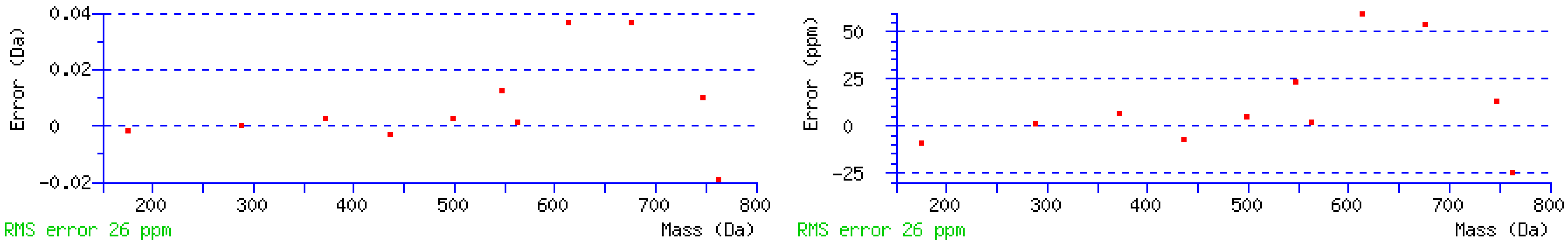
Match to Query 6731: 875.457688 from(438.736120,2+) rtinseconds(1452) index(9354)
Title: Locus:1.1.1.1820.15
Data file 2011-11-10 - TFD - EP 3-6.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 1100 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 875.453476
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P3      : Oxidation (P)
M5      : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 54  Expect: 6.2e-005
Matches : 11/84 fragment ions using 14 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.091340	57.549308					L							7
2	201.123368	101.065322			183.112803	92.060039	S	*763.376701*	382.191989	746.350152	373.678714	745.366136	373.186706	6
3	314.171047	157.589161			296.160482	148.583879	P	*676.344673*	338.675975	659.318124	330.162700			5
4	442.229625	221.618450	425.203076	213.105176	424.219060	212.613168	Q	*563.296994*	282.152135	546.270445	273.638861			4
5	589.265025	295.136151	572.238476	286.622876	571.254460	286.130868	M	*435.238416*	218.122846	418.211867	209.609571			3
6	702.349089	351.678183	685.322540	343.164908	684.338524	342.672900	L	*288.203016*	144.605146	271.176467	136.091871			2
7							R	*175.118952*	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.5	875.453476	0.004212	LSPQMLR
36.2	875.453461	0.004227	EALQMLR
29.1	875.450104	0.007584	LAEQFPR
20.4	875.453476	0.004212	SPIMQIR
17.4	875.453476	0.004212	LNDVMLR
13.5	875.453461	0.004227	LSMQELR
9.2	875.453476	0.004212	IAGSLPMR
8.7	875.461349	-0.003661	LHPQPPR
6.4	875.461349	-0.003661	HPPKPPR
6.4	875.461349	-0.003661	HPPKPPR

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

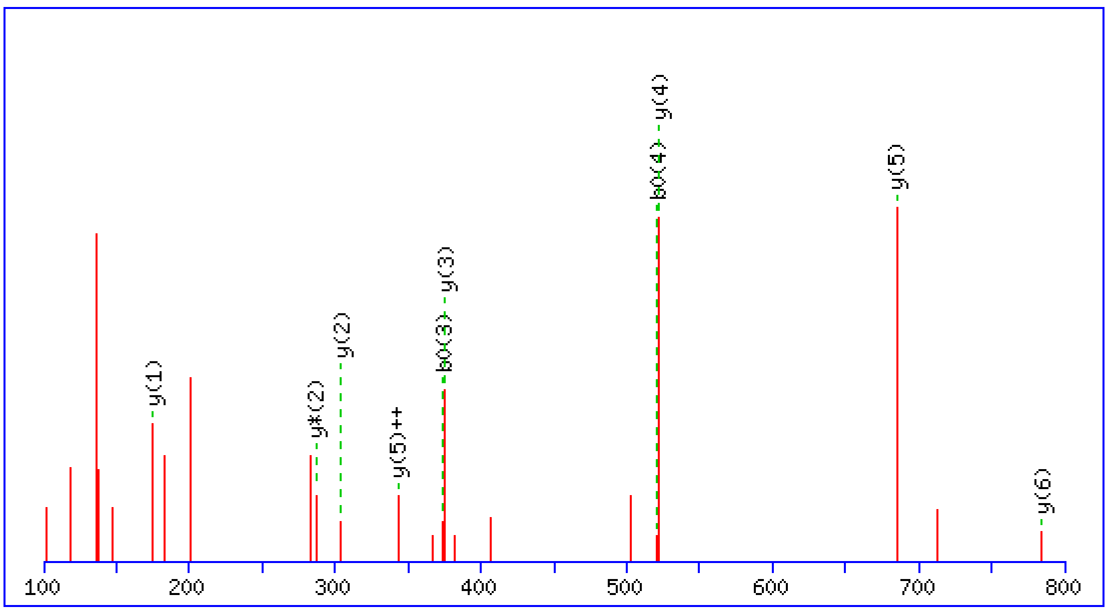
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EVYFAER**
Found in **CRIP1_HUMAN**, Cysteine-rich protein 1 OS=Homo sapiens GN=CRIP1 PE=1 SV=3

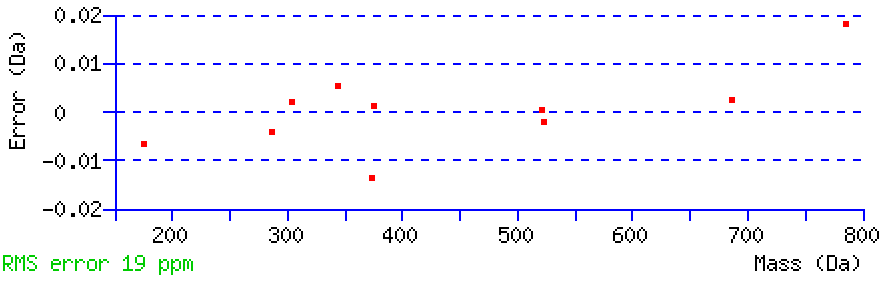
Match to Query 143433: 912.437128 from(457.225840,2+) rtinseconds(1798) index(912144)
Title: Locus:1.1.1.1085.11
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

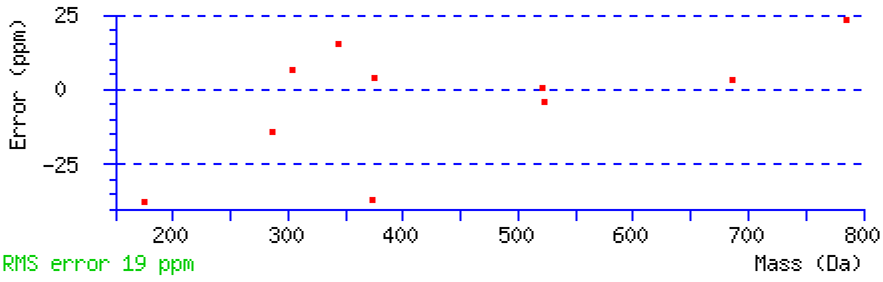
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 912.434113
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 36  Expect: 0.0029
Matches : 10/58 fragment ions using 17 most intense peaks   (help)
```

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	130.049869	65.528572	112.039304	56.523290	E							7
2	229.118283	115.062780	211.107718	106.057497	V	***784.398816***	392.703046	767.372267	384.189772	766.388251	383.697764	6
3	392.181612	196.594444	374.171047	187.589162	Y	***685.330402***	343.168839	668.303853	334.655565	667.319837	334.163557	5
4	539.250026	270.128651	521.239461	261.123369	F	***522.267073***	261.637175	505.240524	253.123900	504.256508	252.631892	4
5	610.287140	305.647208	592.276575	296.641926	A	***375.198659***	188.102967	358.172110	179.589693	357.188094	179.097685	3
6	739.329733	370.168505	721.319168	361.163222	E	***304.161545***	152.584410	287.134996	144.071136	286.150980	143.579128	2
7					R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.6	912.434113	0.003015	EVYFAER
11.6	912.441330	-0.004202	EVSSHAQR
8.0	912.437485	-0.000357	YLDMISR
5.5	912.430954	0.006174	MPHLMER
5.0	912.445389	-0.008261	GGPPFPGPR
3.4	912.445343	-0.008215	ASAPWPER
3.0	912.434128	0.003000	PDYSIFR
2.9	912.437485	-0.000357	DILSYMR
2.9	912.437485	-0.000357	IDLSMYR
2.8	912.430084	0.007044	EAAGPPEAR

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

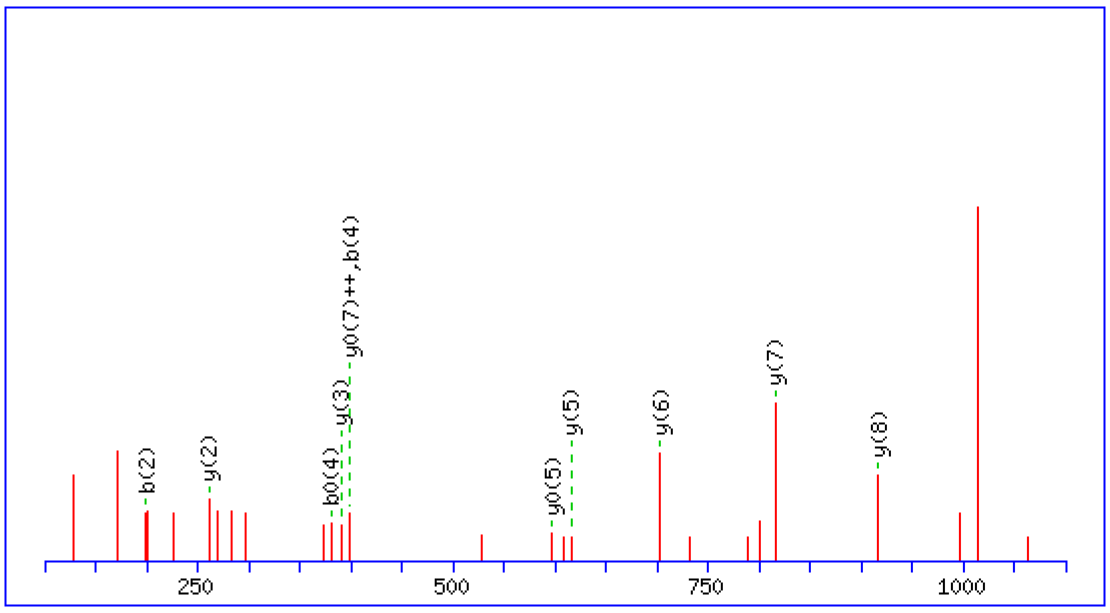
Mascot Search Results

Peptide View

MS/MS Fragmentation of **PTISLIENK**
Found in **CYB_HUMAN**, Cytochrome b OS=Homo sapiens GN=MT-CYB PE=1 SV=1

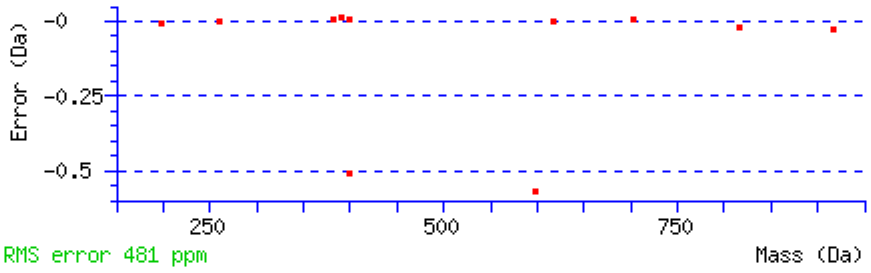
Match to Query 279503: 1013.576128 from(507.795340,2+) rtinseconds(2121) index(597167)
Title: Locus:1.1.1.1133.8
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

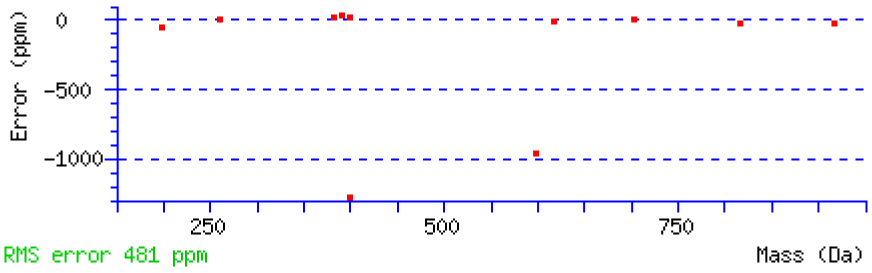
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1013.575684
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 34 **Expect:** 0.002
Matches : 11/76 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	98.060040	49.533658					**P**							9
2	**199.107719**	100.057497			181.097154	91.052215	**T**	***917.530223***	459.268750	900.503674	450.755475	899.519658	450.263467	8
3	312.191783	156.599529			294.181218	147.594247	**I**	***816.482544***	408.744910	799.455995	400.231636	798.471979	399.739628	7
4	**399.223811**	200.115544			381.213246	191.110261	**S**	***703.398480***	352.202878	686.371931	343.689604	685.387915	343.197596	6
5	512.307875	256.657576			494.297310	247.652293	**L**	***616.366452***	308.686864	599.339903	300.173590	598.355887	299.681582	5
6	625.391939	313.199608			607.381374	304.194325	**I**	503.282388	252.144832	486.255839	243.631557	485.271823	243.139549	4
7	754.434532	377.720904			736.423967	368.715622	**E**	***390.198324***	195.602800	373.171775	187.089525	372.187759	186.597517	3
8	868.477459	434.742368	851.450910	426.229093	850.466894	425.737085	**N**	***261.155731***	131.081503	244.129182	122.568229			2
9							**K**	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.4	1013.575684	0.000444	PTISLIENK
5.5	1013.575699	0.000429	GLLDGIELGK
1.9	1013.575714	0.000414	VVIVNPETK

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

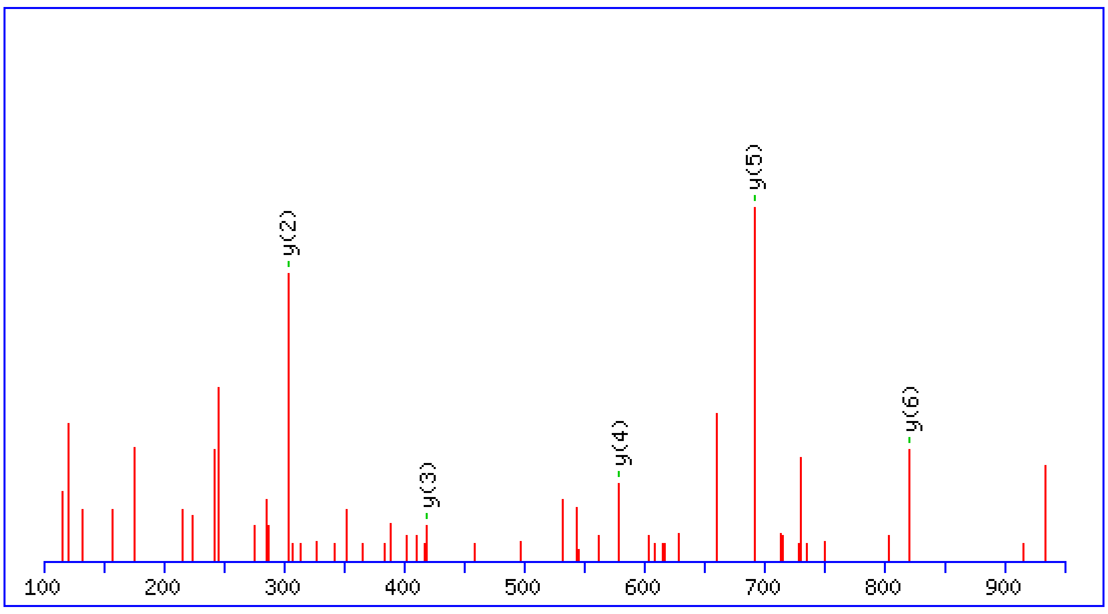
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LELCDER**
Found in **QCR6_HUMAN**, Cytochrome b-c1 complex subunit 6, mitochondrial OS=Homo sapiens GN=UQCRH PE=1 SV=2

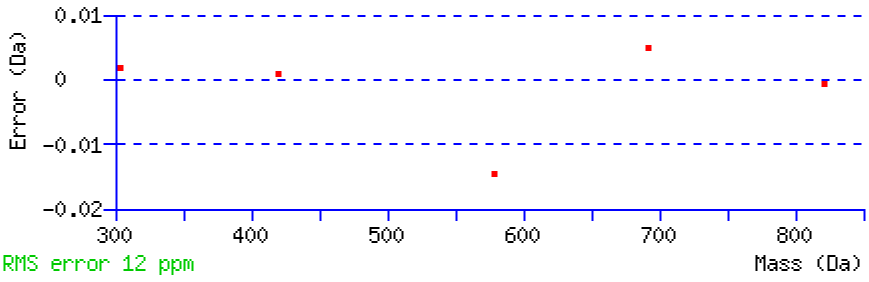
Match to Query 172290: 933.423428 from(467.718990,2+) rtinseconds(1518) index(502740)
Title: Locus:1.1.1.907.11
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

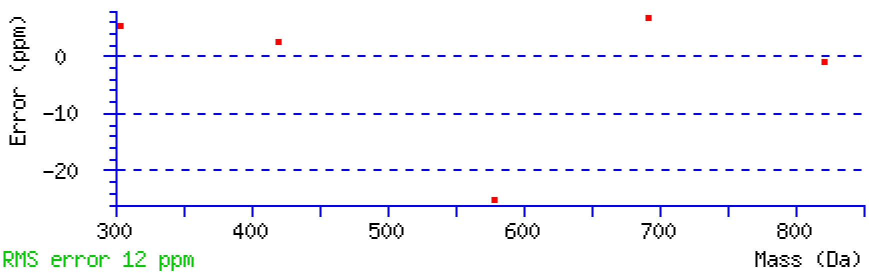
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 933.422562
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33  Expect: 0.0057
Matches : 5/56 fragment ions using 9 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							7
2	243.133933	122.070605	225.123368	113.065322	E	***821.345794***	411.176535	804.319245	402.663261	803.335229	402.171253	6
3	356.217997	178.612637	338.207432	169.607354	L	***692.303201***	346.655239	675.276652	338.141964	674.292636	337.649956	5
4	516.248646	258.627961	498.238081	249.622679	C	***579.219137***	290.113207	562.192588	281.599932	561.208572	281.107924	4
5	631.275589	316.141433	613.265024	307.136150	D	***419.188488***	210.097882	402.161939	201.584608	401.177923	201.092600	3
6	760.318182	380.662729	742.307617	371.657447	E	***304.161545***	152.584411	287.134996	144.071136	286.150980	143.579128	2
7					R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of LELCDER
(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	933.422562	0.000866	LELCDER
19.6	933.422562	0.000866	CIELDER
5.9	933.427277	-0.003849	MSPCGRAR
4.8	933.430450	-0.007022	WSVNGDTR
4.2	933.422577	0.000851	IPECQGSK
3.1	933.422562	0.000866	CLEEEVR
2.2	933.422546	0.000882	IQEMEER
0.0	933.422562	0.000866	EIIDECR

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

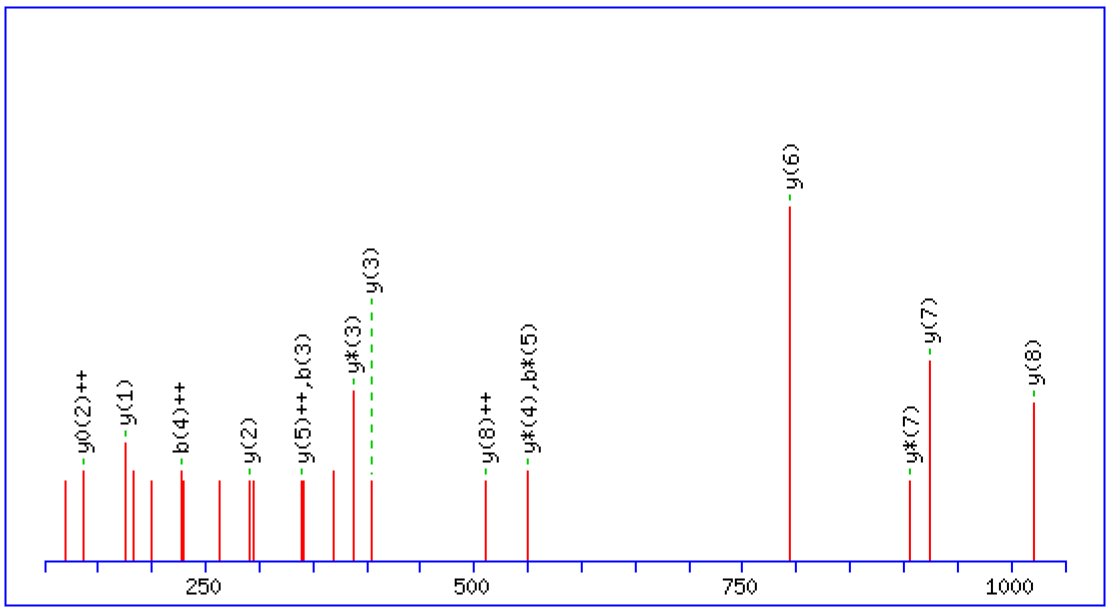
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LPENLYNDR**
Found in **QCR7_HUMAN**, Cytochrome b-c1 complex subunit 7 OS=Homo sapiens GN=UQCRB PE=1 SV=2

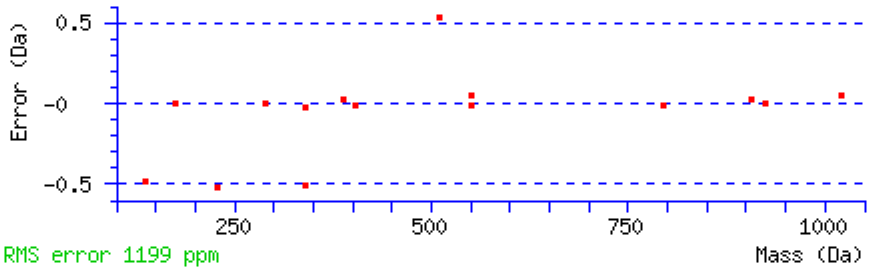
Match to Query 24324: 1132.548988 from(567.281770,2+) rtinseconds(1935) index(13961)
Title: Locus:1.1.1.2194.33
Data file 2011-11-10 - TFD - EP 4-7.mgf

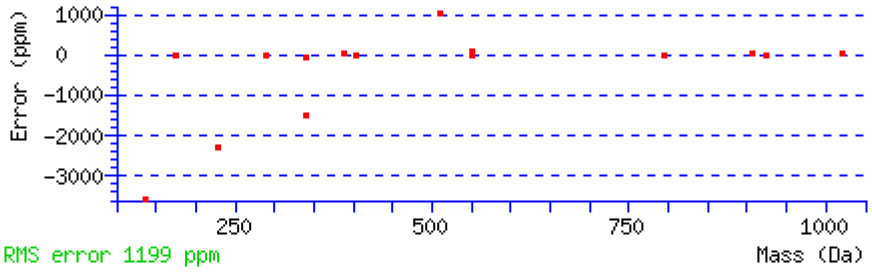
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1132.551254
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 39  Expect: 0.00069
Matches : 15/84 fragment ions using 22 most intense peaks   (help)
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							9
2	211.144104	106.075690					P	1020.474499	510.740888	1003.447950	502.227613	1002.463934	501.735605	8
3	340.186697	170.596986			322.176132	161.591704	E	923.421735	462.214506	906.395186	453.701231	905.411170	453.209223	7
4	454.229624	227.618450	437.203075	219.105176	436.219059	218.613168	N	794.379142	397.693209	777.352593	389.179935	776.368577	388.687927	6
5	567.313688	284.160482	550.287139	275.647208	549.303123	275.155200	L	680.336215	340.671746	663.309666	332.158471	662.325650	331.666463	5
6	730.377017	365.692147	713.350468	357.178872	712.366452	356.686864	Y	567.252151	284.129714	550.225602	275.616439	549.241586	275.124431	4
7	844.419944	422.713610	827.393395	414.200335	826.409379	413.708328	N	404.188822	202.598049	387.162273	194.084774	386.178257	193.592766	3
8	959.446887	480.227082	942.420338	471.713807	941.436322	471.221799	D	290.145895	145.576585	273.119346	137.063311	272.135330	136.571303	2
9							R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of LPENLYNDR
(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	1132.551254	-0.002266	LPENLYNDR
5.1	1132.548767	0.000221	IMWHIDYR
0.0	1132.543381	0.005607	MLKENPEEK

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

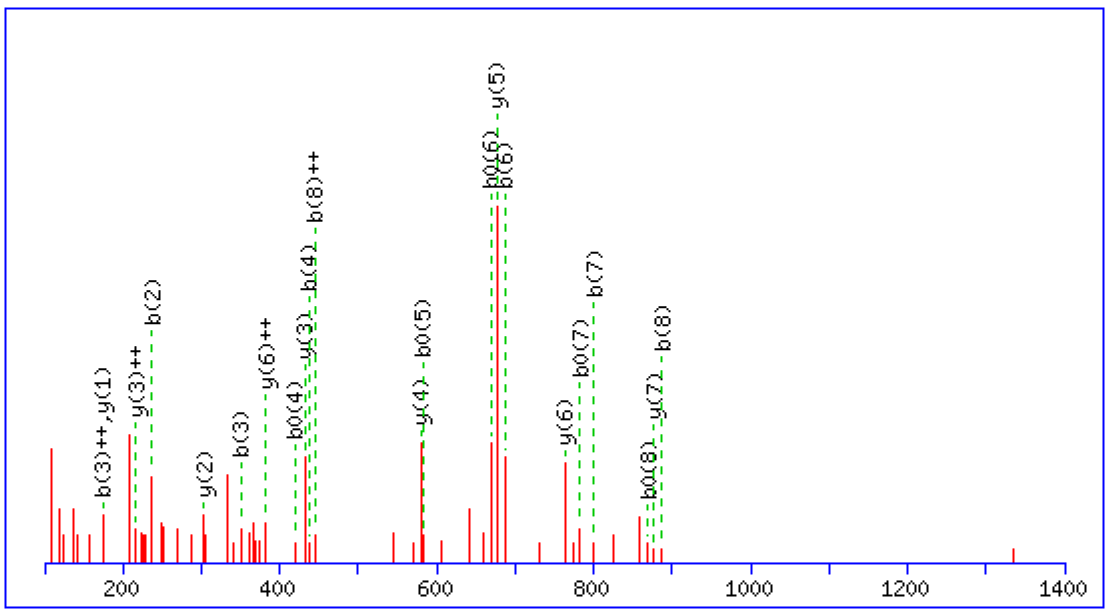
Mascot Search Results

Peptide View

MS/MS Fragmentation of **HVISYSLSPFEQR**
Found in **QCR8_HUMAN**, Cytochrome b-c1 complex subunit 8 OS=Homo sapiens GN=UQCRQ PE=1 SV=4

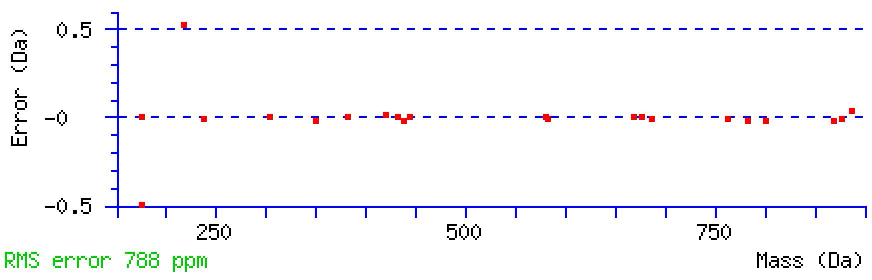
Match to Query 41732: 1561.785072 from(521.602300,3+) rtinseconds(2578) index(27508)
Title: Locus:1.1.1.2314.21
Data file 2011-11-12 - TFD - EP 6-7.mgf

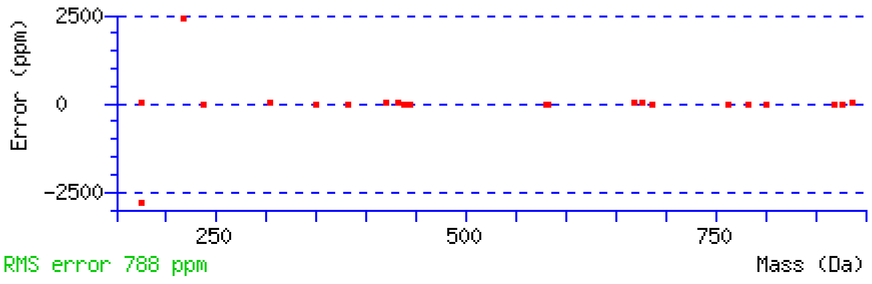
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1561.788879
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.0018
Matches : 22/112 fragment ions using 41 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	138.066188	69.536732					**H**							13
2	***237.134602***	119.070939					**V**	1425.737256	713.372266	1408.710707	704.858992	1407.726691	704.366984	12
3	***350.218666***	175.612971					**I**	1326.668842	663.838059	1309.642293	655.324785	1308.658277	654.832777	11
4	***437.250694***	219.128985			419.240129	210.123703	**S**	1213.584778	607.296027	1196.558229	598.782753	1195.574213	598.290745	10
5	600.314023	300.660650			582.303458	291.655367	**Y**	1126.552750	563.780013	1109.526201	555.266739	1108.542185	554.774731	9
6	***687.346051***	344.176664			669.335486	335.171381	**S**	963.489421	482.248349	946.462872	473.735074	945.478856	473.243066	8
7	***800.430115***	400.718696			782.419550	391.713413	**L**	***876.457393***	438.732335	859.430844	430.219060	858.446828	429.727052	7
8	***887.462143***	444.234710			869.451578	435.229427	**S**	***763.373329***	382.190303	746.346780	373.677028	745.362764	373.185020	6
9	984.514907	492.761092			966.504342	483.755809	**P**	***676.341301***	338.674289	659.314752	330.161014	658.330736	329.669006	5
10	1131.583321	566.295299			1113.572756	557.290016	**F**	***579.288537***	290.147907	562.261988	281.634632	561.277972	281.142624	4
11	1260.625914	630.816595			1242.615349	621.811312	**E**	***432.220123***	216.613699	415.193574	208.100425	414.209558	207.608417	3
12	1388.684492	694.845884	1371.657943	686.332610	1370.673927	685.840602	**Q**	***303.177530***	152.092403	286.150981	143.579129			2
13							**R**	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.6	1561.788879	-0.003807	HVISYSLSPFEQR
10.3	1561.770447	0.014625	RMQDLNLAMDALR
9.9	1561.784851	0.000221	TSPLYDRLDAQGAR
5.5	1561.781006	0.004066	HLVMKLSYGPEEK
4.1	1561.792267	-0.007195	RTTGAPDITWGMLK
2.6	1561.799637	-0.014565	TALWCALQMTLPK
0.7	1561.774506	0.010566	MLYVPVMPGHAKR
0.5	1561.794769	-0.009697	SSLGSLQTPEAVTTR

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

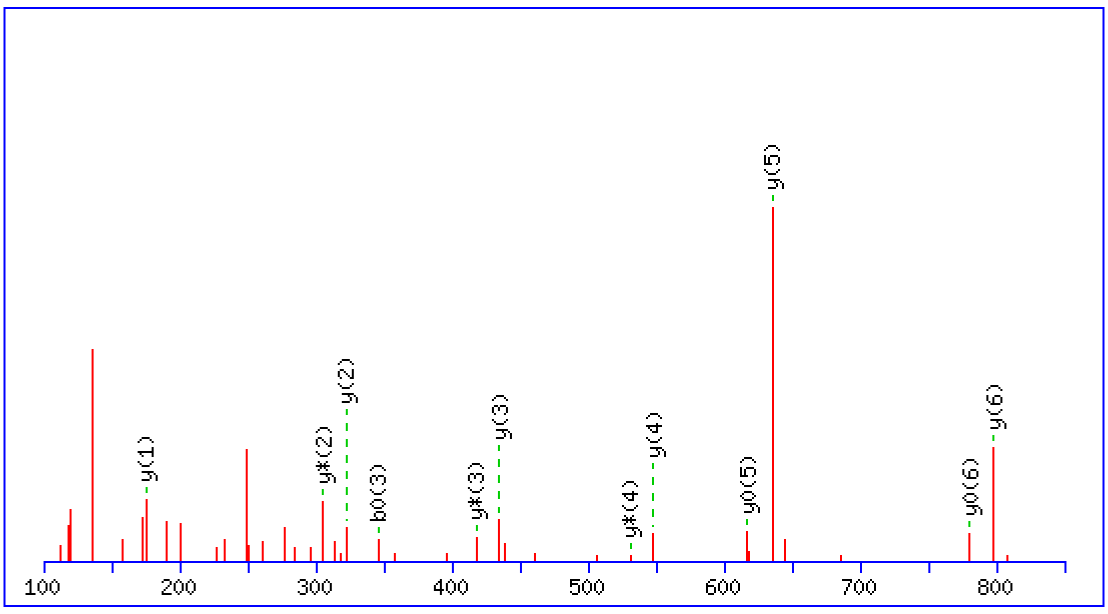
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LYSLLFR**
Found in **QCR9_HUMAN**, Cytochrome b-c1 complex subunit 9 OS=Homo sapiens GN=UQCR10 PE=1 SV=3

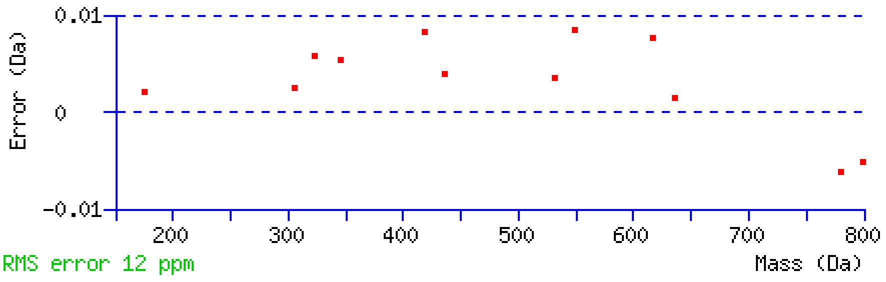
Match to Query 7405: 910.532908 from(456.273730,2+) rtinseconds(3136) index(17807)
Title: Locus:1.1.1.2916.3
Data file 2011-11-14 - TFD - EP 8-8.mgf

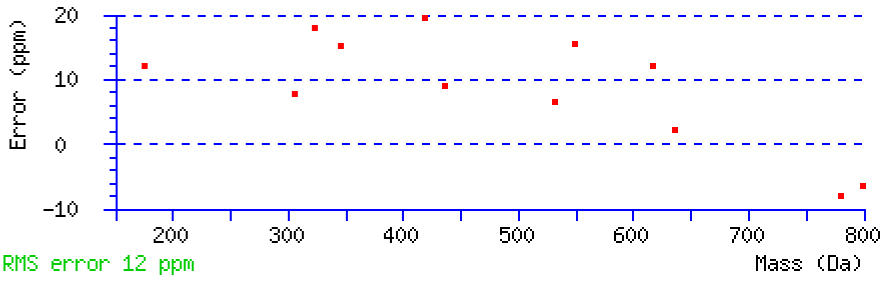
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 910.527618
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 53  Expect: 1.7e-005
Matches : 12/48 fragment ions using 14 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			**L**							7
2	277.154669	139.080973			**Y**	***798.450851***	399.729064	781.424302	391.215789	780.440286	390.723781	6
3	364.186697	182.596987	346.176132	173.591704	**S**	***635.387522***	318.197399	618.360973	309.684125	617.376957	309.192117	5
4	477.270761	239.139019	459.260196	230.133736	**L**	***548.355494***	274.681385	531.328945	266.168111			4
5	590.354825	295.681051	572.344260	286.675768	**L**	***435.271430***	218.139353	418.244881	209.626079			3
6	737.423239	369.215258	719.412674	360.209975	**F**	***322.187366***	161.597321	305.160817	153.084047			2
7					**R**	***175.118952***	88.063114	158.092403	79.549840			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.7	910.527618	0.005290	LYSLLFR
9.5	910.534821	-0.001913	LRQLPER
9.3	910.527618	0.005290	LYIIFSR
5.7	910.534836	-0.001928	IGVNQPKR
4.6	910.538864	-0.005956	IPILHFR
4.3	910.534836	-0.001928	LPRLPQR
0.4	910.538864	-0.005956	LHFPLLR
0.0	910.534821	-0.001913	RGAEILPR

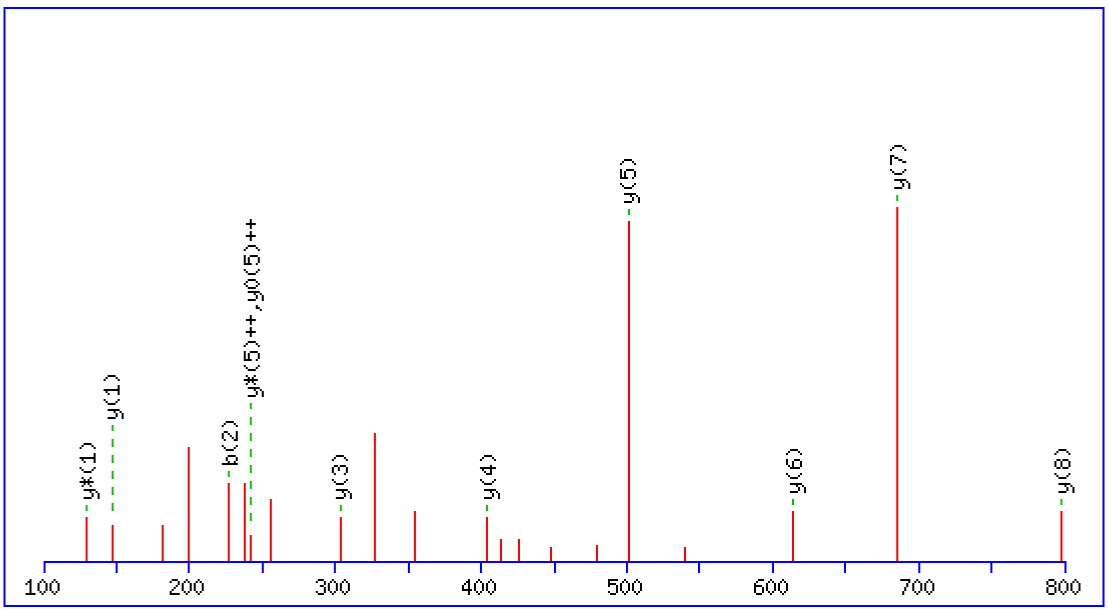
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IIAIPTGVK**
Found in **COX1_HUMAN**, Cytochrome c oxidase subunit 1 OS=Homo sapiens GN=MT-CO1 PE=1 SV=1

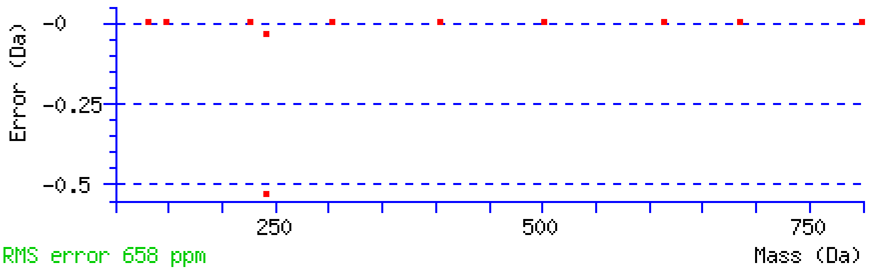
Match to Query 141802: 910.586728 from(456.300640,2+) rtinseconds(2308) index(600750)
Title: Locus:1.1.1.1205.6
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

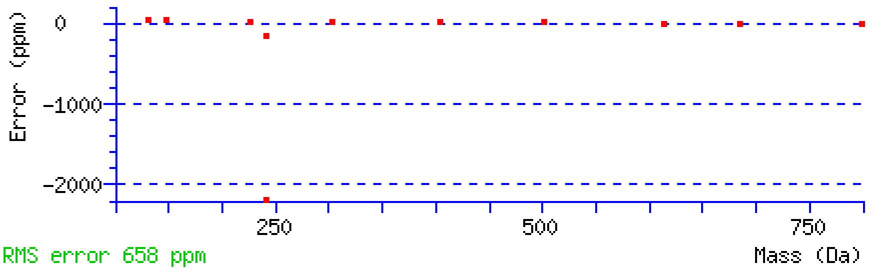
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 910.585144
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 47  Expect: 2e-005
Matches : 11/64 fragment ions using 22 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							9
2	227.175404	114.091340			I	***798.508367***	399.757822	781.481818	391.244547	780.497802	390.752539	8
3	298.212518	149.609897			A	***685.424303***	343.215790	668.397754	334.702515	667.413738	334.210507	7
4	411.296582	206.151929			I	***614.387189***	307.697233	597.360640	299.183958	596.376624	298.691950	6
5	508.349346	254.678311			P	***501.303125***	251.155201	484.276576	242.641926	483.292560	242.149918	5
6	609.397025	305.202151	591.386460	296.196868	T	***404.250361***	202.628818	387.223812	194.115544	386.239796	193.623536	4
7	666.418489	333.712883	648.407924	324.707600	G	***303.202682***	152.104979	286.176133	143.591704			3
8	765.486903	383.247090	747.476338	374.241807	V	246.181218	123.594247	229.154669	115.080972			2
9					K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.1	910.585144	0.001584	IIAIPTGVK
17.6	910.585129	0.001599	LPLAQILK
14.6	910.585129	0.001599	LLQPALLK
8.5	910.585129	0.001599	IKIIAPPK
7.5	910.585144	0.001584	LLVVDPKK
6.7	910.585129	0.001599	IISQLPLK
5.3	910.585144	0.001584	IKLVPPTK
5.1	910.585129	0.001599	LKLPPLSK
5.0	910.585144	0.001584	IKLVPPTK
5.0	910.585129	0.001599	LKLPPLSK

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

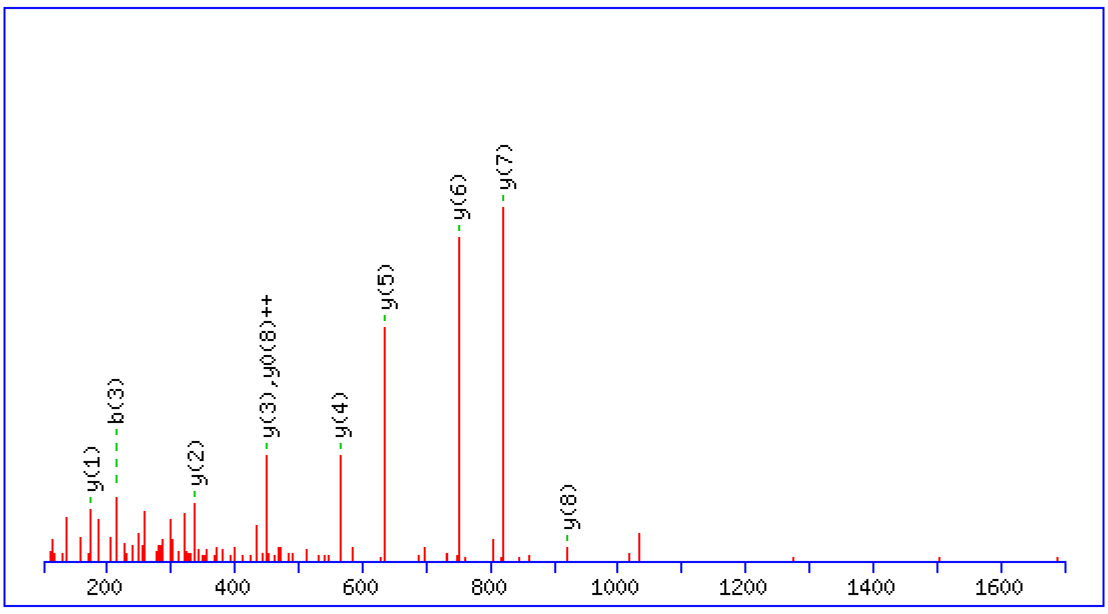
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GGVADALLYR**
Found in **CX7A2_HUMAN**, Cytochrome c oxidase subunit 7A2, mitochondrial OS=Homo sapiens GN=COX7A2 PE=1 SV=1

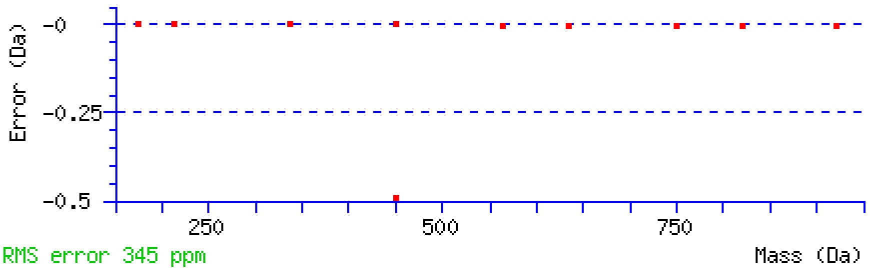
Match to Query 12297: 1033.561228 from(517.787890,2+) rtinseconds(2606) index(14980)
Title: Locus:1.1.1.2505.8
Data file 2011-11-12 - TFD - EP 6-8.mgf

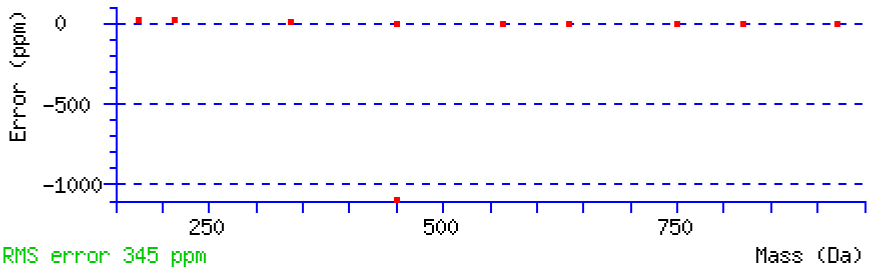
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1033.555634
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 87 **Expect:** 2.4e-008
Matches : 10/72 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008			G							10
2	115.050204	58.028740			G	977.541458	489.274367	960.514909	480.761093	959.530893	480.269085	9
3	214.118618	107.562947			V	***920.519994***	460.763635	903.493445	452.250361	902.509429	451.758353	8
4	285.155732	143.081504			A	***821.451580***	411.229428	804.425031	402.716154	803.441015	402.224146	7
5	400.182675	200.594976	382.172110	191.589693	D	***750.414466***	375.710871	733.387917	367.197597	732.403901	366.705589	6
6	471.219789	236.113533	453.209224	227.108250	A	***635.387523***	318.197400	618.360974	309.684125			5
7	584.303853	292.655565	566.293288	283.650282	L	***564.350409***	282.678843	547.323860	274.165568			4
8	697.387917	349.197597	679.377352	340.192314	L	***451.266345***	226.136810	434.239796	217.623536			3
9	860.451246	430.729261	842.440681	421.723979	Y	***338.182281***	169.594778	321.155732	161.081504			2
10					R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
86.7	1033.555634	0.005594	GGVADALLYR
18.8	1033.566879	-0.005651	NVAVPIPHR
16.7	1033.555634	0.005594	GGLKDLFER
11.8	1033.566864	-0.005636	NVVYERVR
9.4	1033.555634	0.005594	ALDVQGIYR
7.6	1033.555618	0.005610	ELNQVLYR
2.1	1033.566864	-0.005636	AAGPPAGLAPGR

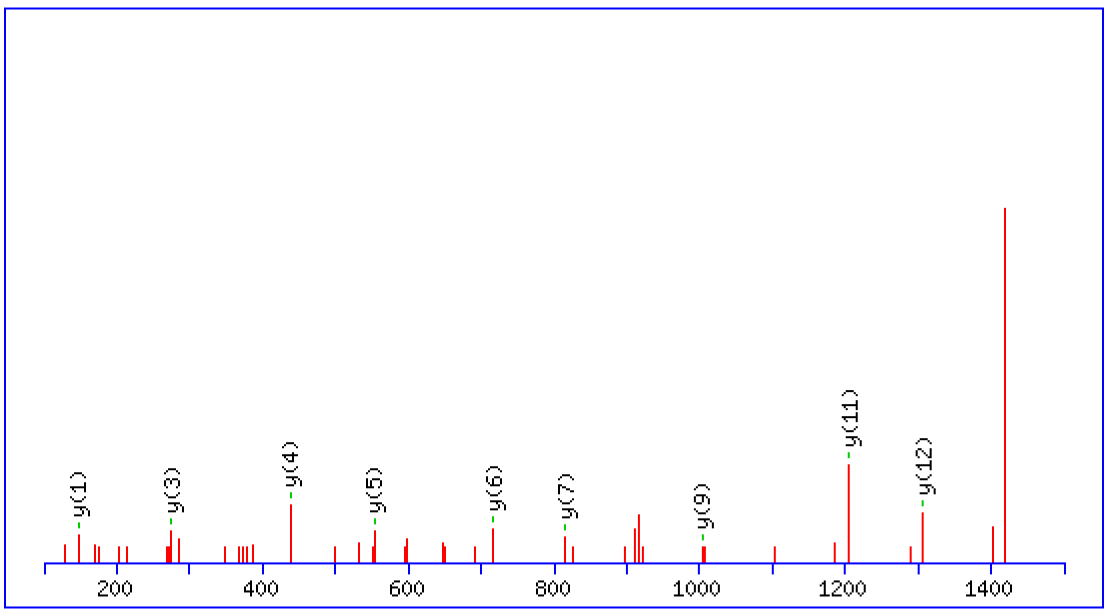
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LTSDSTVYDYAGK**
Found in **COX7R_HUMAN**, Cytochrome c oxidase subunit 7A-related protein, mitochondrial OS=Homo sapiens GN=COX7A2L PE=1 SV=2

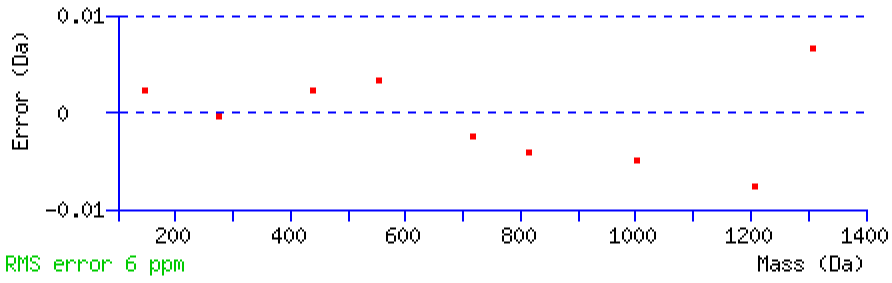
Match to Query 37626: 1418.659468 from(710.337010,2+) rtinseconds(1951) index(16278)
Title: Locus:1.1.1.2074.47
Data file 2011-11-12 - TFD - EP 6-7.mgf

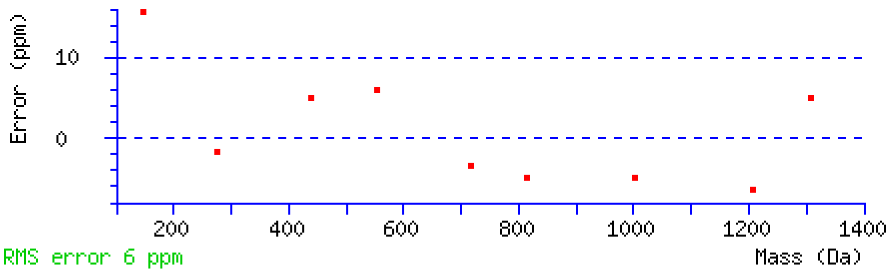
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1418.656540
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 82  Expect: 6.2e-008
Matches : 9/110 fragment ions using 13 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			**L**							**13**
2	215.139019	108.073147	197.128454	99.067865	**T**	***1306.579754***	653.793515	1289.553205	645.280241	1288.569189	644.788233	**12**
3	302.171047	151.589161	284.160482	142.583879	**S**	***1205.532075***	603.269676	1188.505526	594.756401	1187.521510	594.264393	**11**
4	417.197990	209.102633	399.187425	200.097351	**D**	1118.500047	559.753662	1101.473498	551.240387	1100.489482	550.748379	**10**
5	504.230018	252.618647	486.219453	243.613365	**S**	***1003.473104***	502.240190	986.446555	493.726915	985.462539	493.234907	**9**
6	605.277697	303.142487	587.267132	294.137204	**T**	916.441076	458.724176	899.414527	450.210901	898.430511	449.718893	**8**
7	704.346111	352.676694	686.335546	343.671411	**V**	***815.393397***	408.200336	798.366848	399.687062	797.382832	399.195054	**7**
8	867.409440	434.208358	849.398875	425.203076	**Y**	***716.324983***	358.666130	699.298434	350.152855	698.314418	349.660847	**6**
9	982.436383	491.721830	964.425818	482.716547	**D**	***553.261654***	277.134465	536.235105	268.621190	535.251089	268.129182	**5**
10	1145.499712	573.253494	1127.489147	564.248212	**Y**	***438.234711***	219.620993	421.208162	211.107719			**4**
11	1216.536826	608.772051	1198.526261	599.766769	**A**	***275.171382***	138.089329	258.144833	129.576054			**3**
12	1273.558290	637.282783	1255.547725	628.277500	**G**	204.134268	102.570772	187.107719	94.057497			**2**
13					**K**	***147.112804***	74.060040	130.086255	65.546765			**1**





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
82.1	1418.656540	0.002928	LTSDSTVYDYAGK
12.5	1418.671112	-0.011644	DVENMGKEELQK
7.8	1418.657394	0.002074	FYTDLMNMIQK
7.8	1418.657394	0.002074	FYTDLMNMIQK
7.1	1418.671097	-0.011629	RIEEMEDELQK
2.5	1418.664612	-0.005144	NMAMTGGPDPRLK
0.3	1418.664581	-0.005113	LECVEPNCRSK

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

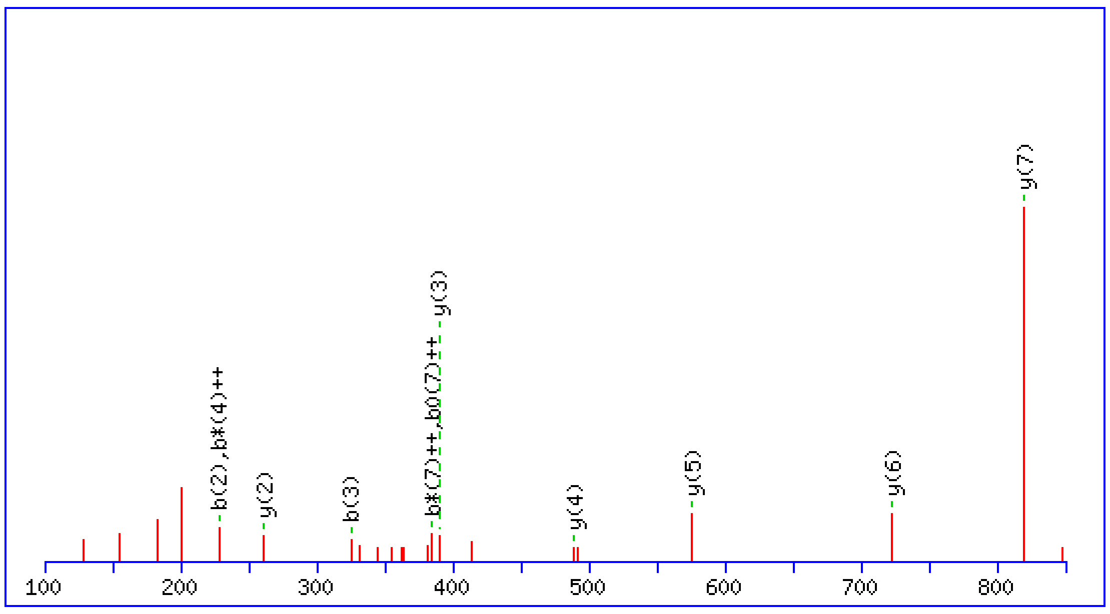
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NLPFSVENK**
Found in **COX7C_HUMAN**, Cytochrome c oxidase subunit 7C, mitochondrial OS=Homo sapiens GN=COX7C PE=1 SV=1

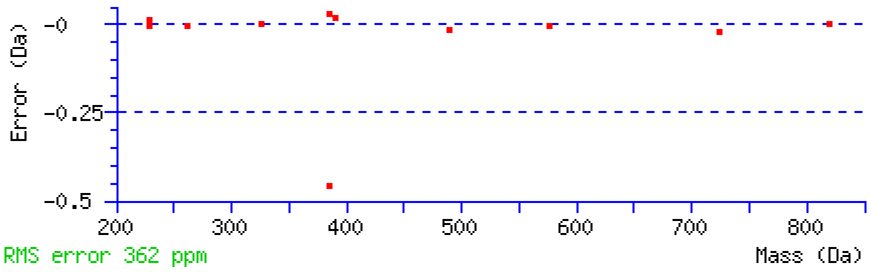
Match to Query 10667: 1046.543848 from(524.279200,2+) rtinseconds(2357) index(9746)
Title: Locus:1.1.1.2547.4
Data file 2011-11-10 - TFD - EP 3-8.mgf

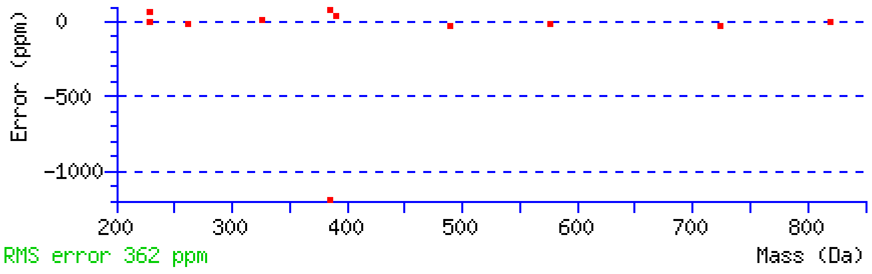
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1046.539642
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 46 **Expect:** 0.00084
Matches : 11/84 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			N							9
2	**228.134267**	114.570771	211.107718	106.057497			L	933.504008	467.255642	916.477459	458.742368	915.493443	458.250360	8
3	**325.187031**	163.097153	308.160482	154.583879			P	***820.419944***	410.713610	803.393395	402.200336	802.409379	401.708328	7
4	472.255445	236.631360	455.228896	228.118086			F	***723.367180***	362.187228	706.340631	353.673954	705.356615	353.181946	6
5	559.287473	280.147375	542.260924	271.634100	541.276908	271.142092	S	***576.298766***	288.653021	559.272217	280.139747	558.288201	279.647739	5
6	658.355887	329.681581	641.329338	321.168307	640.345322	320.676299	V	***489.266738***	245.137007	472.240189	236.623733	471.256173	236.131725	4
7	787.398480	394.202878	770.371931	385.689603	769.387915	385.197595	E	***390.198324***	195.602800	373.171775	187.089526	372.187759	186.597518	3
8	901.441407	451.224341	884.414858	442.711067	883.430842	442.219059	N	***261.155731***	131.081504	244.129182	122.568229			2
9							K	147.112804	74.060040	130.086255	65.546766			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.4	1046.539642	0.004206	NLPFSVENK
2.9	1046.550888	-0.007040	PLNVSFTNR
2.5	1046.550888	-0.007040	GVPYSQRPK
1.7	1046.535629	0.008219	TPGGSQKASSK
0.8	1046.554230	-0.010382	RLQELCSK
0.5	1046.554245	-0.010397	KVAQMVEAR
0.5	1046.554245	-0.010397	KVPSLCSAR
0.5	1046.554245	-0.010397	QVIRTCEK
0.3	1046.550888	-0.007040	INTLGWTSR

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

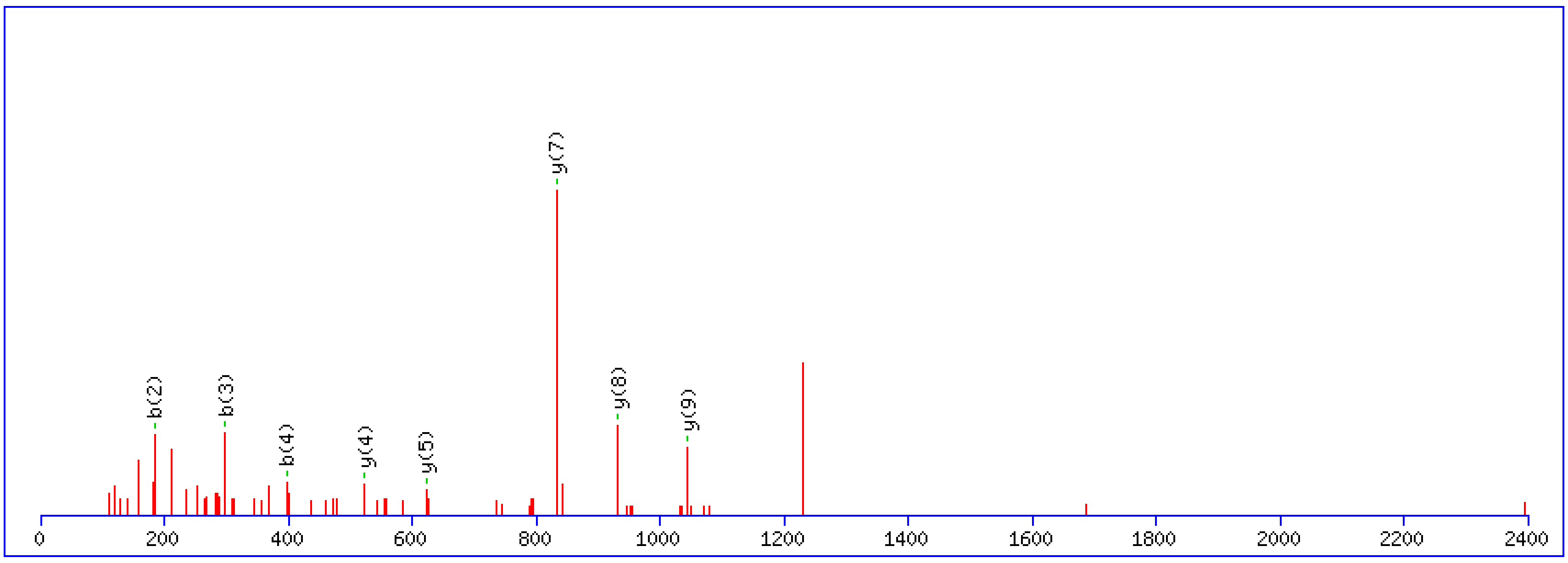
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALLVPLVYTIK**
Found in **CY1_HUMAN**, Cytochrome c1, heme protein, mitochondrial OS=Homo sapiens GN=CYC1 PE=1 SV=3

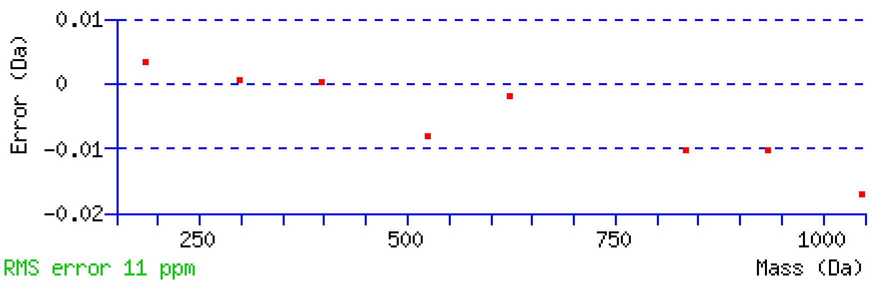
Match to Query 25894: 1228.772348 from(615.393450,2+) rtinseconds(3524) index(51236)
Title: Locus:1.1.1.1780.16
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 3.mgf

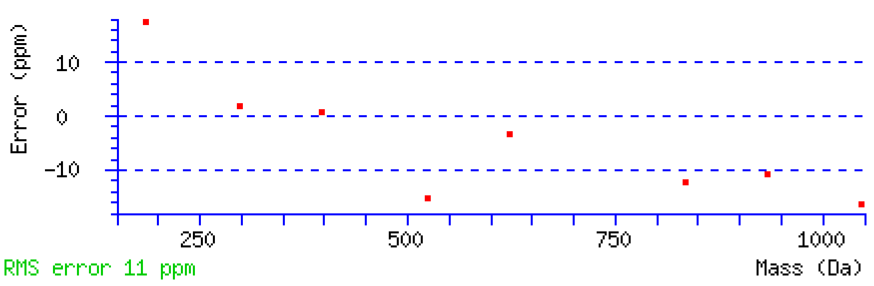
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1228.779480
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.00013
Matches : 8/80 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			A							11
2	**185.128454**	93.067865			L	1158.749660	579.878468	1141.723111	571.365194	1140.739095	570.873185	10
3	**298.212518**	149.609897			L	***1045.665596***	523.336436	1028.639047	514.823162	1027.655031	514.331154	9
4	**397.280932**	199.144104			V	***932.581532***	466.794404	915.554983	458.281129	914.570967	457.789121	8
5	494.333696	247.670486			P	***833.513118***	417.260197	816.486569	408.746922	815.502553	408.254914	7
6	607.417760	304.212518			L	736.460354	368.733815	719.433805	360.220540	718.449789	359.728532	6
7	706.486174	353.746725			V	***623.376290***	312.191783	606.349741	303.678508	605.365725	303.186500	5
8	869.549503	435.278390			Y	***524.307876***	262.657576	507.281327	254.144301	506.297311	253.652293	4
9	970.597182	485.802229	952.586617	476.796946	T	361.244547	181.125911	344.217998	172.612637	343.233982	172.120629	3
10	1083.681246	542.344261	1065.670681	533.338978	I	260.196868	130.602072	243.170319	122.088797			2
11					K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.9	1228.779480	-0.007132	ALLVPLVYTIK

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

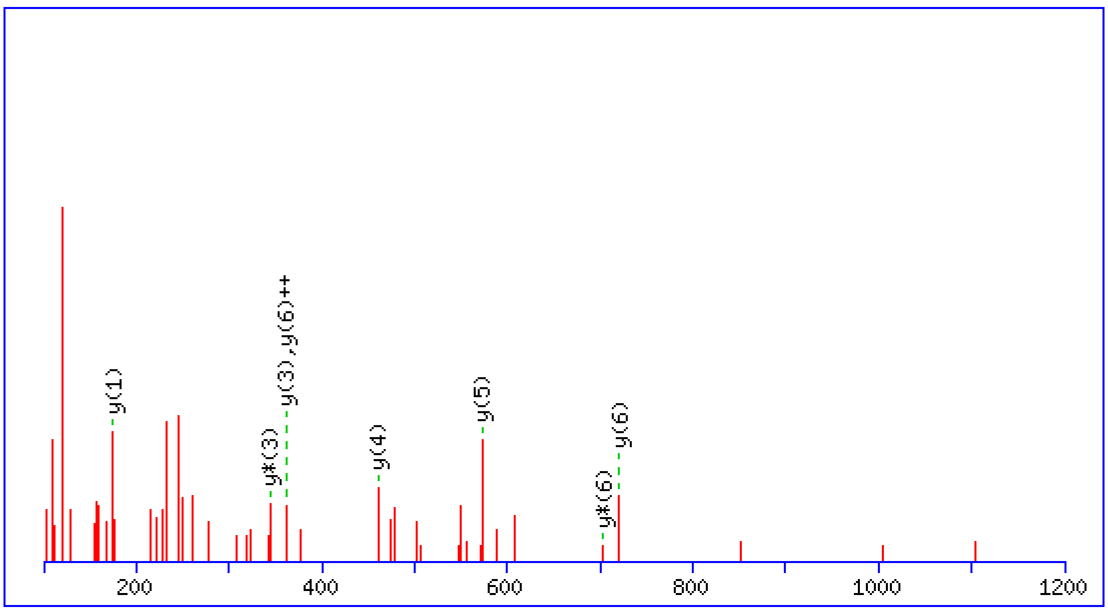
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LFPVVSR**
Found in **CP343_HUMAN**, Cytochrome P450 3A43 OS=Homo sapiens GN=CYP3A43 PE=1 SV=1

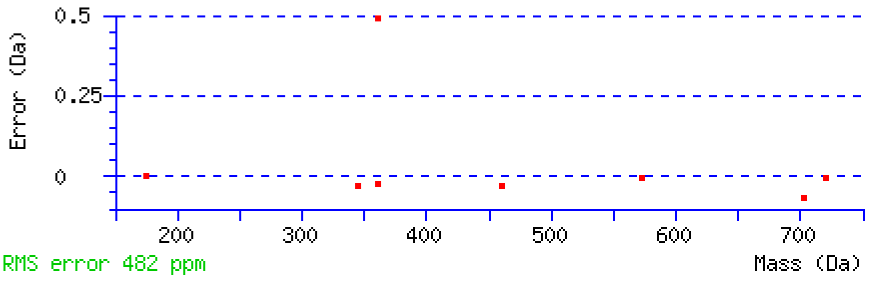
Match to Query 3012: 832.484908 from(417.249730,2+) rtinseconds(2315) index(28526)
Title: Locus:1.1.1.2224.7
Data file 2011-11-10 - TFD - EP 3-4.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●

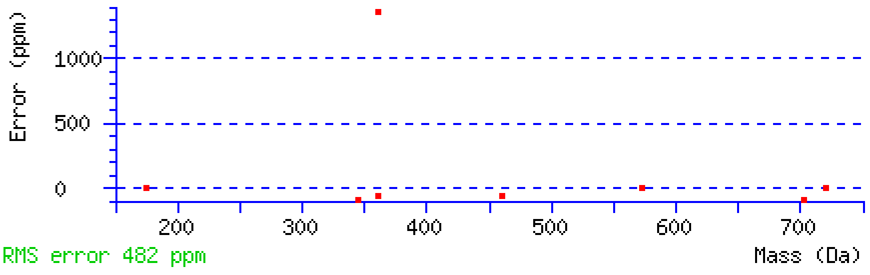


Monoisotopic mass of neutral peptide Mr(calc): 832.480698
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P3 : Oxidation (P)
Ions Score: 30 **Expect:** 0.0066
Matches : 8/48 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			**L**							7
2	261.159754	131.083515			**F**	***720.403901***	360.705589	703.377352	352.192314	702.393336	351.700306	6
3	374.207433	187.607354			**P**	***573.335487***	287.171382	556.308938	278.658107	555.324922	278.166099	5
4	473.275847	237.141561			**V**	***460.287808***	230.647542	443.261259	222.134267	442.277243	221.642259	4
5	572.344261	286.675769			**V**	***361.219394***	181.113335	344.192845	172.600060	343.208829	172.108052	3
6	659.376289	330.191783	641.365724	321.186500	**S**	262.150980	131.579128	245.124431	123.065853	244.140415	122.573845	2
7					**R**	***175.118952***	88.063114	158.092403	79.549839			1



RMS error 482 ppm



RMS error 482 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.4	832.480698	0.004210	LFPVVSR
15.3	832.480682	0.004226	FLLVGER
15.3	832.480698	0.004210	FPLVSVR
14.6	832.480682	0.004226	ILEFVGR
11.3	832.491898	-0.006990	LLREFR
7.8	832.480682	0.004226	IDLGIFR
7.0	832.480682	0.004226	LLSTFPR
5.6	832.491898	-0.006990	LFELRR
5.6	832.491898	-0.006990	LFERLR
5.3	832.484039	0.000869	CAKTIVK

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

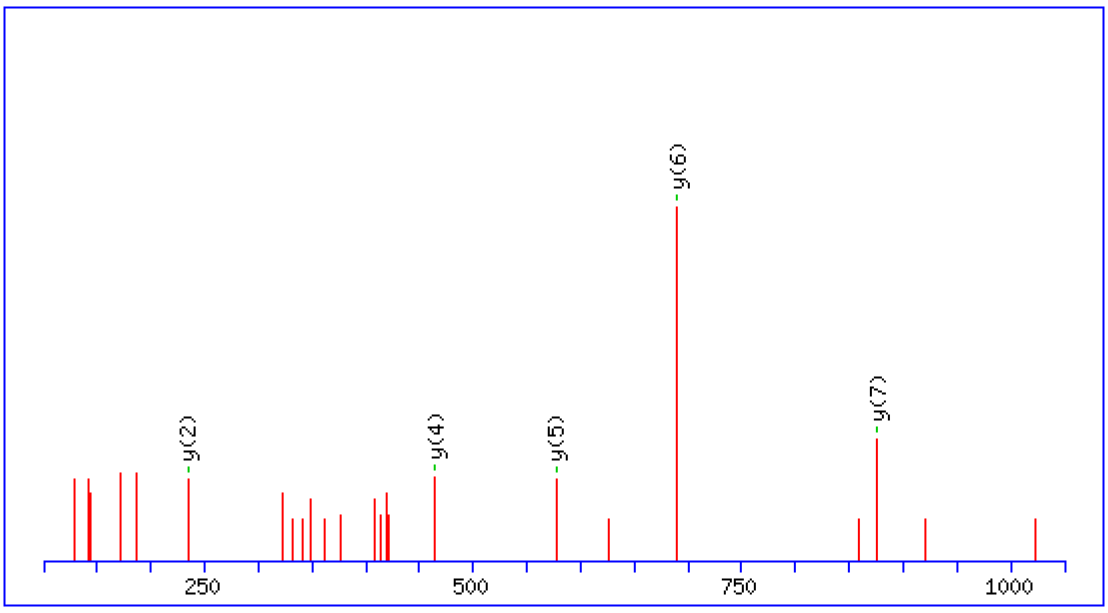
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LWLLDDSK**
Found in **NCK1_HUMAN**, Cytoplasmic protein NCK1 OS=Homo sapiens GN=NCK1 PE=1 SV=1

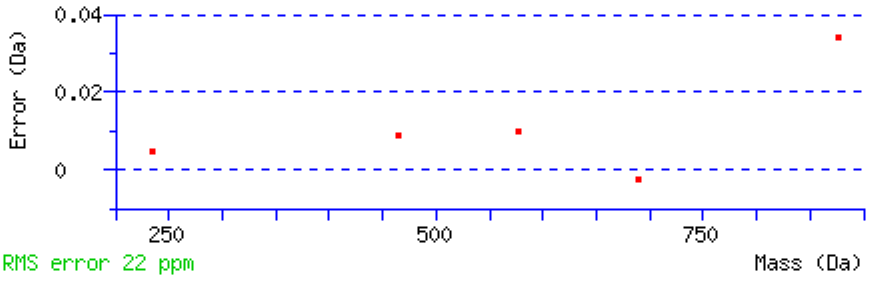
Match to Query 15053: 988.529788 from(495.272170,2+) rtinseconds(3085) index(43073)
Title: Locus:1.1.1.2515.4
Data file 2011-11-10 - TFD - EP 3-4.mgf

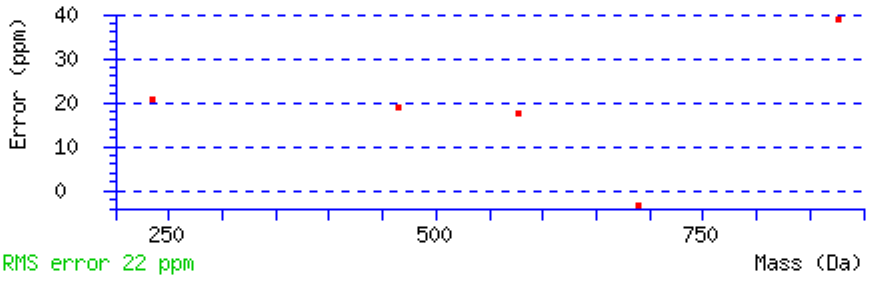
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 988.522934
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.0025
Matches : 5/60 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							8
2	300.170653	150.588965			W	***876.446159***	438.726718	859.419610	430.213443	858.435594	429.721435	7
3	413.254717	207.130997			L	***690.366846***	345.687061	673.340297	337.173786	672.356281	336.681778	6
4	526.338781	263.673029			L	***577.282782***	289.145029	560.256233	280.631755	559.272217	280.139747	5
5	641.365724	321.186500	623.355159	312.181218	D	***464.198718***	232.602997	447.172169	224.089722	446.188153	223.597714	4
6	756.392667	378.699972	738.382102	369.694689	D	349.171775	175.089525	332.145226	166.576251	331.161210	166.084243	3
7	843.424695	422.215985	825.414130	413.210703	S	***234.144832***	117.576054	217.118283	109.062779	216.134267	108.570771	2
8					K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.8	988.522934	0.006854	LWLLDDSK
25.5	988.520432	0.009356	LWIPWMK
13.6	988.520248	0.009540	LGEPHHRK
13.0	988.520432	0.009356	LWIPWMK
1.1	988.534164	-0.004376	QELPLSFR
0.7	988.530151	-0.000363	VPSKAAGSTR

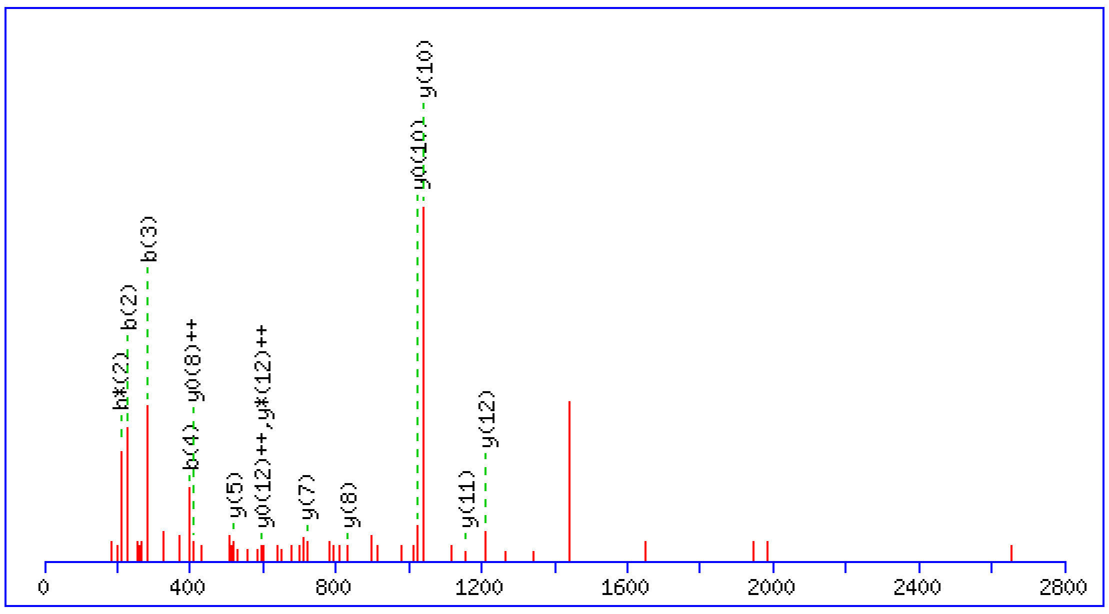
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NLGIPIITVLGDSK**
Found in **CKAP5_HUMAN**, Cytoskeleton-associated protein 5 OS=Homo sapiens GN=CKAP5 PE=1 SV=3

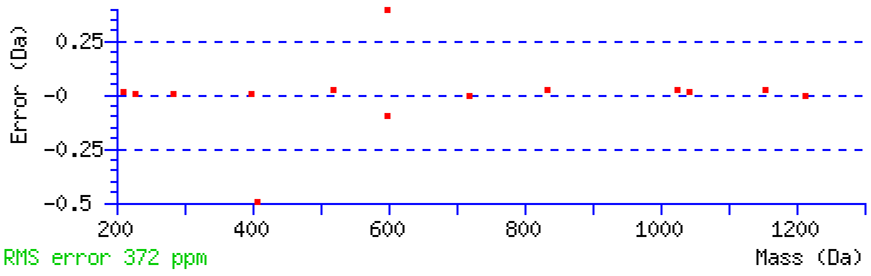
Match to Query 42189: 1438.846668 from(720.430610,2+) rtinseconds(3812) index(55536)
Title: Locus:1.1.1.2862.31
Data file 2011-11-10 - TFD - EP 3-1.mgf

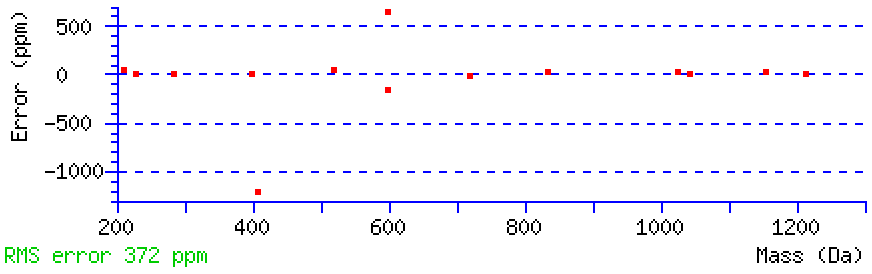
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1438.839523
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 36  Expect: 0.00056
Matches : 14/140 fragment ions using 23 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			N							14
2	**228.134267**	114.570771	211.107718	106.057497			L	1325.803880	663.405578	1308.777331	654.892304	1307.793315	654.400296	13
3	**285.155731**	143.081504	268.129182	134.568229			G	***1212.719816***	606.863546	1195.693267	598.350272	1194.709251	597.858264	12
4	**398.239795**	199.623536	381.213246	191.110261			I	***1155.698352***	578.352814	1138.671803	569.839540	1137.687787	569.347532	11
5	495.292559	248.149918	478.266010	239.636643			P	***1042.614288***	521.810782	1025.587739	513.297508	1024.603723	512.805500	10
6	608.376623	304.691950	591.350074	296.178675			I	945.561524	473.284400	928.534975	464.771126	927.550959	464.279118	9
7	721.460687	361.233982	704.434138	352.720707			I	***832.477460***	416.742368	815.450911	408.229094	814.466895	407.737086	8
8	822.508366	411.757821	805.481817	403.244547	804.497801	402.752539	T	***719.393396***	360.200336	702.366847	351.687062	701.382831	351.195054	7
9	921.576780	461.292028	904.550231	452.778754	903.566215	452.286746	V	618.345717	309.676497	601.319168	301.163222	600.335152	300.671214	6
10	1034.660844	517.834060	1017.634295	509.320786	1016.650279	508.828778	L	***519.277303***	260.142290	502.250754	251.629015	501.266738	251.137007	5
11	1091.682308	546.344792	1074.655759	537.831518	1073.671743	537.339509	G	406.193239	203.600258	389.166690	195.086983	388.182674	194.594975	4
12	1206.709251	603.858264	1189.682702	595.344989	1188.698686	594.852981	D	349.171775	175.089526	332.145226	166.576251	331.161210	166.084243	3
13	1293.741279	647.374278	1276.714730	638.861003	1275.730714	638.368995	S	234.144832	117.576054	217.118283	109.062780	216.134267	108.570772	2
14							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.9	1438.839523	0.007145	NLGIPIITVLGDSK
1.9	1438.850754	-0.004086	LVSRPKPLSAVPK
1.8	1438.839523	0.007145	KPKTISVPDVEVK
1.4	1438.850723	-0.004055	ANVIASALAKIPQK

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

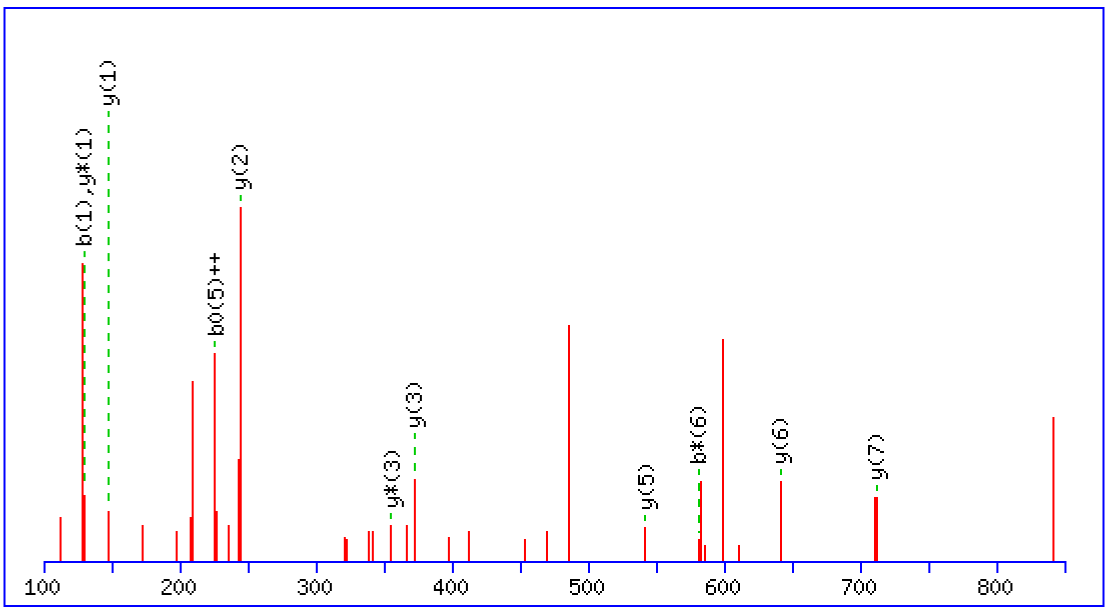
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EAVVAKPK**
Found in **DACT1_HUMAN**, Dapper homolog 1 OS=Homo sapiens GN=DACT1 PE=2 SV=2

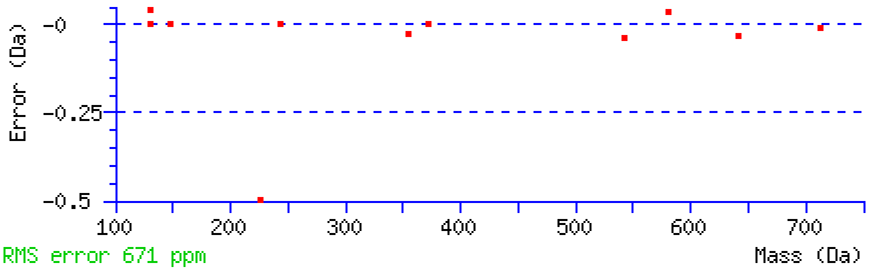
Match to Query 53596: 840.507468 from(421.261010,2+) rtinseconds(1399) index(335965)
Title: Locus:1.1.1.869.2
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

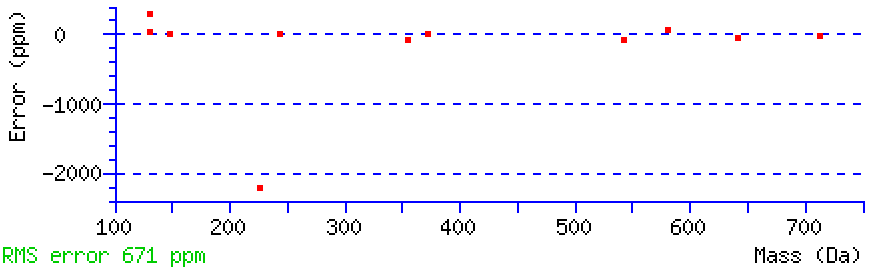
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 840.506882
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 32  Expect: 0.0031
Matches : 11/60 fragment ions using 23 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	130.049869	65.528572			112.039304	56.523290	E					8
2	201.086983	101.047130			183.076418	92.041847	A	*712.471587*	356.739432	695.445038	348.226157	7
3	300.155397	150.581336			282.144832	141.576054	V	*641.434473*	321.220875	624.407924	312.707600	6
4	399.223811	200.115544			381.213246	191.110261	V	*542.366059*	271.686668	525.339510	263.173393	5
5	470.260925	235.634100			452.250360	226.628818	A	443.297645	222.152460	426.271096	213.639186	4
6	598.355888	299.681582	581.329339	291.168308	580.345323	290.676300	K	*372.260531*	186.633904	355.233982	178.120629	3
7	695.408652	348.207964	678.382103	339.694690	677.398087	339.202682	P	*244.165568*	122.586422	227.139019	114.073148	2
8							K	*147.112804*	74.060040	130.086255	65.546765	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.8	840.506882	0.000586	EAVVAKPK
30.5	840.506866	0.000602	KNEPIIK
21.4	840.506882	0.000586	EVAGKIPK
21.1	840.506866	0.000602	KNLPLEK
20.4	840.506912	0.000556	VTVLGQPK
15.2	840.506897	0.000571	QQVLPLK
12.3	840.506866	0.000602	KENIPLK
8.6	840.506866	0.000602	LKNLEPK
5.6	840.506882	0.000586	LLKGEGPK
5.0	840.506897	0.000571	LVGISQPK

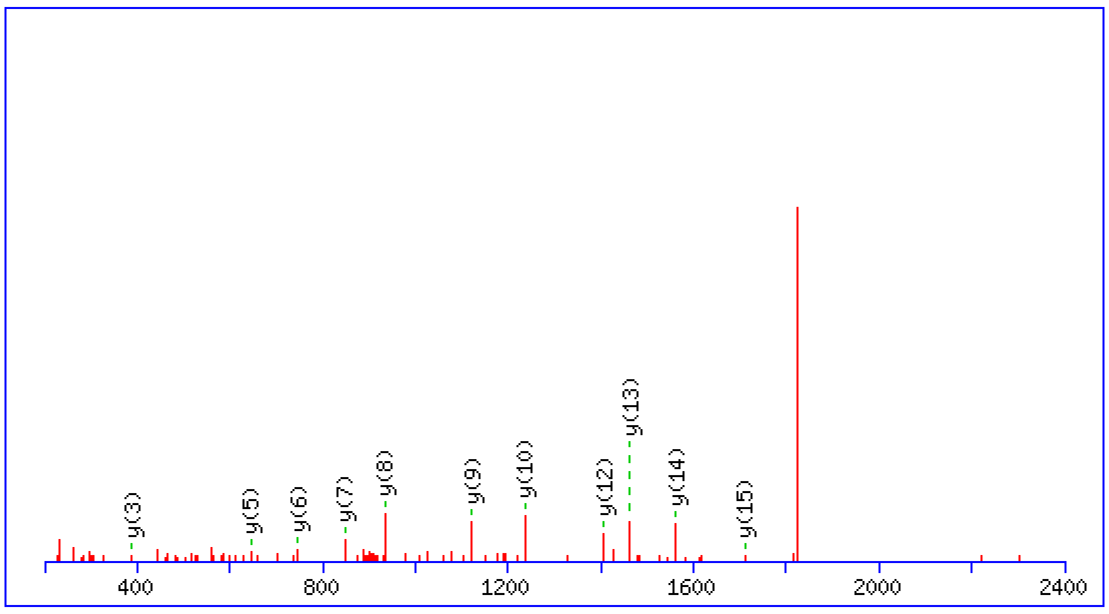
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LFVGGLDWSTTQETLR**
Found in **DAZP1_HUMAN**, DAZ-associated protein 1 OS=Homo sapiens GN=DAZAP1 PE=1 SV=1

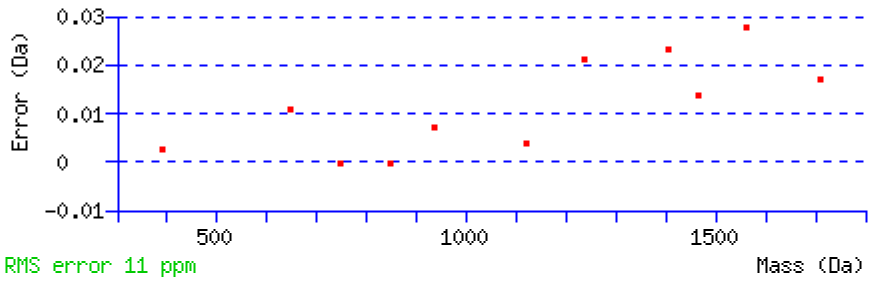
Match to Query 54736: 1821.932468 from(911.973510,2+) rtinseconds(3447) index(50302)
Title: Locus:1.1.1.2800.36
Data file 2011-11-10 - TFD - EP 4-3.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●

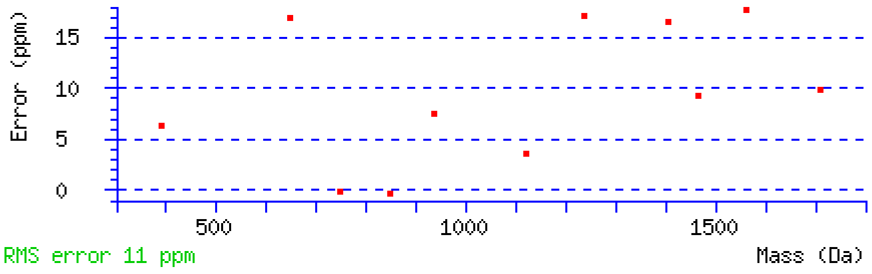


Monoisotopic mass of neutral peptide Mr(calc): 1821.926132
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 92 **Expect:** 6.7e-009
Matches : 11/142 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							16
2	261.159754	131.083515					F	*1709.849328*	855.428302	1692.822779	846.915027	1691.838763	846.423019	15
3	360.228168	180.617722					V	*1562.780914*	781.894095	1545.754365	773.380820	1544.770349	772.888812	14
4	417.249632	209.128454					G	*1463.712500*	732.359888	1446.685951	723.846613	1445.701935	723.354605	13
5	474.271096	237.639186					G	*1406.691036*	703.849156	1389.664487	695.335881	1388.680471	694.843873	12
6	587.355160	294.181218					L	1349.669572	675.338424	1332.643023	666.825149	1331.659007	666.333141	11
7	702.382103	351.694689			684.371538	342.689407	D	*1236.585508*	618.796392	1219.558959	610.283118	1218.574943	609.791109	10
8	888.461416	444.734346			870.450851	435.729063	W	*1121.558565*	561.282920	1104.532016	552.769646	1103.548000	552.277638	9
9	975.493444	488.250360			957.482879	479.245077	S	*935.479252*	468.243264	918.452703	459.729989	917.468687	459.237981	8
10	1076.541123	538.774199			1058.530558	529.768917	T	*848.447224*	424.727250	831.420675	416.213975	830.436659	415.721967	7
11	1177.588802	589.298039			1159.578237	580.292756	T	*747.399545*	374.203411	730.372996	365.690136	729.388980	365.198128	6
12	1305.647380	653.327328	1288.620831	644.814053	1287.636815	644.322045	Q	*646.351866*	323.679571	629.325317	315.166296	628.341301	314.674288	5
13	1434.689973	717.848624	1417.663424	709.335350	1416.679408	708.843342	E	518.293288	259.650282	501.266739	251.137008	500.282723	250.645000	4
14	1535.737652	768.372464	1518.711103	759.859189	1517.727087	759.367181	T	*389.250695*	195.128985	372.224146	186.615711	371.240130	186.123703	3
15	1648.821716	824.914496	1631.795167	816.401221	1630.811151	815.909213	L	288.203016	144.605146	271.176467	136.091871			2
16							R	175.118952	88.063114	158.092403	79.549839			1



RMS error 11 ppm



RMS error 11 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
92.2	1821.926132	0.006336	LFVGGLDWSTTQETLR

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

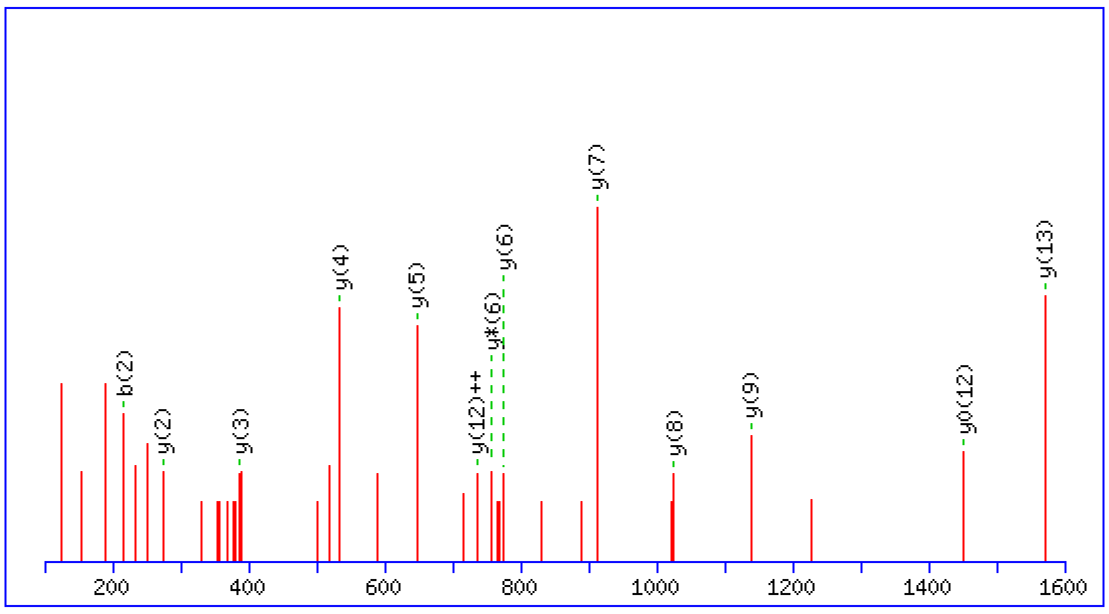
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SETEDSILHQLFIVR**
Found in **DP13A_HUMAN**, DCC-interacting protein 13-alpha OS=Homo sapiens GN=APPL1 PE=1 SV=1

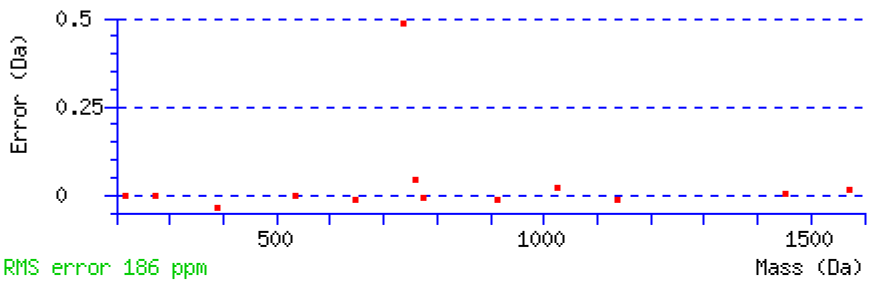
Match to Query 55401: 1785.926532 from(596.316120,3+) rtinseconds(3657) index(52014)
Title: Locus:1.1.1.2838.6
Data file 2011-11-14 - TFD - EP 7-2.mgf

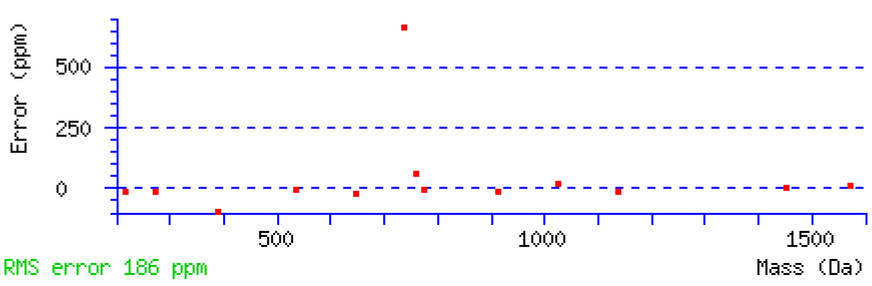
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1600] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1785.926102
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 47 **Expect:** 7.7e-005
Matches : 13/132 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							15
2	217.081897	109.044586			199.071332	100.039304	E	1699.901362	850.454319	1682.874813	841.941044	1681.890797	841.449036	14
3	318.129576	159.568426			300.119011	150.563144	T	***1570.858769***	785.933022	1553.832220	777.419748	1552.848204	776.927740	13
4	447.172169	224.089722			429.161604	215.084440	E	1469.811090	735.409183	1452.784541	726.895909	1451.800525	726.403900	12
5	562.199112	281.603194			544.188547	272.597912	D	1340.768497	670.887886	1323.741948	662.374612	1322.757932	661.882604	11
6	649.231140	325.119208			631.220575	316.113925	S	1225.741554	613.374415	1208.715005	604.861141	1207.730989	604.369132	10
7	762.315204	381.661240			744.304639	372.655958	I	***1138.709526***	569.858401	1121.682977	561.345126			9
8	875.399268	438.203272			857.388703	429.197990	L	***1025.625462***	513.316369	1008.598913	504.803094			8
9	1012.458180	506.732728			994.447615	497.727445	H	***912.541398***	456.774337	895.514849	448.261062			7
10	1140.516758	570.762017	1123.490209	562.248743	1122.506193	561.756734	Q	***775.482486***	388.244881	758.455937	379.731607			6
11	1253.600822	627.304049	1236.574273	618.790775	1235.590257	618.298766	L	***647.423908***	324.215592	630.397359	315.702317			5
12	1400.669236	700.838256	1383.642687	692.324982	1382.658671	691.832973	F	***534.339844***	267.673560	517.313295	259.160286			4
13	1513.753300	757.380288	1496.726751	748.867013	1495.742735	748.375005	I	***387.271430***	194.139353	370.244881	185.626078			3
14	1612.821714	806.914495	1595.795165	798.401221	1594.811149	797.909212	V	***274.187366***	137.597321	257.160817	129.084047			2
15							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of SETEDSILHQLFIVR
(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	1785.926102	0.000430	SETEDSILHQLFIVR
2.5	1785.937317	-0.010785	HLEINPDHSIIETLR
0.4	1785.940704	-0.014172	TSPQQKLIIVEGCQR

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

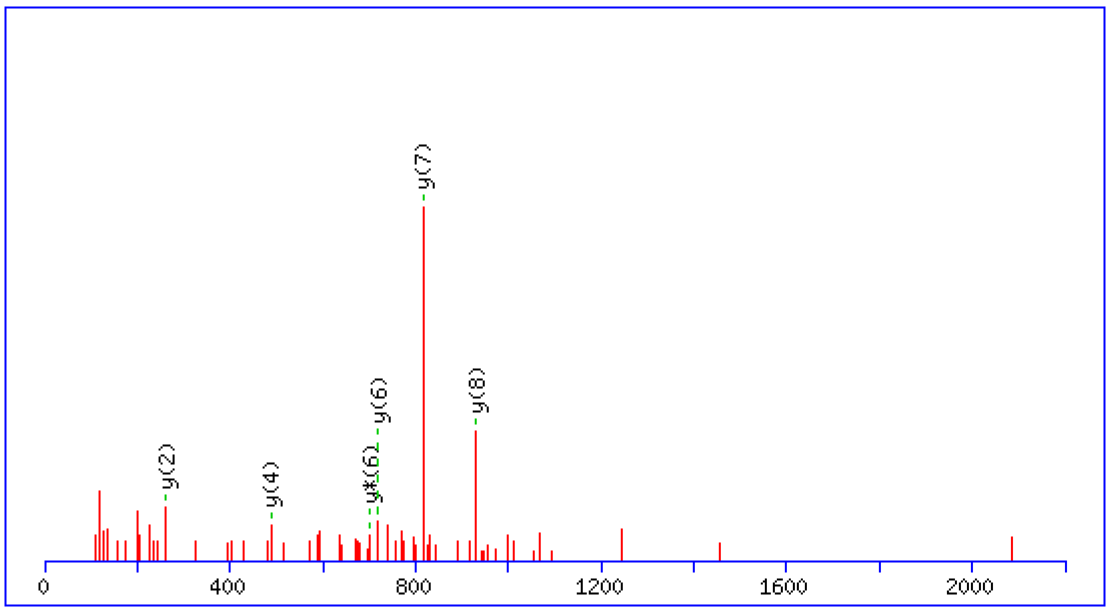
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LIDPQTQVSR**
Found in **DP13B_HUMAN**, DCC-interacting protein 13-beta OS=Homo sapiens GN=APPL2 PE=1 SV=3

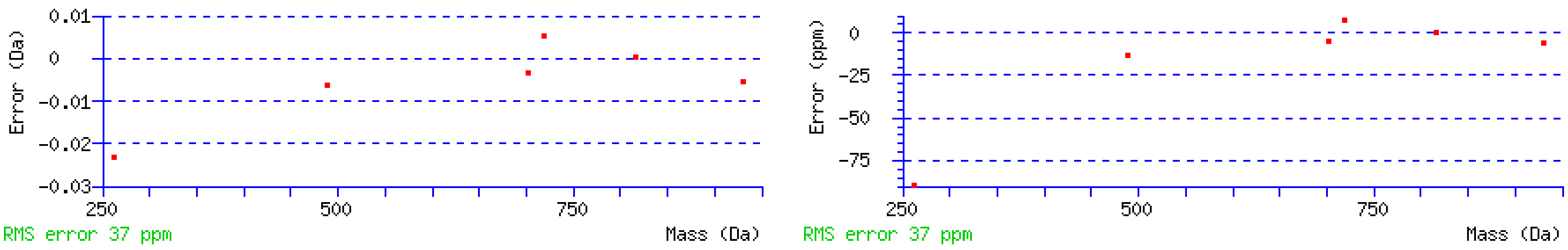
Match to Query 27220: 1155.630748 from(578.822650,2+) rtinseconds(1616) index(15200)
Title: Locus:1.1.1.2059.33
Data file 2011-11-10 - TFD - EP 3-2.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1155.624786
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 32  Expect: 0.0011
Matches : 6/94 fragment ions using 10 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							10
2	227.175404	114.091340					I	1043.548000	522.277638	1026.521451	513.764364	1025.537435	513.272356	9
3	342.202347	171.604811			324.191782	162.599529	D	***930.463936***	465.735606	913.437387	457.222332	912.453371	456.730324	8
4	439.255111	220.131193			421.244546	211.125911	P	***815.436993***	408.222135	798.410444	399.708860	797.426428	399.216852	7
5	567.313689	284.160483	550.287140	275.647208	549.303124	275.155200	Q	***718.384229***	359.695753	701.357680	351.182478	700.373664	350.690470	6
6	668.361368	334.684322	651.334819	326.171048	650.350803	325.679040	T	590.325651	295.666464	573.299102	287.153189	572.315086	286.661181	5
7	796.419946	398.713611	779.393397	390.200337	778.409381	389.708329	Q	***489.277972***	245.142624	472.251423	236.629349	471.267407	236.137341	4
8	895.488360	448.247818	878.461811	439.734544	877.477795	439.242536	V	361.219394	181.113335	344.192845	172.600060	343.208829	172.108052	3
9	982.520388	491.763832	965.493839	483.250558	964.509823	482.758550	S	***262.150980***	131.579128	245.124431	123.065854	244.140415	122.573846	2
10							R	175.118952	88.063114	158.092403	79.549840			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.4	1155.624786	0.005962	LIDPQTQVSR
0.7	1155.636002	-0.005254	VPKNSLQQSR

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

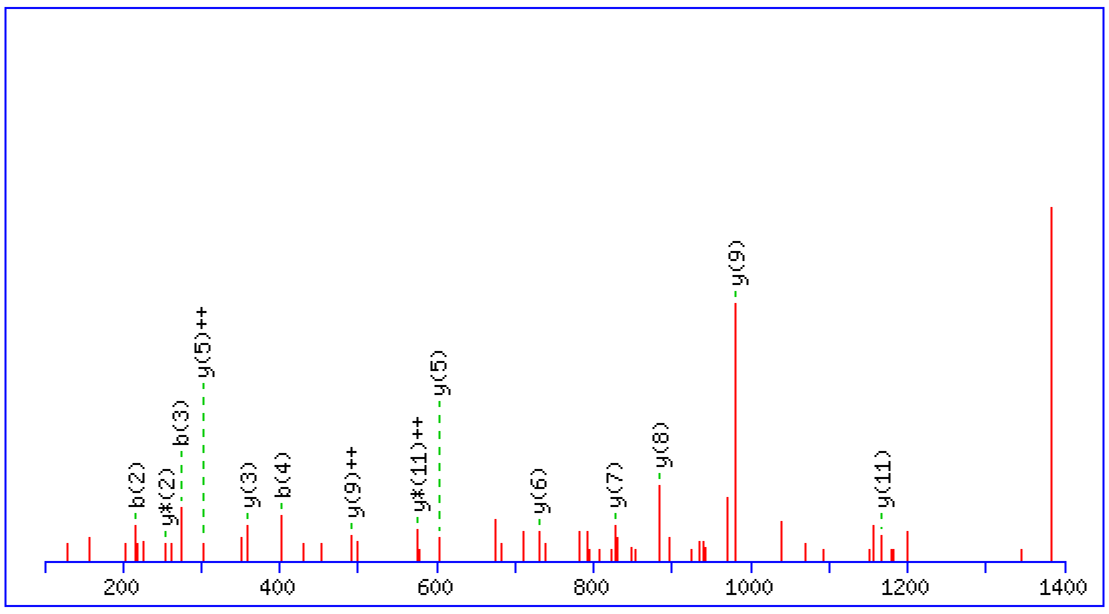
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TDGEPGPQGWSPR**
Found in **DCTP1_HUMAN**, dCTP pyrophosphatase 1 OS=Homo sapiens GN=DCTPP1 PE=1 SV=1

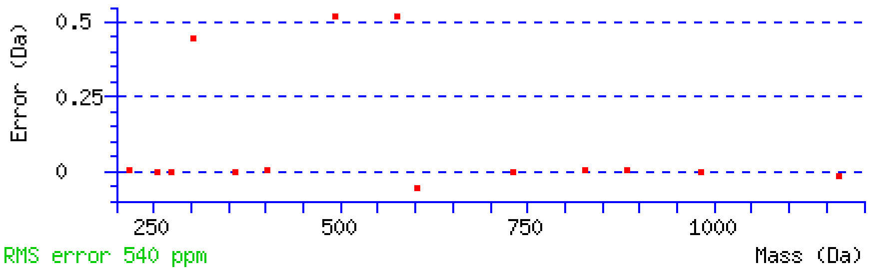
Match to Query 38342: 1382.631548 from(692.323050,2+) rtinseconds(1902) index(17911)
Title: Locus:1.1.1.1991.50
Data file 2011-11-10 - TFD - EP 3-6.mgf

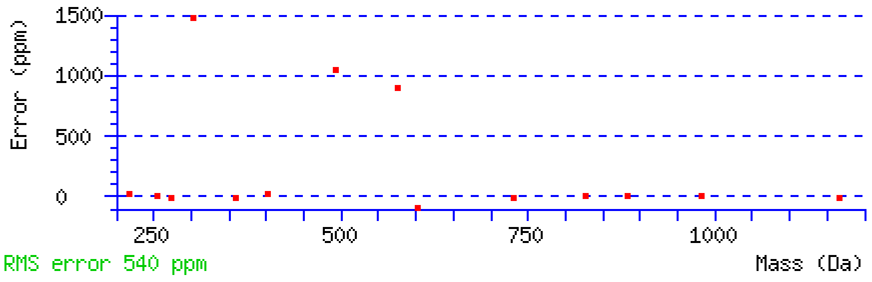
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1382.621506
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 35 **Expect:** 0.00071
Matches : 14/126 fragment ions using 34 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							13
2	**217.081898**	109.044587			199.071333	100.039304	D	1282.581091	641.794184	1265.554542	633.280909	1264.570526	632.788901	12
3	**274.103362**	137.555319			256.092797	128.550037	G	***1167.554148***	584.280712	1150.527599	575.767438	1149.543583	575.275430	11
4	**403.145955**	202.076616			385.135390	193.071333	E	1110.532684	555.769980	1093.506135	547.256706	1092.522119	546.764698	10
5	500.198719	250.602998			482.188154	241.597715	P	***981.490091***	491.248684	964.463542	482.735409	963.479526	482.243401	9
6	557.220183	279.113730			539.209618	270.108447	G	***884.437327***	442.722302	867.410778	434.209027	866.426762	433.717019	8
7	654.272947	327.640112			636.262382	318.634829	P	***827.415863***	414.211570	810.389314	405.698295	809.405298	405.206287	7
8	782.331525	391.669401	765.304976	383.156126	764.320960	382.664118	Q	***730.363099***	365.685188	713.336550	357.171913	712.352534	356.679905	6
9	839.352989	420.180133	822.326440	411.666858	821.342424	411.174850	G	***602.304521***	301.655899	585.277972	293.142624	584.293956	292.650616	5
10	1025.432302	513.219789	1008.405753	504.706515	1007.421737	504.214507	W	545.283057	273.145167	528.256508	264.631892	527.272492	264.139884	4
11	1112.464330	556.735803	1095.437781	548.222529	1094.453765	547.730521	S	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.100228	3
12	1209.517094	605.262185	1192.490545	596.748911	1191.506529	596.256903	P	272.171716	136.589496	255.145167	128.076221			2
13							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.9	1382.621506	0.010042	TDGEPGPQGWSPR
1.3	1382.628891	0.002657	MWVFEETVNGR
0.0	1382.644135	-0.012587	SWMLWNFVER

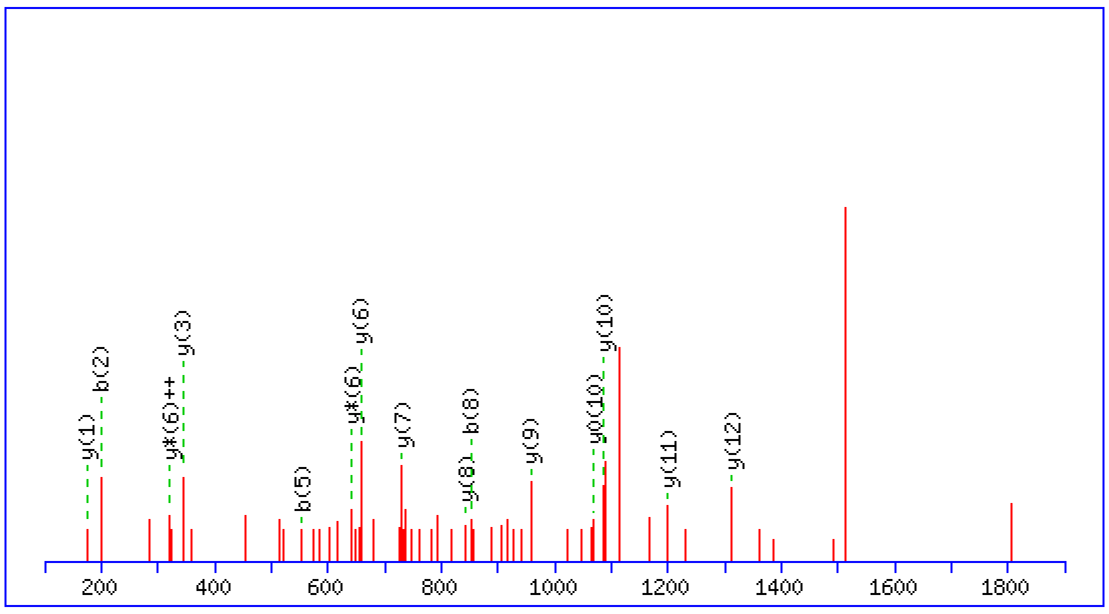
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVLLEDLASQVGLR**
Found in **DDRGK_HUMAN**, DDRGK domain-containing protein 1 OS=Homo sapiens GN=DDRGK1 PE=1 SV=2

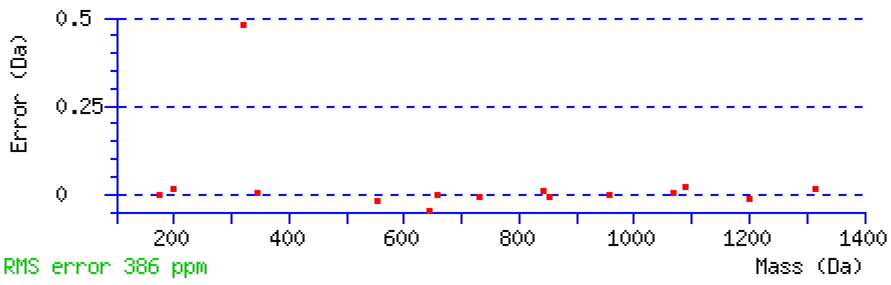
Match to Query 47359: 1510.877128 from(756.445840,2+) rtinseconds(3977) index(59972)
Title: Locus:1.1.1.2804.25
Data file 2011-11-12 - TFD - EP 6-4.mgf

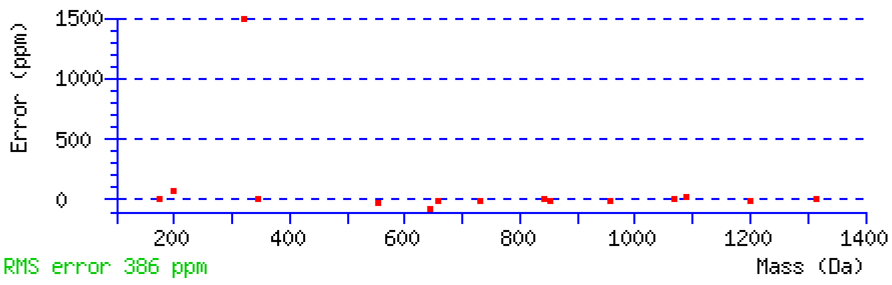
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1510.871887
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 54 **Expect:** 1.1e-005
Matches : 15/120 fragment ions using 33 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							14
2	**199.144104**	100.075690					V	1412.810756	706.909016	1395.784207	698.395741	1394.800191	697.903733	13
3	312.228168	156.617722					L	***1313.742342***	657.374809	1296.715793	648.861535	1295.731777	648.369527	12
4	425.312232	213.159754					L	***1200.658278***	600.832777	1183.631729	592.319503	1182.647713	591.827494	11
5	**554.354825**	277.681051			536.344260	268.675768	E	***1087.574214***	544.290745	1070.547665	535.777471	1069.563649	535.285462	10
6	669.381768	335.194522			651.371203	326.189240	D	***958.531621***	479.769448	941.505072	471.256174	940.521056	470.764166	9
7	782.465832	391.736554			764.455267	382.731272	L	***843.504678***	422.255977	826.478129	413.742702	825.494113	413.250694	8
8	**853.502946**	427.255111			835.492381	418.249829	A	***730.420614***	365.713945	713.394065	357.200670	712.410049	356.708662	7
9	940.534974	470.771125			922.524409	461.765843	S	***659.383500***	330.195388	642.356951	321.682113	641.372935	321.190105	6
10	1068.593552	534.800414	1051.567003	526.287140	1050.582987	525.795132	Q	572.351472	286.679374	555.324923	278.166099			5
11	1167.661966	584.334621	1150.635417	575.821347	1149.651401	575.329339	V	444.292894	222.650085	427.266345	214.136810			4
12	1224.683430	612.845353	1207.656881	604.332079	1206.672865	603.840071	G	***345.224480***	173.115878	328.197931	164.602603			3
13	1337.767494	669.387385	1320.740945	660.874111	1319.756929	660.382102	L	288.203016	144.605146	271.176467	136.091871			2
14							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.2	1510.871887	0.005241	VVLLEDLASQVGLR

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

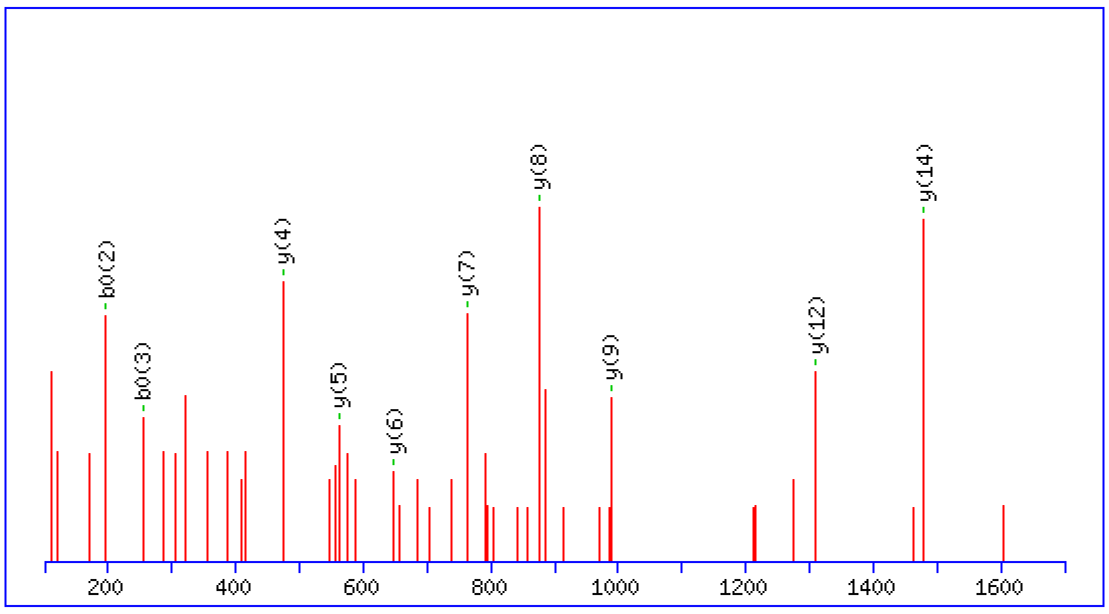
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LTGIPSHILNSSPSDR**
Found in **CRADD_HUMAN**, Death domain-containing protein CRADD OS=Homo sapiens GN=CRADD PE=1 SV=1

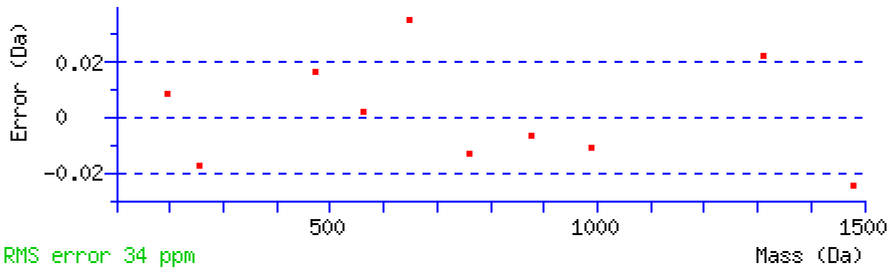
Match to Query 48424: 1692.878622 from(565.300150,3+) rtinseconds(2301) index(25248)
Title: Locus:1.1.1.2167.29
Data file 2011-11-13 - TFD - EP 7-6.mgf

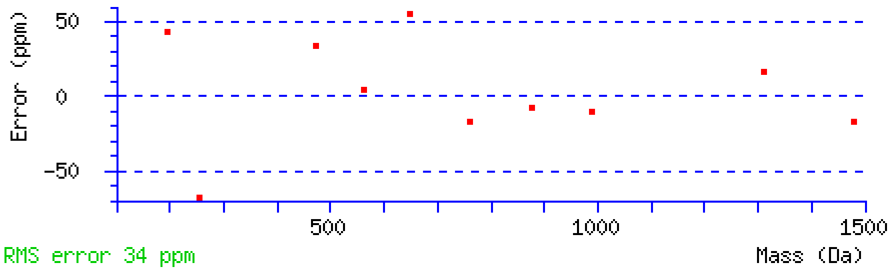
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1692.879486
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 59 **Expect:** 1.2e-005
Matches : 10/158 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							16
2	215.139019	108.073147			197.128454	99.067865	T	1580.802709	790.904993	1563.776160	782.391718	1562.792144	781.899710	15
3	272.160483	136.583879			254.149918	127.578597	G	***1479.755030***	740.381153	1462.728481	731.867879	1461.744465	731.375871	14
4	385.244547	193.125912			367.233982	184.120629	I	1422.733566	711.870421	1405.707017	703.357147	1404.723001	702.865139	13
5	482.297311	241.652293			464.286746	232.647011	P	***1309.649502***	655.328389	1292.622953	646.815115	1291.638937	646.323107	12
6	569.329339	285.168308			551.318774	276.163025	S	1212.596738	606.802007	1195.570189	598.288733	1194.586173	597.796725	11
7	706.388251	353.697764			688.377686	344.692481	H	1125.564710	563.285993	1108.538161	554.772719	1107.554145	554.280711	10
8	819.472315	410.239796			801.461750	401.234513	I	***988.505798***	494.756537	971.479249	486.243263	970.495233	485.751255	9
9	932.556379	466.781828			914.545814	457.776545	L	***875.421734***	438.214505	858.395185	429.701231	857.411169	429.209223	8
10	1046.599306	523.803291	1029.572757	515.290017	1028.588741	514.798009	N	***762.337670***	381.672473	745.311121	373.159199	744.327105	372.667191	7
11	1133.631334	567.319305	1116.604785	558.806031	1115.620769	558.314023	S	***648.294743***	324.651010	631.268194	316.137735	630.284178	315.645727	6
12	1220.663362	610.835319	1203.636813	602.322045	1202.652797	601.830037	S	***561.262715***	281.134996	544.236166	272.621721	543.252150	272.129713	5
13	1317.716126	659.361701	1300.689577	650.848427	1299.705561	650.356419	P	***474.230687***	237.618982	457.204138	229.105707	456.220122	228.613699	4
14	1404.748154	702.877715	1387.721605	694.364441	1386.737589	693.872433	S	377.177923	189.092600	360.151374	180.579325	359.167358	180.087317	3
15	1519.775097	760.391187	1502.748548	751.877912	1501.764532	751.385904	D	290.145895	145.576585	273.119346	137.063311	272.135330	136.571303	2
16							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
59.3	1692.879486	-0.000864	LTGIPSHILNSSPSDR

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

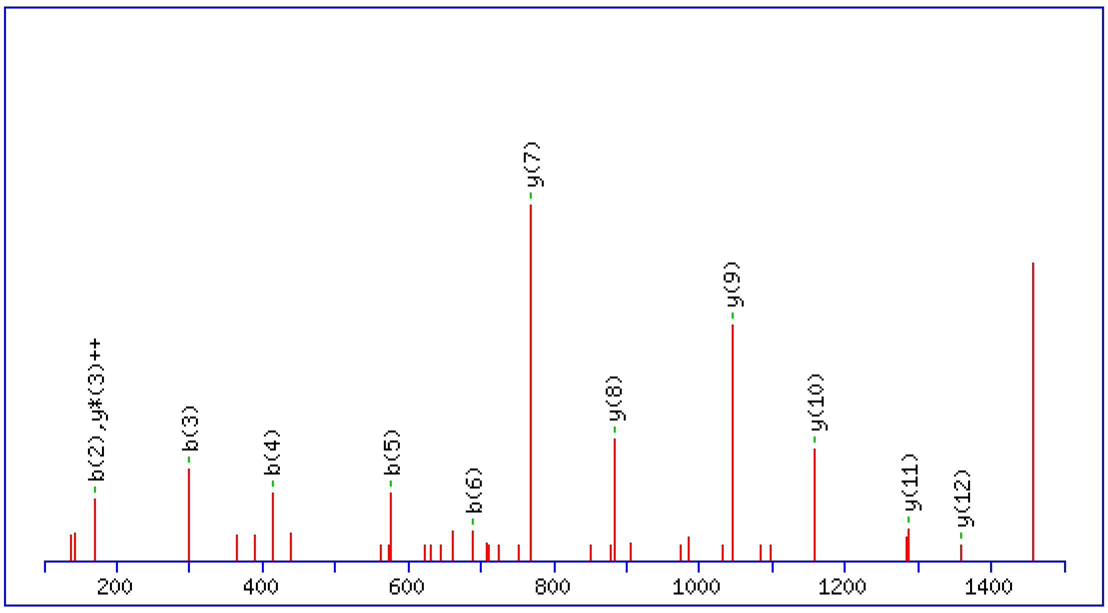
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VAELYLPLLSIAR**
Found in **DOCK6_HUMAN**, Dedicator of cytokinesis protein 6 OS=Homo sapiens GN=DOCK6 PE=1 SV=3

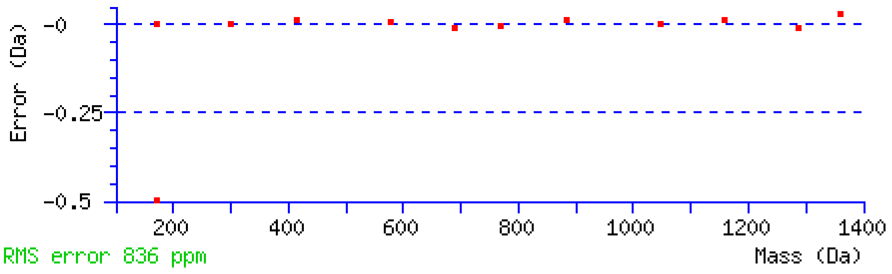
Match to Query 43094: 1456.871808 from(729.443180,2+) rtinseconds(4207) index(61944)
Title: Locus:1.1.1.3009.29
Data file 2011-11-10 - TFD - EP 3-1.mgf

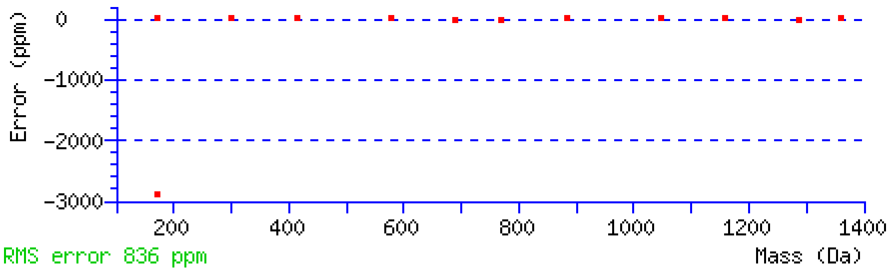
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1456.865311
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 51  Expect: 1e-005
Matches : 12/110 fragment ions using 13 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483			V							13
2	**171.112804**	86.060040			A	***1358.804214***	679.905745	1341.777665	671.392471	1340.793649	670.900463	12
3	**300.155397**	150.581336	282.144832	141.576054	E	***1287.767100***	644.387188	1270.740551	635.873914	1269.756535	635.381906	11
4	**413.239461**	207.123369	395.228896	198.118086	L	***1158.724507***	579.865892	1141.697958	571.352617	1140.713942	570.860609	10
5	**576.302790**	288.655033	558.292225	279.649751	Y	***1045.640443***	523.323860	1028.613894	514.810585	1027.629878	514.318577	9
6	**689.386854**	345.197065	671.376289	336.191783	L	***882.577114***	441.792195	865.550565	433.278921	864.566549	432.786913	8
7	786.439618	393.723447	768.429053	384.718165	P	***769.493050***	385.250163	752.466501	376.736889	751.482485	376.244881	7
8	899.523682	450.265479	881.513117	441.260197	L	672.440286	336.723781	655.413737	328.210507	654.429721	327.718499	6
9	1012.607746	506.807511	994.597181	497.802229	L	559.356222	280.181749	542.329673	271.668475	541.345657	271.176467	5
10	1099.639774	550.323525	1081.629209	541.318243	S	446.272158	223.639717	429.245609	215.126442	428.261593	214.634434	4
11	1212.723838	606.865557	1194.713273	597.860275	I	359.240130	180.123703	342.213581	171.610428			3
12	1283.760952	642.384114	1265.750387	633.378832	A	246.156066	123.581671	229.129517	115.068396			2
13					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of VAELYLPLLSIAR
(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	1456.865311	0.006497	VAELYLPLLSIAR

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

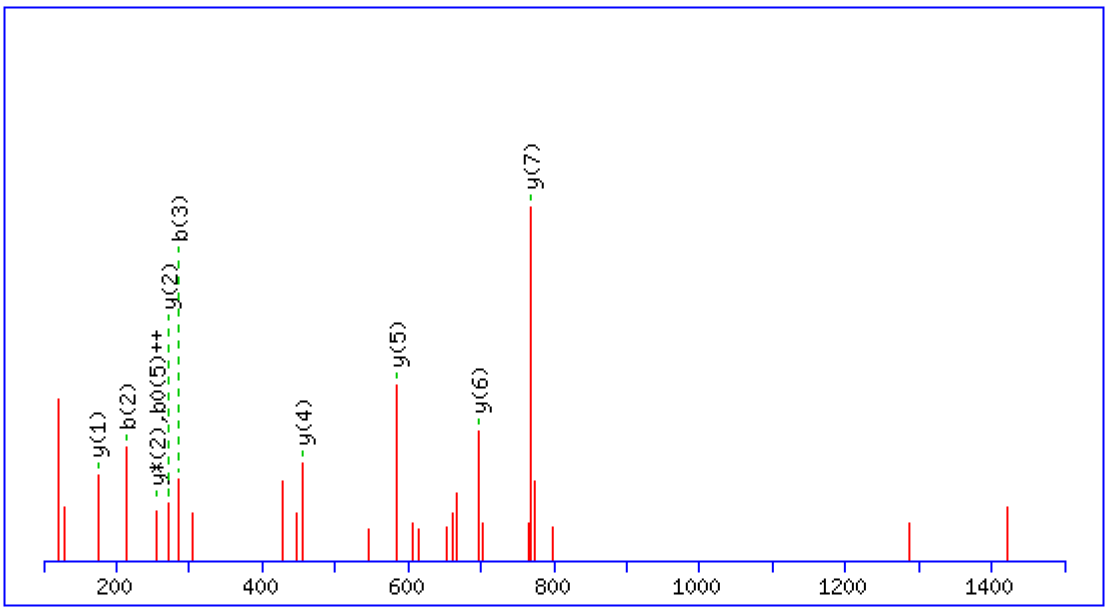
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLAIELAPR**
Found in **DHRS4_HUMAN**, Dehydrogenase/reductase SDR family member 4 OS=Homo sapiens GN=DHRS4 PE=1 SV=3

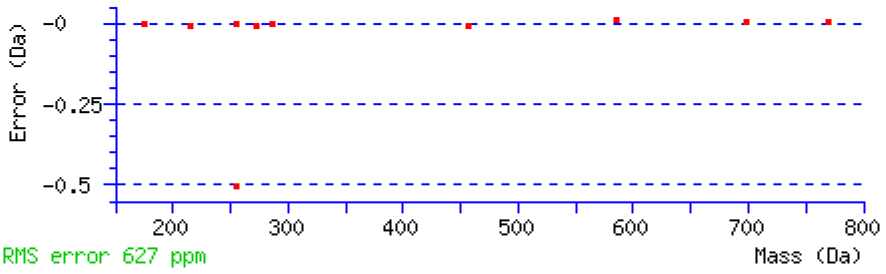
Match to Query 14727: 982.571928 from(492.293240,2+) rtinseconds(2410) index(29793)
Title: Locus:1.1.1.2334.7
Data file 2011-11-12 - TFD - EP 5-4.mgf

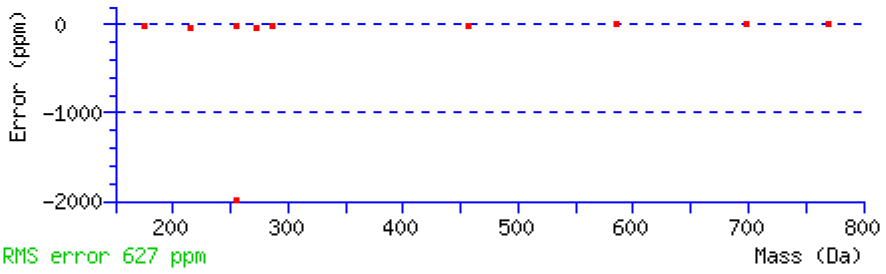
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 982.581100
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 40  Expect: 0.00083
Matches : 10/72 fragment ions using 18 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116	84.044390	42.525833	T							9
2	**215.139019**	108.073147	197.128454	99.067865	L	882.540729	441.774003	865.514180	433.260728	864.530164	432.768720	8
3	**286.176133**	143.591704	268.165568	134.586422	A	***769.456665***	385.231971	752.430116	376.718696	751.446100	376.226688	7
4	399.260197	200.133737	381.249632	191.128454	I	***698.419551***	349.713414	681.393002	341.200139	680.408986	340.708131	6
5	528.302790	264.655033	510.292225	255.649751	E	***585.335487***	293.171382	568.308938	284.658107	567.324922	284.166099	5
6	641.386854	321.197065	623.376289	312.191783	L	***456.292894***	228.650085	439.266345	220.136810			4
7	712.423968	356.715622	694.413403	347.710340	A	343.208830	172.108053	326.182281	163.594778			3
8	809.476732	405.242004	791.466167	396.236722	P	***272.171716***	136.589496	255.145167	128.076221			2
9					R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.7	982.581100	-0.009172	TLAIELAPR
6.4	982.581131	-0.009203	TPITLLGPR
0.4	982.569901	0.002027	DGLPVLIPK

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

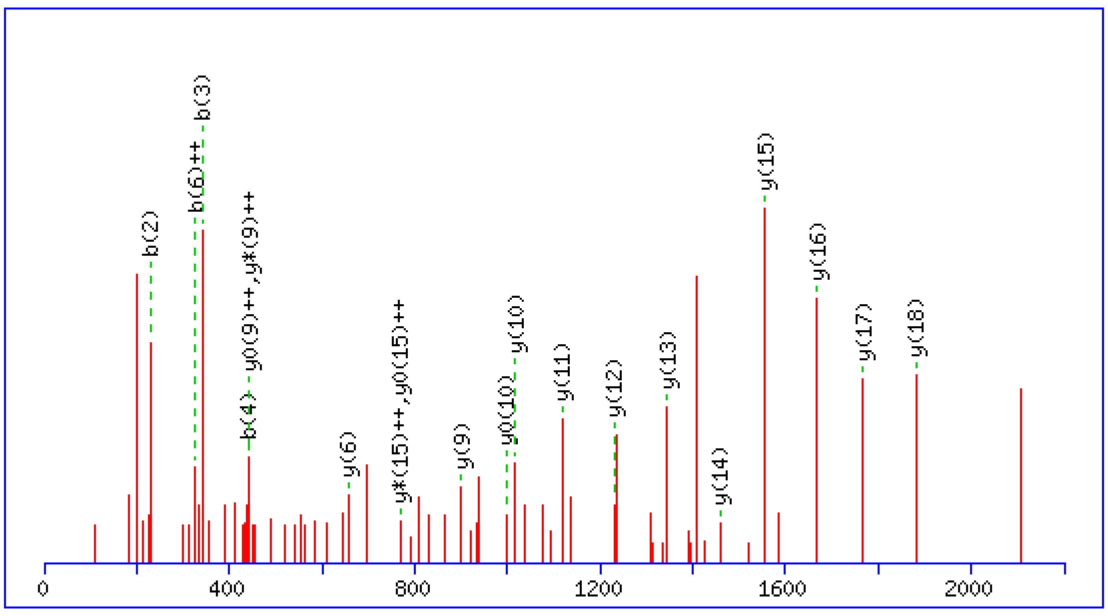
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DILVLPLDLTDTGSHEAATK**
Found in **DHRS7_HUMAN**, Dehydrogenase/reductase SDR family member 7 OS=Homo sapiens GN=DHRS7 PE=1 SV=1

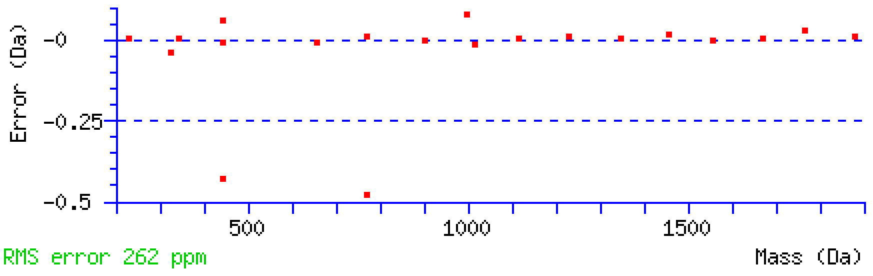
Match to Query 66212: 2108.094612 from(703.705480,3+) rtinseconds(3502) index(51353)
Title: Locus:1.1.1.2656.25
Data file 2011-11-10 - TFD - EP 4-4.mgf

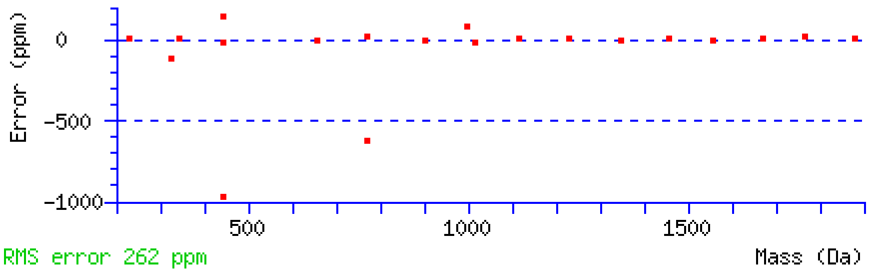
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2108.100113
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 67   Expect: 1.3e-006
Matches : 20/188 fragment ions using 33 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.034219	58.520748	98.023654	49.515465	D							20
2	**229.118283**	115.062779	211.107718	106.057497	I	1994.080450	997.543863	1977.053901	989.030589	1976.069885	988.538581	19
3	**342.202347**	171.604811	324.191782	162.599529	L	***1880.996386***	941.001831	1863.969837	932.488557	1862.985821	931.996549	18
4	**441.270761**	221.139018	423.260196	212.133736	V	***1767.912322***	884.459799	1750.885773	875.946525	1749.901757	875.454517	17
5	554.354825	277.681051	536.344260	268.675768	L	***1668.843908***	834.925592	1651.817359	826.412318	1650.833343	825.920310	16
6	651.407589	326.207433	633.397024	317.202150	P	***1555.759844***	778.383560	1538.733295	769.870286	1537.749279	769.378278	15
7	764.491653	382.749465	746.481088	373.744182	L	***1458.707080***	729.857178	1441.680531	721.343904	1440.696515	720.851896	14
8	879.518596	440.262936	861.508031	431.257654	D	***1345.623016***	673.315146	1328.596467	664.801872	1327.612451	664.309864	13
9	992.602660	496.804968	974.592095	487.799686	L	***1230.596073***	615.801675	1213.569524	607.288400	1212.585508	606.796392	12
10	1093.650339	547.328808	1075.639774	538.323525	T	***1117.512009***	559.259643	1100.485460	550.746368	1099.501444	550.254360	11
11	1208.677282	604.842279	1190.666717	595.836997	D	***1016.464330***	508.735803	999.437781	500.222529	998.453765	499.730521	10
12	1309.724961	655.366119	1291.714396	646.360836	T	***901.437387***	451.222332	884.410838	442.709057	883.426822	442.217049	9
13	1366.746425	683.876851	1348.735860	674.871568	G	800.389708	400.698492	783.363159	392.185218	782.379143	391.693210	8
14	1453.778453	727.392865	1435.767888	718.387582	S	743.368244	372.187760	726.341695	363.674486	725.357679	363.182478	7
15	1590.837365	795.922321	1572.826800	786.917038	H	***656.336216***	328.671746	639.309667	320.158472	638.325651	319.666464	6
16	1719.879958	860.443617	1701.869393	851.438335	E	519.277304	260.142290	502.250755	251.629016	501.266739	251.137008	5
17	1790.917072	895.962174	1772.906507	886.956892	A	390.234711	195.620994	373.208162	187.107719	372.224146	186.615711	4
18	1861.954186	931.480731	1843.943621	922.475449	A	319.197597	160.102437	302.171048	151.589162	301.187032	151.097154	3
19	1963.001865	982.004571	1944.991300	972.999288	T	248.160483	124.583880	231.133934	116.070605	230.149918	115.578597	2
20					K	147.112804	74.060040	130.086255	65.546766			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
67.3	2108.100113	-0.005501	DILVLPLDLTDTGSHEAATK
4.4	2108.090210	0.004402	LAKQVGYENAGTVEFLVDR
1.7	2108.076294	0.018318	HSESFPSVNSRPNVILPGR

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

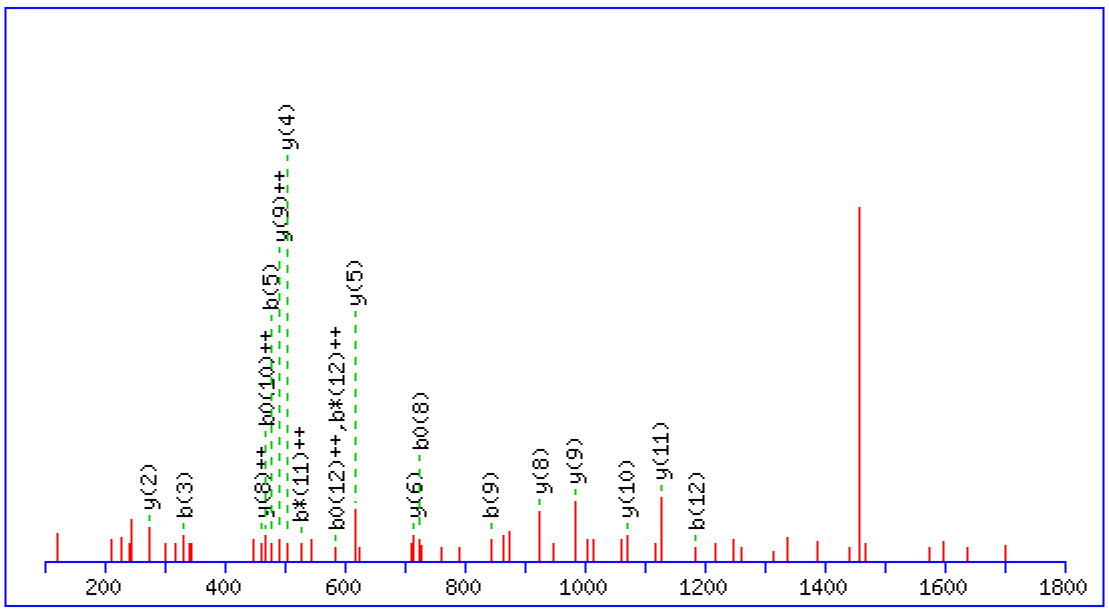
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FGQGSGPIVLDDVR**
Found in **DMBT1_HUMAN**, Deleted in malignant brain tumors 1 protein OS=Homo sapiens GN=DMBT1 PE=1 SV=2

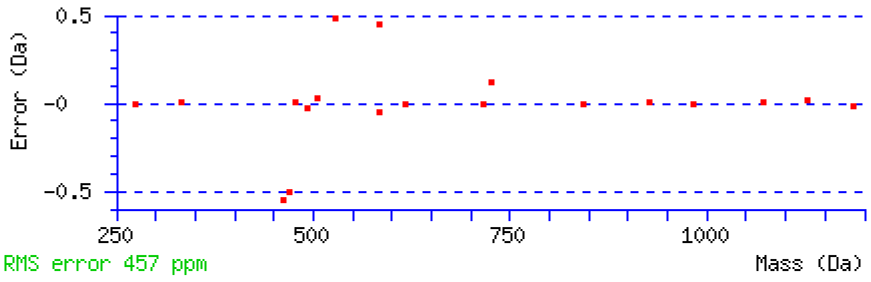
Match to Query 43190: 1458.738388 from(730.376470,2+) rtinseconds(2687) index(34751)
Title: Locus:1.1.1.2446.42
Data file 2011-11-10 - TFD - EP 3-1.mgf

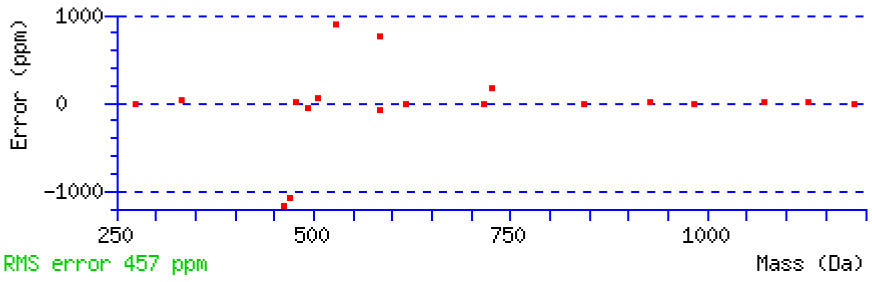
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1458.746719
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 30   Expect: 0.0032
Matches : 19/140 fragment ions using 51 most intense peaks    (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.075690	74.541483					F							14
2	205.097154	103.052215					G	1312.685556	656.846416	1295.659007	648.333142	1294.674991	647.841134	13
3	**333.155732**	167.081504	316.129183	158.568230			Q	1255.664092	628.335684	1238.637543	619.822410	1237.653527	619.330402	12
4	390.177196	195.592236	373.150647	187.078961			G	***1127.605514***	564.306395	1110.578965	555.793121	1109.594949	555.301113	11
5	**477.209224**	239.108250	460.182675	230.594976	459.198659	230.102968	S	***1070.584050***	535.795663	1053.557501	527.282389	1052.573485	526.790381	10
6	534.230688	267.618982	517.204139	259.105708	516.220123	258.613700	G	***983.552022***	492.279649	966.525473	483.766375	965.541457	483.274367	9
7	631.283452	316.145364	614.256903	307.632090	613.272887	307.140082	P	***926.530558***	463.768917	909.504009	455.255643	908.519993	454.763635	8
8	744.367516	372.687396	727.340967	364.174122	726.356951	363.682114	I	829.477794	415.242535	812.451245	406.729261	811.467229	406.237253	7
9	**843.435930**	422.221603	826.409381	413.708329	825.425365	413.216321	V	***716.393730***	358.700503	699.367181	350.187229	698.383165	349.695221	6
10	956.519994	478.763635	939.493445	470.250361	938.509429	469.758353	L	***617.325316***	309.166296	600.298767	300.653022	599.314751	300.161014	5
11	1071.546937	536.277107	1054.520388	527.763832	1053.536372	527.271824	D	***504.241252***	252.624264	487.214703	244.110990	486.230687	243.618982	4
12	**1186.573880**	593.790578	1169.547331	585.277304	1168.563315	584.785296	D	389.214309	195.110793	372.187760	186.597518	371.203744	186.105510	3
13	1285.642294	643.324785	1268.615745	634.811511	1267.631729	634.319503	V	***274.187366***	137.597321	257.160817	129.084047			2
14							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.4	1458.746719	-0.008331	FGQGSGPIVLDDVR
3.7	1458.746674	-0.008286	DPEFNPNLIRTK

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

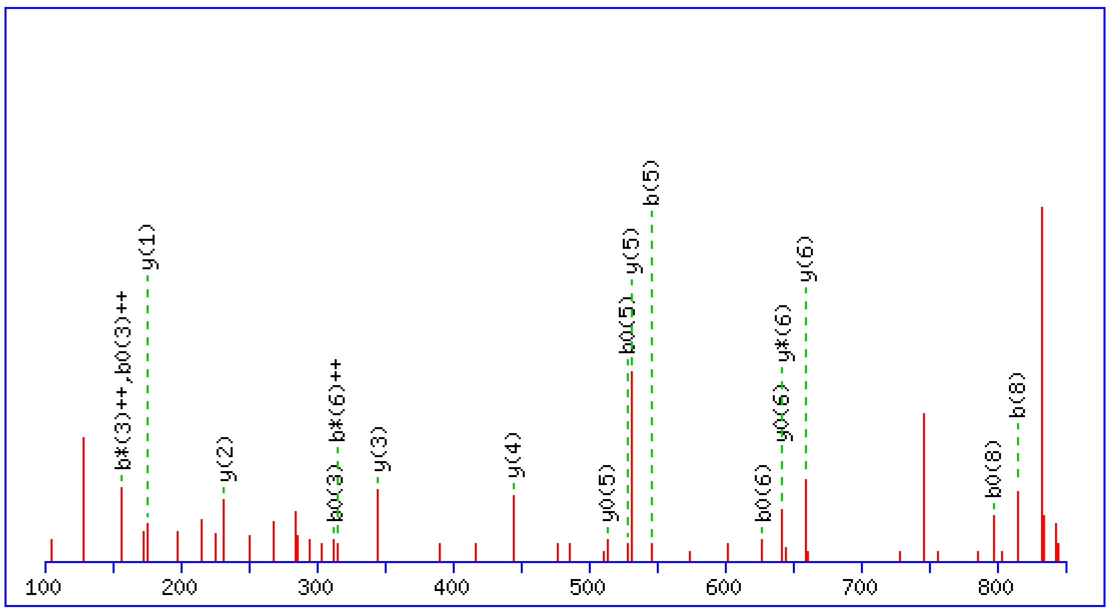
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NDTKSVLGR**
Found in **DNS2B_HUMAN**, Deoxyribonuclease-2-beta OS=Homo sapiens GN=DNASE2B PE=2 SV=1

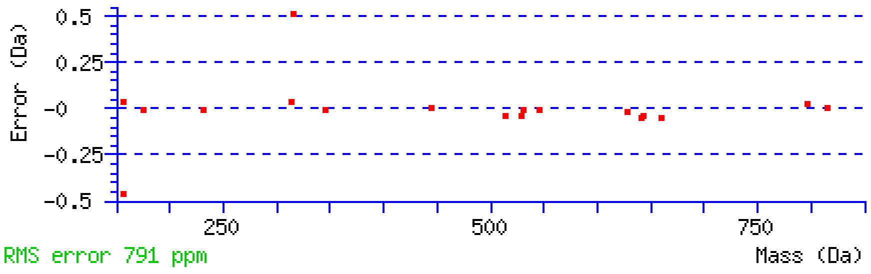
Match to Query 246806: 988.532128 from(495.273340,2+) rtinseconds(2246) index(267274)
Title: Locus:1.1.1.1305.13
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●

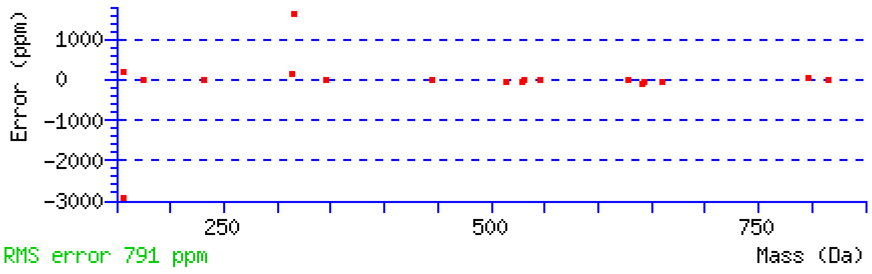


Monoisotopic mass of neutral peptide Mr(calc): 988.530151
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 37 **Expect:** 0.0033
Matches : 18/86 fragment ions using 32 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			**N**							9
2	230.077146	115.542211	213.050597	107.028937	212.066581	106.536928	**D**	875.494507	438.250892	858.467958	429.737617	857.483942	429.245609	8
3	331.124825	166.066050	314.098276	157.552776	313.114260	157.060768	**T**	760.467564	380.737420	743.441015	372.224146	742.456999	371.732138	7
4	459.219788	230.113532	442.193239	221.600258	441.209223	221.108250	**K**	***659.419885***	330.213581	642.393336	321.700306	641.409320	321.208298	6
5	**546.251816**	273.629546	529.225267	265.116272	528.241251	264.624264	**S**	***531.324922***	266.166099	514.298373	257.652825	513.314357	257.160817	5
6	645.320230	323.163753	628.293681	314.650479	627.309665	314.158471	**V**	***444.292894***	222.650085	427.266345	214.136810			4
7	758.404294	379.705785	741.377745	371.192511	740.393729	370.700503	**L**	***345.224480***	173.115878	328.197931	164.602603			3
8	**815.425758**	408.216517	798.399209	399.703243	797.415193	399.211235	**G**	***232.140416***	116.573846	215.113867	108.060571			2
9							**R**	***175.118952***	88.063114	158.092403	79.549839			1



RMS error 791 ppm



RMS error 791 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.4	988.530151	0.001977	NDTKSVLGR
26.9	988.523621	0.008507	CALVSRQR
11.7	988.523621	0.008507	GCLIRNTR
11.5	988.530151	0.001977	SSVAAGGQKGK
7.2	988.530151	0.001977	QTDLKATGR
6.9	988.530151	0.001977	NTVTQALSR
6.1	988.541382	-0.009254	VSGRPSSRK
5.5	988.530136	0.001992	TENQTIKR
5.3	988.530121	0.002007	SEISELRR
4.5	988.523621	0.008507	RAICVNTR

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

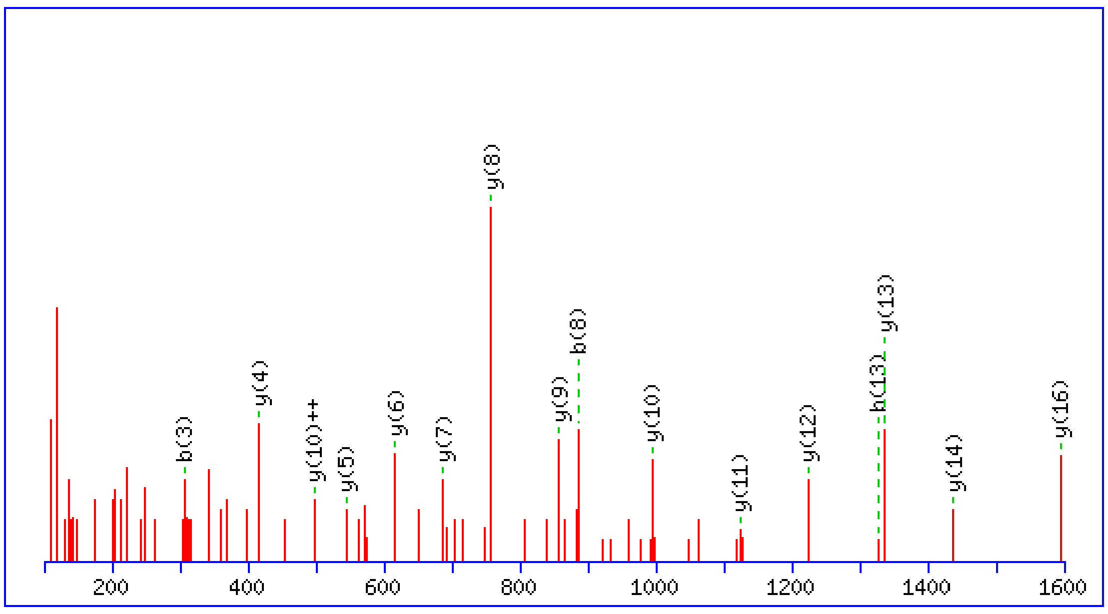
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FGTVLTEHVAAAELGAR**
Found in **RCL_HUMAN**, Deoxyribonucleoside 5'-monophosphate N-glycosidase OS=Homo sapiens GN=RCL PE=1 SV=1

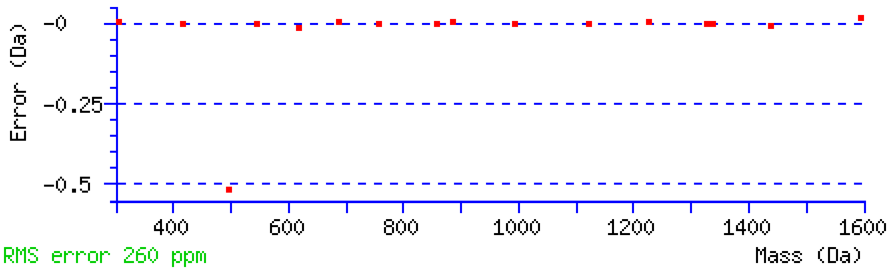
Match to Query 52996: 1740.907752 from(581.309860,3+) rtinseconds(2723) index(34965)
Title: Locus:1.1.1.2357.26
Data file 2011-11-14 - TFD - EP 8-5.mgf

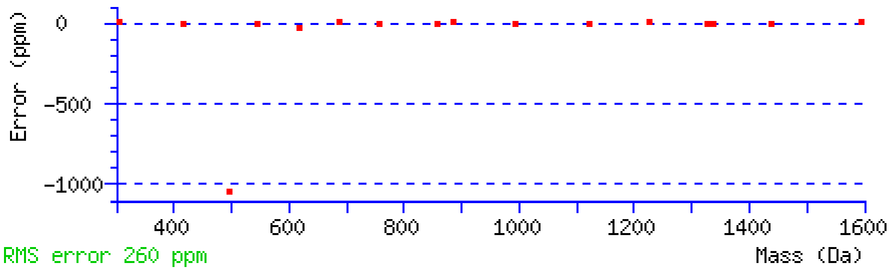
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1740.915878
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 87 **Expect:** 2.1e-008
Matches : 16/148 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.075690	74.541483			F							17
2	205.097154	103.052215			G	***1594.854748***	797.931012	1577.828199	789.417737	1576.844183	788.925729	16
3	**306.144833**	153.576055	288.134268	144.570772	T	1537.833284	769.420280	1520.806735	760.907005	1519.822719	760.414997	15
4	405.213247	203.110262	387.202682	194.104979	V	***1436.785605***	718.896440	1419.759056	710.383166	1418.775040	709.891158	14
5	518.297311	259.652294	500.286746	250.647011	L	***1337.717191***	669.362233	1320.690642	660.848959	1319.706626	660.356951	13
6	619.344990	310.176133	601.334425	301.170851	T	***1224.633127***	612.820201	1207.606578	604.306927	1206.622562	603.814919	12
7	748.387583	374.697430	730.377018	365.692147	E	***1123.585448***	562.296362	1106.558899	553.783087	1105.574883	553.291079	11
8	**885.446495**	443.226886	867.435930	434.221603	H	***994.542855***	497.775065	977.516306	489.261791	976.532290	488.769783	10
9	984.514909	492.761093	966.504344	483.755810	V	***857.483943***	429.245609	840.457394	420.732335	839.473378	420.240327	9
10	1055.552023	528.279650	1037.541458	519.274367	A	***758.415529***	379.711402	741.388980	371.198128	740.404964	370.706120	8
11	1126.589137	563.798206	1108.578572	554.792924	A	***687.378415***	344.192845	670.351866	335.679571	669.367850	335.187563	7
12	1197.626251	599.316763	1179.615686	590.311481	A	***616.341301***	308.674288	599.314752	300.161014	598.330736	299.669006	6
13	**1326.668844**	663.838060	1308.658279	654.832778	E	***545.304187***	273.155732	528.277638	264.642457	527.293622	264.150449	5
14	1439.752908	720.380092	1421.742343	711.374809	L	***416.261594***	208.634435	399.235045	200.121160			4
15	1496.774372	748.890824	1478.763807	739.885541	G	303.177530	152.092403	286.150981	143.579128			3
16	1567.811486	784.409381	1549.800921	775.404098	A	246.156066	123.581671	229.129517	115.068396			2
17					R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
87.0	1740.915878	-0.008126	FGTVLTEHVAAAELGAR

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

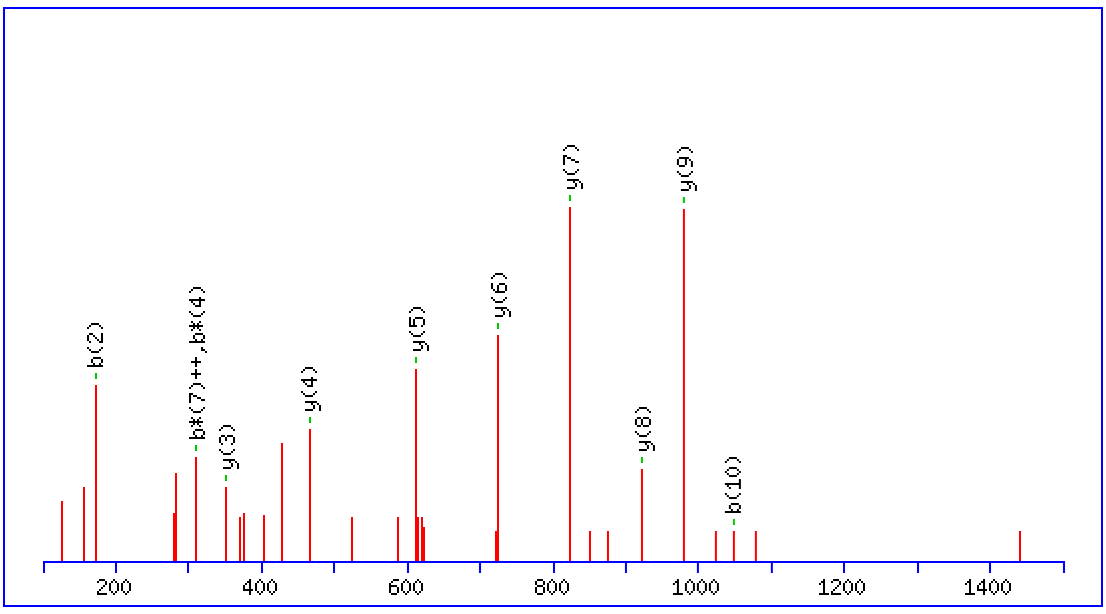
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GNVGVVLFNFGK**
Found in **DUT_HUMAN**, Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial OS=Homo sapiens GN=DUT PE=1 SV=4

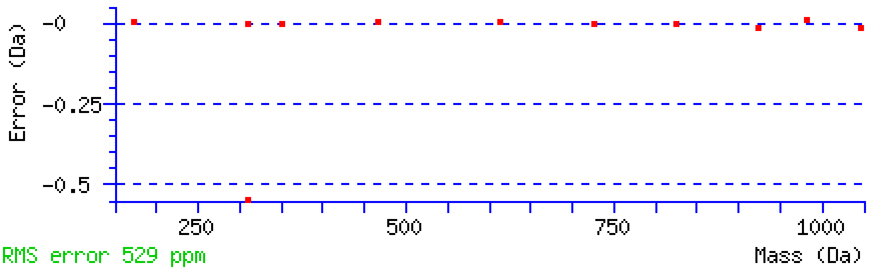
Match to Query 31769: 1249.681068 from(625.847810,2+) rtinseconds(3426) index(45171)
Title: Locus:1.1.1.2594.14
Data file 2011-11-13 - TFD - EP 7-6.mgf

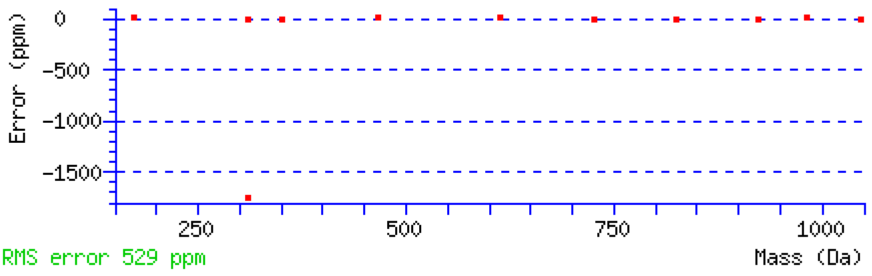
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1249.681931
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 75  Expect: 2.6e-007
Matches : 11/86 fragment ions using 10 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	58.028740	29.518008			G					12
2	172.071667	86.539471	155.045118	78.026197	N	1193.667720	597.337498	1176.641171	588.824224	11
3	271.140081	136.073679	254.113532	127.560404	V	1079.624793	540.316035	1062.598244	531.802760	10
4	328.161545	164.584410	311.134996	156.071136	G	***980.556379***	490.781828	963.529830	482.268553	9
5	427.229959	214.118618	410.203410	205.605343	V	***923.534915***	462.271096	906.508366	453.757821	8
6	526.298373	263.652825	509.271824	255.139550	V	***824.466501***	412.736889	807.439952	404.223614	7
7	639.382437	320.194857	622.355888	311.681582	L	***725.398087***	363.202682	708.371538	354.689407	6
8	786.450851	393.729064	769.424302	385.215789	F	***612.314023***	306.660650	595.287474	298.147375	5
9	900.493778	450.750527	883.467229	442.237253	N	***465.245609***	233.126442	448.219060	224.613168	4
10	1047.562192	524.284734	1030.535643	515.771460	F	***351.202682***	176.104979	334.176133	167.591704	3
11	1104.583656	552.795466	1087.557107	544.282192	G	204.134268	102.570772	187.107719	94.057497	2
12					K	147.112804	74.060040	130.086255	65.546765	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
74.6	1249.681931	-0.000863	GNVGVVLFNFGK
6.9	1249.677902	0.003166	GPPGVRGDPGTLK
0.9	1249.689087	-0.008019	NPSKPPDLRAR

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

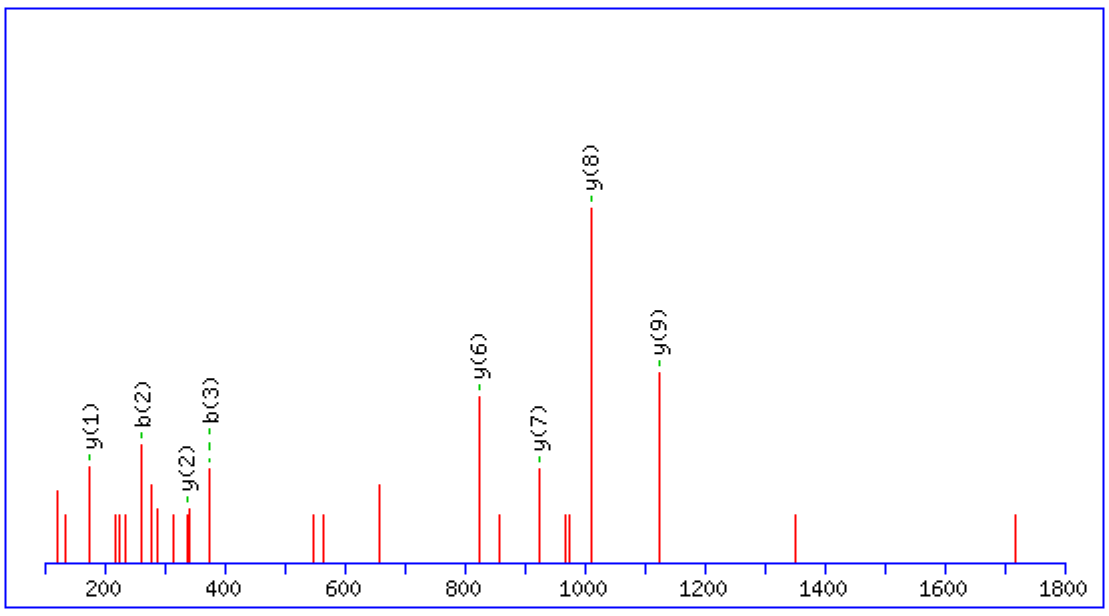
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NFLSTPQFLYR**
Found in **DERL1_HUMAN**, Derlin-1 OS=Homo sapiens GN=DERL1 PE=1 SV=1

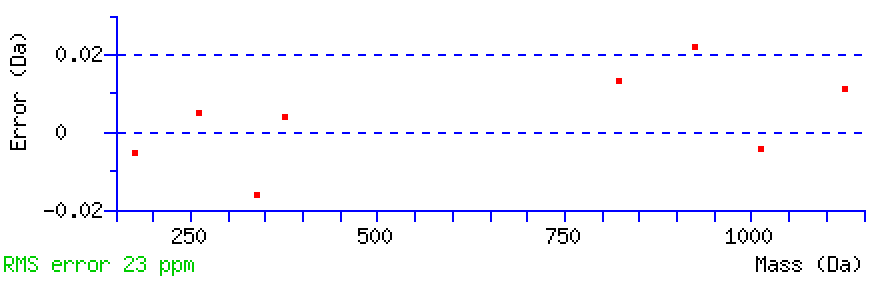
Match to Query 40147: 1384.720088 from(693.367320,2+) rtinseconds(3352) index(44378)
Title: Locus:1.1.1.2548.39
Data file 2011-11-14 - TFD - EP 8-6.mgf

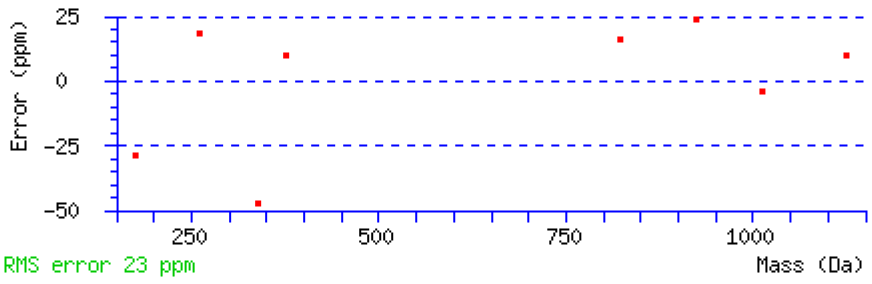
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1384.713928
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.0067
Matches : 8/102 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			N							11
2	**262.118617**	131.562946	245.092068	123.049672			F	1271.678286	636.342781	1254.651737	627.829507	1253.667721	627.337499	10
3	**375.202681**	188.104978	358.176132	179.591704			L	*1124.609872*	562.808574	1107.583323	554.295300	1106.599307	553.803292	9
4	462.234709	231.620993	445.208160	223.107718	444.224144	222.615710	S	*1011.525808*	506.266542	994.499259	497.753268	993.515243	497.261260	8
5	563.282388	282.144832	546.255839	273.631558	545.271823	273.139550	T	*924.493780*	462.750528	907.467231	454.237254	906.483215	453.745246	7
6	660.335152	330.671214	643.308603	322.157940	642.324587	321.665932	P	*823.446101*	412.226689	806.419552	403.713414			6
7	788.393730	394.700503	771.367181	386.187229	770.383165	385.695221	Q	726.393337	363.700307	709.366788	355.187032			5
8	935.462144	468.234710	918.435595	459.721436	917.451579	459.229428	F	598.334759	299.671018	581.308210	291.157743			4
9	1048.546208	524.776742	1031.519659	516.263468	1030.535643	515.771459	L	451.266345	226.136810	434.239796	217.623536			3
10	1211.609537	606.308407	1194.582988	597.795132	1193.598972	597.303124	Y	*338.182281*	169.594778	321.155732	161.081504			2
11							R	*175.118952*	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.7	1384.713928	0.006160	NFLSTPQFLYR
21.0	1384.709900	0.010188	ASSRSVEFFLSR
18.3	1384.721130	-0.001042	VHAEAFSRPLSR
18.2	1384.713272	0.006816	CSLPVPREPLR
18.2	1384.732361	-0.012273	SSSLRPGPSRWR
10.8	1384.713928	0.006160	RPYNFFGILDK
9.8	1384.724487	-0.004399	MSRSPLNPSQLR
8.7	1384.713272	0.006816	MARTAPVEPPLR
8.7	1384.713272	0.006816	MARTAPVEPPLR
7.5	1384.713272	0.006816	MARTAPVEPPLR

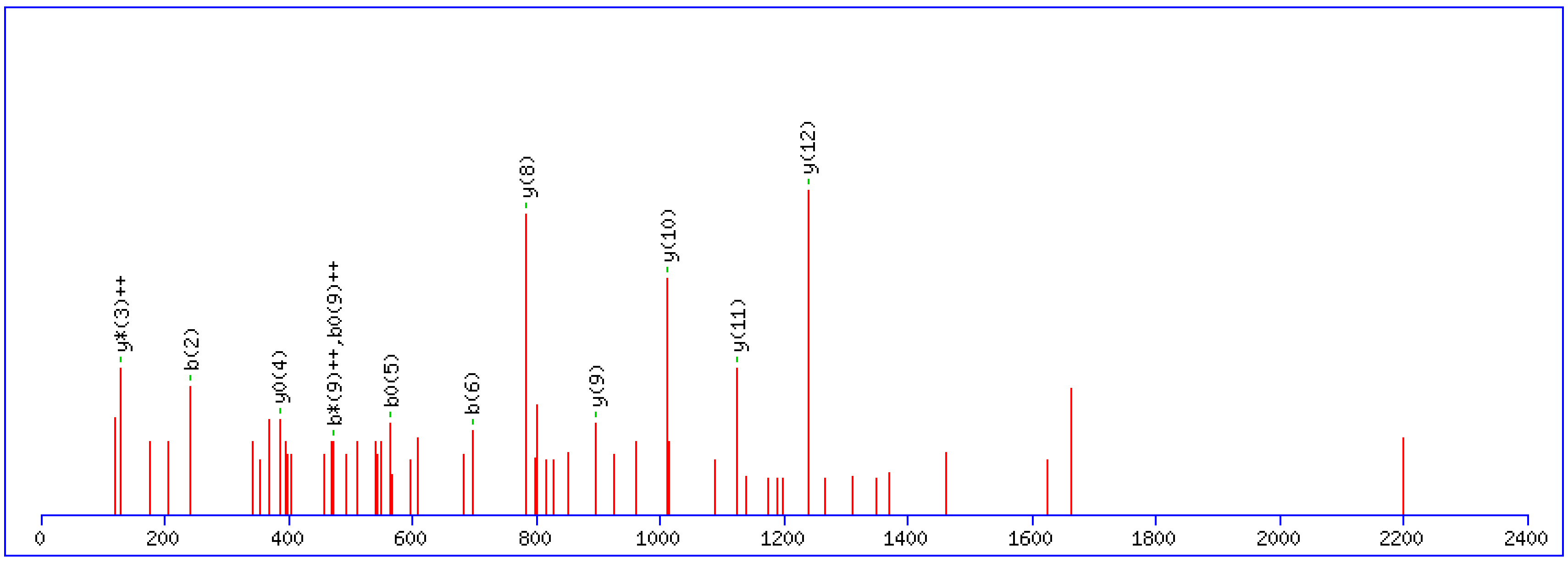
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IQLLDLPGIIEGAK**
Found in **DRG1_HUMAN**, Developmentally-regulated GTP-binding protein 1 OS=Homo sapiens GN=DRG1 PE=1 SV=1

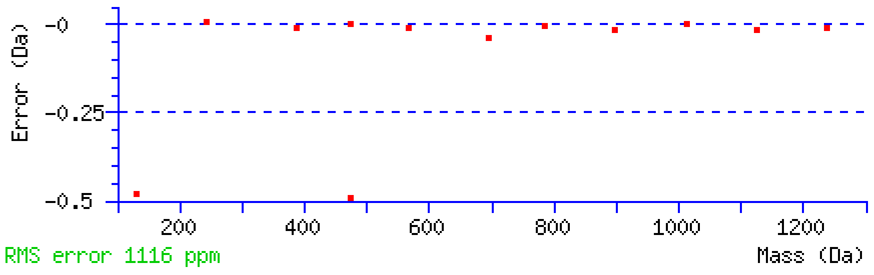
Match to Query 41655: 1478.860148 from(740.437350,2+) rtinseconds(3958) index(59487)
Title: Locus:1.1.1.1879.29
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 2.mgf

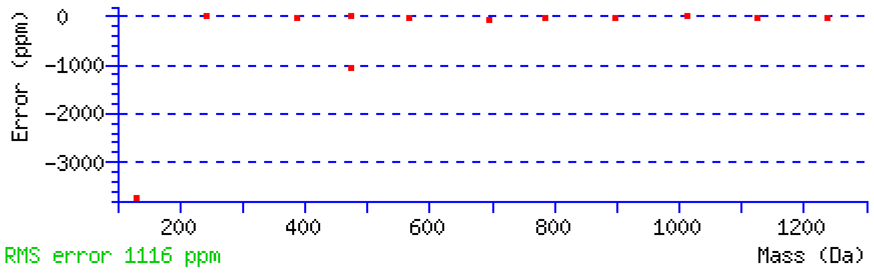
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1478.870804
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 38 **Expect:** 0.00066
Matches : 12/140 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					I							14
2	**242.149918**	121.578597	225.123369	113.065323			Q	1366.794044	683.900660	1349.767495	675.387386	1348.783479	674.895378	13
3	355.233982	178.120629	338.207433	169.607355			L	***1238.735466***	619.871371	1221.708917	611.358096	1220.724901	610.866088	12
4	468.318046	234.662661	451.291497	226.149387			L	***1125.651402***	563.329339	1108.624853	554.816064	1107.640837	554.324056	11
5	583.344989	292.176133	566.318440	283.662858	565.334424	283.170850	D	***1012.567338***	506.787307	995.540789	498.274032	994.556773	497.782024	10
6	**696.429053**	348.718165	679.402504	340.204890	678.418488	339.712882	L	***897.540395***	449.273835	880.513846	440.760561	879.529830	440.268553	9
7	793.481817	397.244547	776.455268	388.731272	775.471252	388.239264	P	***784.456331***	392.731803	767.429782	384.218529	766.445766	383.726521	8
8	850.503281	425.755279	833.476732	417.242004	832.492716	416.749996	G	687.403567	344.205421	670.377018	335.692147	669.393002	335.200139	7
9	963.587345	482.297311	946.560796	473.784036	945.576780	473.292028	I	630.382103	315.694689	613.355554	307.181415	612.371538	306.689407	6
10	1076.671409	538.839343	1059.644860	530.326068	1058.660844	529.834060	I	517.298039	259.152657	500.271490	250.639383	499.287474	250.147375	5
11	1205.714002	603.360639	1188.687453	594.847365	1187.703437	594.355356	E	404.213975	202.610625	387.187426	194.097351	386.203410	193.605343	4
12	1262.735466	631.871371	1245.708917	623.358096	1244.724901	622.866088	G	275.171382	138.089329	258.144833	129.576054			3
13	1333.772580	667.389928	1316.746031	658.876653	1315.762015	658.384645	A	218.149918	109.578597	201.123369	101.065322			2
14							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.6	1478.870804	-0.010656	IQLLDLPGIIEGAK

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

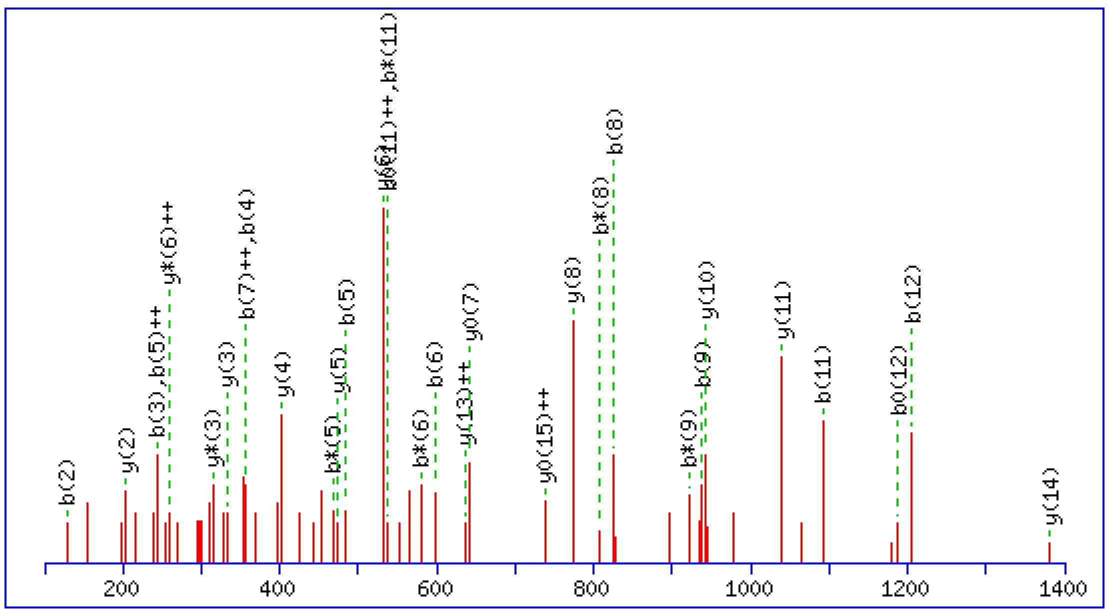
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GANIQLLDLPGIIEGAAQGK**
Found in **DRG2_HUMAN**, Developmentally-regulated GTP-binding protein 2 OS=Homo sapiens GN=DRG2 PE=1 SV=1

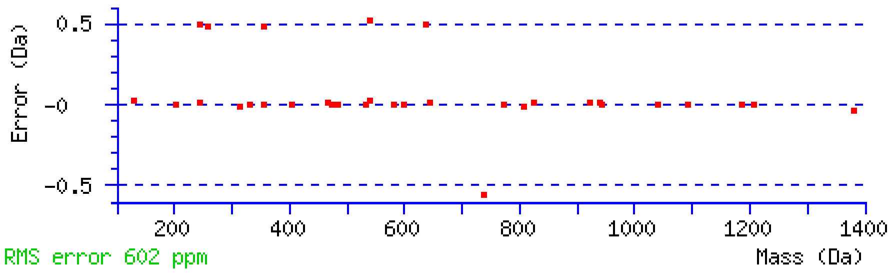
Match to Query 64803: 1977.093102 from(660.038310,3+) rtinseconds(4374) index(66801)
Title: Locus:1.1.1.3040.18
Data file 2011-11-14 - TFD - EP 8-4.mgf

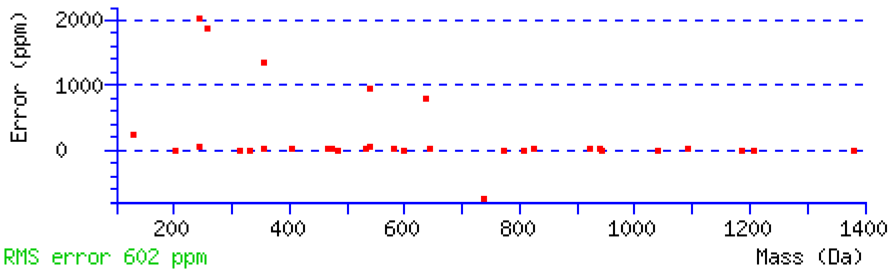
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1977.089462
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 65  Expect: 1.3e-006
Matches : 32/198 fragment ions using 46 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							20
2	***129.065854***	65.036565					A	1921.075305	961.041290	1904.048756	952.528016	1903.064740	952.036008	19
3	***243.108781***	122.058029	226.082232	113.544754			N	1850.038191	925.522733	1833.011642	917.009459	1832.027626	916.517451	18
4	***356.192845***	178.600061	339.166296	170.086786			I	1735.995264	868.501270	1718.968715	859.987995	1717.984699	859.495987	17
5	***484.251423***	242.629350	467.224874	234.116075			Q	1622.911200	811.959238	1605.884651	803.445963	1604.900635	802.953955	16
6	***597.335487***	299.171382	580.308938	290.658107			L	1494.852622	747.929949	1477.826073	739.416674	1476.842057	738.924666	15
7	710.419551	355.713414	693.393002	347.200139			L	***1381.768558***	691.387917	1364.742009	682.874642	1363.757993	682.382634	14
8	***825.446494***	413.226885	808.419945	404.713611	807.435929	404.221603	D	1268.684494	634.845885	1251.657945	626.332610	1250.673929	625.840602	13
9	***938.530558***	469.768917	921.504009	461.255643	920.519993	460.763635	L	1153.657551	577.332413	1136.631002	568.819139	1135.646986	568.327131	12
10	1035.583322	518.295299	1018.556773	509.782024	1017.572757	509.290016	P	***1040.573487***	520.790381	1023.546938	512.277107	1022.562922	511.785099	11
11	***1092.604786***	546.806031	1075.578237	538.292757	1074.594221	537.800748	G	***943.520723***	472.263999	926.494174	463.750725	925.510158	463.258717	10
12	***1205.688850***	603.348063	1188.662301	594.834788	1187.678285	594.342780	I	886.499259	443.753267	869.472710	435.239993	868.488694	434.747985	9
13	1318.772914	659.890095	1301.746365	651.376820	1300.762349	650.884812	I	***773.415195***	387.211235	756.388646	378.697961	755.404630	378.205953	8
14	1447.815507	724.411391	1430.788958	715.898117	1429.804942	715.406109	E	660.331131	330.669203	643.304582	322.155929	642.320566	321.663921	7
15	1504.836971	752.922123	1487.810422	744.408849	1486.826406	743.916841	G	***531.288538***	266.147907	514.261989	257.634633			6
16	1575.874085	788.440680	1558.847536	779.927406	1557.863520	779.435398	A	***474.267074***	237.637175	457.240525	229.123900			5
17	1646.911199	823.959237	1629.884650	815.445963	1628.900634	814.953955	A	***403.229960***	202.118618	386.203411	193.605344			4
18	1774.969777	887.988526	1757.943228	879.475252	1756.959212	878.983244	Q	***332.192846***	166.600061	315.166297	158.086787			3
19	1831.991241	916.499258	1814.964692	907.985984	1813.980676	907.493976	G	***204.134268***	102.570772	187.107719	94.057497			2
20							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
65.3	1977.089462	0.003640	GANIQLLDLPGIIEGAAQGK
6.7	1977.082245	0.010857	YELIADVNKPIIAVFEK

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

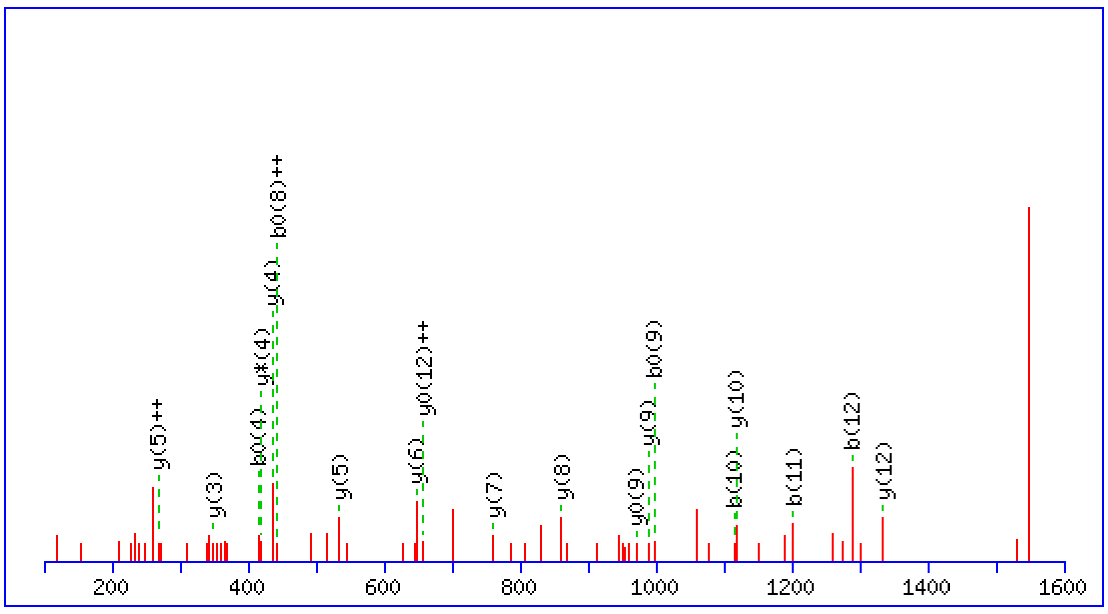
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SESEEEVLLVSSSR**
Found in **NUDT3_HUMAN**, Diphosphoinositol polyphosphate phosphohydrolase 1 OS=Homo sapiens GN=NUDT3 PE=1 SV=1

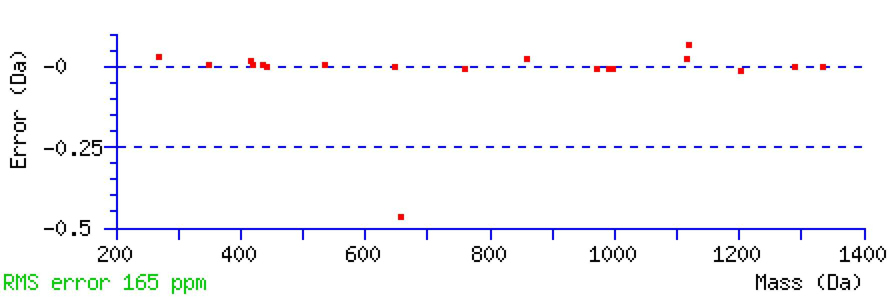
Match to Query 42996: 1549.753748 from(775.884150,2+) rtinseconds(2501) index(29108)
Title: Locus:1.1.1.2220.42
Data file 2011-11-10 - TFD - EP 3-6.mgf

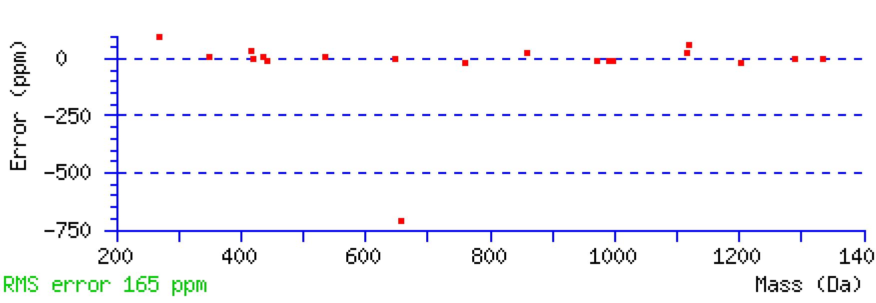
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1549.747116
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 35 **Expect:** 0.0038
Matches : 19/128 fragment ions using 55 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	S							14
2	217.081897	109.044586	199.071332	100.039304	E	1463.722392	732.364834	1446.695843	723.851560	1445.711827	723.359552	13
3	304.113925	152.560600	286.103360	143.555318	S	***1334.679799***	667.843538	1317.653250	659.330263	1316.669234	658.838255	12
4	433.156518	217.081897	415.145953	208.076615	E	1247.647771	624.327524	1230.621222	615.814249	1229.637206	615.322241	11
5	562.199111	281.603194	544.188546	272.597911	E	***1118.605178***	559.806227	1101.578629	551.292953	1100.594613	550.800945	10
6	691.241704	346.124490	673.231139	337.119208	E	***989.562585***	495.284931	972.536036	486.771656	971.552020	486.279648	9
7	790.310118	395.658697	772.299553	386.653415	V	***860.519992***	430.763634	843.493443	422.250360	842.509427	421.758352	8
8	903.394182	452.200729	885.383617	443.195447	L	***761.451578***	381.229427	744.425029	372.716153	743.441013	372.224145	7
9	1016.478246	508.742761	998.467681	499.737479	L	***648.367514***	324.687395	631.340965	316.174121	630.356949	315.682113	6
10	**1115.546660**	558.276968	1097.536095	549.271686	V	***535.283450***	268.145363	518.256901	259.632089	517.272885	259.140081	5
11	**1202.578688**	601.792982	1184.568123	592.787700	S	***436.215036***	218.611156	419.188487	210.097882	418.204471	209.605874	4
12	**1289.610716**	645.308996	1271.600151	636.303714	S	***349.183008***	175.095142	332.156459	166.581868	331.172443	166.089860	3
13	1376.642744	688.825010	1358.632179	679.819728	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
14					R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.9	1549.747116	0.006632	SESEEEVLLVSSSR

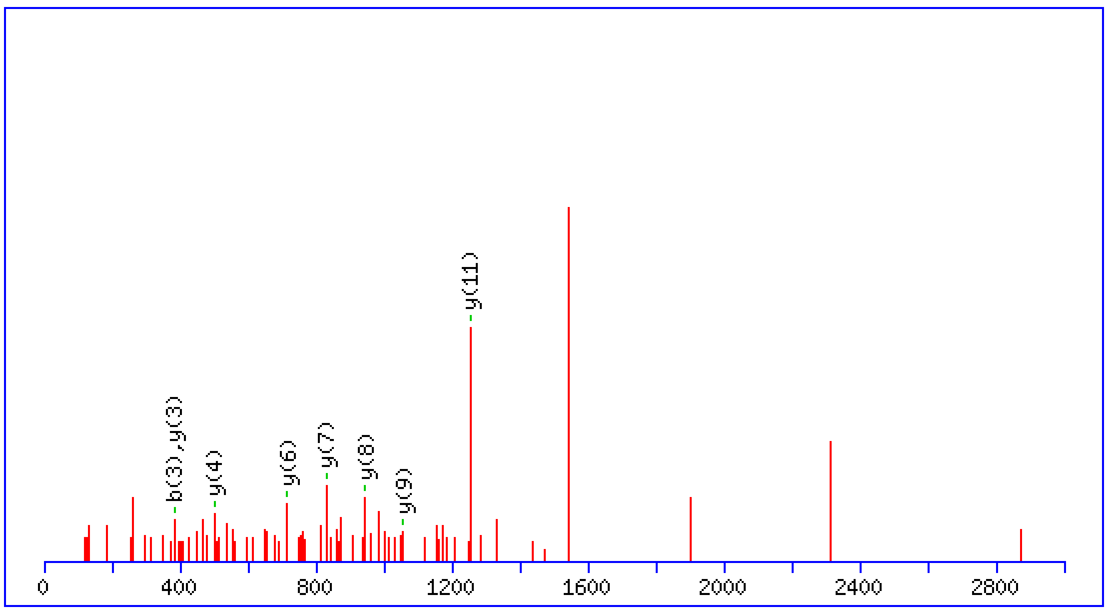
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TWPTIIDTDDLPR**
Found in **DIP2B_HUMAN**, Disco-interacting protein 2 homolog B OS=Homo sapiens GN=DIP2B PE=1 SV=3

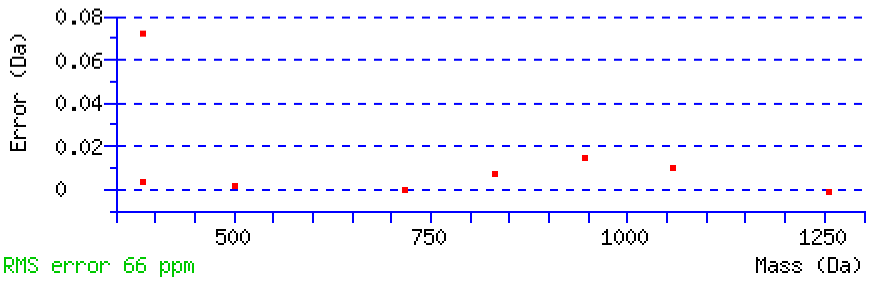
Match to Query 44120: 1541.770728 from(771.892640,2+) rtinseconds(3385) index(45212)
Title: Locus:1.1.1.2833.39
Data file 2011-11-12 - TFD - EP 5-1.mgf

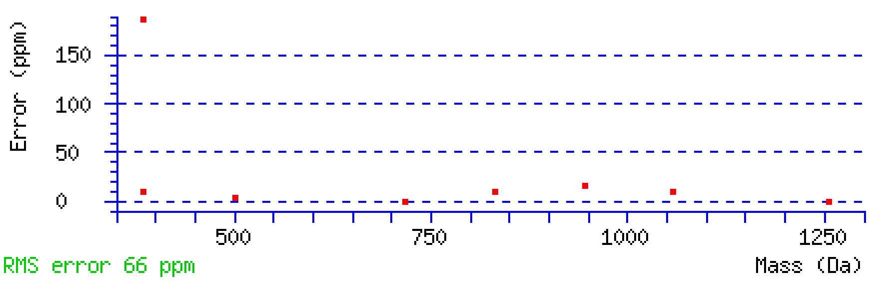
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1541.772583
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.00078
Matches : 8/114 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116	84.044390	42.525833	T							13
2	288.134268	144.570772	270.123703	135.565490	W	1441.732172	721.369724	1424.705623	712.856450	1423.721607	712.364442	12
3	385.187032	193.097154	367.176467	184.091872	P	***1255.652859***	628.330068	1238.626310	619.816793	1237.642294	619.324785	11
4	486.234711	243.620994	468.224146	234.615711	T	1158.600095	579.803686	1141.573546	571.290411	1140.589530	570.798403	10
5	599.318775	300.163026	581.308210	291.157743	I	***1057.552416***	529.279846	1040.525867	520.766572	1039.541851	520.274564	9
6	712.402839	356.705058	694.392274	347.699775	I	***944.468352***	472.737814	927.441803	464.224539	926.457787	463.732531	8
7	827.429782	414.218529	809.419217	405.213247	D	***831.384288***	416.195782	814.357739	407.682507	813.373723	407.190499	7
8	928.477461	464.742369	910.466896	455.737086	T	***716.357345***	358.682311	699.330796	350.169036	698.346780	349.677028	6
9	1043.504404	522.255840	1025.493839	513.250558	D	615.309666	308.158471	598.283117	299.645197	597.299101	299.153189	5
10	1158.531347	579.769312	1140.520782	570.764029	D	***500.282723***	250.644999	483.256174	242.131725	482.272158	241.639717	4
11	1271.615411	636.311344	1253.604846	627.306061	L	***385.255780***	193.131528	368.229231	184.618253			3
12	1368.668175	684.837726	1350.657610	675.832443	P	272.171716	136.589496	255.145167	128.076221			2
13					R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.9	1541.772583	-0.001855	TWPTIIDTDDLPR
1.8	1541.769394	0.001334	LCAGIMITASHNPK
1.6	1541.779755	-0.009027	GNVAKEEVANKPDR

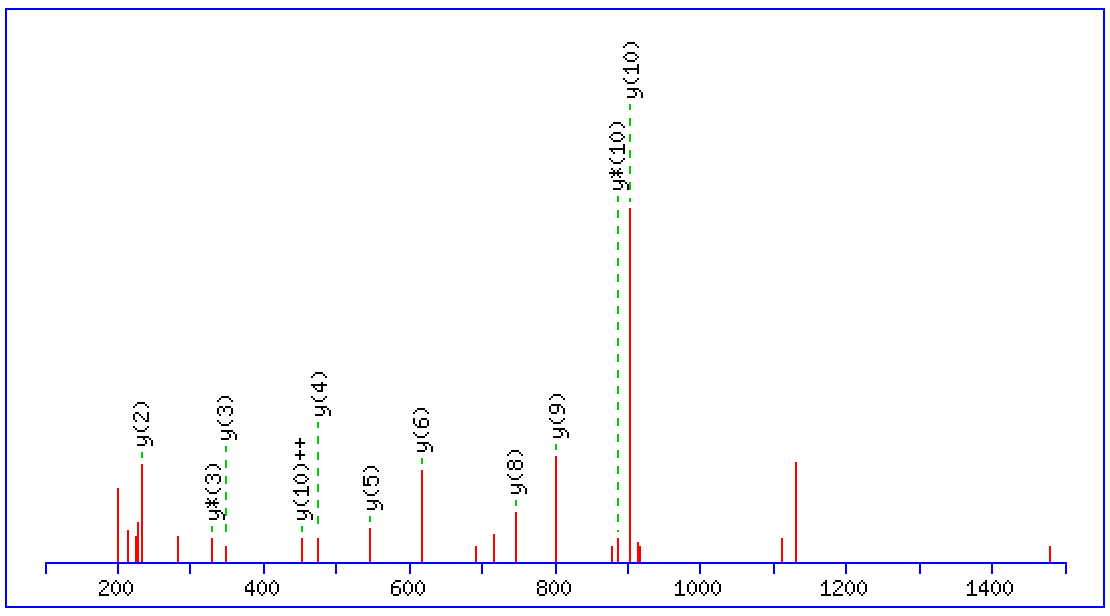
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IITGGAAAQDGR**
Found in **DLG1_HUMAN**, Disks large homolog 1 OS=Homo sapiens GN=DLG1 PE=1 SV=2

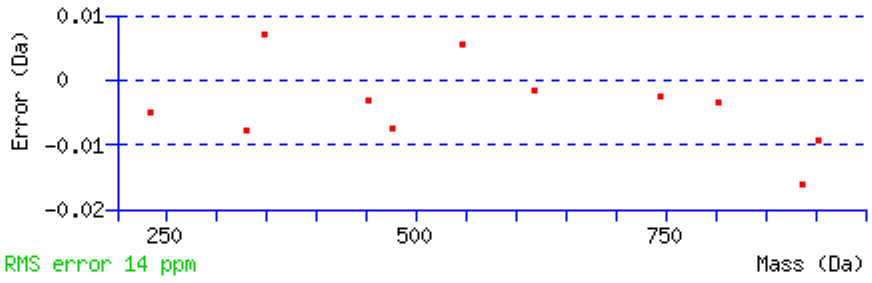
Match to Query 431312: 1128.591348 from(565.302950,2+) rtinseconds(1044) index(329530)
Title: Locus:1.1.1.730.29
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

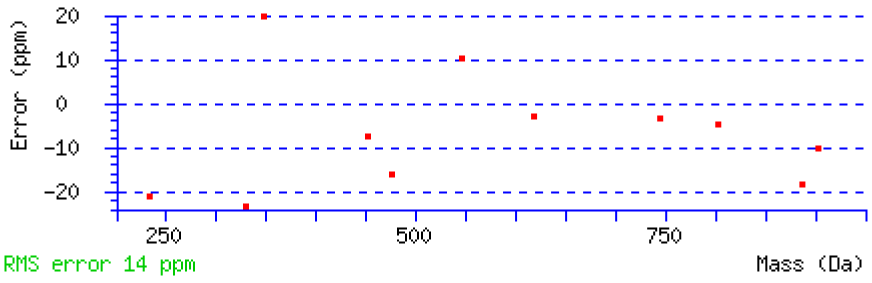
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1128.588730
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 68 **Expect:** 2.7e-006
Matches : 11/108 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					I							12
2	227.175404	114.091340					I	1016.511950	508.759613	999.485401	500.246338	998.501385	499.754330	11
3	328.223083	164.615179			310.212518	155.609897	T	***903.427886***	452.217581	886.401337	443.704306	885.417321	443.212298	10
4	385.244547	193.125911			367.233982	184.120629	G	***802.380207***	401.693741	785.353658	393.180467	784.369642	392.688459	9
5	442.266011	221.636643			424.255446	212.631361	G	***745.358743***	373.183010	728.332194	364.669735	727.348178	364.177727	8
6	513.303125	257.155201			495.292560	248.149918	A	688.337279	344.672278	671.310730	336.159003	670.326714	335.666995	7
7	584.340239	292.673758			566.329674	283.668475	A	***617.300165***	309.153721	600.273616	300.640446	599.289600	300.148438	6
8	655.377353	328.192315			637.366788	319.187032	A	***546.263051***	273.635164	529.236502	265.121889	528.252486	264.629881	5
9	783.435931	392.221604	766.409382	383.708329	765.425366	383.216321	Q	***475.225937***	238.116606	458.199388	229.603332	457.215372	229.111324	4
10	898.462874	449.735075	881.436325	441.221800	880.452309	440.729792	D	***347.167359***	174.087317	330.140810	165.574043	329.156794	165.082035	3
11	955.484338	478.245807	938.457789	469.732532	937.473773	469.240524	G	***232.140416***	116.573846	215.113867	108.060571			2
12							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
67.8	1128.588730	0.002618	IITGGAAAQDGR
11.6	1128.588928	0.002420	LTLFAATFVM
4.1	1128.602631	-0.011283	LIPDPKSESK
2.3	1128.592758	-0.001410	EPVTLGAWTR
1.6	1128.588715	0.002633	IIDERSPQR
1.6	1128.600128	-0.008780	LILMYHPDK
0.8	1128.602631	-0.011283	LPISNEPISK
0.3	1128.596115	-0.004767	ILPDMLQQR

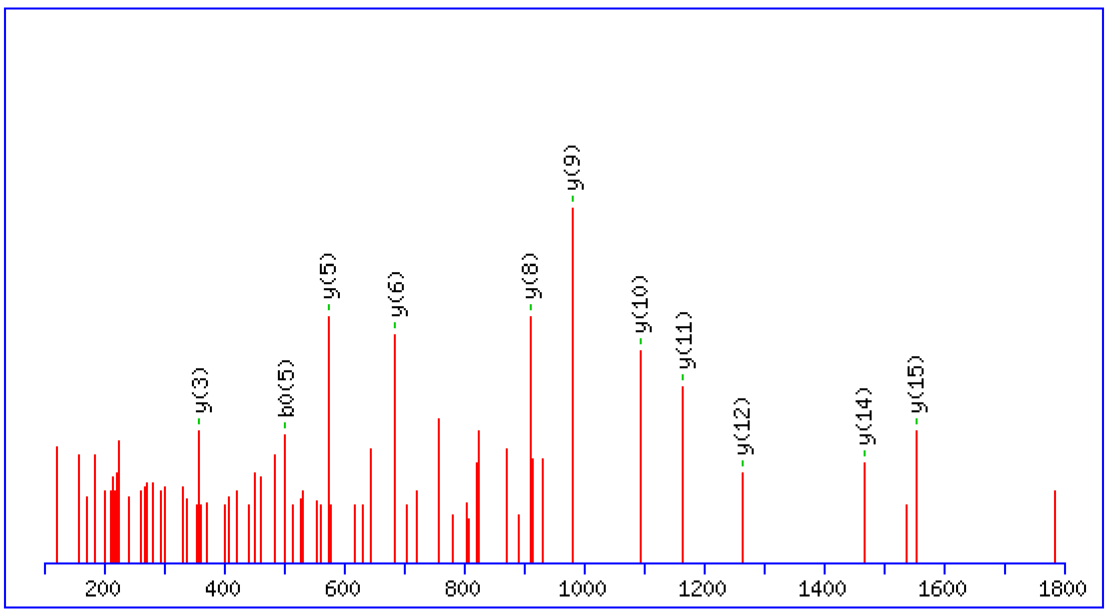
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ETSSDVALASHILTALR**
Found in **DFFA_HUMAN**, DNA fragmentation factor subunit alpha OS=Homo sapiens GN=DFFA PE=1 SV=1

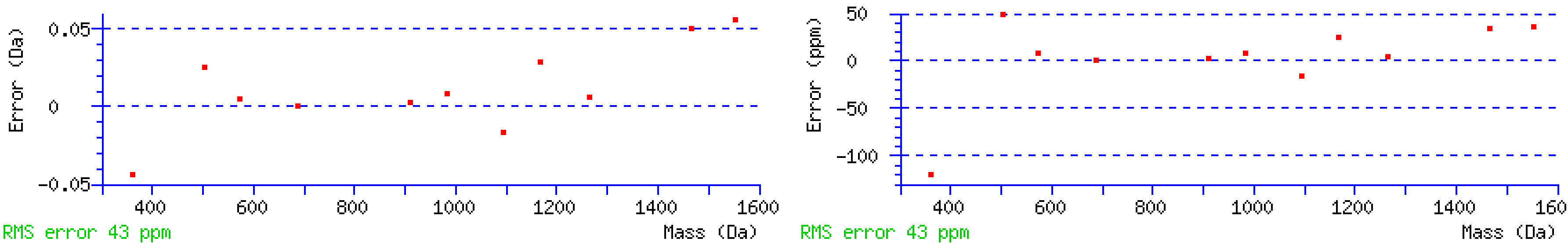
Match to Query 58598: 1782.935772 from(595.319200,3+) rtinseconds(3702) index(54095)
Title: Locus:1.1.1.2820.9
Data file 2011-11-12 - TFD - EP 5-4.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1782.947556
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 82  Expect: 2.6e-008
Matches : 11/154 fragment ions using 14 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572	112.039304	56.523290	E							17
2	231.097548	116.052412	213.086983	107.047130	T	1654.912261	827.959768	1637.885712	819.446494	1636.901696	818.954486	16
3	318.129576	159.568426	300.119011	150.563144	S	***1553.864582***	777.435929	1536.838033	768.922654	1535.854017	768.430646	15
4	405.161604	203.084440	387.151039	194.079157	S	***1466.832554***	733.919915	1449.806005	725.406640	1448.821989	724.914632	14
5	520.188547	260.597912	502.177982	251.592629	D	1379.800526	690.403901	1362.773977	681.890626	1361.789961	681.398618	13
6	619.256961	310.132118	601.246396	301.126836	V	***1264.773583***	632.890429	1247.747034	624.377155	1246.763018	623.885147	12
7	690.294075	345.650675	672.283510	336.645393	A	***1165.705169***	583.356222	1148.678620	574.842948	1147.694604	574.350940	11
8	803.378139	402.192707	785.367574	393.187425	L	***1094.668055***	547.837665	1077.641506	539.324391	1076.657490	538.832383	10
9	874.415253	437.711264	856.404688	428.705982	A	***981.583991***	491.295633	964.557442	482.782359	963.573426	482.290351	9
10	961.447281	481.227278	943.436716	472.221996	S	***910.546877***	455.777076	893.520328	447.263802	892.536312	446.771794	8
11	1098.506193	549.756734	1080.495628	540.751452	H	823.514849	412.261062	806.488300	403.747788	805.504284	403.255780	7
12	1211.590257	606.298766	1193.579692	597.293484	I	***686.455937***	343.731606	669.429388	335.218332	668.445372	334.726324	6
13	1324.674321	662.840798	1306.663756	653.835516	L	***573.371873***	287.189574	556.345324	278.676300	555.361308	278.184292	5
14	1425.722000	713.364638	1407.711435	704.359355	T	460.287809	230.647542	443.261260	222.134268	442.277244	221.642260	4
15	1496.759114	748.883195	1478.748549	739.877912	A	***359.240130***	180.123703	342.213581	171.610428			3
16	1609.843178	805.425227	1591.832613	796.419944	L	288.203016	144.605146	271.176467	136.091871			2
17					R	175.118952	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
81.7	1782.947556	-0.011784	ETSSDVALASHILTALR
0.8	1782.943726	-0.007954	IPMTNSPLLDPLPSLK
0.6	1782.943726	-0.007954	IPMTNSPLLDPLPSLK

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

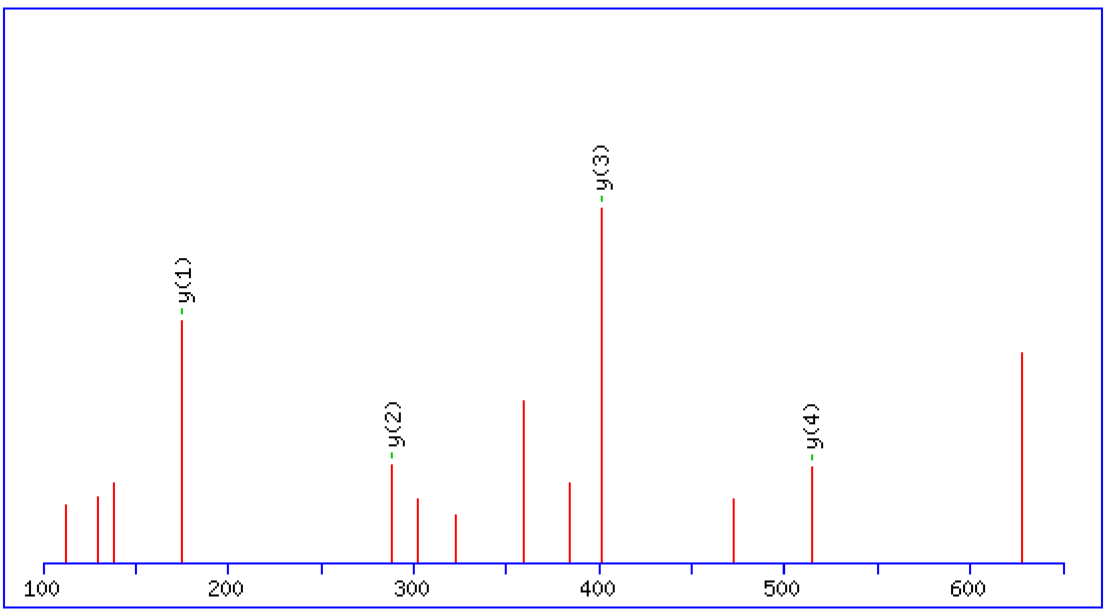
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GGARLPLR**
Found in **B3GA2_HUMAN**, Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase 2 OS=Homo sapiens GN=B3GAT2 PE=1 SV=2

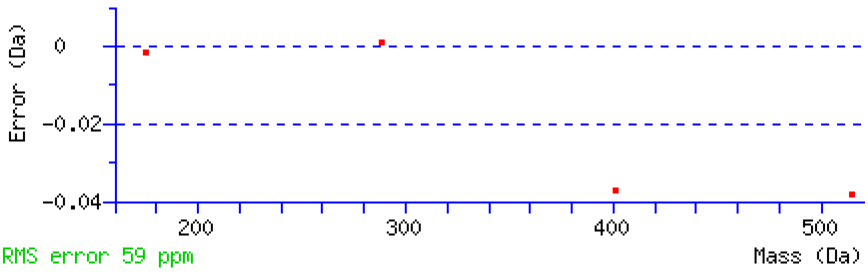
Match to Query 4984: 854.502388 from(428.258470,2+) rtinseconds(1724) index(14499)
Title: Locus:1.1.1.1923.10
Data file 2011-11-10 - TFD - EP 3-6.mgf

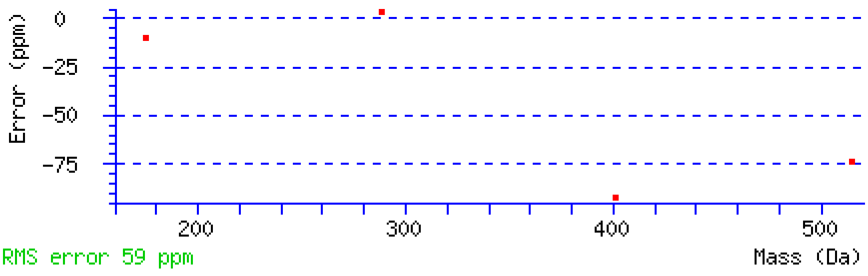
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 650 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 854.508621
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P6 : Oxidation (P)
Ions Score: 31 **Expect:** 0.0054
Matches : 4/50 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	58.028740	29.518008			G					8
2	115.050204	58.028740			G	798.494448	399.750862	781.467899	391.237588	7
3	186.087318	93.547297			A	741.472984	371.240130	724.446435	362.726856	6
4	342.188429	171.597852	325.161880	163.084578	R	670.435870	335.721573	653.409321	327.208299	5
5	455.272493	228.139884	438.245944	219.626610	L	***514.334759***	257.671018	497.308210	249.157743	4
6	568.320172	284.663724	551.293623	276.150450	P	***401.250695***	201.128985	384.224146	192.615711	3
7	681.404236	341.205756	664.377687	332.692482	L	***288.203016***	144.605146	271.176467	136.091871	2
8					R	***175.118952***	88.063114	158.092403	79.549839	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.8	854.508621	-0.006233	GGARLPLR
30.8	854.497391	0.004997	GNLGLIPR
30.8	854.497375	0.005013	LNNLIPR
30.8	854.497391	0.004997	QNVPIIR
30.6	854.508606	-0.006218	RNPALIR
29.5	854.497375	0.005013	AGAAPALLR
16.8	854.508621	-0.006233	VAAGRLPR
14.4	854.497375	0.005013	QAALPSLR
14.4	854.508621	-0.006233	RVKPSPR
10.6	854.508621	-0.006233	VGRPAALR

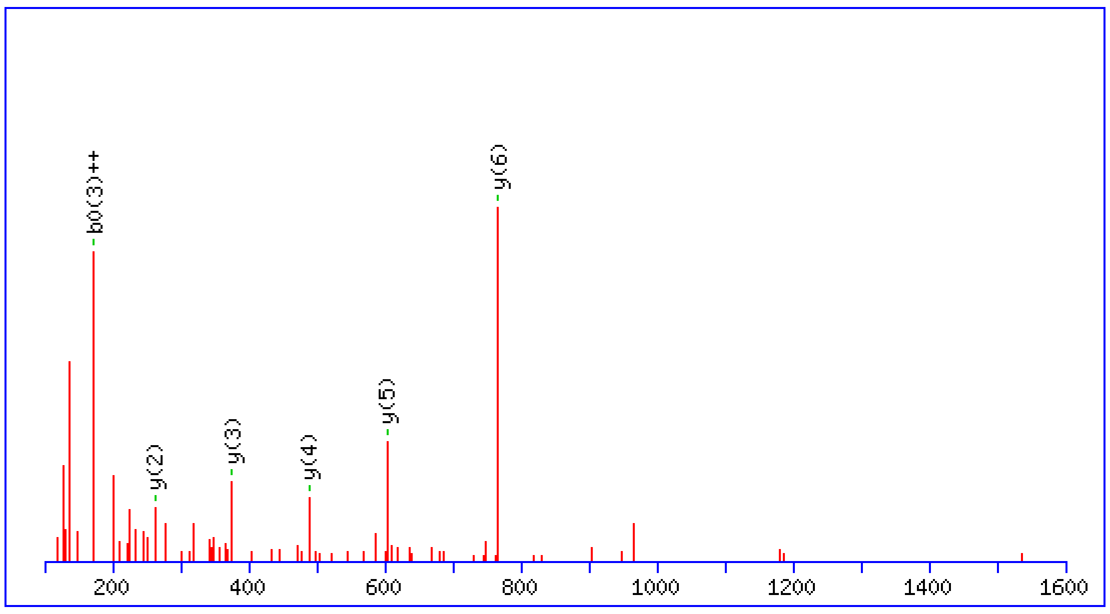
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TVYNLNDK**
Found in **DNLI3_HUMAN**, DNA ligase 3 OS=Homo sapiens GN=LIG3 PE=1 SV=2

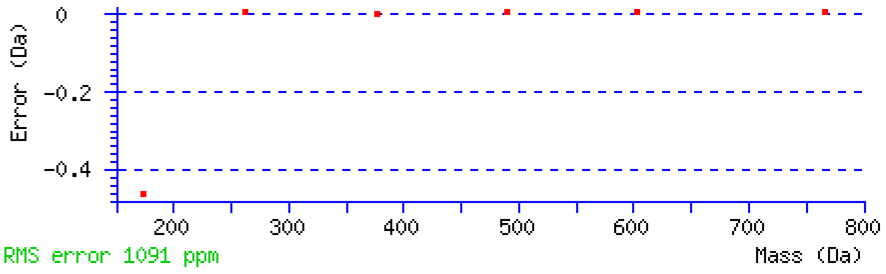
Match to Query 8418: 965.484268 from(483.749410,2+) rtinseconds(1844) index(19206)
Title: Locus:1.1.1.2217.19
Data file 2011-11-12 - TFD - EP 5-3.mgf

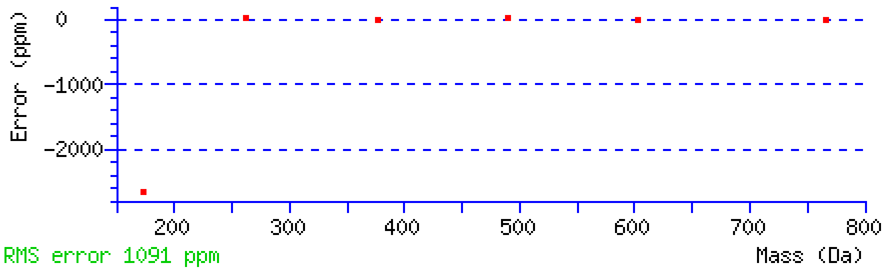
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 1600 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 965.481796
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 35 **Expect:** 0.0036
Matches : 6/76 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							8
2	201.123369	101.065322			183.112804	92.060040	V	865.441408	433.224342	848.414859	424.711068	847.430843	424.219060	7
3	364.186698	182.596987			346.176133	173.591705	Y	***766.372994***	383.690135	749.346445	375.176861	748.362429	374.684853	6
4	478.229625	239.618451	461.203076	231.105176	460.219060	230.613168	N	***603.309665***	302.158471	586.283116	293.645196	585.299100	293.153188	5
5	591.313689	296.160483	574.287140	287.647208	573.303124	287.155200	L	***489.266738***	245.137007	472.240189	236.623732	471.256173	236.131724	4
6	705.356616	353.181946	688.330067	344.668672	687.346051	344.176664	N	***376.182674***	188.594975	359.156125	180.081700	358.172109	179.589692	3
7	820.383559	410.695418	803.357010	402.182143	802.372994	401.690135	D	***262.139747***	131.573511	245.113198	123.060237	244.129182	122.568229	2
8							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.8	965.481796	0.002472	TVYNLNDK
33.1	965.493027	-0.008759	SLYNLGGSR
9.2	965.489197	-0.004929	EVFPIMAK
8.2	965.485153	-0.000885	LSSSMNSIK
4.4	965.481827	0.002441	DGNVVTSFK
4.1	965.489182	-0.004914	EAIEVFMK
3.7	965.493027	-0.008759	EHPDVNKK
1.9	965.485168	-0.000900	SVSTMNLSK
1.8	965.485184	-0.000916	TQTMKTPK
1.7	965.493027	-0.008759	SLYSLGGNR

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

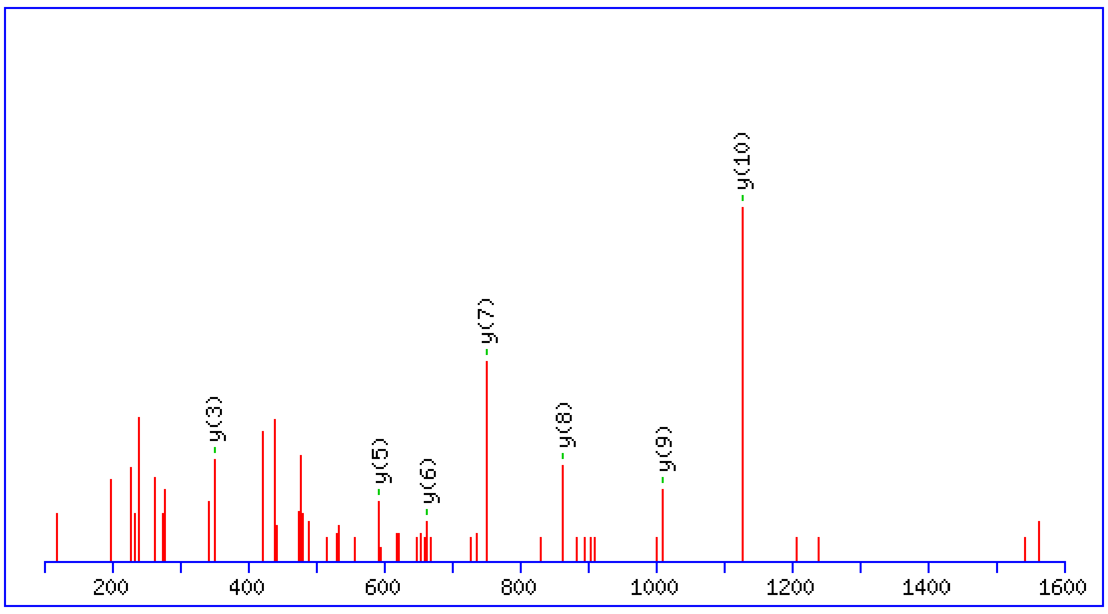
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IIDFLSALEGFK**
Found in **MSH6_HUMAN**, DNA mismatch repair protein Msh6 OS=Homo sapiens GN=MSH6 PE=1 SV=2

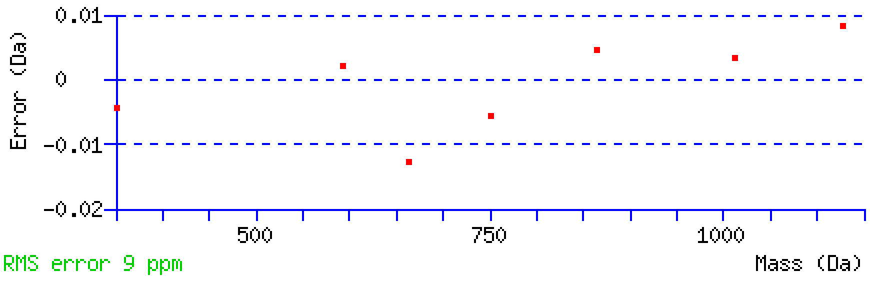
Match to Query 39209: 1351.747768 from(676.881160,2+) rtinseconds(4569) index(68968)
Title: Locus:1.1.1.3031.32
Data file 2011-11-12 - TFD - EP 6-1.mgf

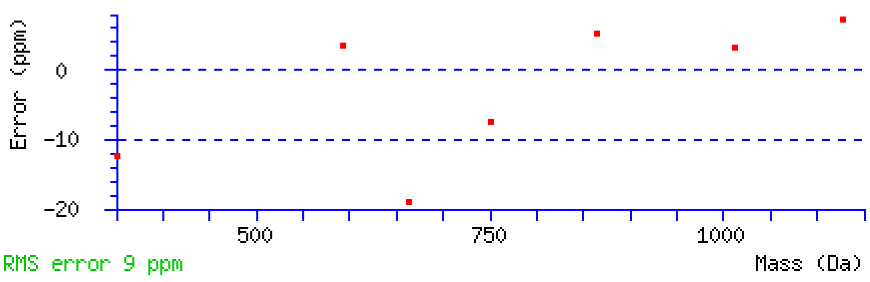
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1351.738739
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 52 **Expect:** 2.7e-005
Matches : 7/100 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							12
2	227.175404	114.091340			I	1239.661966	620.334621	1222.635417	611.821347	1221.651401	611.329339	11
3	342.202347	171.604811	324.191782	162.599529	D	*1126.577902*	563.792589	1109.551353	555.279315	1108.567337	554.787307	10
4	489.270761	245.139018	471.260196	236.133736	F	*1011.550959*	506.279118	994.524410	497.765843	993.540394	497.273835	9
5	602.354825	301.681051	584.344260	292.675768	L	*864.482545*	432.744911	847.455996	424.231636	846.471980	423.739628	8
6	689.386853	345.197065	671.376288	336.191782	S	*751.398481*	376.202879	734.371932	367.689604	733.387916	367.197596	7
7	760.423967	380.715622	742.413402	371.710339	A	*664.366453*	332.686865	647.339904	324.173590	646.355888	323.681582	6
8	873.508031	437.257654	855.497466	428.252371	L	*593.329339*	297.168308	576.302790	288.655033	575.318774	288.163025	5
9	1002.550624	501.778950	984.540059	492.773667	E	480.245275	240.626275	463.218726	232.113001	462.234710	231.620993	4
10	1059.572088	530.289682	1041.561523	521.284399	G	*351.202682*	176.104979	334.176133	167.591704			3
11	1206.640502	603.823889	1188.629937	594.818606	F	294.181218	147.594247	277.154669	139.080973			2
12					K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.6	1351.738739	0.009029	IIDFLSALEGFK
2.7	1351.735565	0.012203	LINFMKMLSQK
0.2	1351.750000	-0.002232	LLVDIHVPDGFK

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

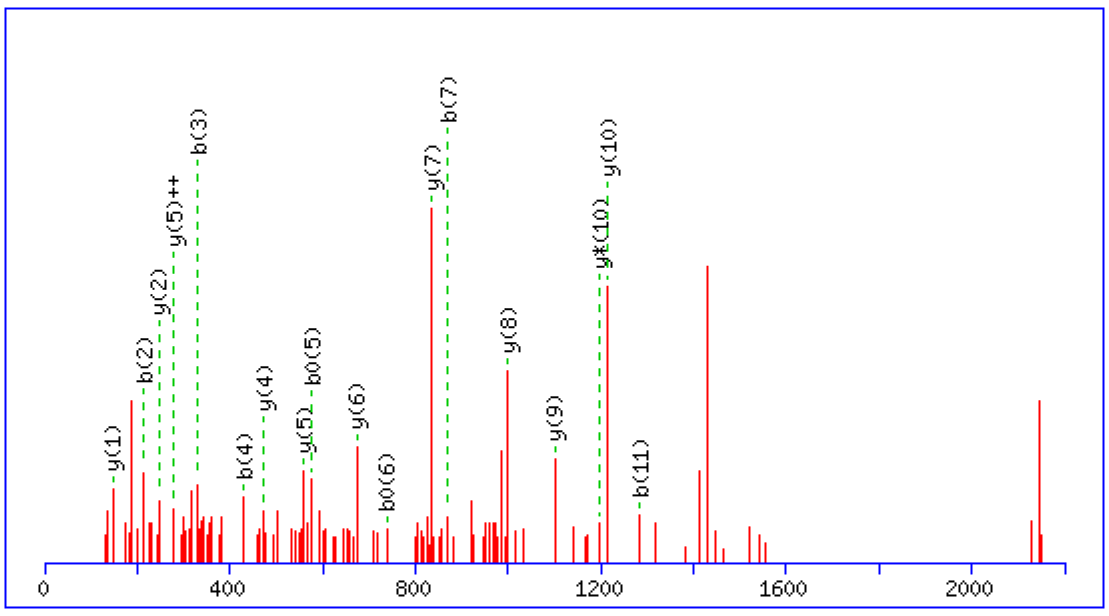
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DVDTYYLSNLVK**
Found in **XPC_HUMAN**, DNA repair protein complementing XP-C cells OS=Homo sapiens GN=XPC PE=1 SV=4

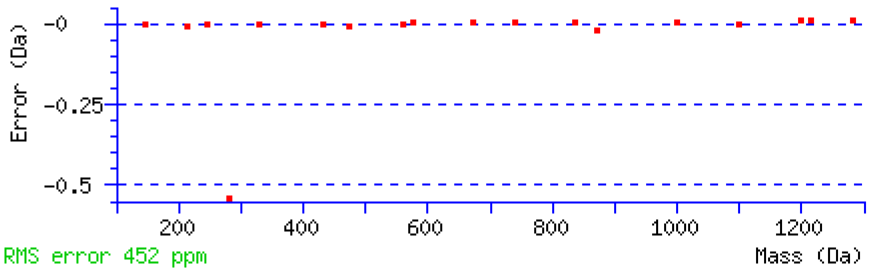
Match to Query 42904: 1428.720268 from(715.367410,2+) rtinseconds(3323) index(47572)
Title: Locus:1.1.1.2571.33
Data file 2011-11-12 - TFD - EP 6-1.mgf

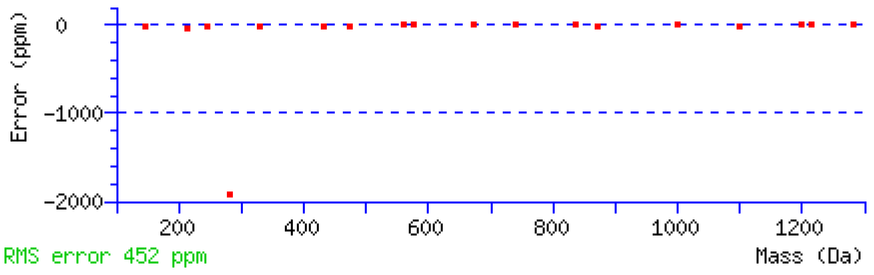
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1428.713654
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 54 **Expect:** 2.7e-005
Matches : 18/108 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	116.034219	58.520748			98.023654	49.515465	D							12
2	**215.102633**	108.054954			197.092068	99.049672	V	1314.693995	657.850636	1297.667446	649.337361	1296.683430	648.845353	11
3	**330.129576**	165.568426			312.119011	156.563144	D	***1215.625581***	608.316429	1198.599032	599.803154	1197.615016	599.311146	10
4	**431.177255**	216.092266			413.166690	207.086983	T	***1100.598638***	550.802957	1083.572089	542.289683	1082.588073	541.797675	9
5	594.240584	297.623930			576.230019	288.618648	Y	***999.550959***	500.279118	982.524410	491.765843	981.540394	491.273835	8
6	757.303913	379.155595			739.293348	370.150312	Y	***836.487630***	418.747453	819.461081	410.234179	818.477065	409.742171	7
7	**870.387977**	435.697627			852.377412	426.692344	L	***673.424301***	337.215789	656.397752	328.702514	655.413736	328.210506	6
8	957.420005	479.213641			939.409440	470.208358	S	***560.340237***	280.673757	543.313688	272.160482	542.329672	271.668474	5
9	1071.462932	536.235104	1054.436383	527.721830	1053.452367	527.229822	N	***473.308209***	237.157742	456.281660	228.644468			4
10	1184.546996	592.777136	1167.520447	584.263862	1166.536431	583.771854	L	359.265282	180.136279	342.238733	171.623004			3
11	**1283.615410**	642.311343	1266.588861	633.798069	1265.604845	633.306061	V	***246.181218***	123.594247	229.154669	115.080973			2
12							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.1	1428.713654	0.006614	DVDTYYLSNLVK
5.0	1428.732269	-0.012001	IDSFNSLYMLVK
3.9	1428.732269	-0.012001	TIMKPLEYQFK
3.7	1428.720871	-0.000603	SPSPSPTSPGSLRK
3.1	1428.720871	-0.000603	SPSPSPTSPGSLRK
2.1	1428.720856	-0.000588	LTDLLQQEEQGR
1.6	1428.728256	-0.007988	GELGMSPPGSKIPK
1.5	1428.732086	-0.011818	ASSSLQPPAKAQGR
1.2	1428.728256	-0.007988	MDLPALLPAPTAR
1.0	1428.724899	-0.004631	AASLLFGPGPAPDK

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

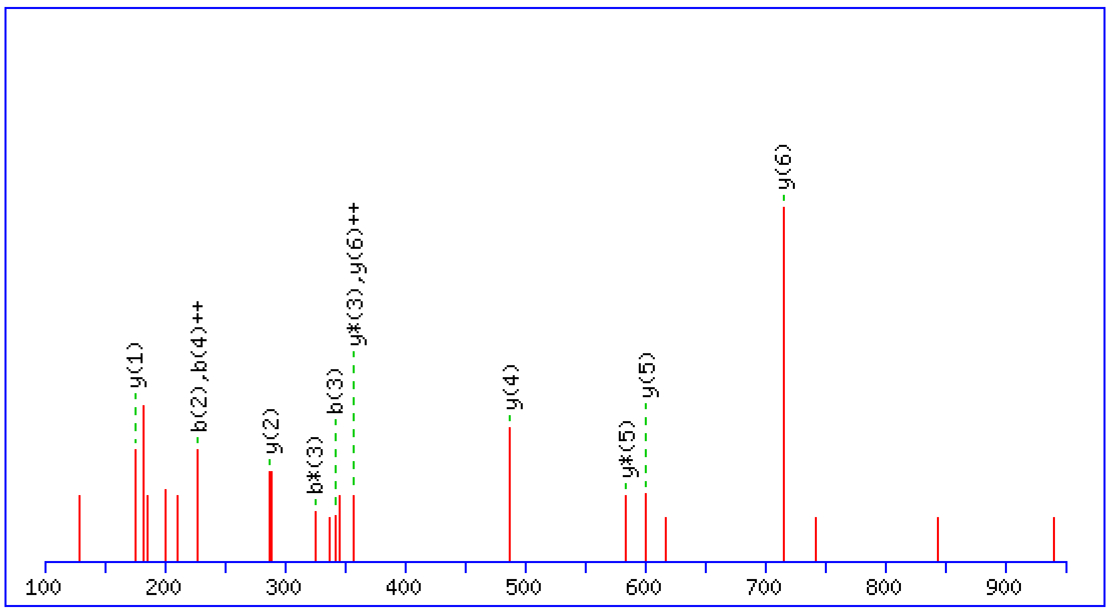
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ARNLISPR**
Found in **CDT1_HUMAN**, DNA replication factor Cdt1 OS=Homo sapiens GN=CDT1 PE=1 SV=3

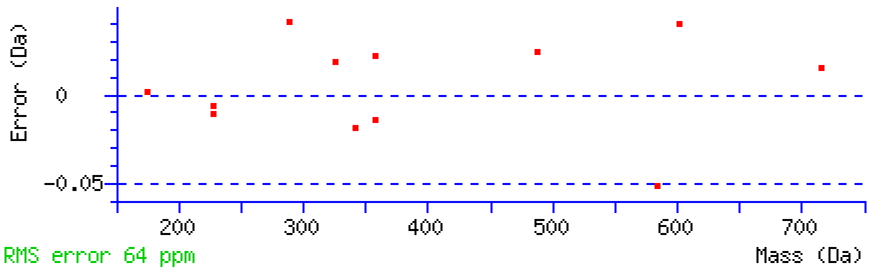
Match to Query 183158: 941.547848 from(471.781200,2+) rtinseconds(1809) index(508285)
Title: Locus:1.1.1.1020.10
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

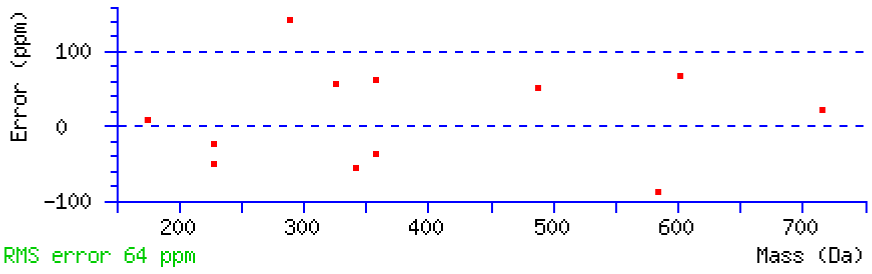
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 941.540634
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
P7      : Oxidation (P)
Ions Score: 33  Expect: 0.007
Matches : 12/68 fragment ions using 17 most intense peaks    (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							8
2	**228.145501**	114.576388	211.118952	106.063114			R	871.510825	436.259051	854.484276	427.745776	853.500260	427.253768	7
3	**342.188428**	171.597852	325.161879	163.084577			N	***715.409714***	358.208495	698.383165	349.695221	697.399149	349.203213	6
4	455.272492	228.139884	438.245943	219.626610			L	***601.366787***	301.187032	584.340238	292.673757	583.356222	292.181749	5
5	568.356556	284.681916	551.330007	276.168642			I	***488.282723***	244.644999	471.256174	236.131725	470.272158	235.639717	4
6	655.388584	328.197930	638.362035	319.684656	637.378019	319.192648	S	375.198659	188.102967	358.172110	179.589693	357.188094	179.097685	3
7	768.436263	384.721770	751.409714	376.208495	750.425698	375.716487	P	***288.166631***	144.586953	271.140082	136.073679			2
8							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.0	941.540634	0.007214	ARNLISPR
16.3	941.554550	-0.006702	IDIIAELR
15.8	941.540634	0.007214	RGQIAELR
11.5	941.554581	-0.006733	VTLVLEPR
11.3	941.554550	-0.006702	EVIEALLR
10.4	941.554550	-0.006702	VLLEAIER
8.5	941.540634	0.007214	PSRNLSLR
8.3	941.554565	-0.006717	DPLILLSR
8.3	941.544678	0.003170	HGFLILSR
6.5	941.540634	0.007214	VQRLEAAR

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

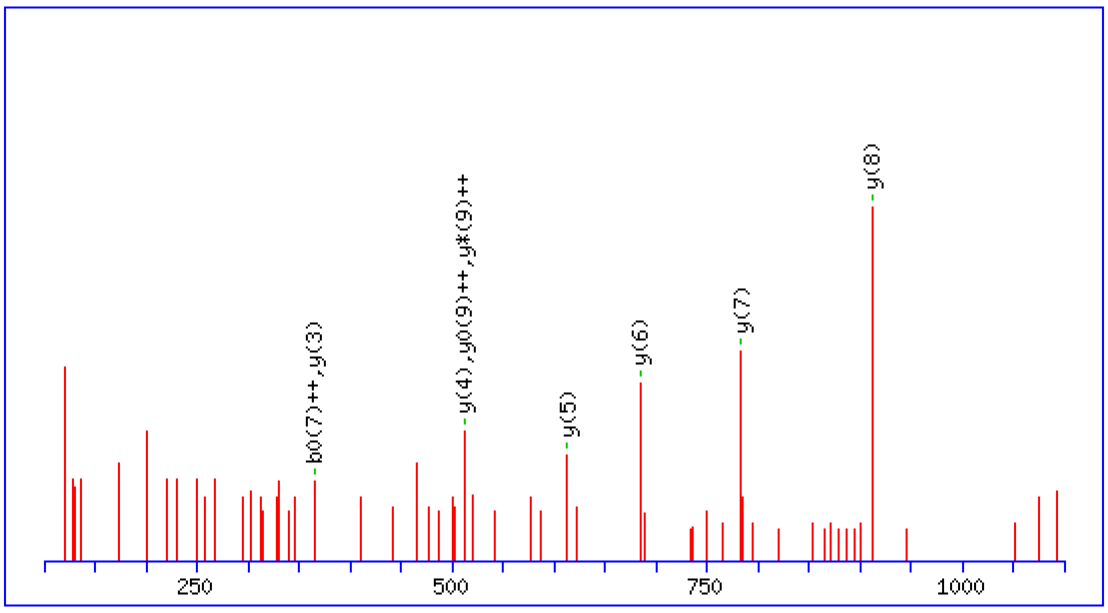
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AEEVATFFAK**
Found in **TOP1_HUMAN**, DNA topoisomerase 1 OS=Homo sapiens GN=TOP1 PE=1 SV=2

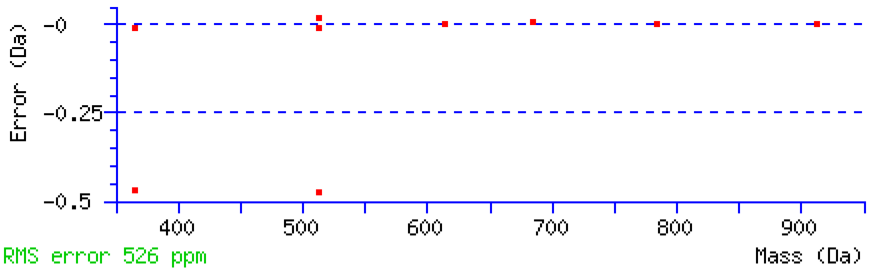
Match to Query 23134: 1111.557768 from(556.786160,2+) rtinseconds(2589) index(30117)
Title: Locus:1.1.1.2625.20
Data file 2011-11-12 - TFD - EP 5-2.mgf

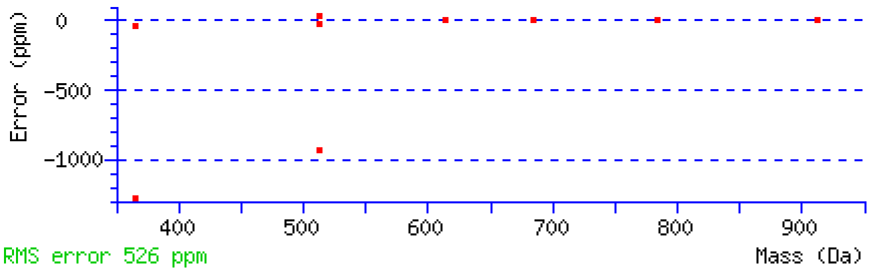
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1111.554962
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 41  Expect: 0.00067
Matches : 9/80 fragment ions using 10 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			A							10
2	201.086983	101.047130	183.076418	92.041847	E	1041.525139	521.266208	1024.498590	512.752933	1023.514574	512.260925	9
3	330.129576	165.568426	312.119011	156.563144	E	***912.482546***	456.744911	895.455997	448.231637	894.471981	447.739629	8
4	429.197990	215.102633	411.187425	206.097351	V	***783.439953***	392.223615	766.413404	383.710340	765.429388	383.218332	7
5	500.235104	250.621190	482.224539	241.615908	A	***684.371539***	342.689408	667.344990	334.176133	666.360974	333.684125	6
6	601.282783	301.145030	583.272218	292.139747	T	***613.334425***	307.170851	596.307876	298.657576	595.323860	298.165568	5
7	748.351197	374.679237	730.340632	365.673954	F	***512.286746***	256.647011	495.260197	248.133737			4
8	895.419611	448.213444	877.409046	439.208161	F	***365.218332***	183.112804	348.191783	174.599529			3
9	966.456725	483.732001	948.446160	474.726718	A	218.149918	109.578597	201.123369	101.065322			2
10					K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.4	1111.554962	0.002806	AEEVATFFAK

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

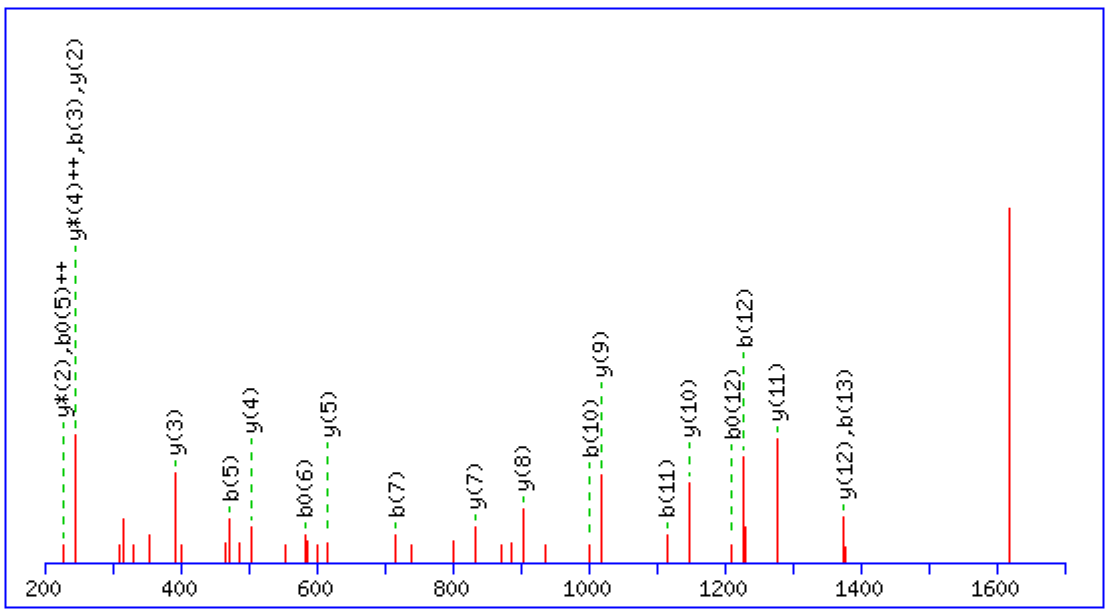
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AGDVEEDASQLIFPK**
Found in **RPB4_HUMAN**, DNA-directed RNA polymerase II subunit RPB4 OS=Homo sapiens GN=POLR2D PE=1 SV=1

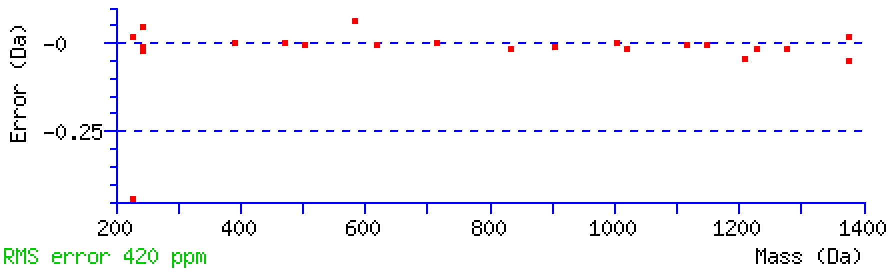
Match to Query 53551: 1617.785988 from(809.900270,2+) rtinseconds(3226) index(43671)
Title: Locus:1.1.1.2484.38
Data file 2011-11-10 - TFD - EP 4-6.mgf

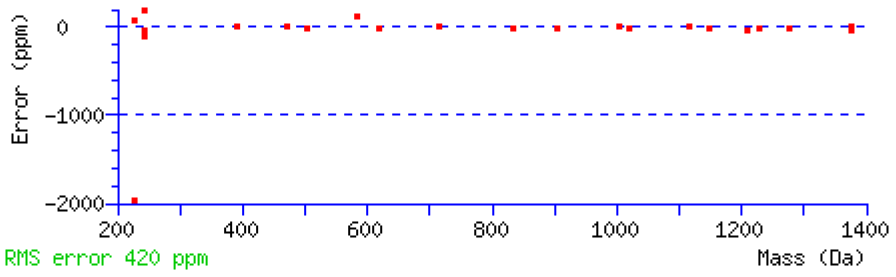
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [1700] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1617.788605
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 77 **Expect:** 2.7e-007
Matches : 22/134 fragment ions using 29 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.044390	36.525833					A							15
2	129.065854	65.036565					G	1547.758780	774.383028	1530.732231	765.869754	1529.748215	765.377746	14
3	**244.092797**	122.550037			226.082232	113.544754	D	1490.737316	745.872296	1473.710767	737.359022	1472.726751	736.867013	13
4	343.161211	172.084244			325.150646	163.078961	V	***1375.710373***	688.358825	1358.683824	679.845550	1357.699808	679.353542	12
5	**472.203804**	236.605540			454.193239	227.600258	E	***1276.641959***	638.824618	1259.615410	630.311343	1258.631394	629.819335	11
6	601.246397	301.126837			583.235832	292.121554	E	***1147.599366***	574.303321	1130.572817	565.790047	1129.588801	565.298039	10
7	**716.273340**	358.640308			698.262775	349.635026	D	***1018.556773***	509.782025	1001.530224	501.268750	1000.546208	500.776742	9
8	787.310454	394.158865			769.299889	385.153583	A	***903.529830***	452.268553	886.503281	443.755279	885.519265	443.263271	8
9	874.342482	437.674879			856.331917	428.669597	S	***832.492716***	416.749996	815.466167	408.236722	814.482151	407.744714	7
10	**1002.401060**	501.704168	985.374511	493.190894	984.390495	492.698886	Q	745.460688	373.233982	728.434139	364.720708			6
11	**1115.485124**	558.246200	1098.458575	549.732926	1097.474559	549.240918	L	***617.402110***	309.204693	600.375561	300.691419			5
12	**1228.569188**	614.788232	1211.542639	606.274958	1210.558623	605.782949	I	***504.318046***	252.662661	487.291497	244.149386			4
13	**1375.637602**	688.322439	1358.611053	679.809165	1357.627037	679.317157	F	***391.233982***	196.120629	374.207433	187.607355			3
14	1472.690366	736.848821	1455.663817	728.335547	1454.679801	727.843539	P	***244.165568***	122.586422	227.139019	114.073148			2
15							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
76.8	1617.788605	-0.002617	AGDVEEDASQLIFPK
9.3	1617.770874	0.015114	YQVPPDCPPLVQK
6.2	1617.785919	0.000069	AAFQGAEGPRGGLESR
2.1	1617.785492	0.000496	TITPGMVCAGVPQGGK
1.2	1617.785492	0.000496	TITPGMVCAGVPQGGK
0.7	1617.800674	-0.014686	IYNISMKHPQEMK
0.4	1617.786102	-0.000114	DQFALAMYFIQQK
0.3	1617.785416	0.000572	NPLMEMEPKALSAR

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

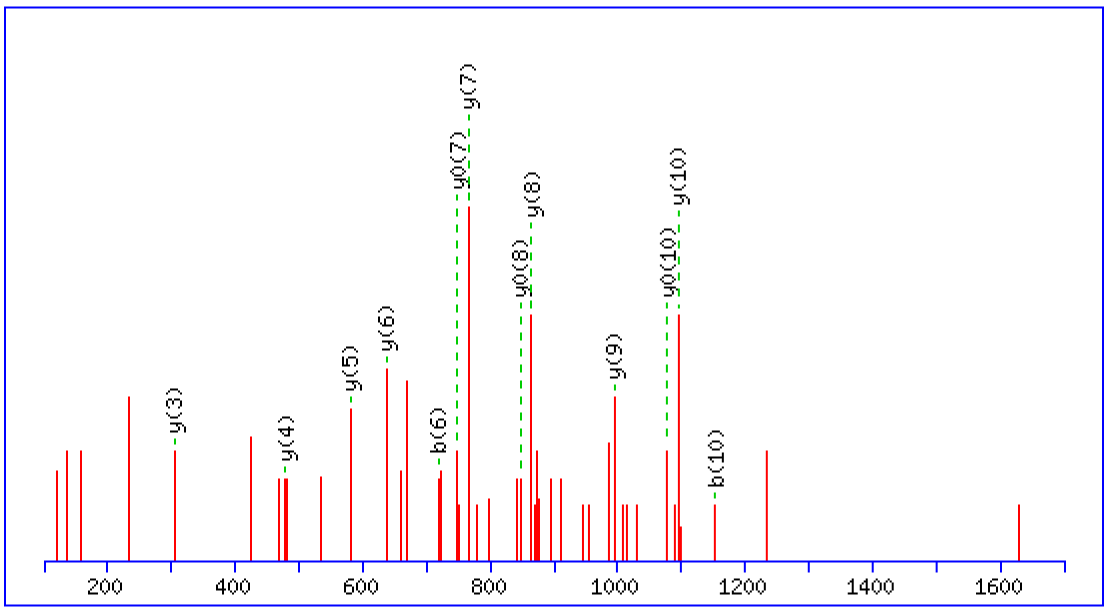
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LFTEVEGTCTGK**
Found in **RPB7_HUMAN**, DNA-directed RNA polymerase II subunit RPB7 OS=Homo sapiens GN=POLR2G PE=1 SV=1

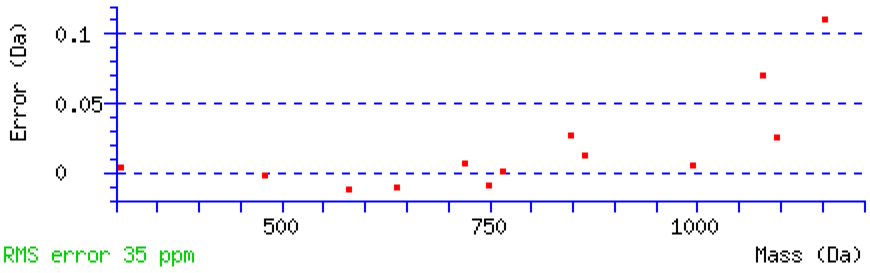
Match to Query 42136: 1354.646608 from(678.330580,2+) rtinseconds(1940) index(19814)
Title: Locus:1.1.1.1957.46
Data file 2011-11-12 - TFD - EP 5-6.mgf

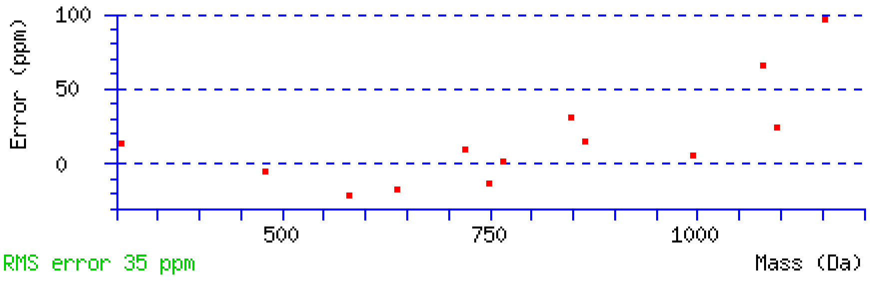
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1354.643875
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 43 **Expect:** 0.00067
Matches : 13/102 fragment ions using 33 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308			L							12
2	261.159754	131.083515			F	1242.567082	621.787179	1225.540533	613.273905	1224.556517	612.781897	11
3	362.207433	181.607354	344.196868	172.602072	T	***1095.498668***	548.252972	1078.472119	539.739698	1077.488103	539.247690	10
4	491.250026	246.128651	473.239461	237.123369	E	***994.450989***	497.729133	977.424440	489.215858	976.440424	488.723850	9
5	590.318440	295.662858	572.307875	286.657576	V	***865.408396***	433.207836	848.381847	424.694562	847.397831	424.202554	8
6	719.361033	360.184155	701.350468	351.178872	E	***766.339982***	383.673629	749.313433	375.160355	748.329417	374.668347	7
7	776.382497	388.694887	758.371932	379.689604	G	***637.297389***	319.152333	620.270840	310.639058	619.286824	310.147050	6
8	877.430176	439.218726	859.419611	430.213444	T	***580.275925***	290.641601	563.249376	282.128326	562.265360	281.636318	5
9	1051.476475	526.241876	1033.465910	517.236593	C	***479.228246***	240.117761	462.201697	231.604487	461.217681	231.112479	4
10	1152.524154	576.765715	1134.513589	567.760433	T	***305.181947***	153.094611	288.155398	144.581337	287.171382	144.089329	3
11	1209.545618	605.276447	1191.535053	596.271165	G	204.134268	102.570772	187.107719	94.057497			2
12					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of LFTEVEGTCTGK
(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	1354.643875	0.002733	LFTEVEGTCTGK

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

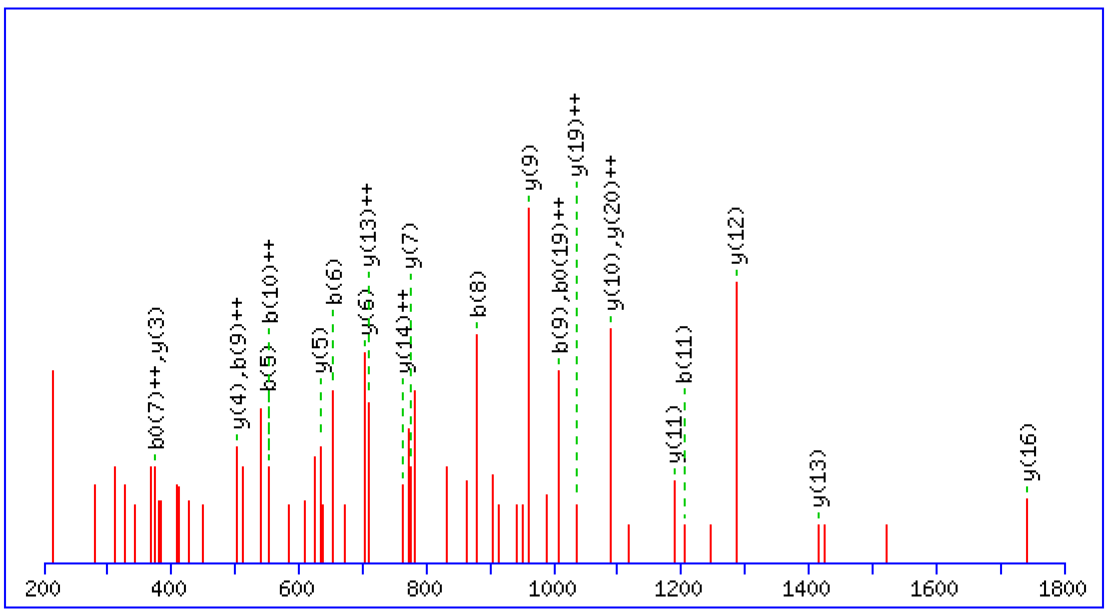
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLPDITLLEPVEGEAAEELSR**
Found in **RPAC1_HUMAN**, DNA-directed RNA polymerases I and III subunit RPAC1 OS=Homo sapiens GN=POLR1C PE=1 SV=1

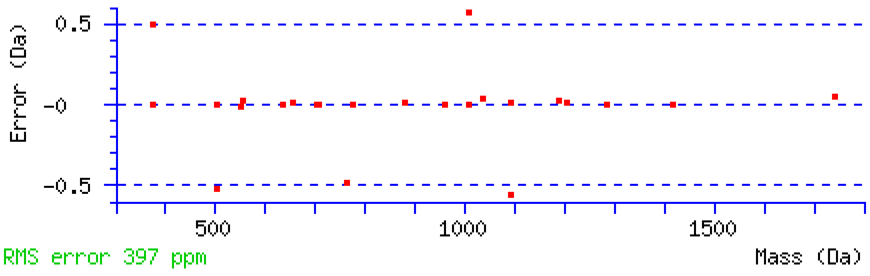
Match to Query 69907: 2293.212852 from(765.411560,3+) rtinseconds(4262) index(64971)
Title: Locus:1.1.1.2998.37
Data file 2011-11-14 - TFD - EP 8-4.mgf

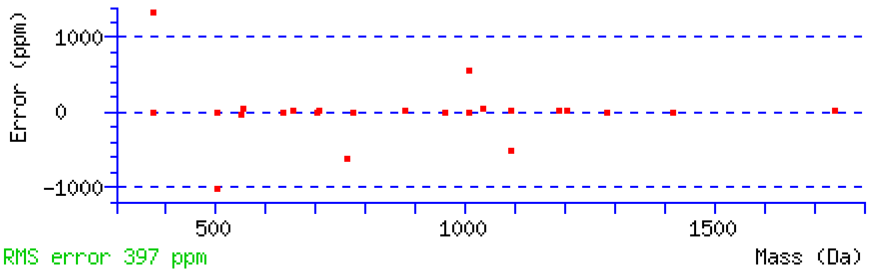
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2293.205261
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 55  Expect: 1.5e-005
Matches : 24/192 fragment ions using 42 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							21
2	227.175404	114.091340			L	2181.128521	1091.067898	2164.101972	1082.554624	2163.117956	1082.062616	20
3	324.228168	162.617722			P	2068.044457	1034.525866	2051.017908	1026.012592	2050.033892	1025.520584	19
4	439.255111	220.131193	421.244546	211.125911	D	1970.991693	985.999484	1953.965144	977.486210	1952.981128	976.994202	18
5	**552.339175**	276.673226	534.328610	267.667943	I	1855.964750	928.486013	1838.938201	919.972738	1837.954185	919.480730	17
6	**653.386854**	327.197065	635.376289	318.191783	T	***1742.880686***	871.943981	1725.854137	863.430707	1724.870121	862.938698	16
7	766.470918	383.739097	748.460353	374.733815	L	1641.833007	821.420142	1624.806458	812.906867	1623.822442	812.414859	15
8	**879.554982**	440.281129	861.544417	431.275847	L	1528.748943	764.878109	1511.722394	756.364835	1510.738378	755.872827	14
9	**1008.597575**	504.802426	990.587010	495.797143	E	***1415.664879***	708.336077	1398.638330	699.822803	1397.654314	699.330795	13
10	1105.650339	553.328808	1087.639774	544.323525	P	***1286.622286***	643.814781	1269.595737	635.301507	1268.611721	634.809499	12
11	**1204.718753**	602.863015	1186.708188	593.857732	V	***1189.569522***	595.288399	1172.542973	586.775125	1171.558957	586.283117	11
12	1333.761346	667.384311	1315.750781	658.379029	E	***1090.501108***	545.754192	1073.474559	537.240918	1072.490543	536.748909	10
13	1390.782810	695.895043	1372.772245	686.889760	G	***961.458515***	481.232896	944.431966	472.719621	943.447950	472.227613	9
14	1519.825403	760.416340	1501.814838	751.411057	E	904.437051	452.722164	887.410502	444.208889	886.426486	443.716881	8
15	1590.862517	795.934897	1572.851952	786.929614	A	***775.394458***	388.200867	758.367909	379.687592	757.383893	379.195585	7
16	1661.899631	831.453454	1643.889066	822.448171	A	***704.357344***	352.682310	687.330795	344.169036	686.346779	343.677028	6
17	1790.942224	895.974750	1772.931659	886.969468	E	***633.320230***	317.163753	616.293681	308.650479	615.309665	308.158471	5
18	1919.984817	960.496047	1901.974252	951.490764	E	***504.277637***	252.642456	487.251088	244.129182	486.267072	243.637174	4
19	2033.068881	1017.038079	2015.058316	1008.032796	L	***375.235044***	188.121160	358.208495	179.607885	357.224479	179.115877	3
20	2120.100909	1060.554092	2102.090344	1051.548810	S	262.150980	131.579128	245.124431	123.065853	244.140415	122.573845	2
21					R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.5	2293.205261	0.007591	LLPDITLLEPVEGEAAEELSR
4.0	2293.206619	0.006233	LPFSAAKSLINSPSQGAFSSLR

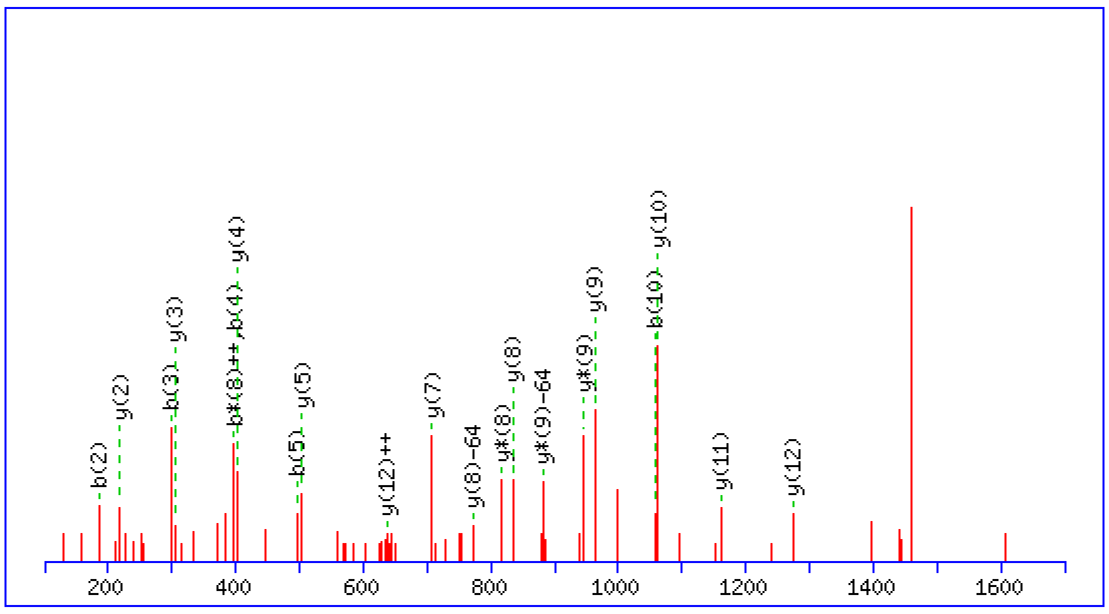
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALIVVQQGMTPSAK**
Found in **RPAB1_HUMAN**, DNA-directed RNA polymerases I, II, and III subunit RPABC1 OS=Homo sapiens GN=POLR2E PE=1 SV=4

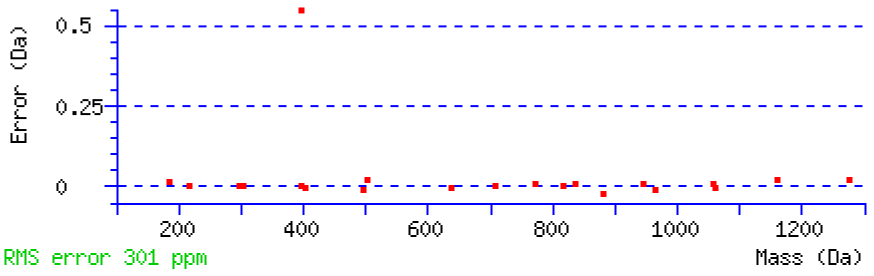
Match to Query 42240: 1457.795268 from(729.904910,2+) rtinseconds(1923) index(17010)
Title: Locus:1.1.1.2318.45
Data file 2011-11-12 - TFD - EP 5-5.mgf

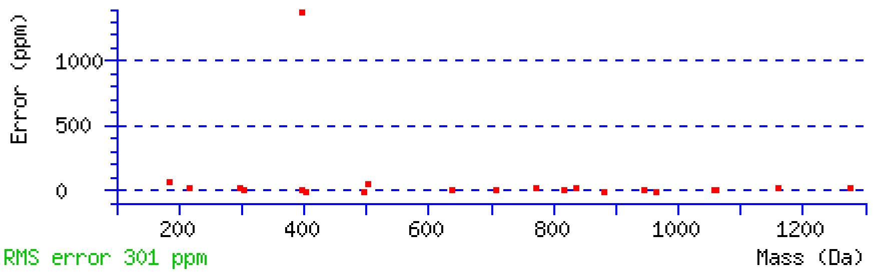
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1457.791199
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M9     : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 83  Expect: 2.3e-008
Matches : 21/200 fragment ions using 27 most intense peaks   (help)
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							14
2	**185.128454**	93.067865					L	1387.761365	694.384321	1370.734816	685.871046	1369.750800	685.379038	13
3	**298.212518**	149.609897					I	***1274.677301***	637.842289	1257.650752	629.329014	1256.666736	628.837006	12
4	**397.280932**	199.144104					V	***1161.593237***	581.300257	1144.566688	572.786982	1143.582672	572.294974	11
5	**496.349346**	248.678311					V	***1062.524823***	531.766050	1045.498274	523.252775	1044.514258	522.760767	10
6	624.407924	312.707600	607.381375	304.194326			Q	***963.456409***	482.231843	946.429860	473.718568	945.445844	473.226560	9
7	752.466502	376.736889	735.439953	368.223615			Q	***835.397831***	418.202554	818.371282	409.689279	817.387266	409.197271	8
8	809.487966	405.247621	792.461417	396.734347			G	***707.339253***	354.173265	690.312704	345.659990	689.328688	345.167982	7
9	956.523366	478.765321	939.496817	470.252047			M	650.317789	325.662533	633.291240	317.149258	632.307224	316.657250	6
10	**1057.571045**	529.289161	1040.544496	520.775886	1039.560480	520.283878	T	***503.282389***	252.144833	486.255840	243.631558	485.271824	243.139550	5
11	1154.623809	577.815543	1137.597260	569.302268	1136.613244	568.810260	P	***402.234710***	201.620993	385.208161	193.107719	384.224145	192.615711	4
12	1241.655837	621.331557	1224.629288	612.818282	1223.645272	612.326274	S	***305.181946***	153.094611	288.155397	144.581337	287.171381	144.089329	3
13	1312.692951	656.850114	1295.666402	648.336839	1294.682386	647.844831	A	***218.149918***	109.578597	201.123369	101.065322			2
14							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
82.6	1457.791199	0.004069	ALIVVQQGMTPSAK
49.9	1457.791199	0.004069	ALIVVQQGMTPSAK
1.1	1457.787796	0.007472	EPAVERVIEFAAK

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

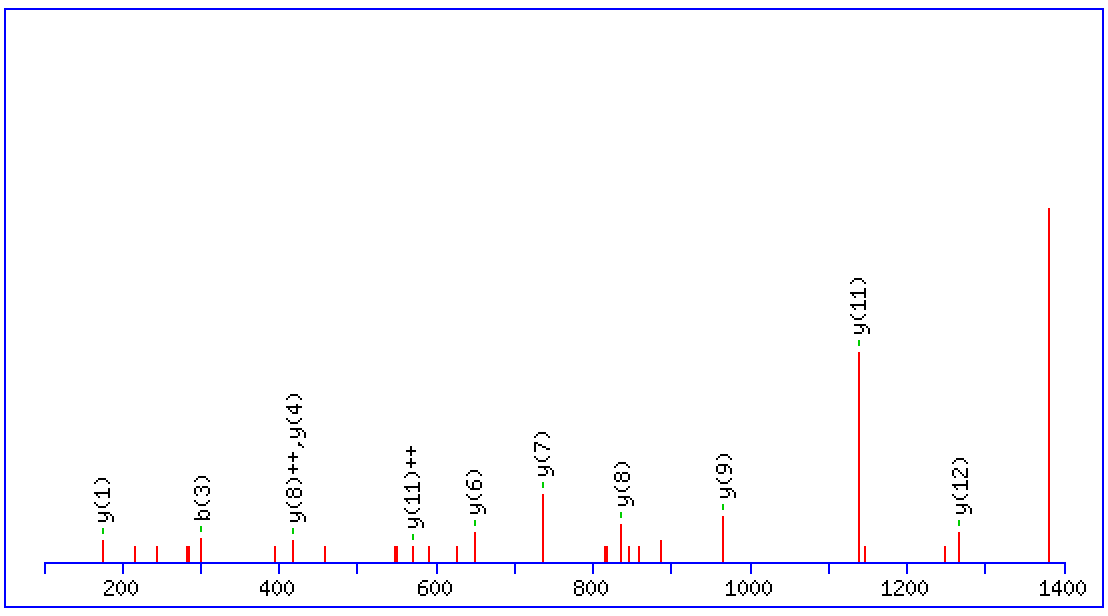
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IEGDETSTEAATR**
Found in **RPAB3_HUMAN**, DNA-directed RNA polymerases I, II, and III subunit RPABC3 OS=Homo sapiens GN=POLR2H PE=1 SV=4

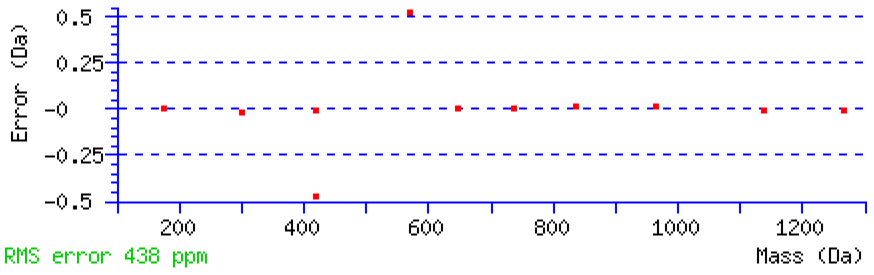
Match to Query 726547: 1378.626428 from(690.320490,2+) rtinseconds(1082) index(245331)
Title: Locus:1.1.1.853.38
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

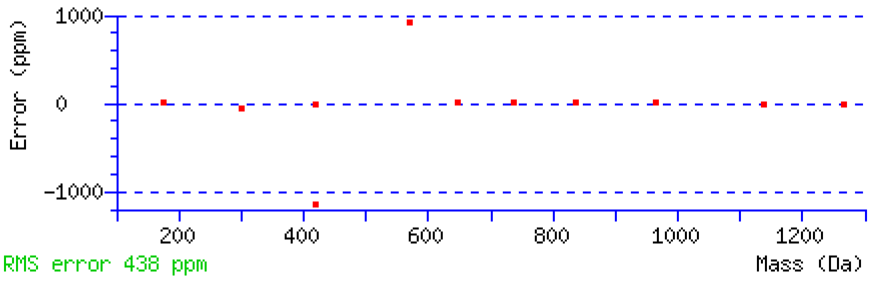
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1378.621201
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 80 **Expect:** 1.4e-007
Matches : 11/116 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							13
2	243.133933	122.070605	225.123368	113.065322	E	***1266.544431***	633.775854	1249.517882	625.262579	1248.533866	624.770571	12
3	300.155397	150.581336	282.144832	141.576054	G	***1137.501838***	569.254557	1120.475289	560.741283	1119.491273	560.249275	11
4	415.182340	208.094808	397.171775	199.089526	D	1080.480374	540.743825	1063.453825	532.230551	1062.469809	531.738543	10
5	544.224933	272.616105	526.214368	263.610822	E	***965.453431***	483.230354	948.426882	474.717079	947.442866	474.225071	9
6	645.272612	323.139944	627.262047	314.134662	T	***836.410838***	418.709057	819.384289	410.195783	818.400273	409.703775	8
7	732.304640	366.655958	714.294075	357.650676	S	***735.363159***	368.185218	718.336610	359.671943	717.352594	359.179935	7
8	833.352319	417.179798	815.341754	408.174515	T	***648.331131***	324.669204	631.304582	316.155929	630.320566	315.663921	6
9	962.394912	481.701094	944.384347	472.695812	E	547.283452	274.145364	530.256903	265.632090	529.272887	265.140082	5
10	1033.432026	517.219651	1015.421461	508.214369	A	***418.240859***	209.624068	401.214310	201.110793	400.230294	200.618785	4
11	1104.469140	552.738208	1086.458575	543.732926	A	347.203745	174.105510	330.177196	165.592236	329.193180	165.100228	3
12	1205.516819	603.262048	1187.506254	594.256765	T	276.166631	138.586953	259.140082	130.073679	258.156066	129.581671	2
13					R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
79.9	1378.621201	0.005227	IEGDETSTEAATR
22.8	1378.617386	0.009042	LESPTTPLLDDM
3.9	1378.621185	0.005243	VSKNDTEEESNK
2.1	1378.628601	-0.002173	IEGVGAATSAELDM
1.7	1378.628586	-0.002158	LEQPDLSSEMSK
0.8	1378.626114	0.000314	IEFCPGGAVDAIM
0.7	1378.625229	0.001199	LEESPDNDGFLK
0.7	1378.628586	-0.002158	LEQPDLSSEMSK
0.7	1378.628601	-0.002173	LETDISQIQGEM
0.5	1378.614670	0.011758	EIDNSAACSSAVR

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

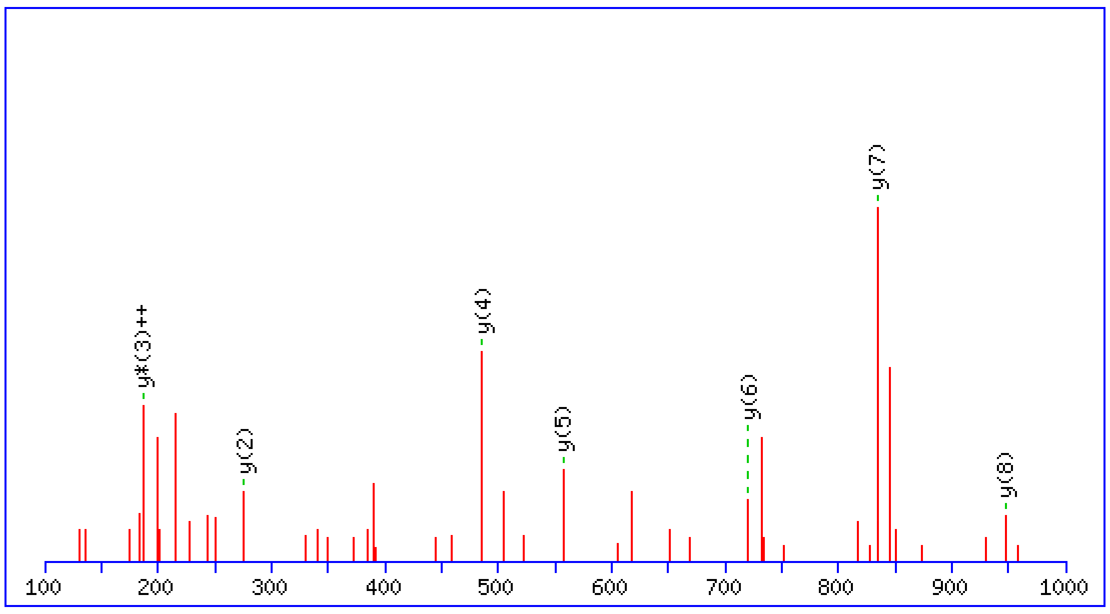
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLNYAPLEK**
Found in **RPAB5_HUMAN**, DNA-directed RNA polymerases I, II, and III subunit RPABC5 OS=Homo sapiens GN=POLR2L PE=1 SV=1

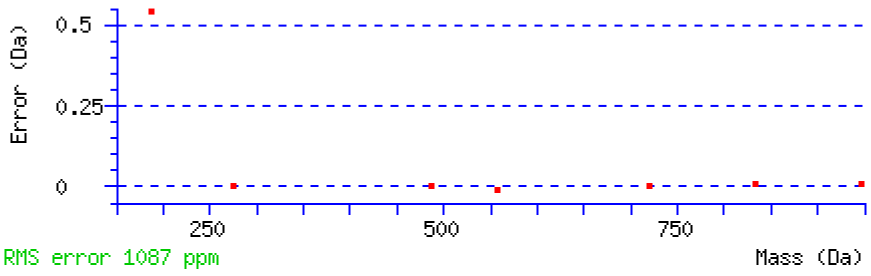
Match to Query 13747: 1059.588848 from(530.801700,2+) rtinseconds(2333) index(13745)
Title: Locus:1.1.1.2612.13
Data file 2011-11-14 - TFD - EP 8-8.mgf

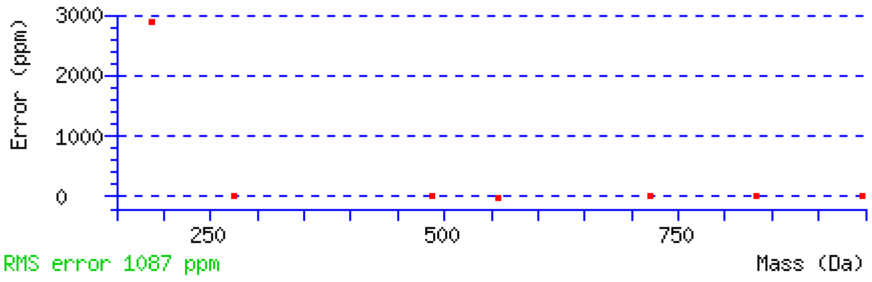
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1059.596405
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 52 **Expect:** 5.7e-005
Matches : 7/76 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							9
2	227.175404	114.091340					L	*947.519659*	474.263468	930.493110	465.750193	929.509094	465.258185	8
3	341.218331	171.112803	324.191782	162.599529			N	*834.435595*	417.721436	817.409046	409.208161	816.425030	408.716153	7
4	504.281660	252.644468	487.255111	244.131193			Y	*720.392668*	360.699972	703.366119	352.186698	702.382103	351.694690	6
5	575.318774	288.163025	558.292225	279.649751			A	*557.329339*	279.168308	540.302790	270.655033	539.318774	270.163025	5
6	672.371538	336.689407	655.344989	328.176133			P	*486.292225*	243.649751	469.265676	235.136476	468.281660	234.644468	4
7	785.455602	393.231439	768.429053	384.718165			L	389.239461	195.123369	372.212912	186.610094	371.228896	186.118086	3
8	914.498195	457.752736	897.471646	449.239461	896.487630	448.747453	E	*276.155397*	138.581336	259.128848	130.068062	258.144832	129.576054	2
9							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.0	1059.596405	-0.007557	LLNYAPLEK
18.3	1059.581177	0.007671	LLTQEVTEK
14.5	1059.581177	0.007671	ITKPTIDEK
7.4	1059.581161	0.007687	LLSAGTIEEK
5.5	1059.596451	-0.007603	LLPAVTFDGK
5.3	1059.596420	-0.007572	ILPGEKPYK
0.9	1059.585876	0.002972	CRSLTGKPK

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

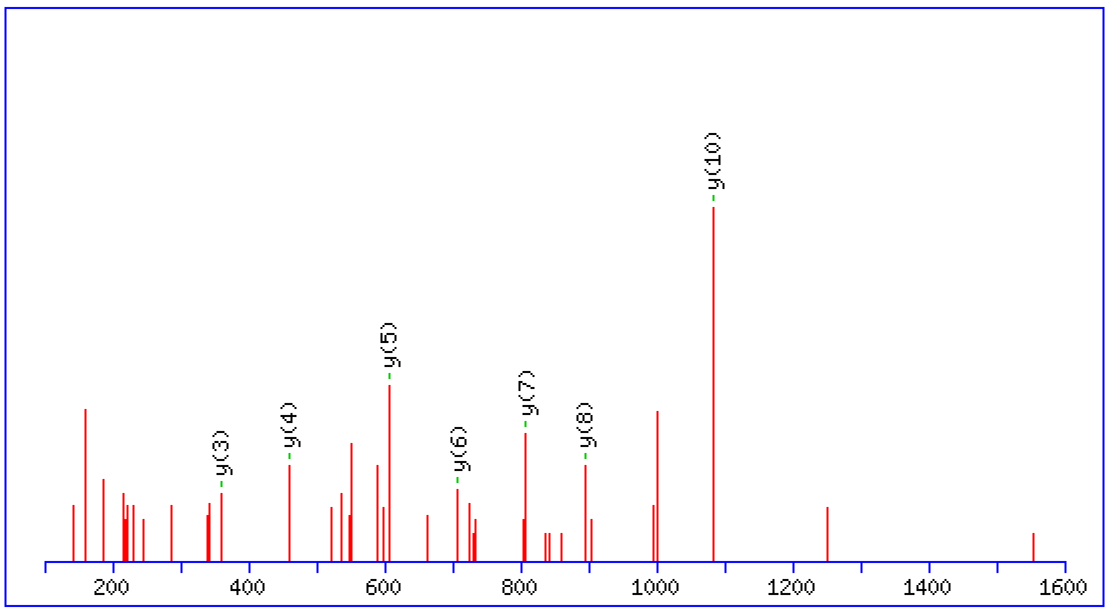
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SVSTSTTFVQGR**
Found in **DNJB2_HUMAN**, DnaJ homolog subfamily B member 2 OS=Homo sapiens GN=DNAJB2 PE=2 SV=3

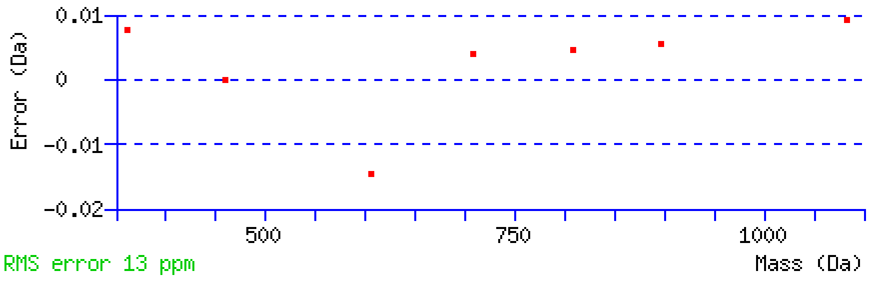
Match to Query 34435: 1268.635828 from(635.325190,2+) rtinseconds(1592) index(14331)
Title: Locus:1.1.1.2024.45
Data file 2011-11-12 - TFD - EP 5-4.mgf

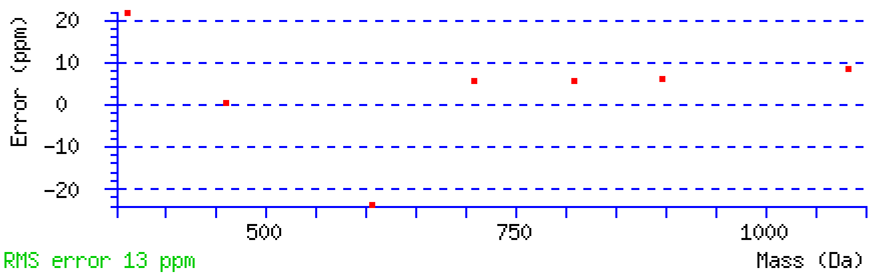
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1268.636108
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 57 **Expect:** 4.8e-006
Matches : 7/104 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							12
2	187.107718	94.057497			169.097153	85.052214	V	1182.611329	591.809302	1165.584780	583.296028	1164.600764	582.804020	11
3	274.139746	137.573511			256.129181	128.568229	S	***1083.542915***	542.275096	1066.516366	533.761821	1065.532350	533.269813	10
4	375.187425	188.097351			357.176860	179.092068	T	996.510887	498.759081	979.484338	490.245807	978.500322	489.753799	9
5	462.219453	231.613364			444.208888	222.608082	S	***895.463208***	448.235242	878.436659	439.721967	877.452643	439.229959	8
6	563.267132	282.137204			545.256567	273.131922	T	***808.431180***	404.719228	791.404631	396.205953	790.420615	395.713945	7
7	664.314811	332.661044			646.304246	323.655761	T	***707.383501***	354.195388	690.356952	345.682114	689.372936	345.190106	6
8	811.383225	406.195251			793.372660	397.189968	F	***606.335822***	303.671549	589.309273	295.158274			5
9	910.451639	455.729458			892.441074	446.724175	V	***459.267408***	230.137342	442.240859	221.624067			4
10	1038.510217	519.758747	1021.483668	511.245472	1020.499652	510.753464	Q	***360.198994***	180.603135	343.172445	172.089860			3
11	1095.531681	548.269478	1078.505132	539.756204	1077.521116	539.264196	G	232.140416	116.573846	215.113867	108.060571			2
12							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
57.4	1268.636108	-0.000280	SVSTSTTFVQGR
0.7	1268.624847	0.010981	GEGPEVDVNLPK
0.4	1268.647293	-0.011465	EGSLPAPAARPR

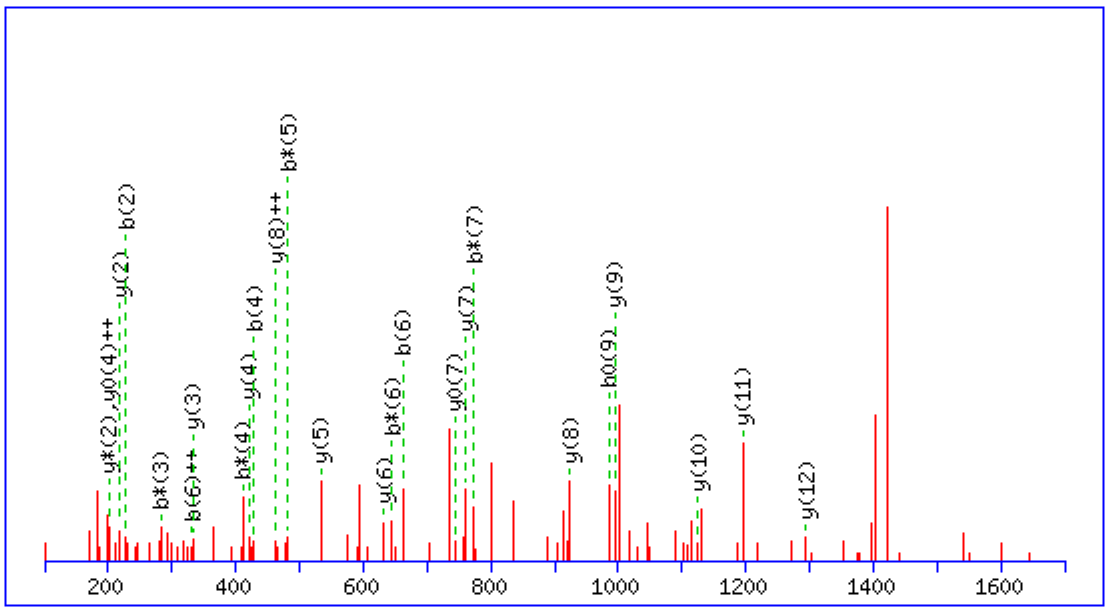
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QVAEAYEVLSDAK**
Found in **DNJB3_HUMAN**, DnaJ homolog subfamily B member 3 OS=Homo sapiens GN=DNAJB3 PE=1 SV=1

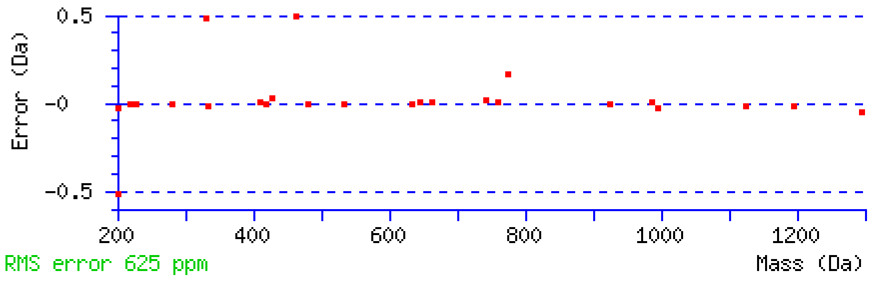
Match to Query 40686: 1421.702088 from(711.858320,2+) rtinseconds(2499) index(27941)
Title: Locus:1.1.1.2537.43
Data file 2011-11-12 - TFD - EP 5-5.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●

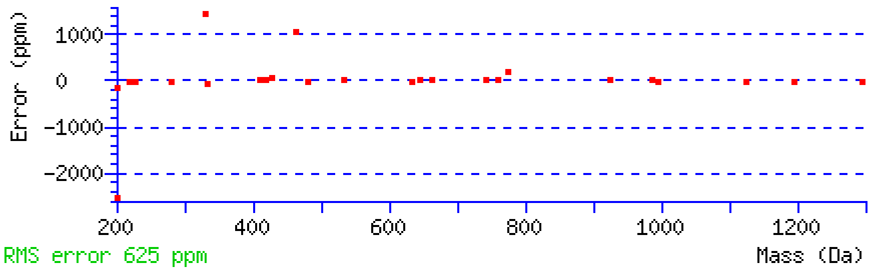


Monoisotopic mass of neutral peptide Mr(calc): 1421.703796
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 56 **Expect:** 3.2e-005
Matches : 25/134 fragment ions using 63 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	129.065854	65.036565	112.039305	56.523291			Q							13
2	**228.134268**	114.570772	211.107719	106.057498			V	***1294.652524***	647.829900	1277.625975	639.316626	1276.641959	638.824618	12
3	299.171382	150.089329	282.144833	141.576055			A	***1195.584110***	598.295693	1178.557561	589.782419	1177.573545	589.290411	11
4	**428.213975**	214.610626	411.187426	206.097351	410.203410	205.605343	E	***1124.546996***	562.777136	1107.520447	554.263862	1106.536431	553.771854	10
5	499.251089	250.129183	482.224540	241.615908	481.240524	241.123900	A	***995.504403***	498.255840	978.477854	489.742565	977.493838	489.250557	9
6	**662.314418**	331.660847	645.287869	323.147573	644.303853	322.655565	Y	***924.467289***	462.737283	907.440740	454.224008	906.456724	453.732000	8
7	791.357011	396.182144	774.330462	387.668869	773.346446	387.176861	E	***761.403960***	381.205618	744.377411	372.692344	743.393395	372.200336	7
8	890.425425	445.716351	873.398876	437.203076	872.414860	436.711068	V	***632.361367***	316.684322	615.334818	308.171047	614.350802	307.679039	6
9	1003.509489	502.258383	986.482940	493.745108	985.498924	493.253100	L	***533.292953***	267.150115	516.266404	258.636840	515.282388	258.144832	5
10	1090.541517	545.774397	1073.514968	537.261122	1072.530952	536.769114	S	***420.208889***	210.608082	403.182340	202.094808	402.198324	201.602800	4
11	1205.568460	603.287868	1188.541911	594.774594	1187.557895	594.282586	D	***333.176861***	167.092069	316.150312	158.578794	315.166296	158.086786	3
12	1276.605574	638.806425	1259.579025	630.293151	1258.595009	629.801143	A	***218.149918***	109.578597	201.123369	101.065322			2
13							K	147.112804	74.060040	130.086255	65.546765			1



RMS error 625 ppm



RMS error 625 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.3	1421.703796	-0.001708	QVAEAYEVLSDAK

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

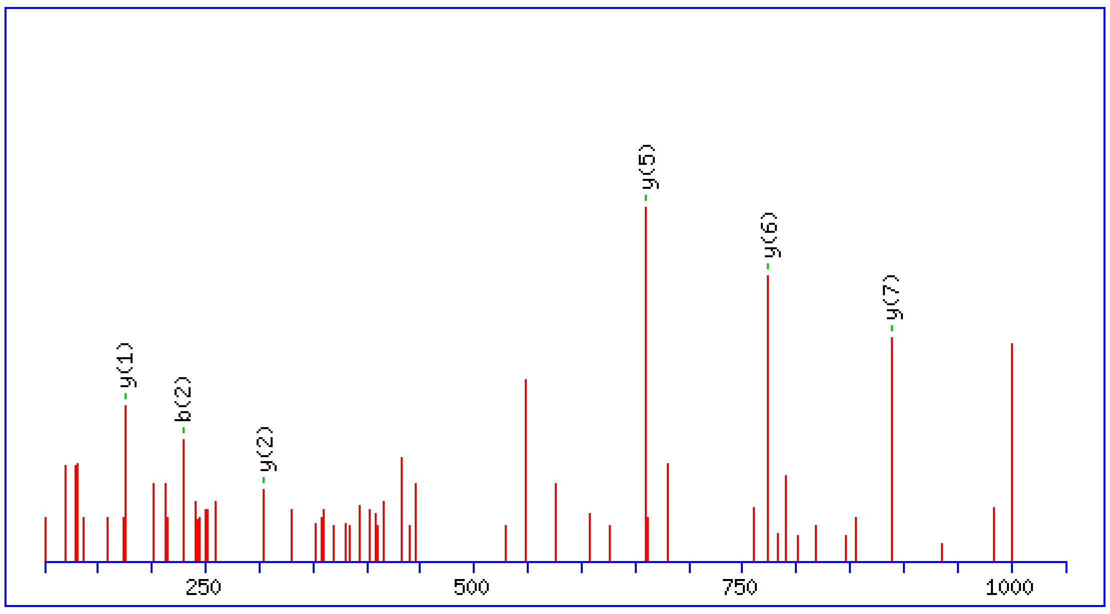
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LDLEARER**
Found in **DJC17_HUMAN**, DnaJ homolog subfamily C member 17 OS=Homo sapiens GN=DNAJC17 PE=1 SV=1

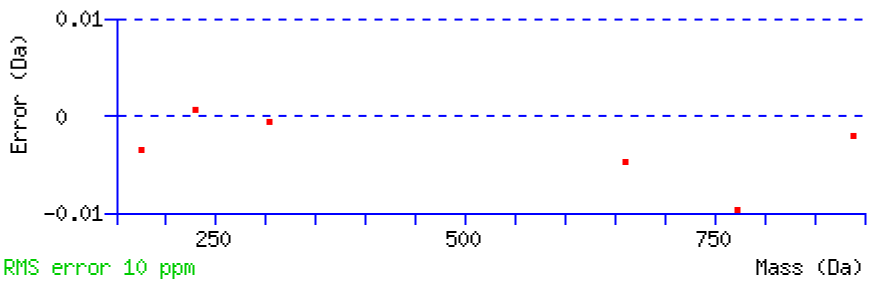
Match to Query 15769: 1000.529008 from(501.271780,2+) rtinseconds(2172) index(25059)
Title: Locus:1.1.1.2175.14
Data file 2011-11-10 - TFD - EP 4-1.mgf

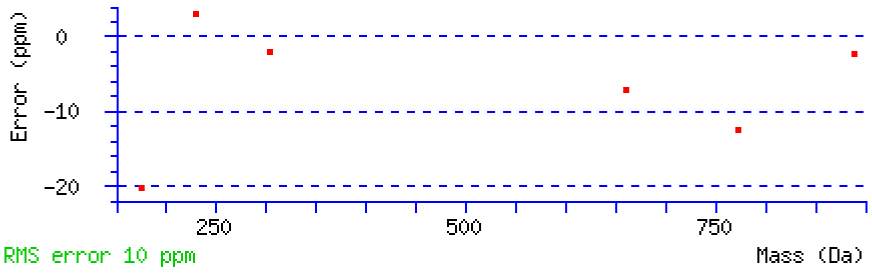
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



`Monoisotopic mass of neutral peptide Mr(calc): 1000.530121`
`Fixed modifications: Propionamide (C) (apply to specified residues or termini only)`
`Ions Score: 36  Expect: 0.0037`
`Matches : 6/70 fragment ions using 9 most intense peaks   (help)`

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.091340	57.549308					**L**							8
2	229.118283	115.062779			211.107718	106.057497	**D**	***888.453370***	444.730323	871.426821	436.217049	870.442805	435.725041	7
3	342.202347	171.604811			324.191782	162.599529	**L**	***773.426427***	387.216852	756.399878	378.703577	755.415862	378.211569	6
4	471.244940	236.126108			453.234375	227.120826	**E**	***660.342363***	330.674820	643.315814	322.161545	642.331798	321.669537	5
5	542.282054	271.644665			524.271489	262.639383	**A**	531.299770	266.153523	514.273221	257.640249	513.289205	257.148241	4
6	698.383165	349.695221	681.356616	341.181946	680.372600	340.689938	**R**	460.262656	230.634966	443.236107	222.121692	442.252091	221.629684	3
7	827.425758	414.216517	810.399209	405.703242	809.415193	405.211234	**E**	***304.161545***	152.584411	287.134996	144.071136	286.150980	143.579128	2
8							**R**	***175.118952***	88.063114	158.092403	79.549840			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.7	1000.530121	-0.001113	LDLEARER
10.0	1000.534180	-0.005172	LDQPFIPR
10.0	1000.534180	-0.005172	LDQPFIPR
9.2	1000.530136	-0.001128	DPSLLRER
8.8	1000.530121	-0.001113	VLEERAER
6.6	1000.530136	-0.001128	KPLSQQER
6.3	1000.530151	-0.001143	AVAGQGELTR
5.9	1000.530151	-0.001143	SPKPSGLQR
3.1	1000.530121	-0.001113	QALNEISAR
1.2	1000.530136	-0.001128	NAGETLLQR

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

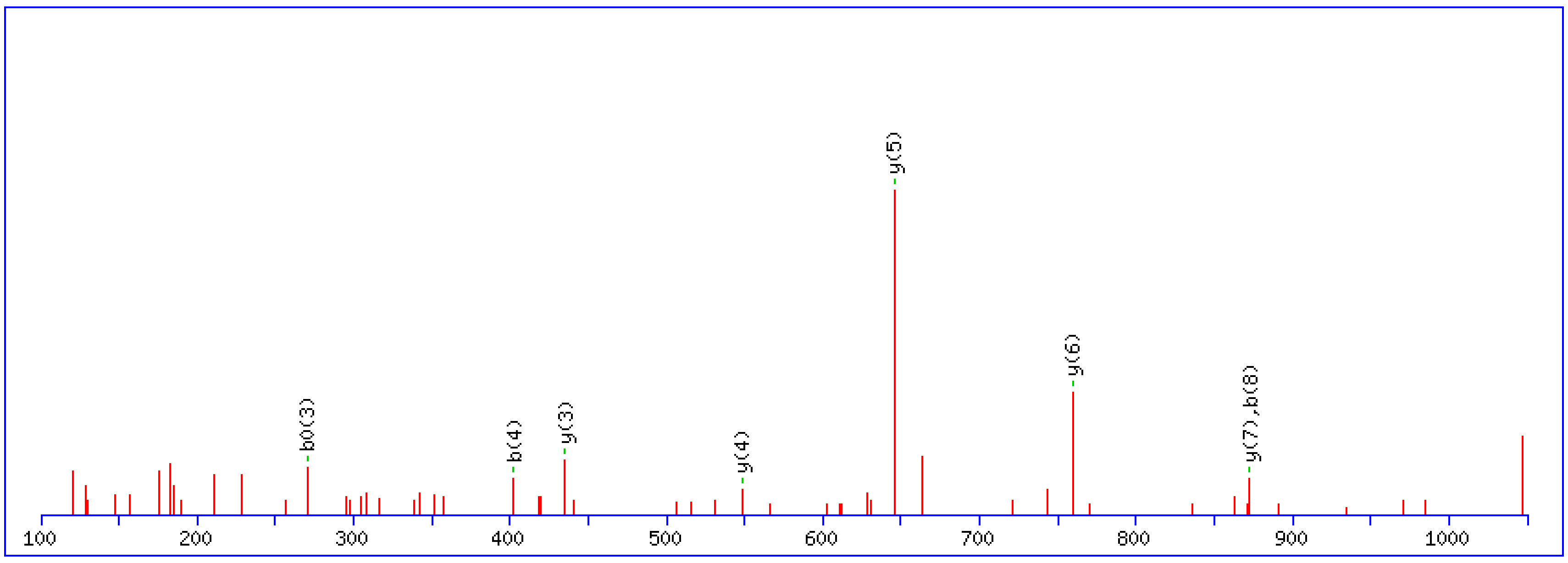
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SSLNPILFR**
Found in **OST48_HUMAN**, Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Homo sapiens GN=DDOST PE=1 SV=4

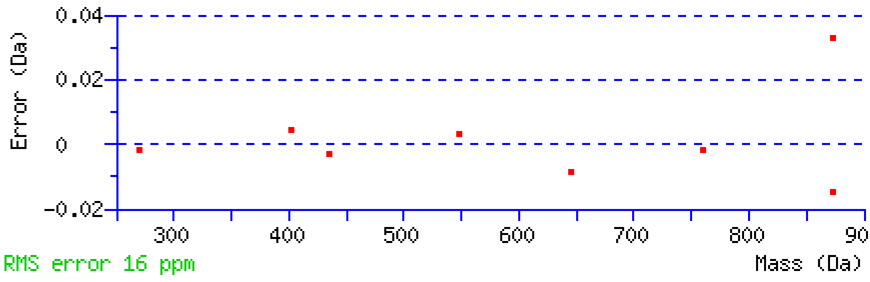
Match to Query 17822: 1045.589108 from(523.801830,2+) rtinseconds(2810) index(38603)
Title: Locus:1.1.1.1459.16
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 1.mgf

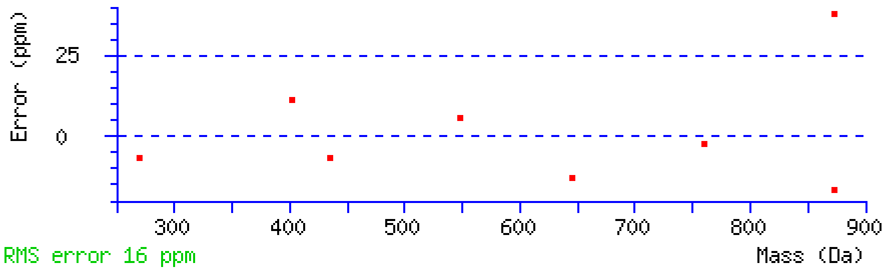
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1050] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1045.592010
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 40  Expect: 0.00085
Matches : 8/76 fragment ions using 9 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	**S**							9
2	175.071332	88.039304			157.060767	79.034021	**S**	959.567277	480.287277	942.540728	471.774002	941.556712	471.281994	8
3	288.155396	144.581336			270.144831	135.576054	**L**	***872.535249***	436.771263	855.508700	428.257988			7
4	**402.198323**	201.602800	385.171774	193.089525	384.187758	192.597517	**N**	***759.451185***	380.229231	742.424636	371.715956			6
5	499.251087	250.129182	482.224538	241.615907	481.240522	241.123899	**P**	***645.408258***	323.207767	628.381709	314.694493			5
6	612.335151	306.671214	595.308602	298.157939	594.324586	297.665931	**I**	***548.355494***	274.681385	531.328945	266.168111			4
7	725.419215	363.213246	708.392666	354.699971	707.408650	354.207963	**L**	***435.271430***	218.139353	418.244881	209.626079			3
8	**872.487629**	436.747453	855.461080	428.234178	854.477064	427.742170	**F**	322.187366	161.597321	305.160817	153.084047			2
9							**R**	175.118952	88.063114	158.092403	79.549840			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.4	1045.592010	-0.002902	SSLNPILFR
11.9	1045.592010	-0.002902	YLAVTNPLR
7.8	1045.592010	-0.002902	NLILSAFPR
7.7	1045.592026	-0.002918	SSLPPPPPVR
6.8	1045.592041	-0.002933	VDVKGIFPR
6.6	1045.587997	0.001111	SRTSLTLPR
3.4	1045.595367	-0.006259	IMASLNLLR
2.4	1045.595383	-0.006275	SLAGVSLMLR
1.3	1045.591995	-0.002887	EKIYQPLR
1.0	1045.592026	-0.002918	NEVVGLIFR

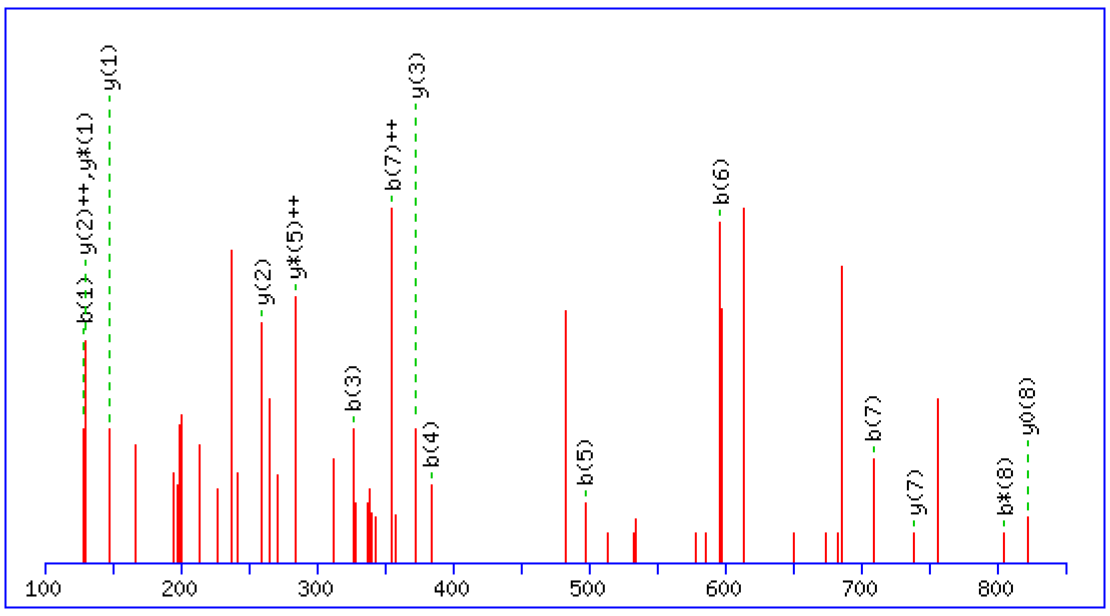
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KTPGPVLPK**
Found in **RED1_HUMAN**, Double-stranded RNA-specific editase 1 OS=Homo sapiens GN=ADARB1 PE=1 SV=1

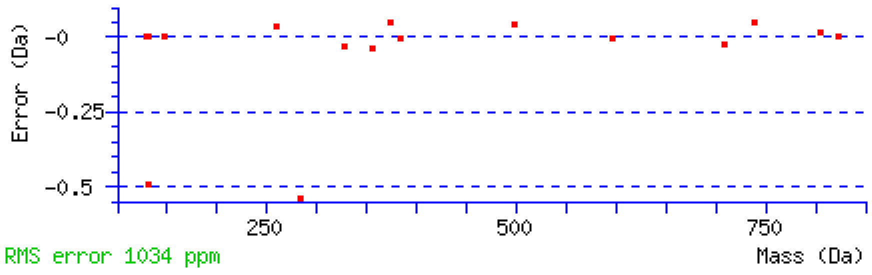
Match to Query 13553: 967.576568 from(484.795560,2+) rtinseconds(2931) index(40172)
Title: Locus:1.1.1.2457.3
Data file 2011-11-10 - TFD - EP 3-4.mgf

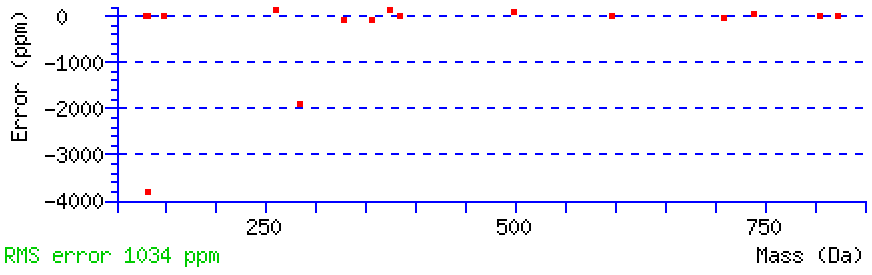
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 967.570236
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P5      : Oxidation (P)
P8      : Oxidation (P)
Ions Score: 40  Expect: 0.00042
Matches : 17/80 fragment ions using 32 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	***129.102239***	65.054757	112.075690	56.541483			K							9
2	230.149918	115.578597	213.123369	107.065323	212.139353	106.573315	T	840.482547	420.744912	823.455998	412.231637	822.471982	411.739629	8
3	***327.202682***	164.104979	310.176133	155.591705	309.192117	155.099697	P	**739.434868**	370.221072	722.408319	361.707798			7
4	***384.224146***	192.615711	367.197597	184.102437	366.213581	183.610429	G	642.382104	321.694690	625.355555	313.181416			6
5	***497.271825***	249.139550	480.245276	240.626276	479.261260	240.134268	P	585.360640	293.183958	568.334091	284.670684			5
6	***596.340239***	298.673758	579.313690	290.160483	578.329674	289.668475	V	472.312961	236.660118	455.286412	228.146844			4
7	***709.424303***	355.215790	692.397754	346.702515	691.413738	346.210507	L	**373.244547**	187.125912	356.217998	178.612637			3
8	***822.471982***	411.739629	805.445433	403.226355	804.461417	402.734347	P	**260.160483**	130.583879	243.133934	122.070605			2
9							K	**147.112804**	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.2	967.570236	0.006332	KTPGPVLPK
26.1	967.570221	0.006347	AVLNPTPIK
24.3	967.570221	0.006347	KPPGSLLPK
22.8	967.570221	0.006347	KLKPPPPK
22.1	967.570236	0.006332	KTPGPVLPK
21.1	967.570221	0.006347	KPPGSLLPK
19.4	967.570221	0.006347	VSPKLAPPK
15.4	967.570221	0.006347	APGKLPLPK
15.0	967.570221	0.006347	AKTVPVPEK
14.4	967.570221	0.006347	KIPPPKPK

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

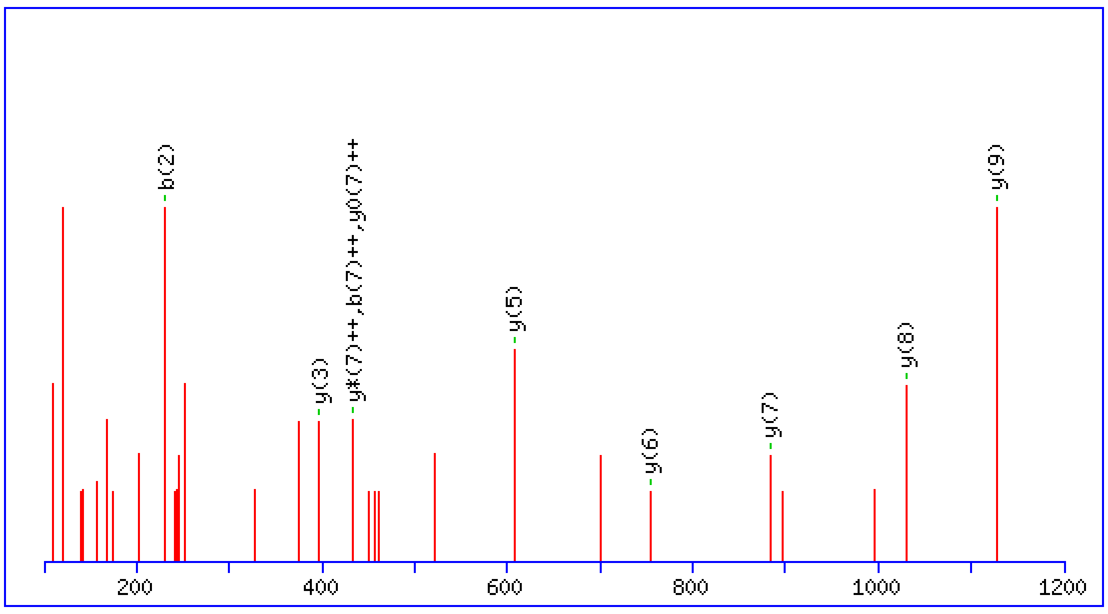
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TEIPFEFPLHLK**
Found in **DSCR3_HUMAN**, Down syndrome critical region protein 3 OS=Homo sapiens GN=DSCR3 PE=1 SV=1

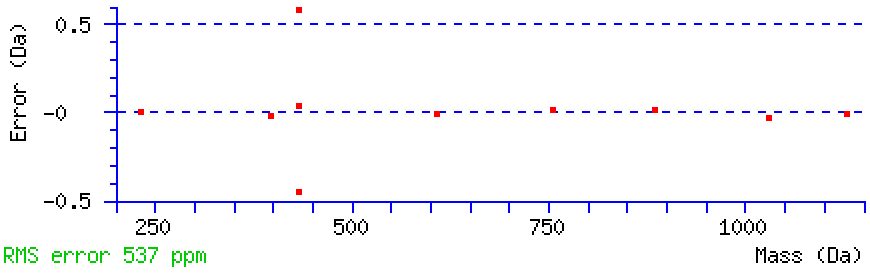
Match to Query 43565: 1469.789982 from(490.937270,3+) rtinseconds(3548) index(50312)
Title: Locus:1.1.1.2640.11
Data file 2011-11-12 - TFD - EP 6-5.mgf

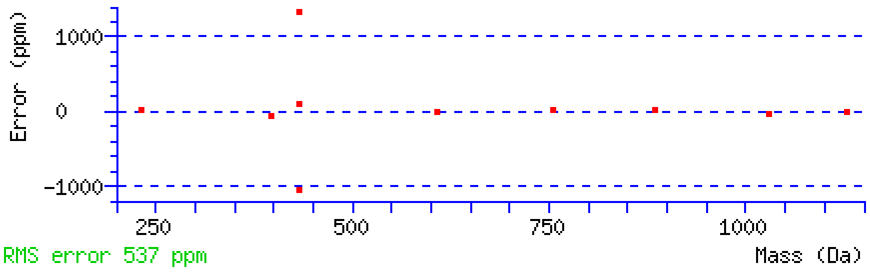
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1469.791840
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.00023
Matches : 10/98 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	102.054955	51.531116	84.044390	42.525833	T							12
2	231.097548	116.052412	213.086983	107.047130	E	1369.751450	685.379363	1352.724901	676.866089	1351.740885	676.374080	11
3	344.181612	172.594444	326.171047	163.589162	I	1240.708857	620.858066	1223.682308	612.344792	1222.698292	611.852784	10
4	441.234376	221.120826	423.223811	212.115544	P	***1127.624793***	564.316035	1110.598244	555.802760	1109.614228	555.310752	9
5	588.302790	294.655033	570.292225	285.649751	F	***1030.572029***	515.789652	1013.545480	507.276378	1012.561464	506.784370	8
6	717.345383	359.176330	699.334818	350.171047	E	***883.503615***	442.255446	866.477066	433.742171	865.493050	433.250163	7
7	864.413797	432.710537	846.403232	423.705254	F	***754.461022***	377.734149	737.434473	369.220874			6
8	961.466561	481.236919	943.455996	472.231636	P	***607.392608***	304.199942	590.366059	295.686668			5
9	1074.550625	537.778951	1056.540060	528.773668	L	510.339844	255.673560	493.313295	247.160285			4
10	1211.609537	606.308407	1193.598972	597.303124	H	***397.255780***	199.131528	380.229231	190.618253			3
11	1324.693601	662.850439	1306.683036	653.845156	L	260.196868	130.602072	243.170319	122.088797			2
12					K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.6	1469.791840	-0.001858	TEIPFEFPLHLK
1.7	1469.783783	0.006199	ASGKSPQPQLLSNK
1.7	1469.783783	0.006199	ASGKSPQPQLLSNK
0.1	1469.783783	0.006199	IEAQDGPGLLSRAK

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

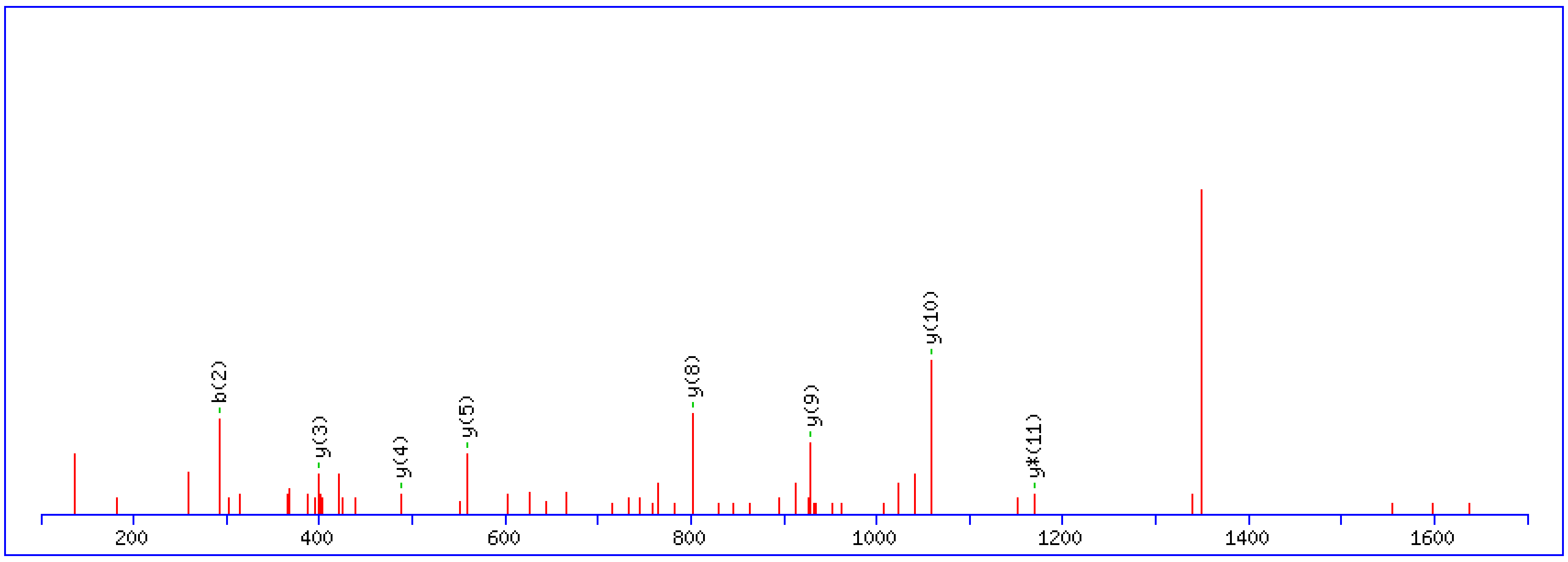
{MATRIX}{SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YQEQGGEASPQR**
Found in **DBNL_HUMAN**, Drebrin-like protein OS=Homo sapiens GN=DBNL PE=1 SV=1

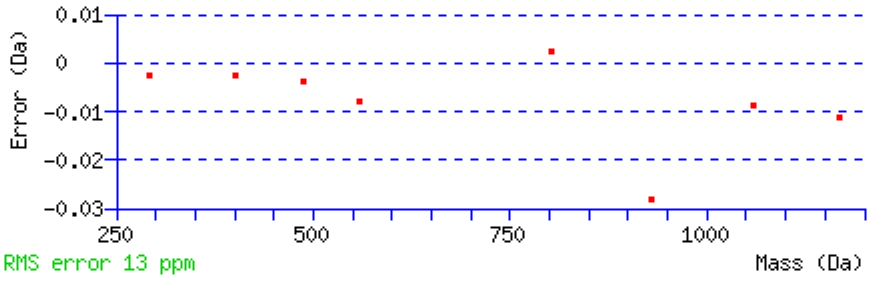
Match to Query 43280: 1348.594268 from(675.304410,2+) rtinseconds(847) index(1312)
Title: Locus:1.1.1.709.17
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 1.mgf

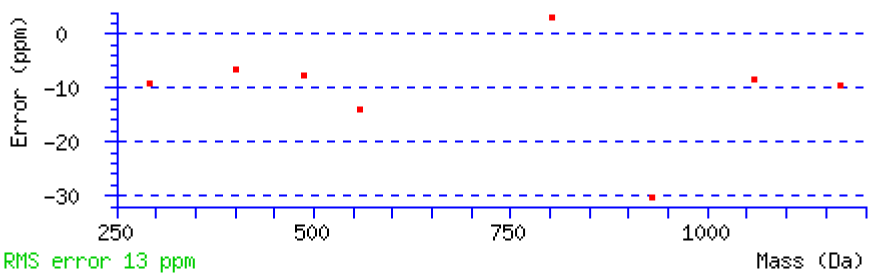
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1348.600739
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 42 **Expect:** 0.0005
Matches : 8/120 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	164.070605	82.538940					Y							12
2	292.129183	146.568230	275.102634	138.054955			Q	1186.544706	593.775991	1169.518157	585.262717	1168.534141	584.770708	11
3	421.171776	211.089526	404.145227	202.576252	403.161211	202.084244	E	***1058.486128***	529.746702	1041.459579	521.233428	1040.475563	520.741420	10
4	549.230354	275.118815	532.203805	266.605541	531.219789	266.113533	Q	***929.443535***	465.225405	912.416986	456.712131	911.432970	456.220123	9
5	606.251818	303.629547	589.225269	295.116273	588.241253	294.624265	G	***801.384957***	401.196117	784.358408	392.682842	783.374392	392.190834	8
6	663.273282	332.140279	646.246733	323.627005	645.262717	323.134997	G	744.363493	372.685385	727.336944	364.172110	726.352928	363.680102	7
7	792.315875	396.661576	775.289326	388.148301	774.305310	387.656293	E	687.342029	344.174652	670.315480	335.661378	669.331464	335.169370	6
8	863.352989	432.180133	846.326440	423.666858	845.342424	423.174850	A	***558.299436***	279.653356	541.272887	271.140081	540.288871	270.648073	5
9	950.385017	475.696147	933.358468	467.182872	932.374452	466.690864	S	***487.262322***	244.134799	470.235773	235.621524	469.251757	235.129516	4
10	1047.437781	524.222529	1030.411232	515.709254	1029.427216	515.217246	P	***400.230294***	200.618785	383.203745	192.105510			3
11	1175.496359	588.251818	1158.469810	579.738543	1157.485794	579.246535	Q	303.177530	152.092403	286.150981	143.579128			2
12							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.4	1348.600739	-0.006471	YQEQGGEASPQR

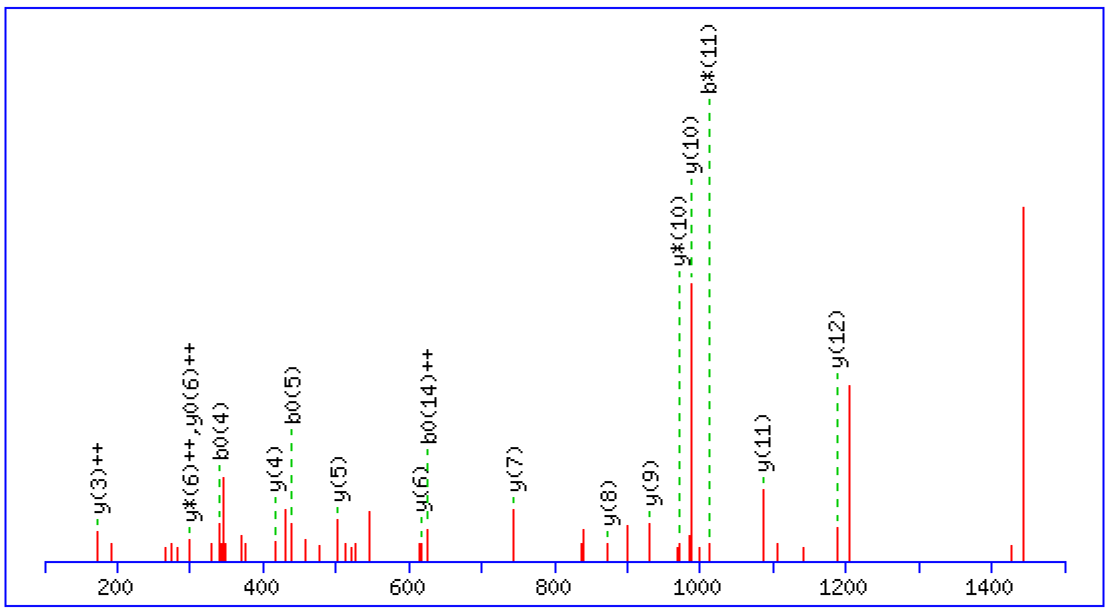
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ASVTVGGEQISAIGR**
Found in **DTD1_HUMAN**, D-tyrosyl-tRNA(Tyr) deacylase 1 OS=Homo sapiens GN=DTD1 PE=1 SV=2

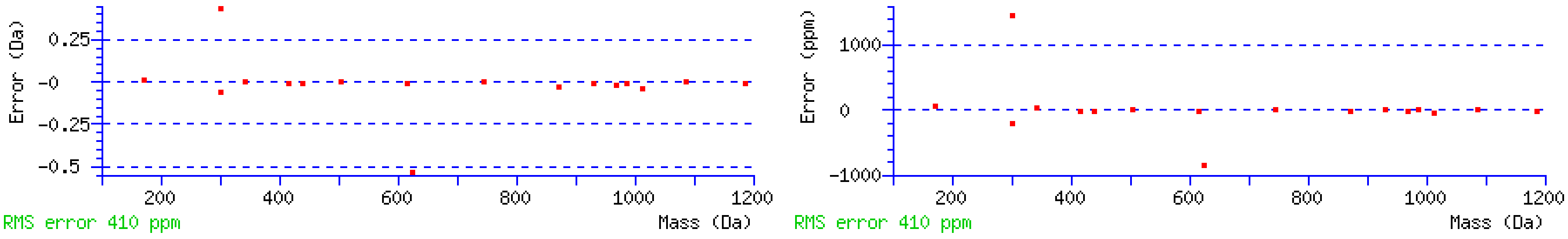
Match to Query 38494: 1443.763728 from(722.889140,2+) rtinseconds(2332) index(24081)
Title: Locus:1.1.1.2509.45
Data file 2011-11-10 - TFD - EP 3-5.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1443.768158
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 38   Expect: 0.00042
Matches : 17/142 fragment ions using 37 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.044390	36.525833					A							15
2	159.076418	80.041847			141.065853	71.036564	S	1373.738320	687.372798	1356.711771	678.859524	1355.727755	678.367515	14
3	258.144832	129.576054			240.134267	120.570772	V	1286.706292	643.856784	1269.679743	635.343509	1268.695727	634.851501	13
4	359.192511	180.099894			341.181946	171.094611	T	***1187.637878***	594.322577	1170.611329	585.809302	1169.627313	585.317294	12
5	458.260925	229.634101			440.250360	220.628818	V	***1086.590199***	543.798738	1069.563650	535.285463	1068.579634	534.793455	11
6	515.282389	258.144833			497.271824	249.139550	G	***987.521785***	494.264530	970.495236	485.751256	969.511220	485.259248	10
7	572.303853	286.655565			554.293288	277.650282	G	***930.500321***	465.753798	913.473772	457.240524	912.489756	456.748516	9
8	701.346446	351.176861			683.335881	342.171579	E	***873.478857***	437.243066	856.452308	428.729792	855.468292	428.237784	8
9	829.405024	415.206150	812.378475	406.692876	811.394459	406.200868	Q	***744.436264***	372.721770	727.409715	364.208495	726.425699	363.716487	7
10	942.489088	471.748182	925.462539	463.234908	924.478523	462.742900	I	***616.377686***	308.692481	599.351137	300.179206	598.367121	299.687198	6
11	1029.521116	515.264196	1012.494567	506.750922	1011.510551	506.258914	S	***503.293622***	252.150449	486.267073	243.637174	485.283057	243.145166	5
12	1100.558230	550.782753	1083.531681	542.269479	1082.547665	541.777471	A	***416.261594***	208.634435	399.235045	200.121160			4
13	1213.642294	607.324785	1196.615745	598.811511	1195.631729	598.319503	I	345.224480	173.115878	328.197931	164.602603			3
14	1270.663758	635.835517	1253.637209	627.322243	1252.653193	626.830234	G	232.140416	116.573846	215.113867	108.060571			2
15							R	175.118952	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.3	1443.768158	-0.004430	ASVTVGGEQISAIGR
2.2	1443.760956	0.002772	FPTALVLDPTPNK

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

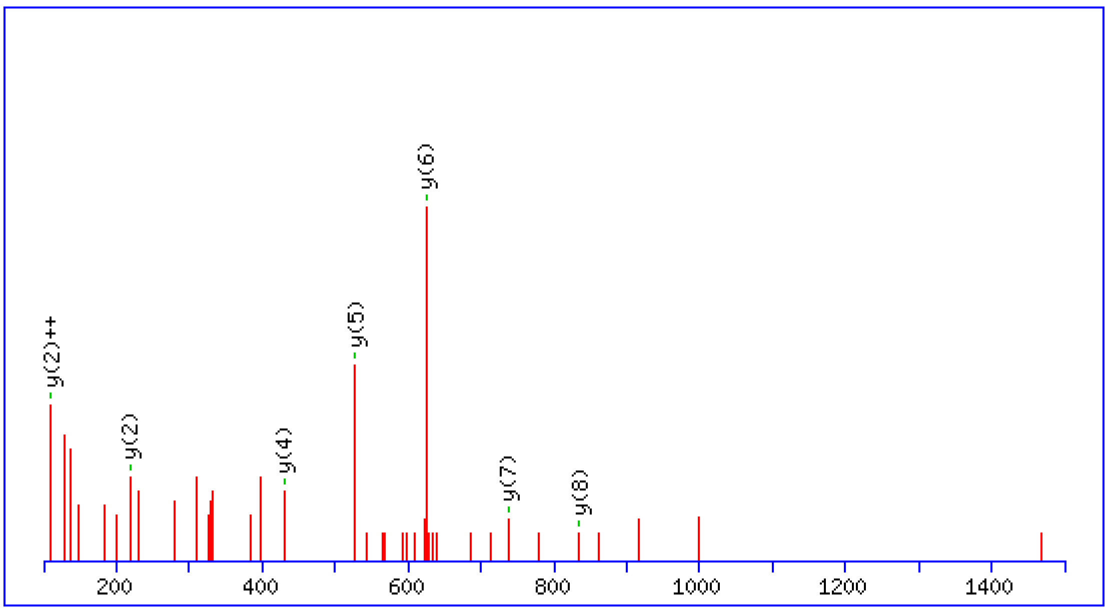
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YPIPPPDAK**
Found in **MP2K1_HUMAN**, Dual specificity mitogen-activated protein kinase kinase 1 OS=Homo sapiens GN=MAP2K1 PE=1 SV=2

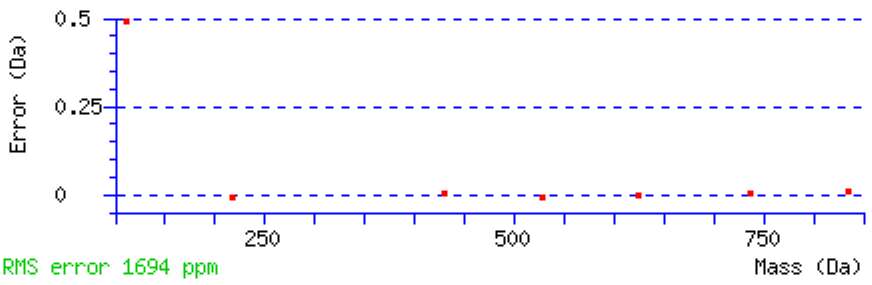
Match to Query 16508: 996.528108 from(499.271330,2+) rtinseconds(1634) index(15779)
Title: Locus:1.1.1.2009.24
Data file 2011-11-14 - TFD - EP 8-4.mgf

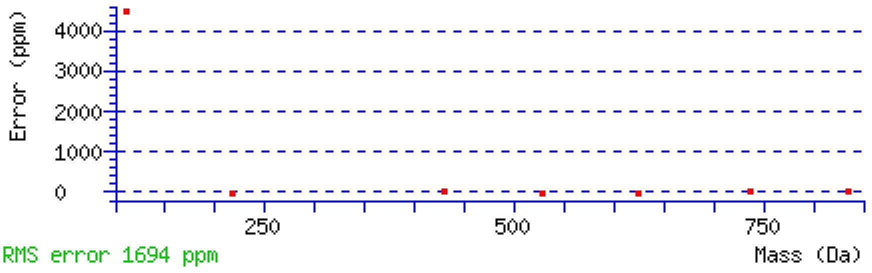
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 996.528015
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 50  Expect: 6.6e-005
Matches : 7/64 fragment ions using 9 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.070605	82.538940			Y							9
2	261.123369	131.065322			P	*834.471981*	417.739629	817.445432	409.226354	816.461416	408.734346	8
3	374.207433	187.607354			I	*737.419217*	369.213247	720.392668	360.699972	719.408652	360.207964	7
4	471.260197	236.133737			P	*624.335153*	312.671215	607.308604	304.157940	606.324588	303.665932	6
5	568.312961	284.660119			P	*527.282389*	264.144833	510.255840	255.631558	509.271824	255.139550	5
6	665.365725	333.186501			P	*430.229625*	215.618450	413.203076	207.105176	412.219060	206.613168	4
7	780.392668	390.699972	762.382103	381.694690	D	333.176861	167.092068	316.150312	158.578794	315.166296	158.086786	3
8	851.429782	426.218529	833.419217	417.213247	A	*218.149918*	109.578597	201.123369	101.065322			2
9					K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.5	996.528015	0.000093	YPIPPPDAK
4.7	996.531372	-0.003264	KMIEGLYK
3.4	996.524033	0.004075	QGSVVPGPPK
1.1	996.535233	-0.007125	HPVSTKANK

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

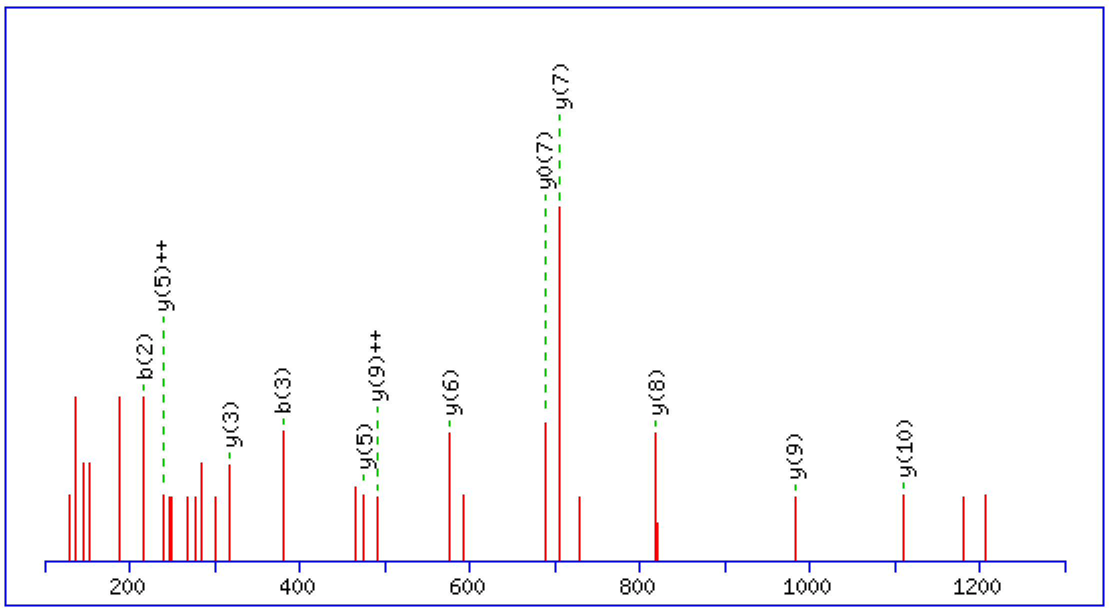
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SEYIETASGNK**
Found in **DCTN5_HUMAN**, Dynactin subunit 5 OS=Homo sapiens GN=DCTN5 PE=1 SV=1

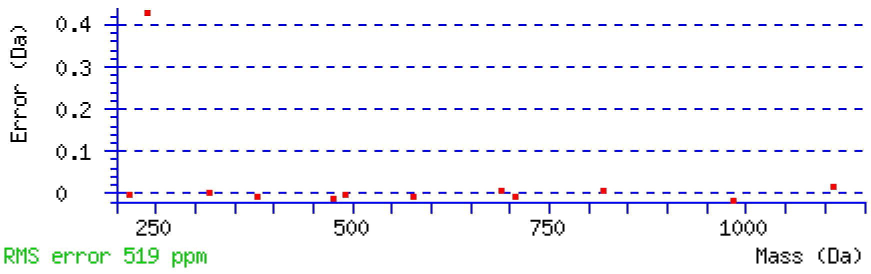
Match to Query 29422: 1197.555968 from(599.785260,2+) rtinseconds(1236) index(5272)
Title: Locus:1.1.1.1737.42
Data file 2011-11-10 - TFD - EP 3-6.mgf

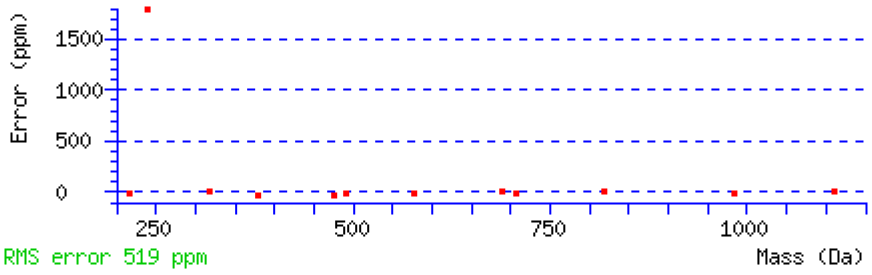
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 1300 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1197.551315
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 52  Expect: 1.6e-005
Matches : 12/96 fragment ions using 20 most intense peaks    (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	**S**							11
2	**217.081897**	109.044586			199.071332	100.039304	**E**	***1111.526595***	556.266936	1094.500046	547.753661	1093.516030	547.261653	10
3	**380.145226**	190.576251			362.134661	181.570969	**Y**	***982.484002***	491.745639	965.457453	483.232365	964.473437	482.740357	9
4	493.229290	247.118283			475.218725	238.113001	**I**	***819.420673***	410.213975	802.394124	401.700700	801.410108	401.208692	8
5	622.271883	311.639580			604.261318	302.634297	**E**	***706.336609***	353.671943	689.310060	345.158668	688.326044	344.666660	7
6	723.319562	362.163419			705.308997	353.158137	**T**	***577.294016***	289.150646	560.267467	280.637372	559.283451	280.145364	6
7	794.356676	397.681976			776.346111	388.676694	**A**	***476.246337***	238.626806	459.219788	230.113532	458.235772	229.621524	5
8	881.388704	441.197990			863.378139	432.192708	**S**	405.209223	203.108249	388.182674	194.594975	387.198658	194.102967	4
9	938.410168	469.708722			920.399603	460.703440	**G**	***318.177195***	159.592235	301.150646	151.078961			3
10	1052.453095	526.730186	1035.426546	518.216911	1034.442530	517.724903	**N**	261.155731	131.081503	244.129182	122.568229			2
11							**K**	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.5	1197.551315	0.004653	SEYIETASGNK
1.4	1197.560074	-0.004106	DTKMSFQWR

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

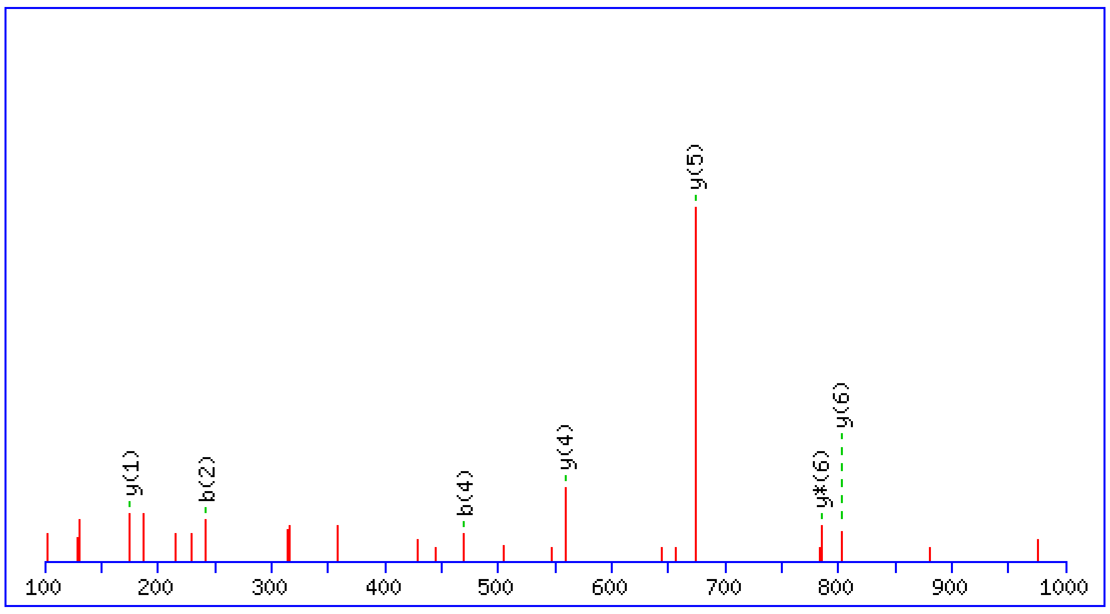
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IQDLDRR**
Found in **DYH17_HUMAN**, Dynein heavy chain 17, axonemal OS=Homo sapiens GN=DNAH17 PE=2 SV=2

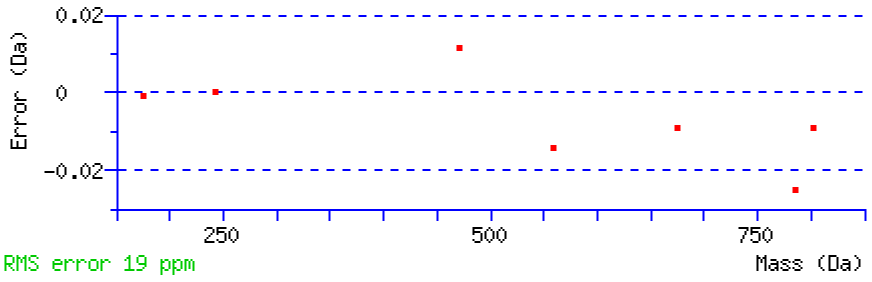
Match to Query 6180: 914.485868 from(458.250210,2+) rtinseconds(1568) index(3733)
Title: Locus:1.1.1.2245.9
Data file 2011-11-10 - TFD - EP 3-8.mgf

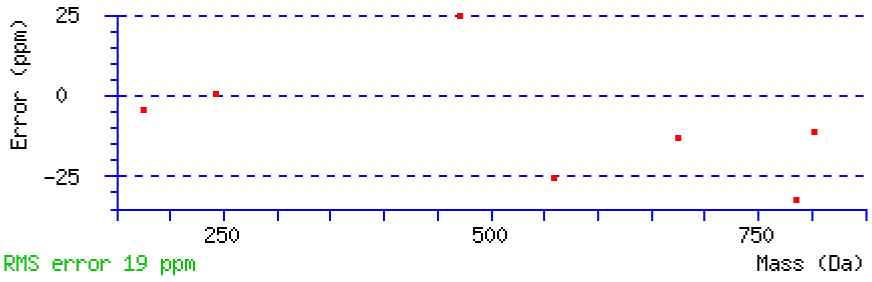
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 914.493362
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 35  Expect: 0.0053
Matches : 7/62 fragment ions using 8 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					I							7
2	**242.149918**	121.578597	225.123369	113.065323			Q	***802.416591***	401.711934	785.390042	393.198659	784.406026	392.706651	6
3	357.176861	179.092069	340.150312	170.578794	339.166296	170.086786	D	***674.358013***	337.682645	657.331464	329.169370	656.347448	328.677362	5
4	**470.260925**	235.634101	453.234376	227.120826	452.250360	226.628818	L	***559.331070***	280.169173	542.304521	271.655898	541.320505	271.163890	4
5	585.287868	293.147572	568.261319	284.634298	567.277303	284.142290	D	446.247006	223.627141	429.220457	215.113866	428.236441	214.621858	3
6	741.388979	371.198128	724.362430	362.684853	723.378414	362.192845	R	331.220063	166.113669	314.193514	157.600395			2
7							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.0	914.493362	-0.007494	IQDLDRR
31.5	914.482117	0.003751	LQDAEIAR
22.2	914.482147	0.003721	LQIDVDGR
19.7	914.482132	0.003736	KPDPASLR
16.6	914.493362	-0.007494	LSRSPSPR
15.7	914.482117	0.003751	IQEELQR
15.7	914.493378	-0.007510	IQTVGQNR
15.7	914.482117	0.003751	LQEIQER
15.7	914.482117	0.003751	LQQELER
15.7	914.482147	0.003721	LQVTPEGR

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

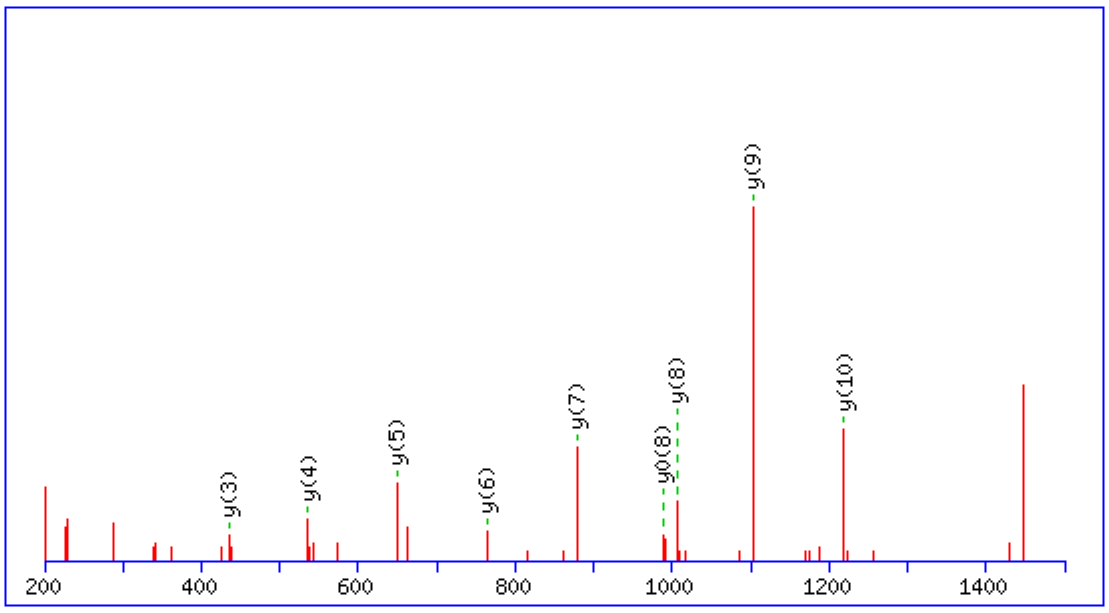
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DIDPQNDLTFLR**
Found in **DLRB1_HUMAN**, Dynein light chain roadblock-type 1 OS=Homo sapiens GN=DYNLRB1 PE=1 SV=3

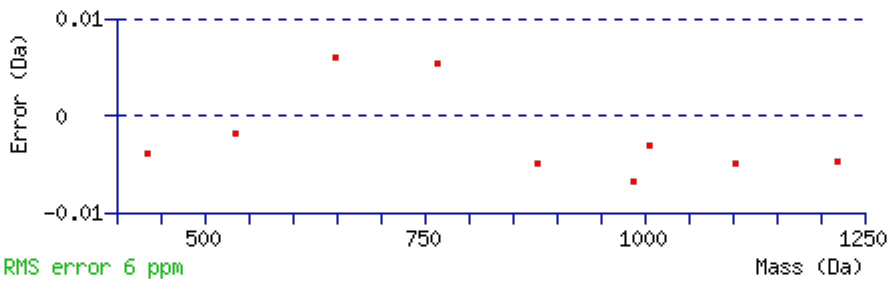
Match to Query 38781: 1445.714088 from(723.864320,2+) rtinseconds(3265) index(38359)
Title: Locus:1.1.1.2578.22
Data file 2011-11-12 - TFD - EP 6-7.mgf

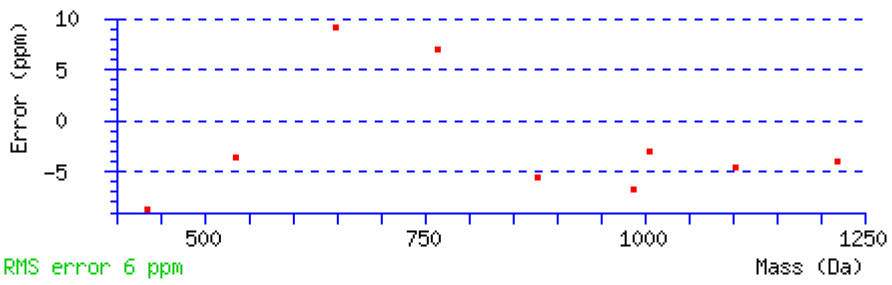
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1445.715057
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 74 **Expect:** 1.2e-007
Matches : 9/118 fragment ions using 12 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	116.034219	58.520748			98.023654	49.515465	D							12
2	229.118283	115.062779			211.107718	106.057497	I	1331.695392	666.351334	1314.668843	657.838059	1313.684827	657.346051	11
3	344.145226	172.576251			326.134661	163.570968	D	***1218.611328***	609.809302	1201.584779	601.296028	1200.600763	600.804019	10
4	441.197990	221.102633			423.187425	212.097350	P	***1103.584385***	552.295830	1086.557836	543.782556	1085.573820	543.290548	9
5	569.256568	285.131922	552.230019	276.618648	551.246003	276.126640	Q	***1006.531621***	503.769449	989.505072	495.256174	988.521056	494.764166	8
6	683.299495	342.153386	666.272946	333.640111	665.288930	333.148103	N	***878.473043***	439.740160	861.446494	431.226885	860.462478	430.734877	7
7	798.326438	399.666857	781.299889	391.153582	780.315873	390.661574	D	***764.430116***	382.718696	747.403567	374.205422	746.419551	373.713414	6
8	911.410502	456.208889	894.383953	447.695614	893.399937	447.203606	L	***649.403173***	325.205225	632.376624	316.691950	631.392608	316.199942	5
9	1012.458181	506.732729	995.431632	498.219454	994.447616	497.727446	T	***536.319109***	268.663193	519.292560	260.149918	518.308544	259.657910	4
10	1159.526595	580.266936	1142.500046	571.753661	1141.516030	571.261653	F	***435.271430***	218.139353	418.244881	209.626078			3
11	1272.610659	636.808967	1255.584110	628.295693	1254.600094	627.803685	L	288.203016	144.605146	271.176467	136.091871			2
12							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
73.7	1445.715057	-0.000969	DIDPQNDLTFLR
0.0	1445.699814	0.014274	TEIDSPTNVVTDR

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

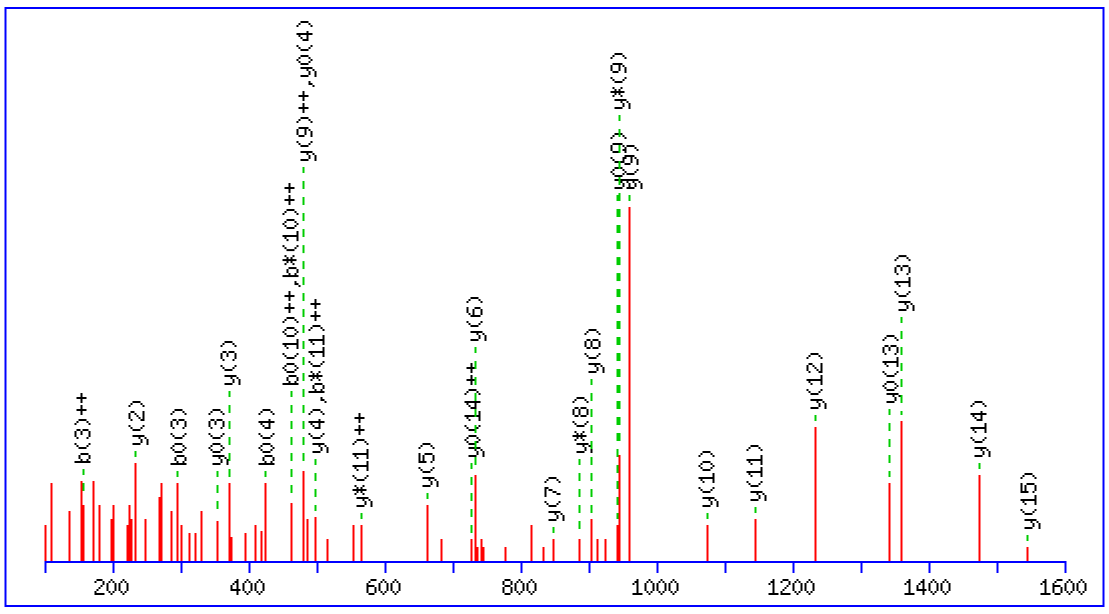
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EAIESAIGGNAYQHSK**
Found in **DYLT1_HUMAN**, Dynein light chain Tctex-type 1 OS=Homo sapiens GN=DYNLT1 PE=1 SV=1

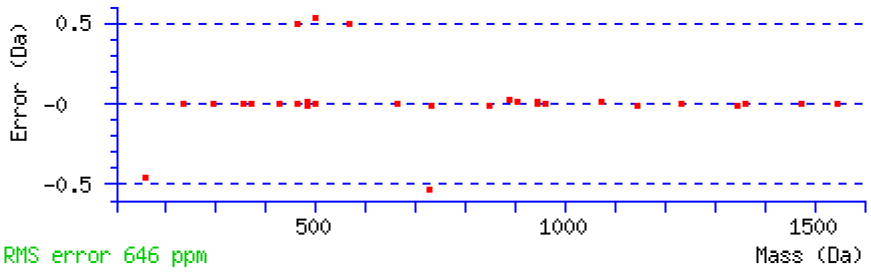
Match to Query 43895: 1673.798112 from(558.939980,3+) rtinseconds(1811) index(13643)
Title: Locus:1.1.1.2020.35
Data file 2011-11-12 - TFD - EP 6-7.mgf

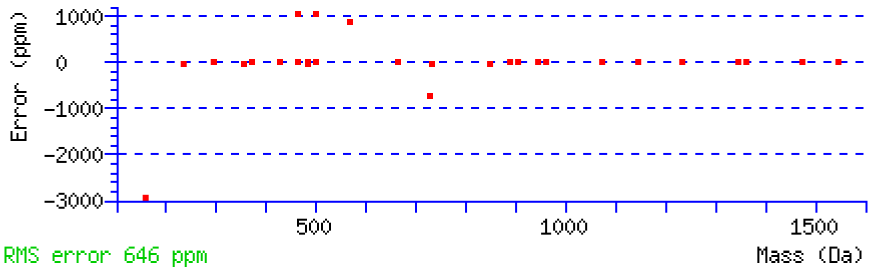
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1673.800873
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 105  Expect: 2.5e-010
Matches : 29/160 fragment ions using 42 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	E							16
2	201.086983	101.047130			183.076418	92.041847	A	***1545.765597***	773.386436	1528.739048	764.873162	1527.755032	764.381154	15
3	314.171047	157.589161			296.160482	148.583879	I	***1474.728483***	737.867879	1457.701934	729.354605	1456.717918	728.862597	14
4	443.213640	222.110458			425.203075	213.105176	E	***1361.644419***	681.325848	1344.617870	672.812573	1343.633854	672.320565	13
5	530.245668	265.626472			512.235103	256.621190	S	***1232.601826***	616.804551	1215.575277	608.291276	1214.591261	607.799268	12
6	601.282782	301.145029			583.272217	292.139747	A	***1145.569798***	573.288537	1128.543249	564.775263	1127.559233	564.283255	11
7	714.366846	357.687061			696.356281	348.681779	I	***1074.532684***	537.769980	1057.506135	529.256706	1056.522119	528.764698	10
8	771.388310	386.197793			753.377745	377.192511	G	***961.448620***	481.227948	944.422071	472.714674	943.438055	472.222666	9
9	828.409774	414.708525			810.399209	405.703243	G	***904.427156***	452.717216	887.400607	444.203941	886.416591	443.711933	8
10	942.452701	471.729989	925.426152	463.216714	924.442136	462.724706	N	***847.405692***	424.206484	830.379143	415.693209	829.395127	415.201201	7
11	1013.489815	507.248546	996.463266	498.735271	995.479250	498.243263	A	***733.362765***	367.185021	716.336216	358.671746	715.352200	358.179738	6
12	1176.553144	588.780210	1159.526595	580.266936	1158.542579	579.774927	Y	***662.325651***	331.666464	645.299102	323.153189	644.315086	322.661181	5
13	1304.611722	652.809499	1287.585173	644.296224	1286.601157	643.804216	Q	***499.262322***	250.134799	482.235773	241.621524	481.251757	241.129516	4
14	1441.670634	721.338955	1424.644085	712.825680	1423.660069	712.333672	H	***371.203744***	186.105510	354.177195	177.592236	353.193179	177.100228	3
15	1528.702662	764.854969	1511.676113	756.341695	1510.692097	755.849686	S	***234.144832***	117.576054	217.118283	109.062780	216.134267	108.570772	2
16							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
104.7	1673.800873	-0.002761	EAIESAIGGNAYQHSK
2.2	1673.799561	-0.001449	VLESTPAESSEGLDPK

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

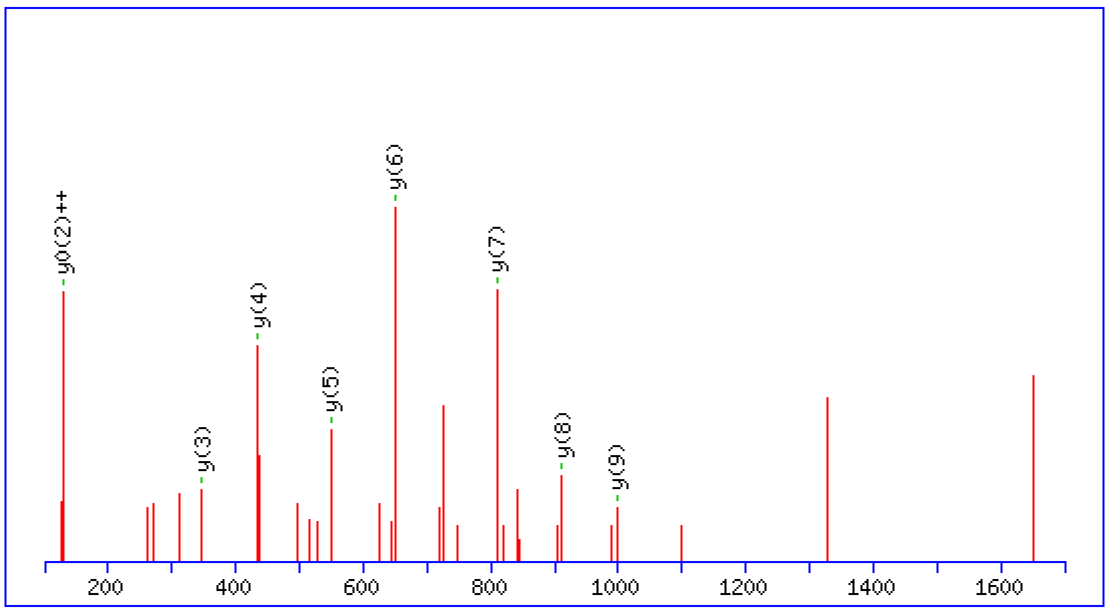
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AKPPSSSSTCTDSATR**
Found in **DTBP1_HUMAN**, Dysbindin OS=Homo sapiens GN=DTNBP1 PE=1 SV=1

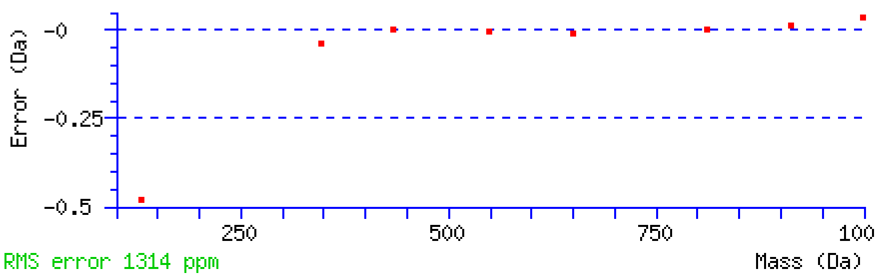
Match to Query 937944: 1651.750032 from(551.590620,3+) rtinseconds(734) index(324782)
Title: Locus:1.1.1.610.10
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

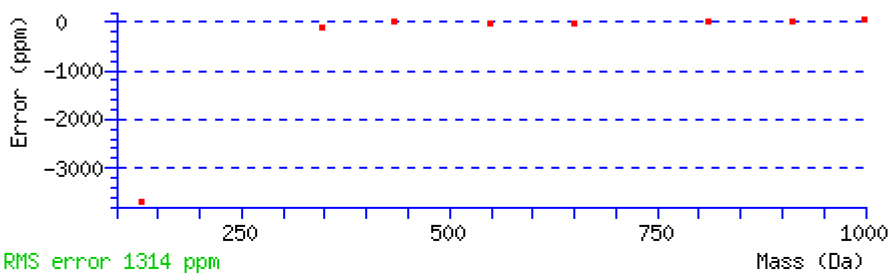
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1651.747162
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 54  Expect: 1.3e-005
Matches : 8/168 fragment ions using 11 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							16
2	200.139353	100.573315	183.112804	92.060040			K	1581.717326	791.362301	1564.690777	782.849027	1563.706761	782.357019	15
3	297.192117	149.099696	280.165568	140.586422			P	1453.622363	727.314820	1436.595814	718.801545	1435.611798	718.309537	14
4	394.244881	197.626079	377.218332	189.112804			P	1356.569599	678.788438	1339.543050	670.275163	1338.559034	669.783155	13
5	481.276909	241.142092	464.250360	232.628818	463.266344	232.136810	S	1259.516835	630.262056	1242.490286	621.748781	1241.506270	621.256773	12
6	568.308937	284.658107	551.282388	276.144832	550.298372	275.652824	S	1172.484807	586.746042	1155.458258	578.232767	1154.474242	577.740759	11
7	655.340965	328.174121	638.314416	319.660846	637.330400	319.168838	S	1085.452779	543.230028	1068.426230	534.716753	1067.442214	534.224745	10
8	742.372993	371.690135	725.346444	363.176860	724.362428	362.684852	S	***998.420751***	499.714014	981.394202	491.200739	980.410186	490.708731	9
9	843.420672	422.213974	826.394123	413.700699	825.410107	413.208691	T	***911.388723***	456.198000	894.362174	447.684725	893.378158	447.192717	8
10	1003.451321	502.229299	986.424772	493.716024	985.440756	493.224016	C	***810.341044***	405.674160	793.314495	397.160886	792.330479	396.668878	7
11	1104.499000	552.753138	1087.472451	544.239864	1086.488435	543.747856	T	***650.310395***	325.658836	633.283846	317.145561	632.299830	316.653553	6
12	1219.525943	610.266610	1202.499394	601.753335	1201.515378	601.261327	D	***549.262716***	275.134996	532.236167	266.621722	531.252151	266.129714	5
13	1306.557971	653.782624	1289.531422	645.269349	1288.547406	644.777341	S	***434.235773***	217.621524	417.209224	209.108250	416.225208	208.616242	4
14	1377.595085	689.301181	1360.568536	680.787906	1359.584520	680.295898	A	***347.203745***	174.105510	330.177196	165.592236	329.193180	165.100228	3
15	1478.642764	739.825020	1461.616215	731.311746	1460.632199	730.819738	T	276.166631	138.586953	259.140082	130.073679	258.156066	129.581671	2
16							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.0	1651.747162	0.002870	AKPPSSSSTCTDSATR
1.6	1651.748688	0.001344	ACLFSSVAQGYFRM
0.5	1651.738785	0.011247	WHVCPYCAKEFR

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

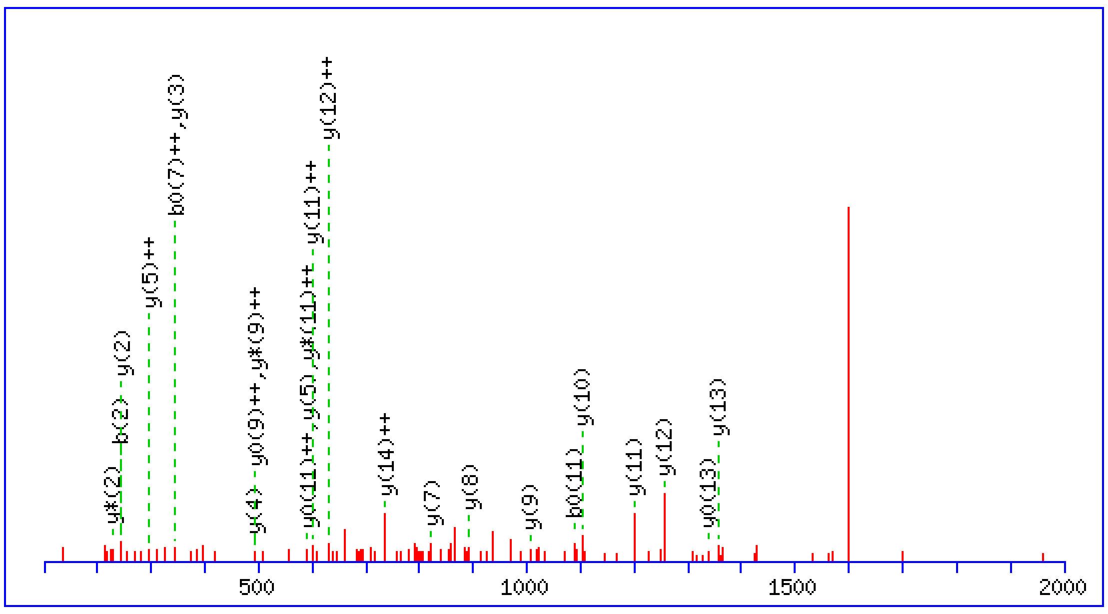
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELVGPPLAETVFTPK**
Found in **RBP2_HUMAN**, E3 SUMO-protein ligase RanBP2 OS=Homo sapiens GN=RANBP2 PE=1 SV=2

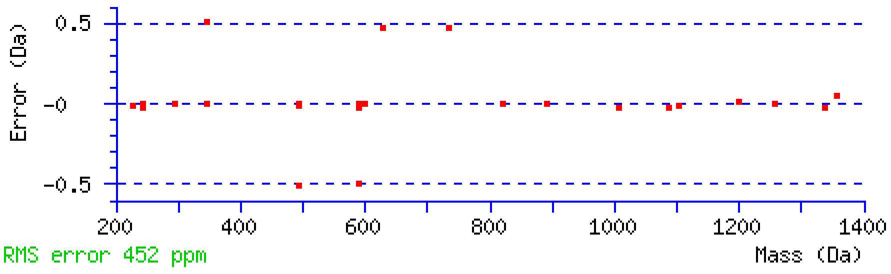
Match to Query 46513: 1596.881048 from(799.447800,2+) rtinseconds(3318) index(43964)
Title: Locus:1.1.1.2808.41
Data file 2011-11-12 - TFD - EP 5-1.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●

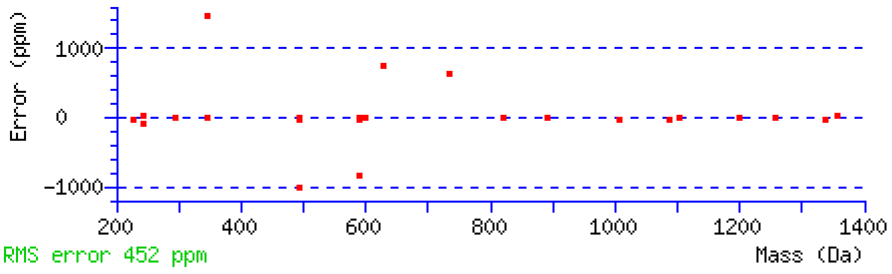


```
Monoisotopic mass of neutral peptide Mr(calc): 1596.876312
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 51   Expect: 1.7e-005
Matches : 24/136 fragment ions using 54 most intense peaks   (help)
```

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	130.049869	65.528572	112.039304	56.523290	E							15
2	243.133933	122.070605	225.123368	113.065322	L	1468.840995	734.924136	1451.814446	726.410861	1450.830430	725.918853	14
3	342.202347	171.604812	324.191782	162.599529	V	***1355.756931***	678.382104	1338.730382	669.868829	1337.746366	669.376821	13
4	399.223811	200.115544	381.213246	191.110261	G	***1256.688517***	628.847897	1239.661968	620.334622	1238.677952	619.842614	12
5	496.276575	248.641926	478.266010	239.636643	P	***1199.667053***	600.337165	1182.640504	591.823890	1181.656488	591.331882	11
6	593.329339	297.168308	575.318774	288.163025	P	***1102.614289***	551.810783	1085.587740	543.297508	1084.603724	542.805500	10
7	706.413403	353.710340	688.402838	344.705057	L	***1005.561525***	503.284401	988.534976	494.771126	987.550960	494.279118	9
8	777.450517	389.228897	759.439952	380.223614	A	***892.477461***	446.742369	875.450912	438.229094	874.466896	437.737086	8
9	906.493110	453.750193	888.482545	444.744911	E	***821.440347***	411.223812	804.413798	402.710537	803.429782	402.218529	7
10	1007.540789	504.274033	989.530224	495.268750	T	692.397754	346.702515	675.371205	338.189241	674.387189	337.697233	6
11	1106.609203	553.808240	1088.598638	544.802957	V	***591.350075***	296.178676	574.323526	287.665401	573.339510	287.173393	5
12	1253.677617	627.342447	1235.667052	618.337164	F	***492.281661***	246.644469	475.255112	238.131194	474.271096	237.639186	4
13	1354.725296	677.866286	1336.714731	668.861004	T	***345.213247***	173.110262	328.186698	164.596987	327.202682	164.104979	3
14	1451.778060	726.392668	1433.767495	717.387386	P	***244.165568***	122.586422	227.139019	114.073148			2
15					K	147.112804	74.060040	130.086255	65.546765			1



RMS error 452 ppm



RMS error 452 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.3	1596.876312	0.004736	ELVGPPLAETVFTPK
0.6	1596.872284	0.008764	EPVVGGTLSPLALANK

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

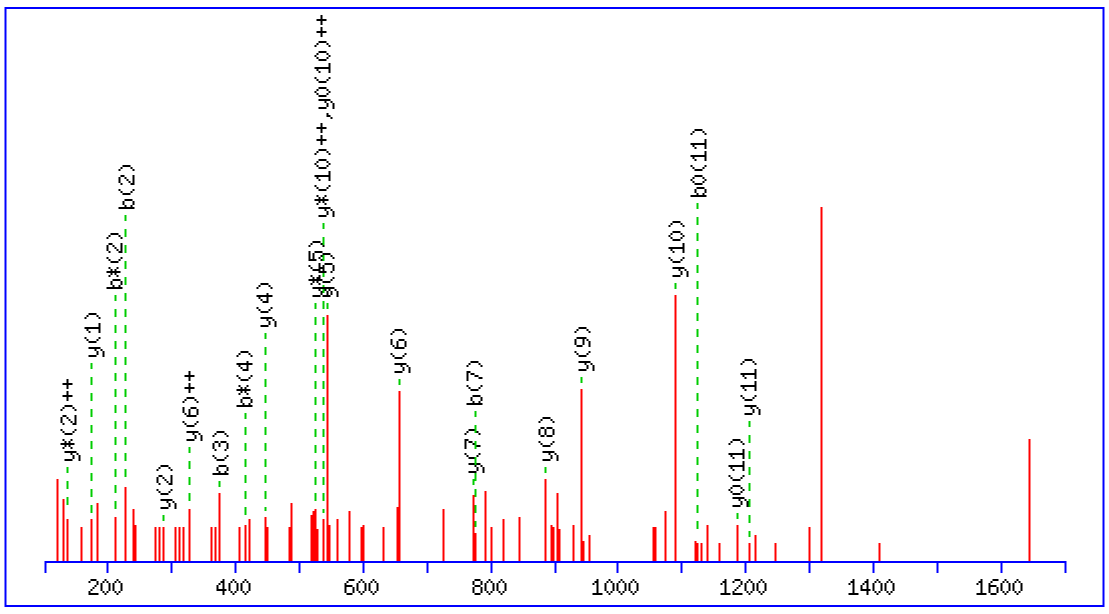
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LNFGDDIPSALR**
Found in **CHIP_HUMAN**, E3 ubiquitin-protein ligase CHIP OS=Homo sapiens GN=STUB1 PE=1 SV=2

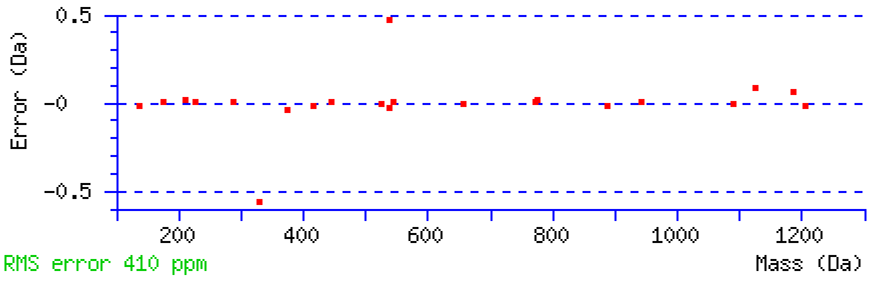
Match to Query 36347: 1316.685308 from(659.349930,2+) rtinseconds(3096) index(43702)
Title: Locus:1.1.1.2503.23
Data file 2011-11-10 - TFD - EP 4-4.mgf

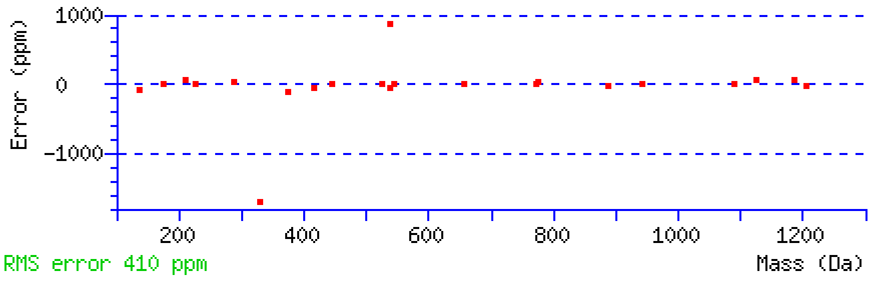
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1316.672455
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 45 **Expect:** 0.00025
Matches : 22/116 fragment ions using 66 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					L							12
2	**228.134267**	114.570771	211.107718	106.057497			N	***1204.595677***	602.801477	1187.569128	594.288202	1186.585112	593.796194	11
3	**375.202681**	188.104978	358.176132	179.591704			F	***1090.552750***	545.780013	1073.526201	537.266738	1072.542185	536.774730	10
4	432.224145	216.615710	415.197596	208.102436			G	***943.484336***	472.245806	926.457787	463.732531	925.473771	463.240523	9
5	547.251088	274.129182	530.224539	265.615907	529.240523	265.123899	D	***886.462872***	443.735074	869.436323	435.221799	868.452307	434.729791	8
6	662.278031	331.642653	645.251482	323.129379	644.267466	322.637371	D	***771.435929***	386.221603	754.409380	377.708328	753.425364	377.216320	7
7	**775.362095**	388.184686	758.335546	379.671411	757.351530	379.179403	I	***656.408986***	328.708131	639.382437	320.194857	638.398421	319.702849	6
8	872.414859	436.711068	855.388310	428.197793	854.404294	427.705785	P	***543.324922***	272.166099	526.298373	263.652825	525.314357	263.160817	5
9	959.446887	480.227082	942.420338	471.713807	941.436322	471.221799	S	***446.272158***	223.639717	429.245609	215.126442	428.261593	214.634434	4
10	1030.484001	515.745639	1013.457452	507.232364	1012.473436	506.740356	A	359.240130	180.123703	342.213581	171.610428			3
11	1143.568065	572.287670	1126.541516	563.774396	1125.557500	563.282388	L	***288.203016***	144.605146	271.176467	136.091871			2
12							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.3	1316.672455	0.012853	LNFGDDIPSALR
1.9	1316.675842	0.009466	NSVPVTVAMVER
1.2	1316.675827	0.009481	QVQLMQSGAEVK

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

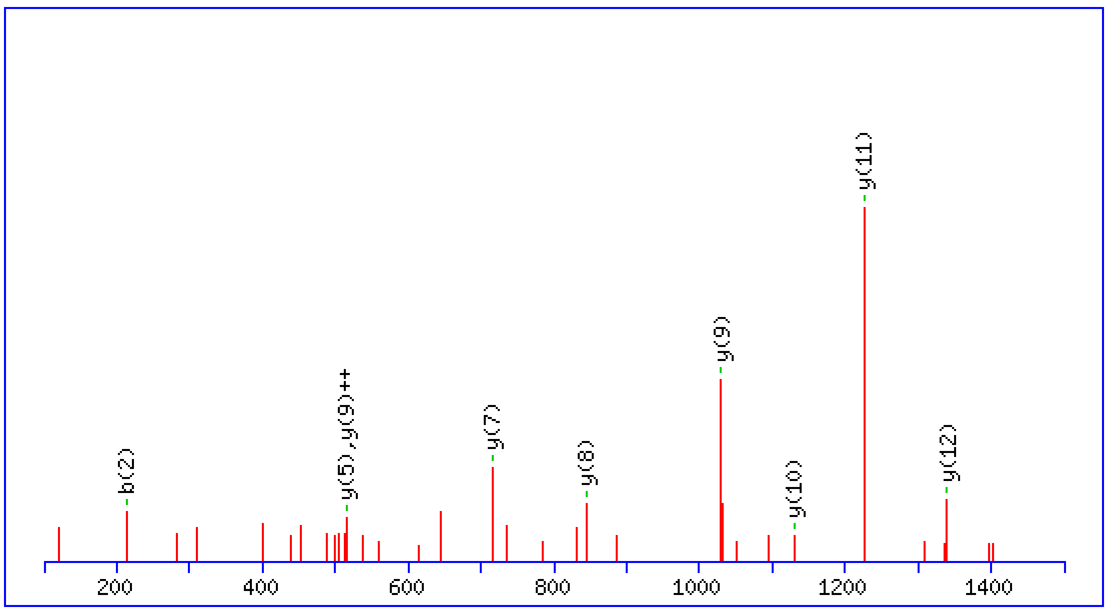
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLLPVWEAEGLGLR**
Found in **HECD3_HUMAN**, E3 ubiquitin-protein ligase HECTD3 OS=Homo sapiens GN=HECTD3 PE=1 SV=1

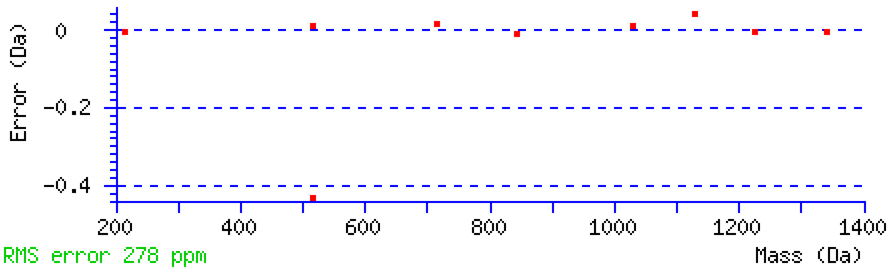
Match to Query 49672: 1550.889988 from(776.452270,2+) rtinseconds(3894) index(57725)
Title: Locus:1.1.1.2910.40
Data file 2011-11-10 - TFD - EP 3-2.mgf

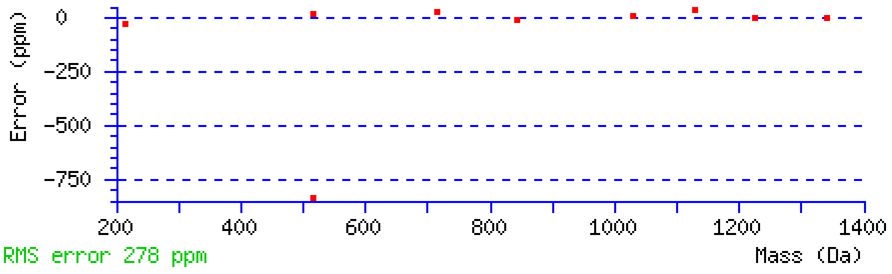
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1550.882050
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 49 **Expect:** 3.7e-005
Matches : 9/108 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	100.075690	50.541483			V							14
2	213.159754	107.083515			L	1452.820927	726.914101	1435.794378	718.400827	1434.810362	717.908819	13
3	326.243818	163.625547			L	*1339.736863*	670.372069	1322.710314	661.858795	1321.726298	661.366787	12
4	423.296582	212.151929			P	*1226.652799*	613.830037	1209.626250	605.316763	1208.642234	604.824755	11
5	522.364996	261.686136			V	*1129.600035*	565.303655	1112.573486	556.790381	1111.589470	556.298373	10
6	708.444309	354.725793			W	*1030.531621*	515.769448	1013.505072	507.256174	1012.521056	506.764166	9
7	837.486902	419.247089	819.476337	410.241807	E	*844.452308*	422.729792	827.425759	414.216517	826.441743	413.724509	8
8	908.524016	454.765646	890.513451	445.760363	A	*715.409715*	358.208495	698.383166	349.695221	697.399150	349.203213	7
9	1037.566609	519.286943	1019.556044	510.281660	E	644.372601	322.689938	627.346052	314.176664	626.362036	313.684656	6
10	1094.588073	547.797674	1076.577508	538.792392	G	*515.330008*	258.168642	498.303459	249.655367			5
11	1207.672137	604.339706	1189.661572	595.334424	L	458.308544	229.657910	441.281995	221.144635			4
12	1264.693601	632.850438	1246.683036	623.845156	G	345.224480	173.115878	328.197931	164.602603			3
13	1377.777665	689.392470	1359.767100	680.387188	L	288.203016	144.605146	271.176467	136.091871			2
14					R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.5	1550.882050	0.007938	VLLPVWEAEGLGLR

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

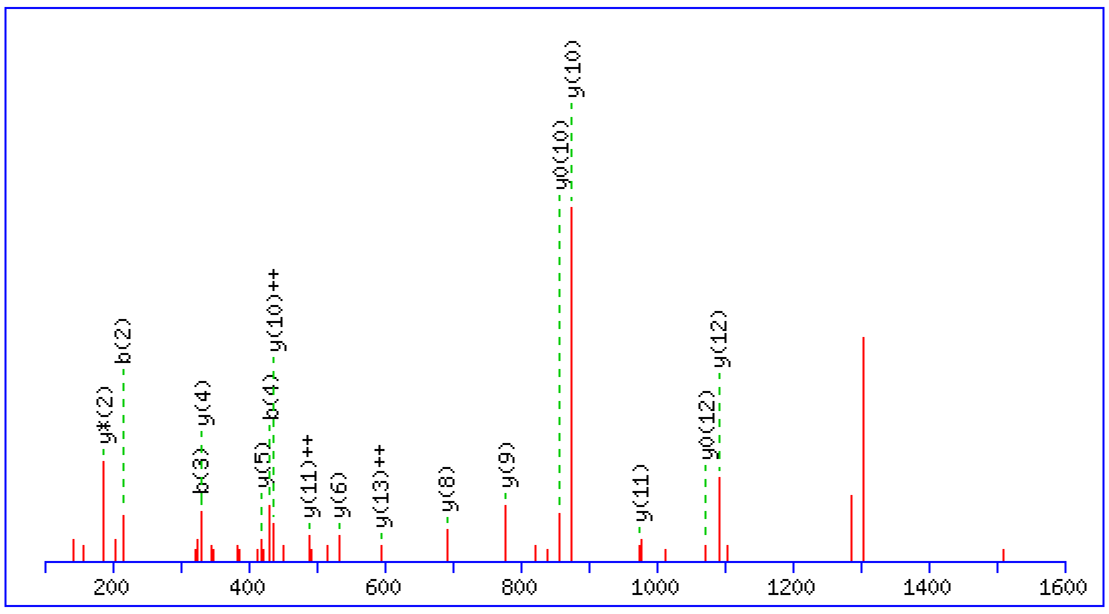
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DVDTPSGTNSGAGK**
Found in **RBX1_HUMAN**, E3 ubiquitin-protein ligase RBX1 OS=Homo sapiens GN=RBX1 PE=1 SV=1

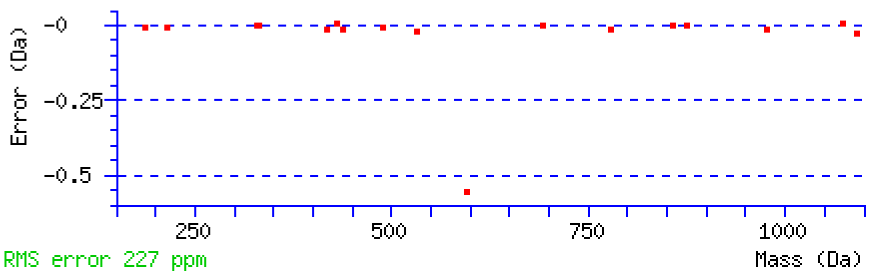
Match to Query 645175: 1304.587808 from(653.301180,2+) rtinseconds(874) index(157642)
Title: Locus:1.1.1.1018.8
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

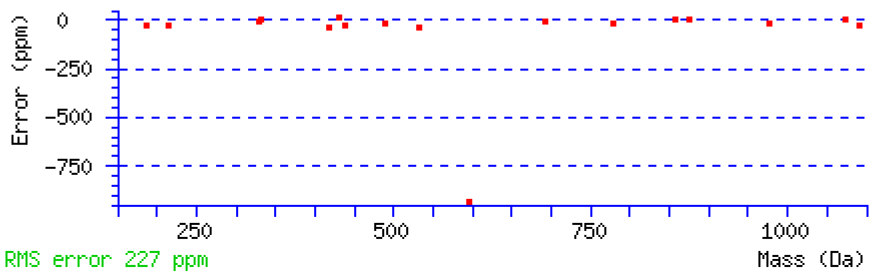
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1304.584457
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 60  Expect: 1e-005
Matches : 17/132 fragment ions using 26 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	116.034219	58.520748			98.023654	49.515465	D							14
2	**215.102633**	108.054954			197.092068	99.049672	V	1190.564772	595.786024	1173.538223	587.272750	1172.554207	586.780741	13
3	**330.129576**	165.568426			312.119011	156.563144	D	***1091.496358***	546.251817	1074.469809	537.738543	1073.485793	537.246535	12
4	**431.177255**	216.092266			413.166690	207.086983	T	***976.469415***	488.738346	959.442866	480.225071	958.458850	479.733063	11
5	528.230019	264.618648			510.219454	255.613365	P	***875.421736***	438.214506	858.395187	429.701232	857.411171	429.209224	10
6	615.262047	308.134662			597.251482	299.129379	S	***778.368972***	389.688124	761.342423	381.174849	760.358407	380.682841	9
7	672.283511	336.645394			654.272946	327.640111	G	***691.336944***	346.172110	674.310395	337.658836	673.326379	337.166828	8
8	773.331190	387.169233			755.320625	378.163951	T	634.315480	317.661378	617.288931	309.148103	616.304915	308.656095	7
9	887.374117	444.190697	870.347568	435.677422	869.363552	435.185414	N	***533.267801***	267.137539	516.241252	258.624264	515.257236	258.132256	6
10	974.406145	487.706711	957.379596	479.193436	956.395580	478.701428	S	***419.224874***	210.116075	402.198325	201.602800	401.214309	201.110792	5
11	1031.427609	516.217443	1014.401060	507.704168	1013.417044	507.212160	G	***332.192846***	166.600061	315.166297	158.086786			4
12	1102.464723	551.736000	1085.438174	543.222725	1084.454158	542.730717	A	275.171382	138.089329	258.144833	129.576054			3
13	1159.486187	580.246732	1142.459638	571.733457	1141.475622	571.241449	G	204.134268	102.570772	187.107719	94.057497			2
14							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
59.7	1304.584457	0.003351	DVDTPSGTNSGAGK

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

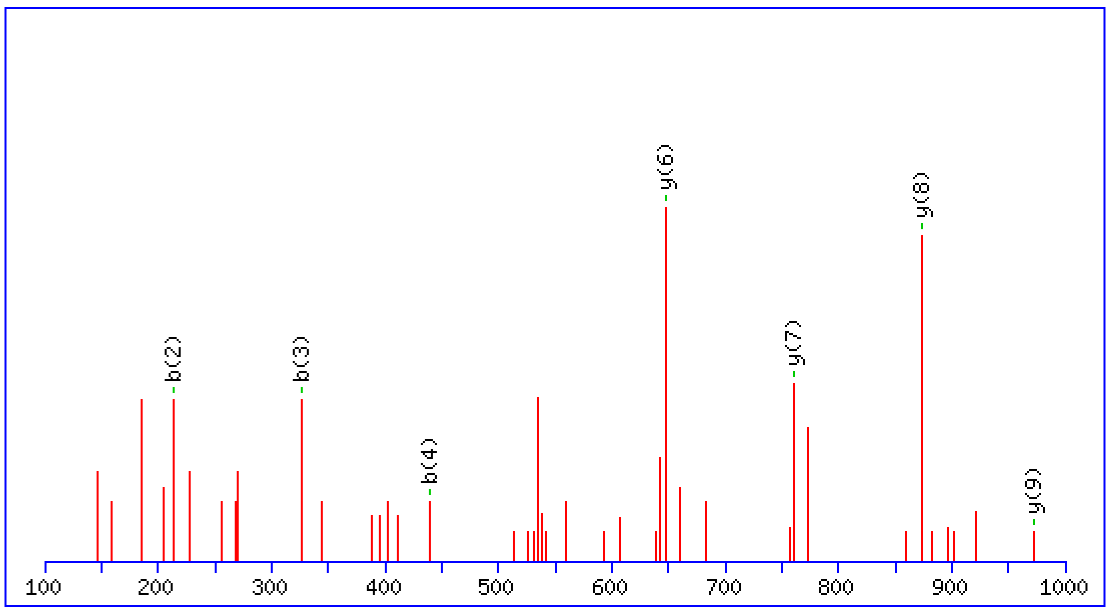
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IVLLSANSIR**
Found in **UBR5_HUMAN**, E3 ubiquitin-protein ligase UBR5 OS=Homo sapiens GN=UBR5 PE=1 SV=2

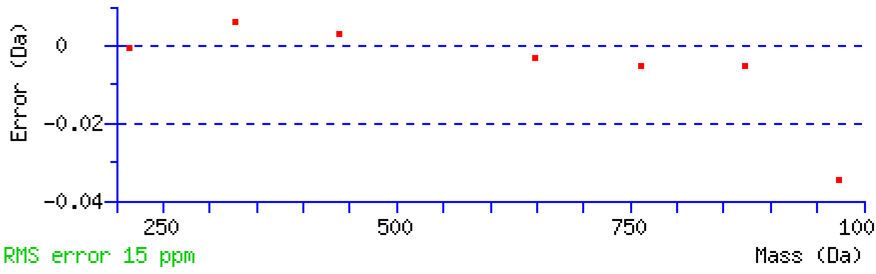
Match to Query 22384: 1084.652008 from(543.333280,2+) rtinseconds(2521) index(29449)
Title: Locus:1.1.1.2228.19
Data file 2011-11-10 - TFD - EP 3-6.mgf

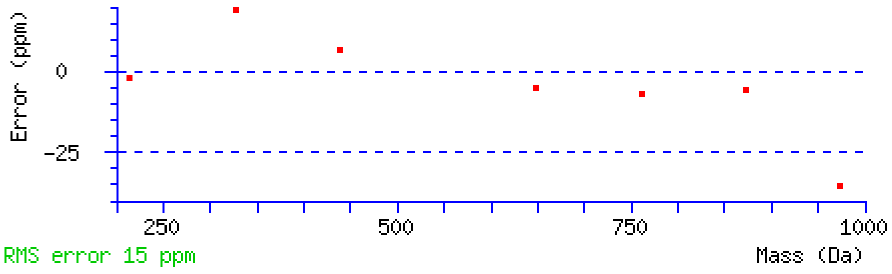
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1084.660416
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 33  Expect: 0.0028
Matches : 7/84 fragment ions using 9 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					I							10
2	**213.159754**	107.083515					V	*972.583655*	486.795466	955.557106	478.282191	954.573090	477.790183	9
3	**326.243818**	163.625547					L	*873.515241*	437.261259	856.488692	428.747984	855.504676	428.255976	8
4	**439.327882**	220.167579					L	*760.431177*	380.719227	743.404628	372.205952	742.420612	371.713944	7
5	526.359910	263.683593			508.349345	254.678311	S	*647.347113*	324.177195	630.320564	315.663920	629.336548	315.171912	6
6	597.397024	299.202150			579.386459	290.196868	A	560.315085	280.661181	543.288536	272.147906	542.304520	271.655898	5
7	711.439951	356.223614	694.413402	347.710339	693.429386	347.218331	N	489.277971	245.142623	472.251422	236.629349	471.267406	236.137341	4
8	798.471979	399.739627	781.445430	391.226353	780.461414	390.734345	S	375.235044	188.121160	358.208495	179.607886	357.224479	179.115878	3
9	911.556043	456.281659	894.529494	447.768385	893.545478	447.276377	I	288.203016	144.605146	271.176467	136.091872			2
10							R	175.118952	88.063114	158.092403	79.549840			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.7	1084.660416	-0.008408	IVLLSANSIR
31.9	1084.649200	0.002808	LVLLGESAVGK
7.2	1084.660416	-0.008408	VIIKTENIR
7.2	1084.642670	0.009338	VPLKGCLLR
6.3	1084.649200	0.002808	ILIIGESGVGK
3.5	1084.649231	0.002777	VIVVGDLSVGK
3.1	1084.649185	0.002823	LTPLELKQK

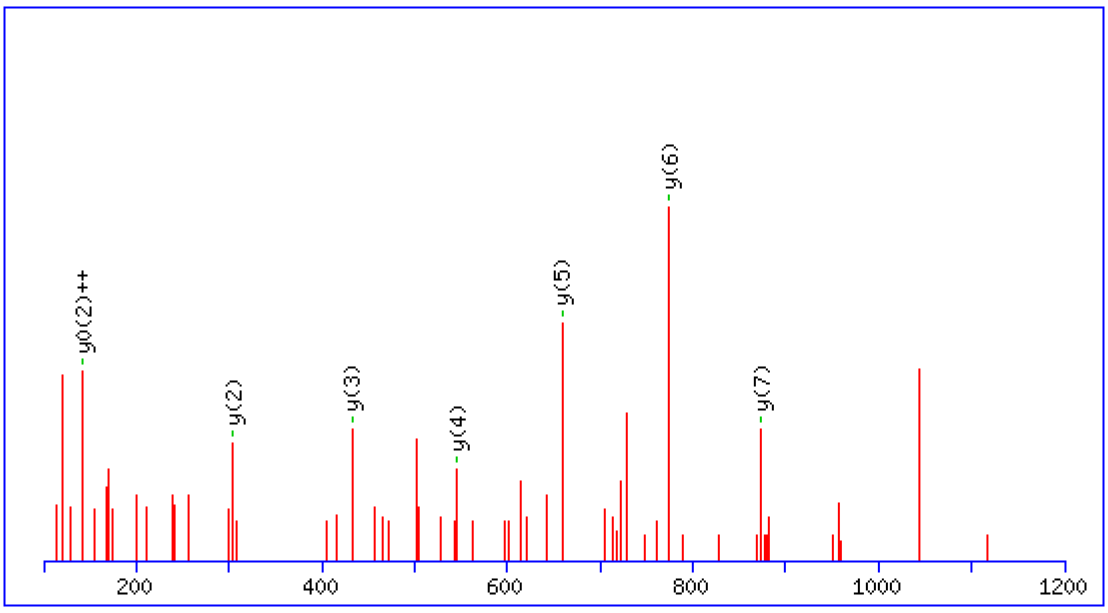
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GIVDLIEER**
Found in **EFGM_HUMAN**, Elongation factor G, mitochondrial OS=Homo sapiens GN=GFM1 PE=1 SV=2

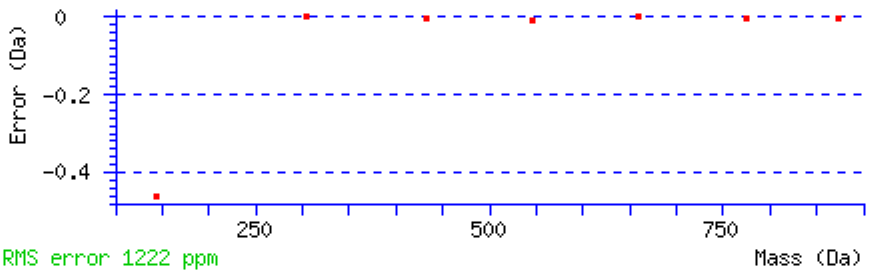
Match to Query 19958: 1042.569788 from(522.292170,2+) rtinseconds(3015) index(41428)
Title: Locus:1.1.1.2584.11
Data file 2011-11-10 - TFD - EP 3-2.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●

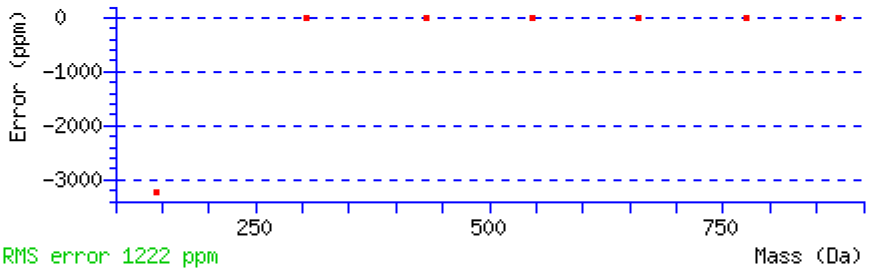


```
Monoisotopic mass of neutral peptide Mr(calc): 1042.565857
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 51  Expect: 0.00015
Matches : 7/72 fragment ions using 9 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008			G							9
2	171.112804	86.060040			I	986.551687	493.779482	969.525138	485.266207	968.541122	484.774199	8
3	270.181218	135.594247			V	***873.467623***	437.237450	856.441074	428.724175	855.457058	428.232167	7
4	385.208161	193.107719	367.197596	184.102436	D	***774.399209***	387.703243	757.372660	379.189968	756.388644	378.697960	6
5	498.292225	249.649751	480.281660	240.644468	L	***659.372266***	330.189771	642.345717	321.676497	641.361701	321.184489	5
6	611.376289	306.191783	593.365724	297.186500	I	***546.288202***	273.647739	529.261653	265.134464	528.277637	264.642456	4
7	740.418882	370.713079	722.408317	361.707797	E	***433.204138***	217.105707	416.177589	208.592432	415.193573	208.100424	3
8	869.461475	435.234376	851.450910	426.229093	E	***304.161545***	152.584410	287.134996	144.071136	286.150980	143.579128	2
9					R	175.118952	88.063114	158.092403	79.549839			1



RMS error 1222 ppm



RMS error 1222 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.5	1042.565857	0.003931	GIVDLIEER
10.1	1042.577072	-0.007284	LRVLEEER
9.0	1042.577072	-0.007284	LGLKQAEER

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

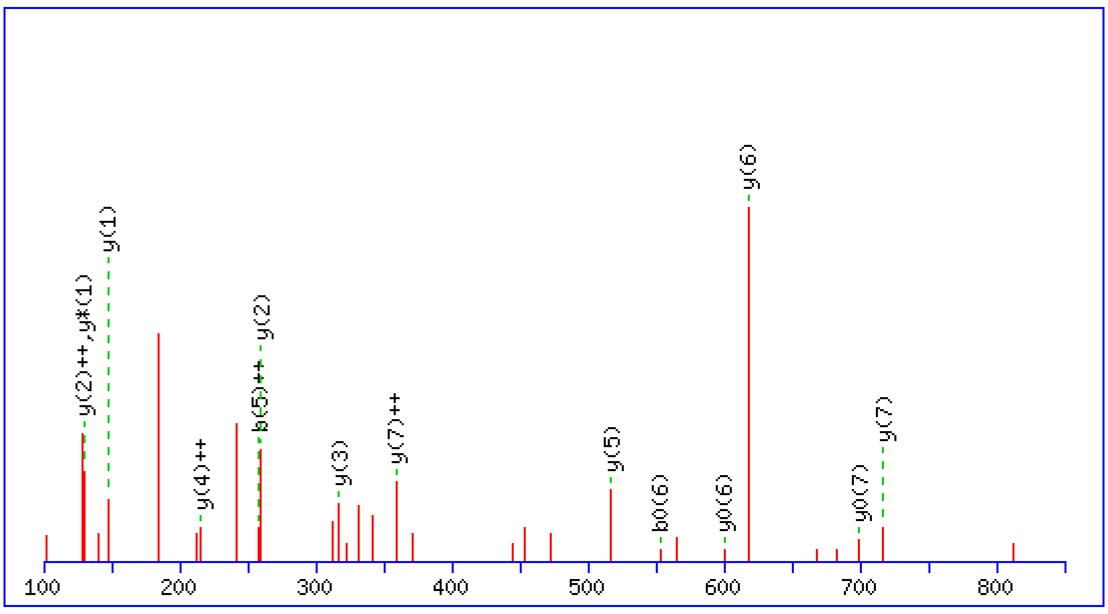
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IVTSLGLK**
Found in **ETUD1_HUMAN**, Elongation factor Tu GTP-binding domain-containing protein 1 OS=Homo sapiens GN=EFTUD1 PE=1 SV=2

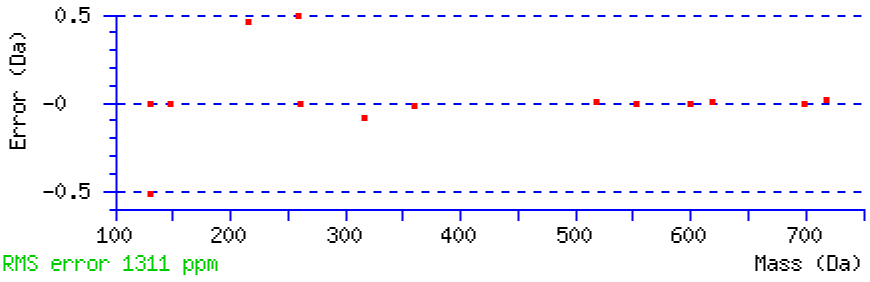
Match to Query 2467: 829.528988 from(415.771770,2+) rtinseconds(1716) index(15046)
Title: Locus:1.1.1.2072.9
Data file 2011-11-13 - TFD - EP 7-5.mgf

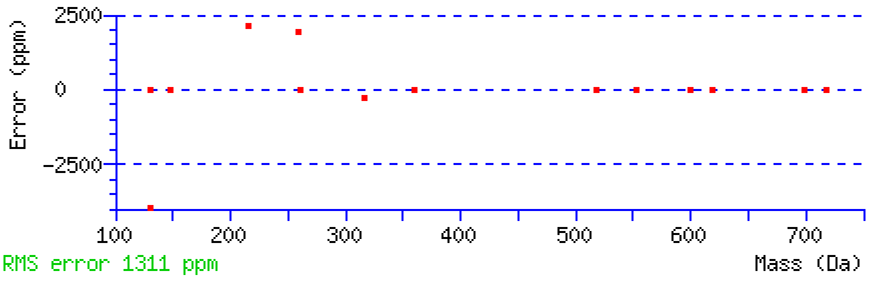
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [850] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 829.527298
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 38  Expect: 0.00046
Matches : 14/58 fragment ions using 25 most intense peaks    (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							8
2	213.159754	107.083515			V	***717.450517***	359.228897	700.423968	350.715622	699.439952	350.223614	7
3	314.207433	157.607354	296.196868	148.602072	T	***618.382103***	309.694690	601.355554	301.181415	600.371538	300.689407	6
4	401.239461	201.123368	383.228896	192.118086	S	***517.334424***	259.170850	500.307875	250.657576	499.323859	250.165568	5
5	514.323525	257.665401	496.312960	248.660118	L	430.302396	215.654836	413.275847	207.141562			4
6	571.344989	286.176133	553.334424	277.170850	G	***317.218332***	159.112804	300.191783	150.599530			3
7	684.429053	342.718165	666.418488	333.712882	L	***260.196868***	130.602072	243.170319	122.088798			2
8					K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.6	829.527298	0.001690	IVTSLGLK
37.4	829.527313	0.001675	LVTTGVLK
23.2	829.527283	0.001705	ETKLVLK
22.9	829.527283	0.001705	KETIVLK
13.8	829.520752	0.008236	VMRIAIK
13.3	829.527283	0.001705	ETLKVLK
11.8	829.527283	0.001705	IEKTVIK
11.2	829.527267	0.001721	ILSEKLK
7.6	829.527283	0.001705	KTEVLLK
5.8	829.527267	0.001721	LESKLLK

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

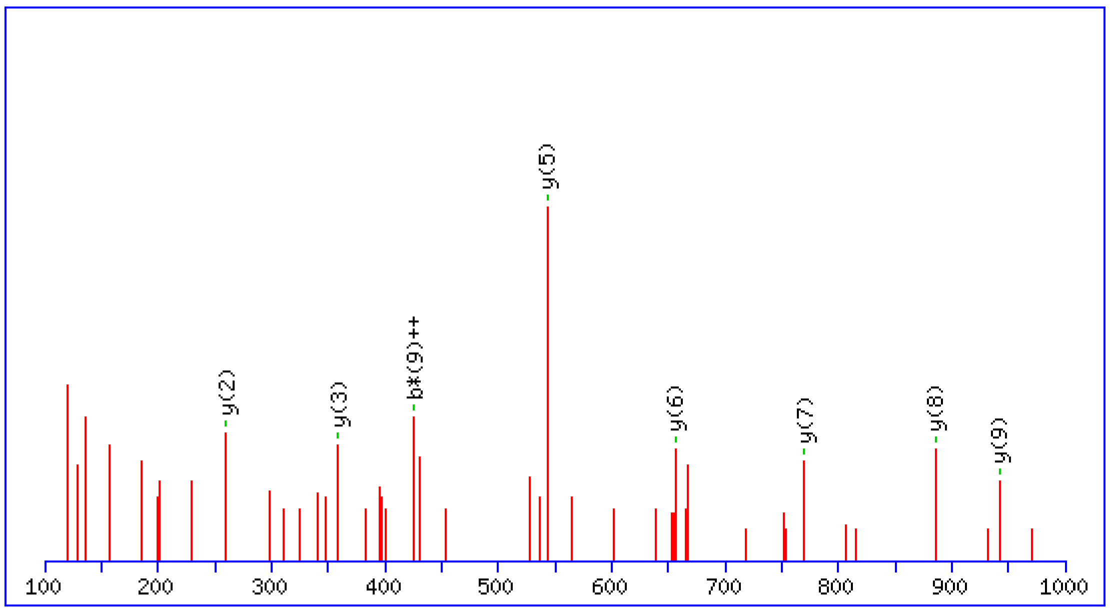
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AGDNILAVLK**
Found in **ERMP1_HUMAN**, Endoplasmic reticulum metallopeptidase 1 OS=Homo sapiens GN=ERMP1 PE=1 SV=2

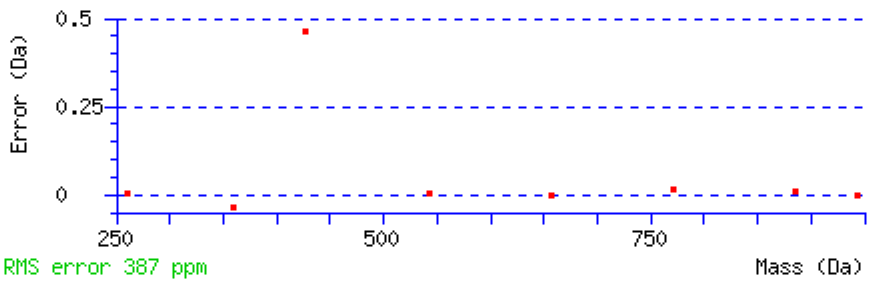
Match to Query 15986: 1012.592388 from(507.303470,2+) rtinseconds(2945) index(39519)
Title: Locus:1.1.1.2542.10
Data file 2011-11-10 - TFD - EP 3-1.mgf

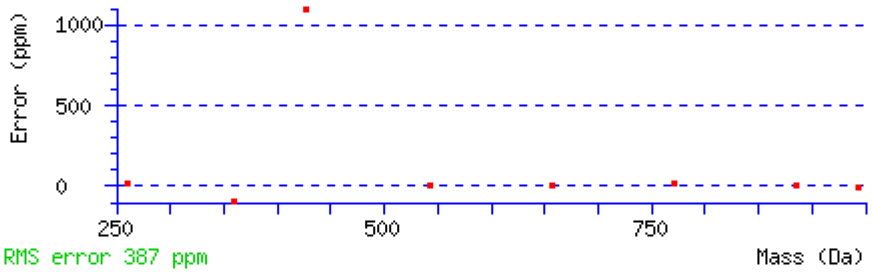
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1012.591675
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 64 **Expect:** 3e-006
Matches : 8/84 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							10
2	129.065854	65.036565					G	***942.561858***	471.784567	925.535309	463.271293	924.551293	462.779285	9
3	244.092797	122.550037			226.082232	113.544754	D	***885.540394***	443.273835	868.513845	434.760561	867.529829	434.268553	8
4	358.135724	179.571500	341.109175	171.058226	340.125159	170.566218	N	***770.513451***	385.760364	753.486902	377.247089			7
5	471.219788	236.113532	454.193239	227.600258	453.209223	227.108250	I	***656.470524***	328.738900	639.443975	320.225626			6
6	584.303852	292.655564	567.277303	284.142290	566.293287	283.650282	L	***543.386460***	272.196868	526.359911	263.683594			5
7	655.340966	328.174121	638.314417	319.660847	637.330401	319.168839	A	430.302396	215.654836	413.275847	207.141561			4
8	754.409380	377.708328	737.382831	369.195054	736.398815	368.703046	V	***359.265282***	180.136279	342.238733	171.623004			3
9	867.493444	434.250360	850.466895	425.737086	849.482879	425.245078	L	***260.196868***	130.602072	243.170319	122.088798			2
10							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
63.5	1012.591675	0.000713	AGDNILAVLK
8.1	1012.591705	0.000683	TGTVGKLPPK
4.3	1012.591690	0.000698	AGEVPKVGLK

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

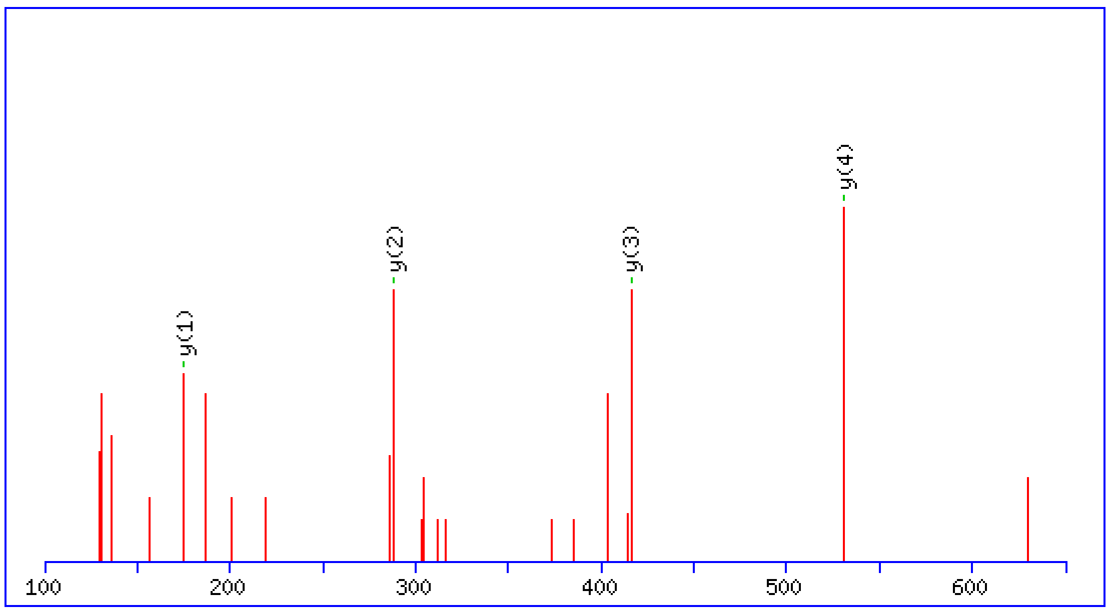
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VMADQLR**
Found in **ECE2_HUMAN**, Endothelin-converting enzyme 2 OS=Homo sapiens GN=ECE2 PE=1 SV=4

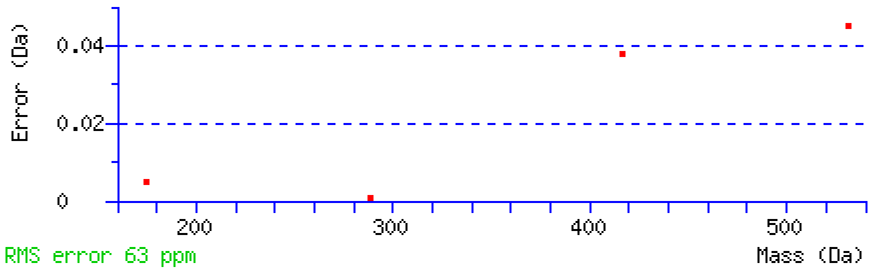
Match to Query 3846: 847.421048 from(424.717800,2+) rtinseconds(922) index(2490)
Title: Locus:1.1.1.1679.11
Data file 2011-11-10 - TFD - EP 4-4.mgf

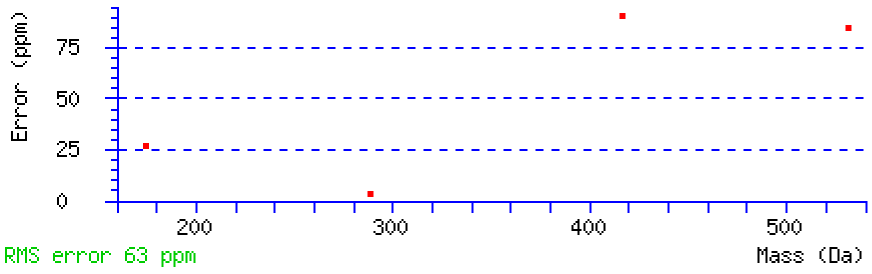
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 650 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 847.422180
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M2 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 34 **Expect:** 0.0044
Matches : 4/78 fragment ions using 5 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					**V**							7
2	247.111090	124.059183					**M**	749.361051	375.184164	732.334502	366.670889	731.350486	366.178881	6
3	318.148204	159.577740					**A**	602.325651	301.666464	585.299102	293.153189	584.315086	292.661181	5
4	433.175147	217.091212			415.164582	208.085929	**D**	***531.288537***	266.147907	514.261988	257.634632	513.277972	257.142624	4
5	561.233725	281.120501	544.207176	272.607226	543.223160	272.115218	**Q**	***416.261594***	208.634435	399.235045	200.121161			3
6	674.317789	337.662533	657.291240	329.149258	656.307224	328.657250	**L**	***288.203016***	144.605146	271.176467	136.091872			2
7							**R**	***175.118952***	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of VMADQLR
(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	847.422180	-0.001132	VMADQLR
21.4	847.422165	-0.001117	MAAASPLR
17.9	847.422165	-0.001117	MADDLKR
16.2	847.422180	-0.001132	MATPPKR
14.9	847.422165	-0.001117	CIDASLR
14.9	847.422165	-0.001117	LACSDIR
12.5	847.422180	-0.001132	DGKPMLR
12.5	847.418808	0.002240	ENGPFLR
12.3	847.422165	-0.001117	ALSCVER
12.3	847.422165	-0.001117	LNSMVER

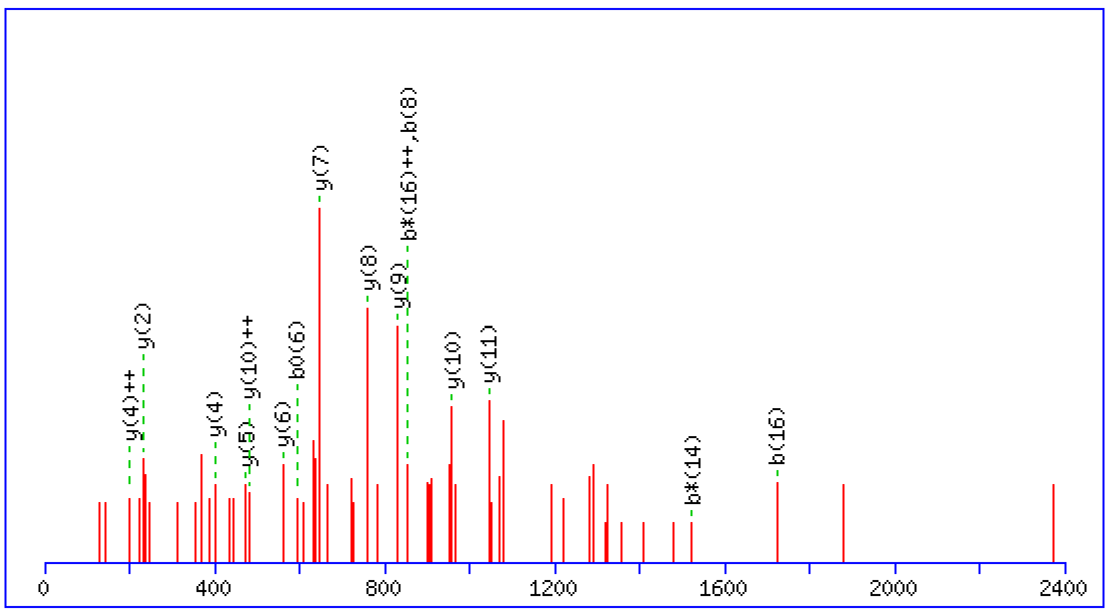
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GGQLQEQLTQQLSQALSSAVAGR**
Found in **EDC4_HUMAN**, Enhancer of mRNA-decapping protein 4 OS=Homo sapiens GN=EDC4 PE=1 SV=1

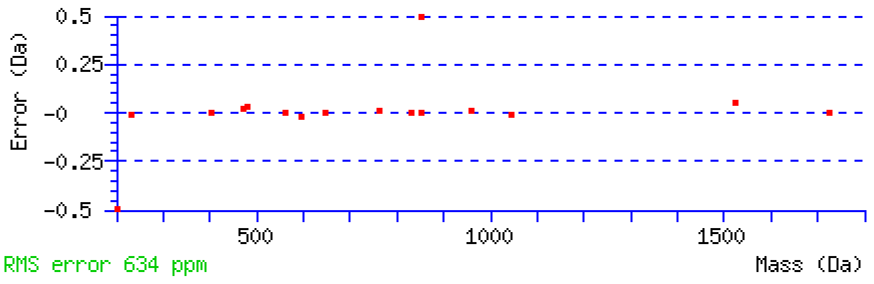
Match to Query 49278: 2369.217582 from(790.746470,3+) rtinseconds(4292) index(64468)
Title: Locus:1.1.1.3020.33
Data file 2011-11-14 - TFD - EP 8-1.mgf

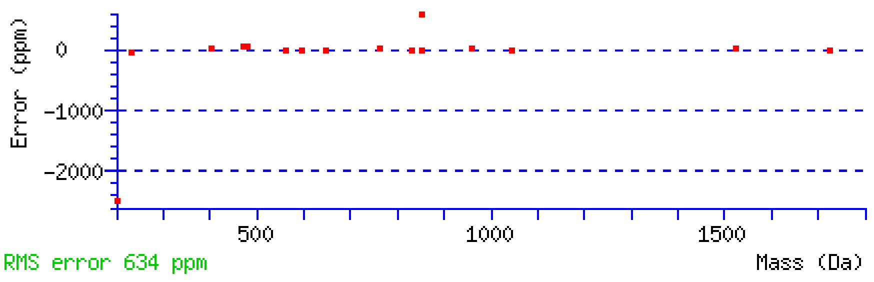
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [0] to [2400] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2369.229889
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 42  Expect: 0.00012
Matches : 16/240 fragment ions using 31 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	58.028740	29.518008					G							23
2	115.050204	58.028740					G	2313.215716	1157.111496	2296.189167	1148.598221	2295.205151	1148.106213	22
3	243.108782	122.058029	226.082233	113.544755			Q	2256.194252	1128.600764	2239.167703	1120.087489	2238.183687	1119.595481	21
4	356.192846	178.600061	339.166297	170.086787			L	2128.135674	1064.571475	2111.109125	1056.058200	2110.125109	1055.566192	20
5	484.251424	242.629350	467.224875	234.116076			Q	2015.051610	1008.029443	1998.025061	999.516169	1997.041045	999.024161	19
6	613.294017	307.150647	596.267468	298.637372	595.283452	298.145364	E	1886.993032	944.000154	1869.966483	935.486880	1868.982467	934.994872	18
7	741.352595	371.179936	724.326046	362.666661	723.342030	362.174653	Q	1757.950439	879.478858	1740.923890	870.965583	1739.939874	870.473575	17
8	**854.436659**	427.721968	837.410110	419.208693	836.426094	418.716685	L	1629.891861	815.449569	1612.865312	806.936294	1611.881296	806.444286	16
9	955.484338	478.245807	938.457789	469.732533	937.473773	469.240525	T	1516.807797	758.907537	1499.781248	750.394262	1498.797232	749.902254	15
10	1083.542916	542.275096	1066.516367	533.761822	1065.532351	533.269814	Q	1415.760118	708.383697	1398.733569	699.870423	1397.749553	699.378415	14
11	1211.601494	606.304385	1194.574945	597.791111	1193.590929	597.299103	Q	1287.701540	644.354408	1270.674991	635.841134	1269.690975	635.349126	13
12	1324.685558	662.846417	1307.659009	654.333143	1306.674993	653.841135	L	1159.642962	580.325119	1142.616413	571.811845	1141.632397	571.319837	12
13	1411.717586	706.362431	1394.691037	697.849157	1393.707021	697.357149	S	***1046.558898***	523.783087	1029.532349	515.269813	1028.548333	514.777805	11
14	1539.776164	770.391720	1522.749615	761.878446	1521.765599	761.386438	Q	***959.526870***	480.267073	942.500321	471.753799	941.516305	471.261791	10
15	1610.813278	805.910277	1593.786729	797.397003	1592.802713	796.904995	A	***831.468292***	416.237784	814.441743	407.724510	813.457727	407.232502	9
16	**1723.897342**	862.452309	1706.870793	853.939035	1705.886777	853.447026	L	***760.431178***	380.719227	743.404629	372.205953	742.420613	371.713945	8
17	1810.929370	905.968323	1793.902821	897.455049	1792.918805	896.963041	S	***647.347114***	324.177195	630.320565	315.663921	629.336549	315.171913	7
18	1897.961398	949.484337	1880.934849	940.971063	1879.950833	940.479055	S	***560.315086***	280.661181	543.288537	272.147907	542.304521	271.655899	6
19	1968.998512	985.002894	1951.971963	976.489620	1950.987947	975.997612	A	***473.283058***	237.145167	456.256509	228.631893			5
20	2068.066926	1034.537101	2051.040377	1026.023826	2050.056361	1025.531818	V	***402.245944***	201.626610	385.219395	193.113336			4
21	2139.104040	1070.055658	2122.077491	1061.542383	2121.093475	1061.050376	A	303.177530	152.092403	286.150981	143.579129			3
22	2196.125504	1098.566390	2179.098955	1090.053115	2178.114939	1089.561107	G	***232.140416***	116.573846	215.113867	108.060571			2
23							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.1	2369.229889	-0.012307	GGQLQEQLTQQLSQALSSAVAGR
0.1	2369.217484	0.000098	MAGQPWLAWGTAAARVSARPTR

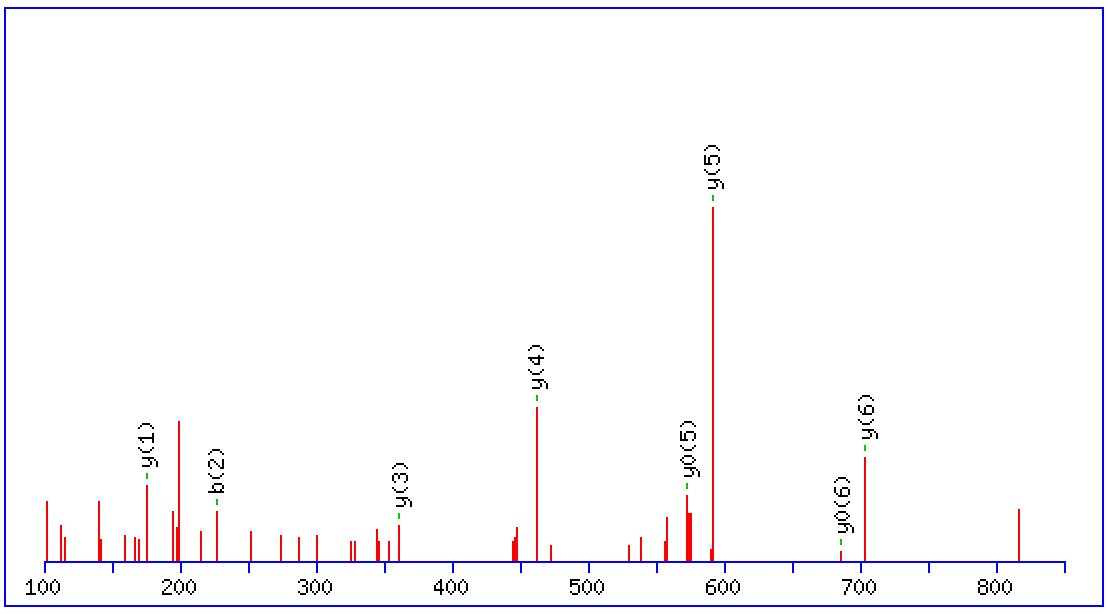
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LIETGER**
Found in **ENY2_HUMAN**, Enhancer of yellow 2 transcription factor homolog OS=Homo sapiens GN=ENY2 PE=1 SV=1

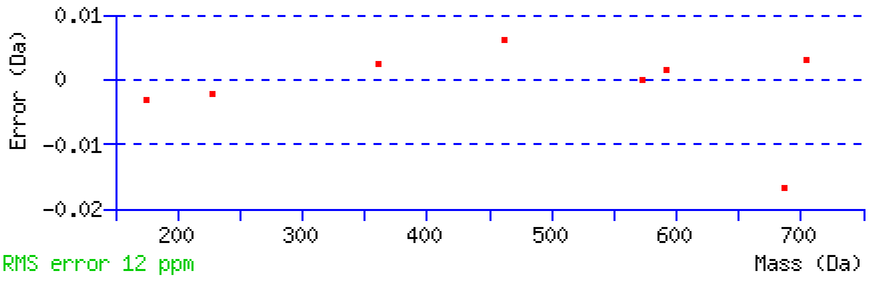
Match to Query 865: 816.437128 from(409.225840,2+) rtinseconds(982) index(352)
Title: Locus:1.1.1.2007.3
Data file 2011-11-12 - TFD - EP 5-8.mgf

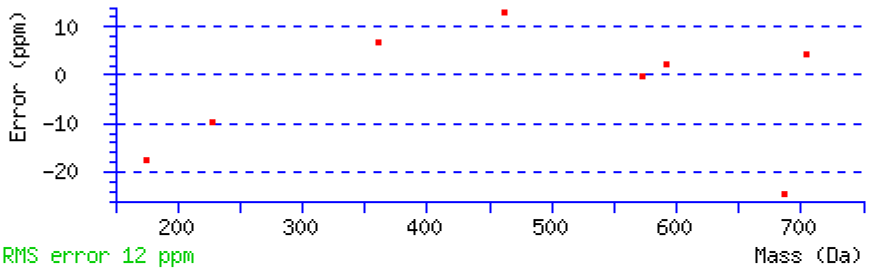
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 816.434113
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.0035
Matches : 8/54 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							7
2	227.175404	114.091340			I	*704.357345*	352.682311	687.330796	344.169036	686.346780	343.677028	6
3	356.217997	178.612637	338.207432	169.607354	E	*591.273281*	296.140279	574.246732	287.627004	573.262716	287.134996	5
4	457.265676	229.136476	439.255111	220.131194	T	*462.230688*	231.618982	445.204139	223.105708	444.220123	222.613700	4
5	514.287140	257.647208	496.276575	248.641926	G	*361.183009*	181.095143	344.156460	172.581868	343.172444	172.089860	3
6	643.329733	322.168505	625.319168	313.163222	E	304.161545	152.584411	287.134996	144.071136	286.150980	143.579128	2
7					R	*175.118952*	88.063114	158.092403	79.549840			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.7	816.434113	0.003015	LIETGER
13.4	816.434128	0.003000	IPLDTSR
11.6	816.434113	0.003015	IPSSELR
11.6	816.434097	0.003031	LLAEESR
11.6	816.434097	0.003031	LLSAEER
7.7	816.438812	-0.001684	LNQMRR
5.5	816.434113	0.003015	IIQDSNK
5.4	816.434113	0.003015	ELEATVR
5.2	816.434128	0.003000	IDEVVSR
4.5	816.434097	0.003031	LEKDNAK

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

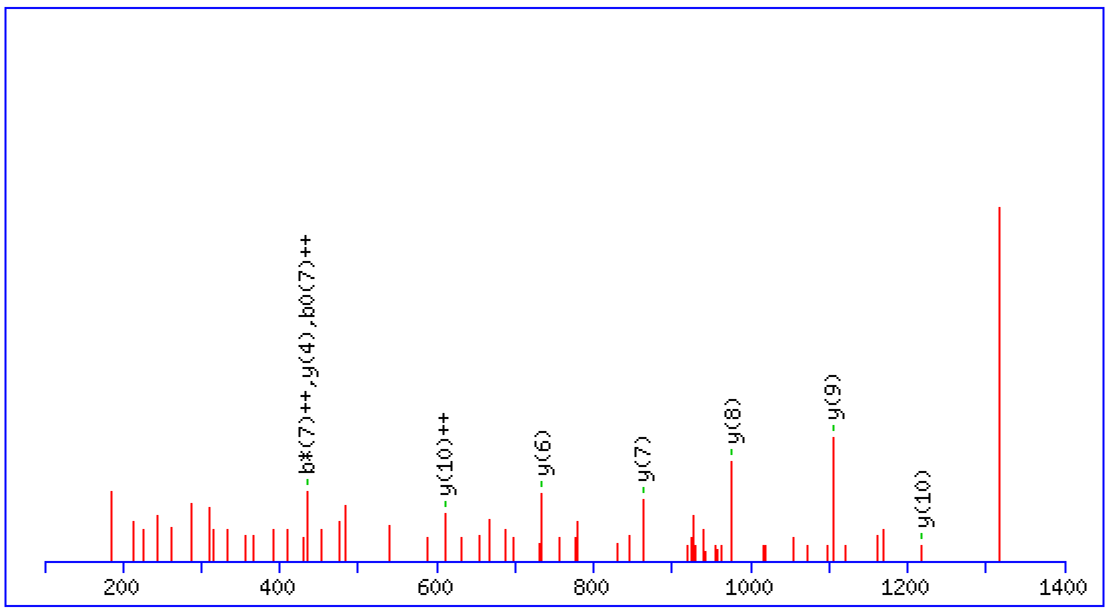
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VIELENWTEGK**
Found in **ECHD1_HUMAN**, Enoyl-CoA hydratase domain-containing protein 1 OS=Homo sapiens GN=ECHDC1 PE=1 SV=2

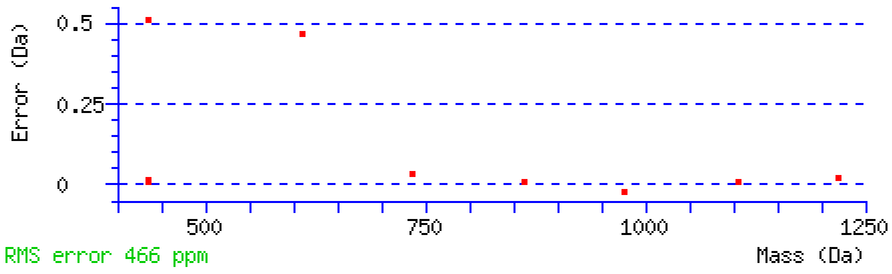
Match to Query 35447: 1316.659248 from(659.336900,2+) rtinseconds(2791) index(33417)
Title: Locus:1.1.1.2647.29
Data file 2011-11-12 - TFD - EP 5-5.mgf

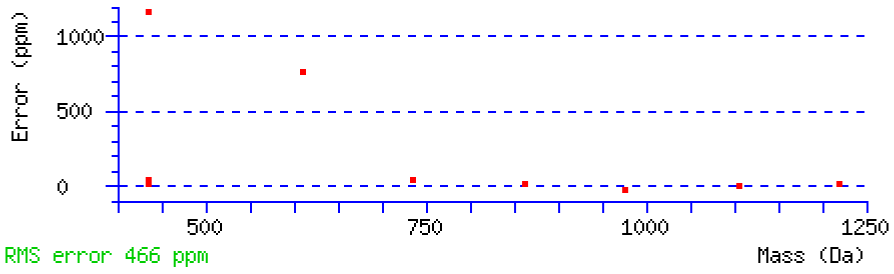
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1316.661209
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 37  Expect: 0.0007
Matches : 9/102 fragment ions using 11 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	100.075690	50.541483					V							11
2	213.159754	107.083515					I	***1218.600094***	609.803685	1201.573545	601.290411	1200.589529	600.798402	10
3	342.202347	171.604811			324.191782	162.599529	E	***1105.516030***	553.261653	1088.489481	544.748379	1087.505465	544.256371	9
4	455.286411	228.146843			437.275846	219.141561	L	***976.473437***	488.740357	959.446888	480.227082	958.462872	479.735074	8
5	584.329004	292.668140			566.318439	283.662858	E	***863.389373***	432.198325	846.362824	423.685050	845.378808	423.193042	7
6	698.371931	349.689604	681.345382	341.176329	680.361366	340.684321	N	***734.346780***	367.677028	717.320231	359.163753	716.336215	358.671745	6
7	884.451244	442.729260	867.424695	434.215986	866.440679	433.723978	W	620.303853	310.655565	603.277304	302.142290	602.293288	301.650282	5
8	985.498923	493.253100	968.472374	484.739825	967.488358	484.247817	T	***434.224540***	217.615908	417.197991	209.102633	416.213975	208.610625	4
9	1114.541516	557.774396	1097.514967	549.261122	1096.530951	548.769114	E	333.176861	167.092068	316.150312	158.578794	315.166296	158.086786	3
10	1171.562980	586.285128	1154.536431	577.771854	1153.552415	577.279845	G	204.134268	102.570772	187.107719	94.057497			2
11							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.3	1316.661209	-0.001961	VIELENWTEGK
3.4	1316.647324	0.011924	VPFNSQGSNPVR
0.9	1316.665924	-0.006676	VLERWSTCPR
0.4	1316.657196	0.002052	VPDNSLLEATSR

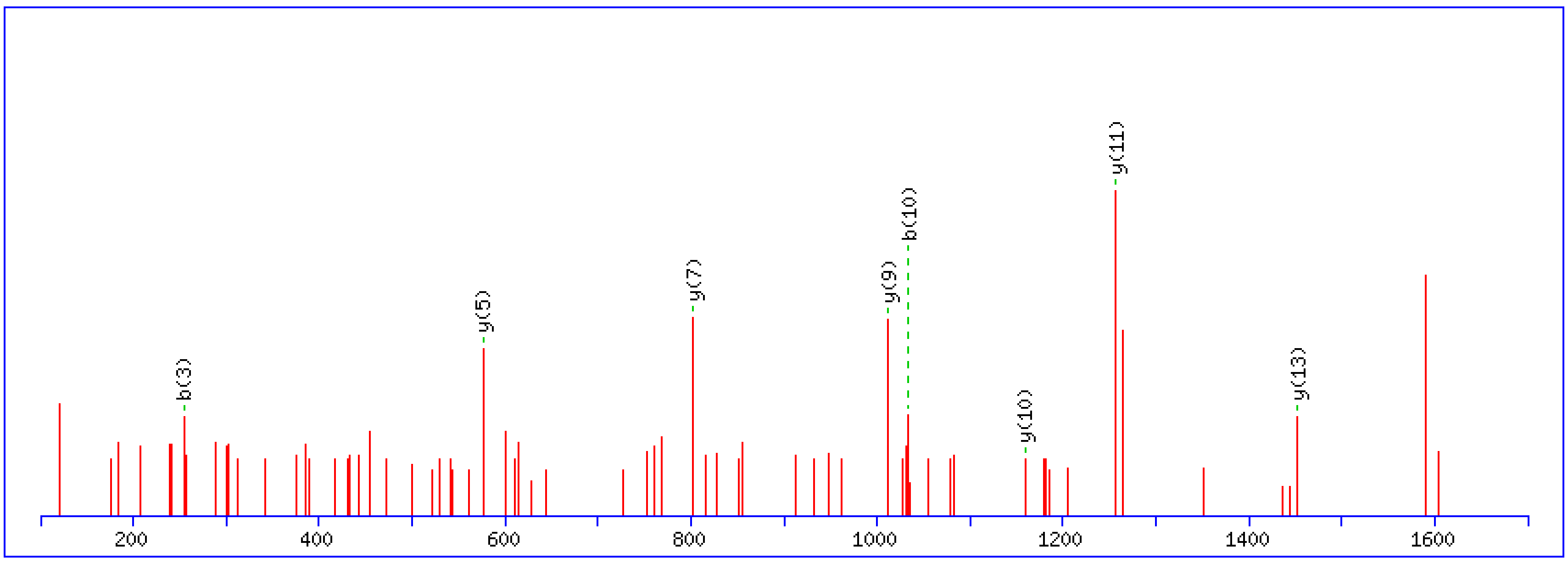
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GVPVPFPIPEPDGCK**
Found in **NPC2_HUMAN**, Epididymal secretory protein E1 OS=Homo sapiens GN=NPC2 PE=1 SV=1

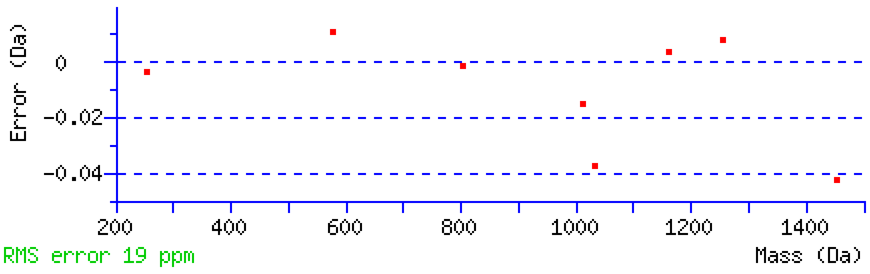
Match to Query 49266: 1607.787908 from(804.901230,2+) rtinseconds(3075) index(42945)
Title: Locus:1.1.1.1548.36
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 2.mgf

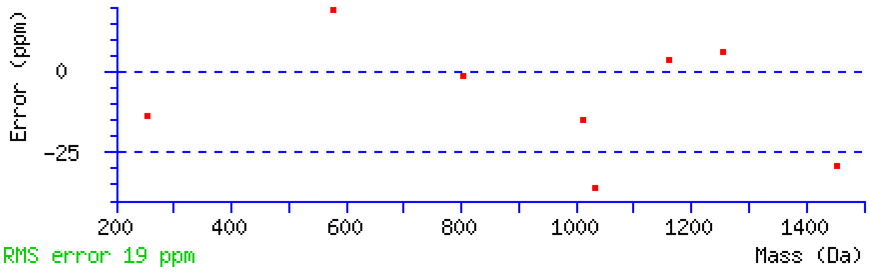
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1607.801788
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 34 **Expect:** 0.0056
Matches : 8/116 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	58.028740	29.518008			G							15
2	157.097154	79.052215			V	1551.787579	776.397428	1534.761030	767.884153	1533.777014	767.392145	14
3	**254.149918**	127.578597			P	***1452.719165***	726.863221	1435.692616	718.349946	1434.708600	717.857938	13
4	353.218332	177.112804			V	1355.666401	678.336839	1338.639852	669.823564	1337.655836	669.331556	12
5	450.271096	225.639186			P	***1256.597987***	628.802632	1239.571438	620.289357	1238.587422	619.797349	11
6	597.339510	299.173393			F	***1159.545223***	580.276250	1142.518674	571.762975	1141.534658	571.270967	10
7	694.392274	347.699775			P	***1012.476809***	506.742043	995.450260	498.228768	994.466244	497.736760	9
8	807.476338	404.241807			I	915.424045	458.215661	898.397496	449.702386	897.413480	449.210378	8
9	904.529102	452.768189			P	***802.339981***	401.673629	785.313432	393.160354	784.329416	392.668346	7
10	**1033.571695**	517.289486	1015.561130	508.284203	E	705.287217	353.147247	688.260668	344.633972	687.276652	344.141964	6
11	1130.624459	565.815868	1112.613894	556.810585	P	***576.244624***	288.625950	559.218075	280.112676	558.234059	279.620668	5
12	1245.651402	623.329339	1227.640837	614.324057	D	479.191860	240.099568	462.165311	231.586294	461.181295	231.094286	4
13	1302.672866	651.840071	1284.662301	642.834789	G	364.164917	182.586096	347.138368	174.072822			3
14	1462.703515	731.855396	1444.692950	722.850113	C	307.143453	154.075365	290.116904	145.562090			2
15					K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.4	1607.801788	-0.013880	GVPVPFPIPEPDGCK

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

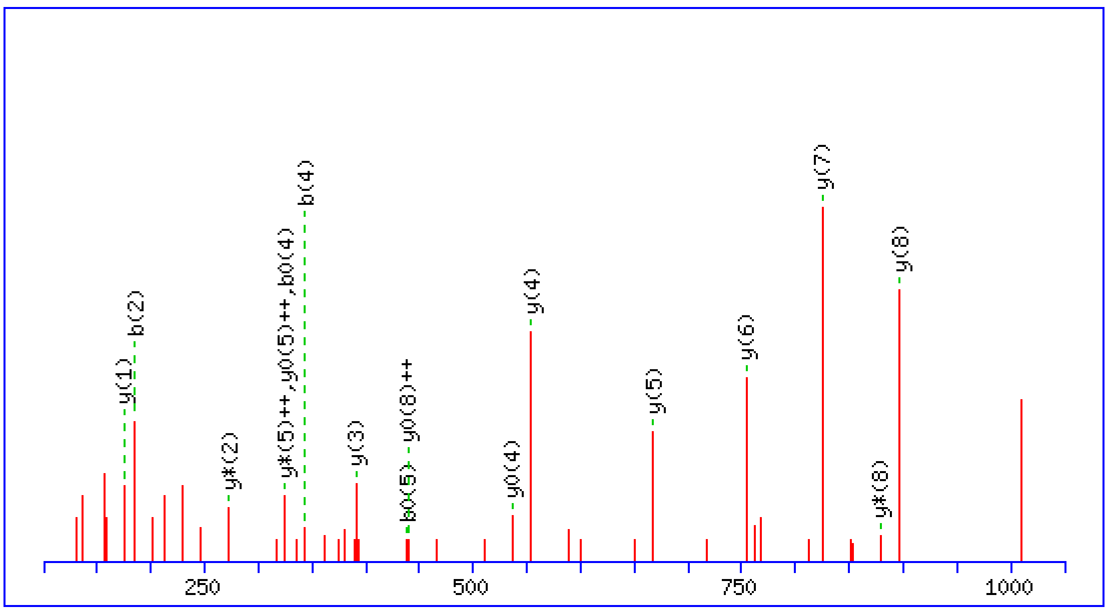
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IAASIYTDR**
Found in **EMP2_HUMAN**, Epithelial membrane protein 2 OS=Homo sapiens GN=EMP2 PE=2 SV=1

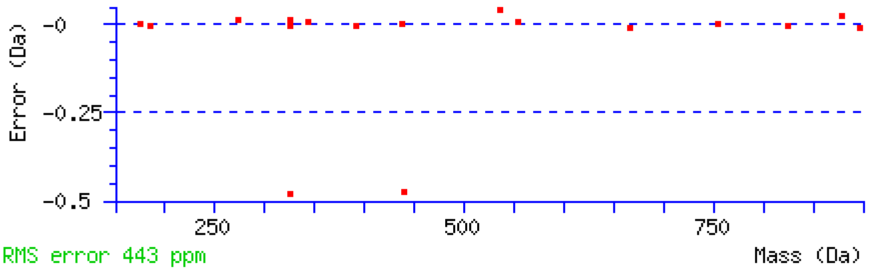
Match to Query 273180: 1008.525008 from(505.269780,2+) rtinseconds(1678) index(588922)
Title: Locus:1.1.1.960.21
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

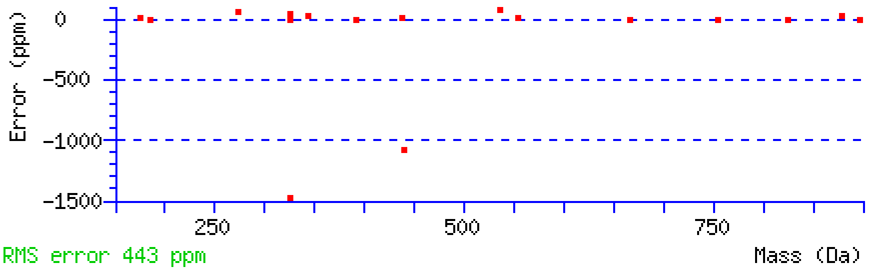
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1008.523987
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 52 **Expect:** 4.7e-005
Matches : 17/72 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							9
2	**185.128454**	93.067865			A	***896.447223***	448.727250	879.420674	440.213975	878.436658	439.721967	8
3	256.165568	128.586422			A	***825.410109***	413.208693	808.383560	404.695418	807.399544	404.203410	7
4	**343.197596**	172.102436	325.187031	163.097153	S	***754.372995***	377.690136	737.346446	369.176861	736.362430	368.684853	6
5	456.281660	228.644468	438.271095	219.639186	I	***667.340967***	334.174122	650.314418	325.660847	649.330402	325.168839	5
6	619.344989	310.176133	601.334424	301.170850	Y	***554.256903***	277.632090	537.230354	269.118815	536.246338	268.626807	4
7	720.392668	360.699972	702.382103	351.694690	T	***391.193574***	196.100425	374.167025	187.587150	373.183009	187.095142	3
8	835.419611	418.213444	817.409046	409.208161	D	290.145895	145.576585	273.119346	137.063311	272.135330	136.571303	2
9					R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.2	1008.523987	0.001021	IAASIYTDR
13.7	1008.523987	0.001021	LATEEPPPR
8.2	1008.531403	-0.006395	LAAAVGFLTM
6.3	1008.521500	0.003508	LPPPPMWR
5.4	1008.521500	0.003508	LPPPPMWR
4.8	1008.521500	0.003508	LPPPPMWR
3.5	1008.523987	0.001021	IKFTEESR
2.9	1008.531387	-0.006379	LAFGSLIASM
1.9	1008.521500	0.003508	RWIAFAVM
0.6	1008.524017	0.000991	TFSSIPVSR

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

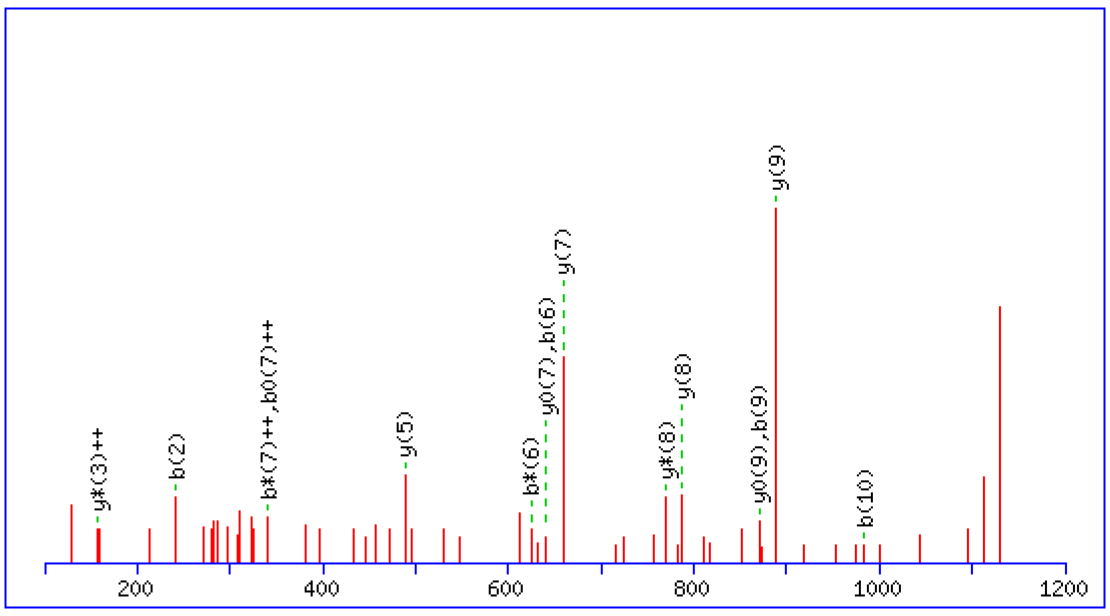
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **LQTQGLGTALK**
Found in **ERO1A_HUMAN**, ERO1-like protein alpha OS=Homo sapiens GN=ERO1L PE=1 SV=2

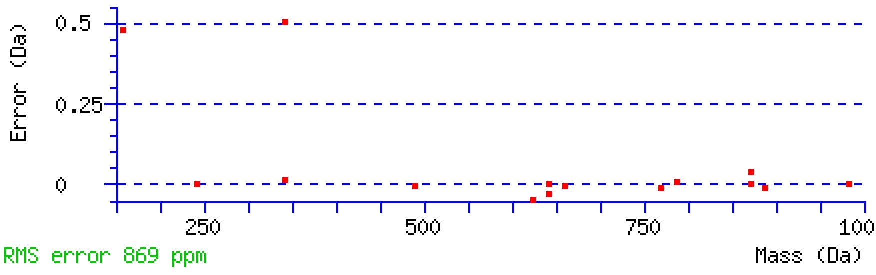
Match to Query 431673: 1128.648388 from(565.331470,2+) rtinseconds(1944) index(428729)
Title: Locus:1.1.1.1083.17
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

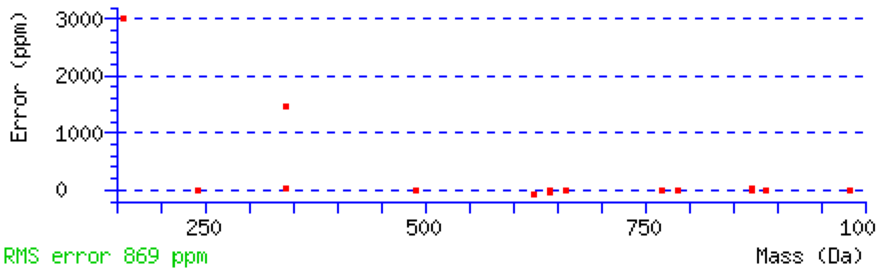
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1128.650269
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.0067
Matches : 15/108 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					L							11
2	***242.149918***	121.578597	225.123369	113.065323			Q	1016.573488	508.790382	999.546939	500.277108	998.562923	499.785100	10
3	343.197597	172.102437	326.171048	163.589162	325.187032	163.097154	T	***888.514910***	444.761093	871.488361	436.247819	870.504345	435.755811	9
4	471.256175	236.131726	454.229626	227.618451	453.245610	227.126443	Q	***787.467231***	394.237254	770.440682	385.723979	769.456666	385.231971	8
5	528.277639	264.642458	511.251090	256.129183	510.267074	255.637175	G	***659.408653***	330.207965	642.382104	321.694690	641.398088	321.202682	7
6	***641.361703***	321.184490	624.335154	312.671215	623.351138	312.179207	L	602.387189	301.697233	585.360640	293.183958	584.376624	292.691950	6
7	698.383167	349.695222	681.356618	341.181947	680.372602	340.689939	G	***489.303125***	245.155201	472.276576	236.641926	471.292560	236.149918	5
8	799.430846	400.219061	782.404297	391.705787	781.420281	391.213779	T	432.281661	216.644469	415.255112	208.131194	414.271096	207.639186	4
9	***870.467960***	435.737618	853.441411	427.224344	852.457395	426.732336	A	331.233982	166.120629	314.207433	157.607355			3
10	***983.552024***	492.279650	966.525475	483.766376	965.541459	483.274368	L	260.196868	130.602072	243.170319	122.088798			2
11							K	147.112804	74.060040	130.086255	65.546766			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.3	1128.650269	-0.001881	LQTQGLGTALK
22.6	1128.639008	0.009380	QLVEASELLK
9.9	1128.639038	0.009350	KVPSDTLPLK
9.2	1128.643723	0.004665	AGLLARLCQK
9.2	1128.654282	-0.005894	AGLSIFSPIPK
9.2	1128.650253	-0.001865	KLLSGQQEVK
2.3	1128.639023	0.009365	PVESLNTLLK
1.7	1128.650238	-0.001850	QRITLEELK
1.5	1128.639038	0.009350	KSPVPVETLK
1.1	1128.639008	0.009380	KETIPLTAEK

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

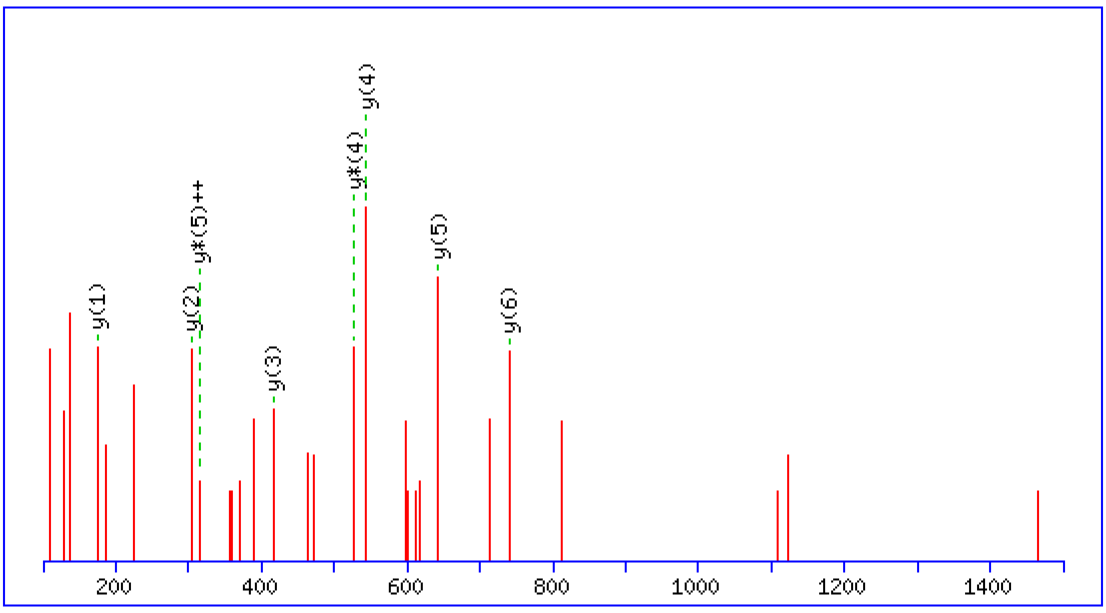
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IPVQLQR**
Found in **STML3_HUMAN**, Stomatin-like protein 3 OS=Homo sapiens GN=STOML3 PE=1 SV=1

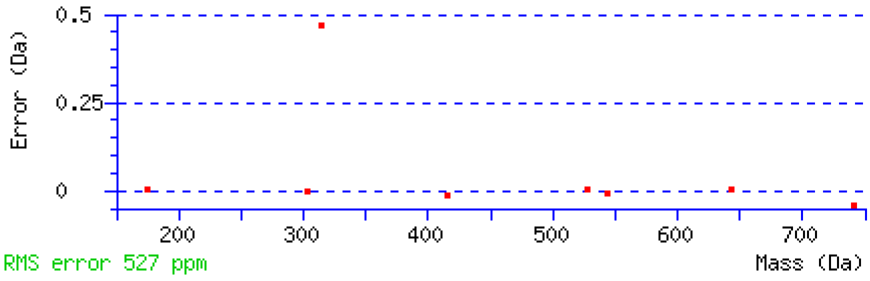
Match to Query 4110: 852.521448 from(427.268000,2+) rtinseconds(1749) index(16572)
Title: Locus:1.1.1.1958.6
Data file 2011-11-12 - TFD - EP 6-5.mgf

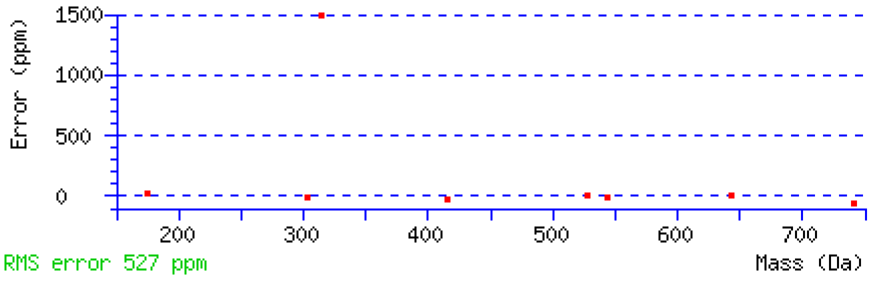
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 852.518127
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 43 **Expect:** 0.00016
Matches : 8/42 fragment ions using 15 most intense peaks (help)

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	114.091340	57.549308			I					7
2	211.144104	106.075690			P	***740.441350***	370.724313	723.414801	362.211039	6
3	310.212518	155.609897			V	***643.388586***	322.197931	626.362037	313.684657	5
4	438.271096	219.639186	421.244547	211.125912	Q	***544.320172***	272.663724	527.293623	264.150450	4
5	551.355160	276.181218	534.328611	267.667944	L	***416.261594***	208.634435	399.235045	200.121161	3
6	679.413738	340.210507	662.387189	331.697233	Q	***303.177530***	152.092403	286.150981	143.579129	2
7					R	***175.118952***	88.063114	158.092403	79.549840	1





NCBI **BLAST** search of IPVQLQR
(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	852.518127	0.003321	IPVQLQR
43.4	852.518127	0.003321	LPVQLQR
32.4	852.518127	0.003321	IPVKQPR
6.9	852.518112	0.003336	LPKDKPR
4.5	852.518127	0.003321	IPVKQPR
4.0	852.518112	0.003336	LLPNAIGR
3.5	852.518112	0.003336	LNIGPAIR

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

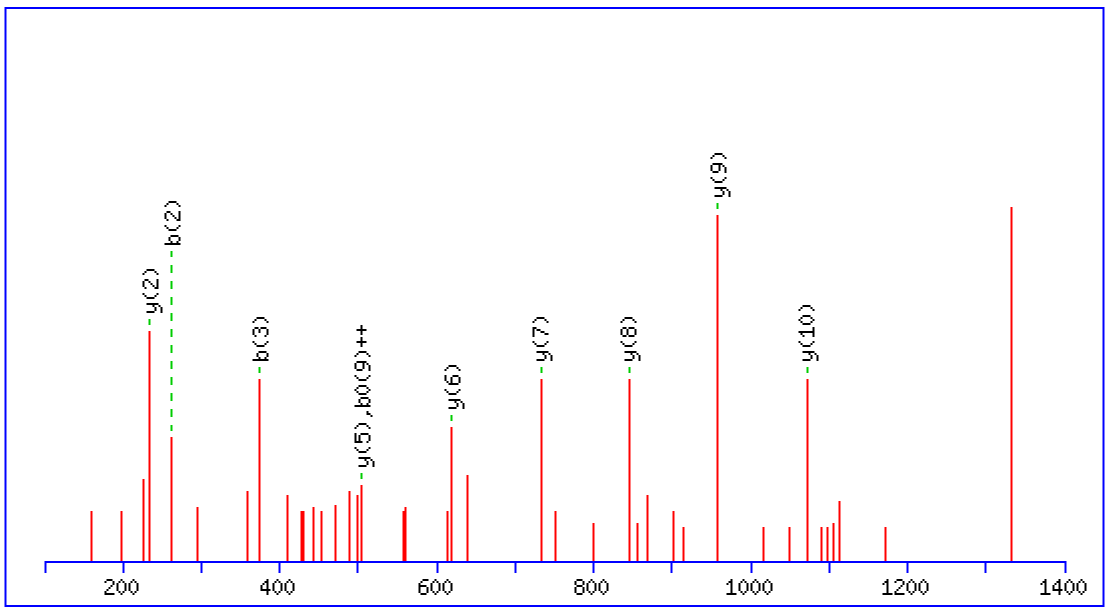
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NFLLLINSLASK**
Found in **DHB2_HUMAN**, Estradiol 17-beta-dehydrogenase 2 OS=Homo sapiens GN=HSD17B2 PE=1 SV=1

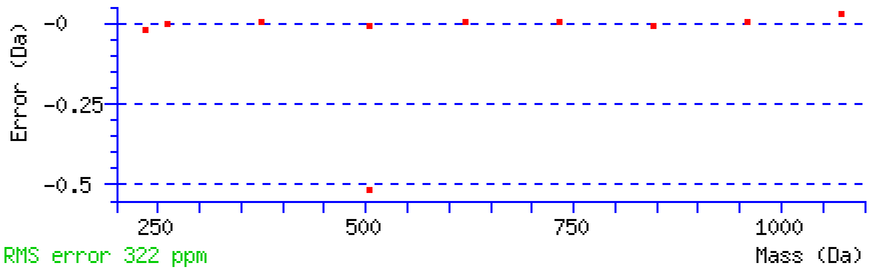
Match to Query 38126: 1331.787788 from(666.901170,2+) rtinseconds(4194) index(63974)
Title: Locus:1.1.1.2884.27
Data file 2011-11-12 - TFD - EP 6-4.mgf

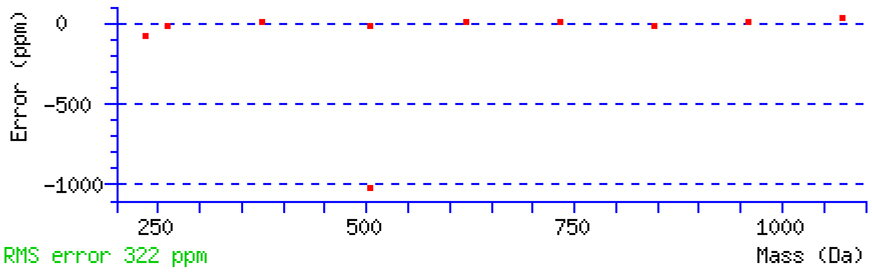
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1331.781250
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 63 **Expect:** 7.4e-007
Matches : 10/116 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			N							12
2	**262.118617**	131.562946	245.092068	123.049672			F	1218.745635	609.876456	1201.719086	601.363181	1200.735070	600.871173	11
3	**375.202681**	188.104978	358.176132	179.591704			L	***1071.677221***	536.342248	1054.650672	527.828974	1053.666656	527.336966	10
4	488.286745	244.647010	471.260196	236.133736			L	***958.593157***	479.800217	941.566608	471.286942	940.582592	470.794934	9
5	601.370809	301.189043	584.344260	292.675768			L	***845.509093***	423.258184	828.482544	414.744910	827.498528	414.252902	8
6	714.454873	357.731075	697.428324	349.217800			I	***732.425029***	366.716153	715.398480	358.202878	714.414464	357.710870	7
7	828.497800	414.752538	811.471251	406.239263			N	***619.340965***	310.174121	602.314416	301.660846	601.330400	301.168838	6
8	915.529828	458.268552	898.503279	449.755277	897.519263	449.263269	S	***505.298038***	253.152657	488.271489	244.639382	487.287473	244.147374	5
9	1028.613892	514.810584	1011.587343	506.297309	1010.603327	505.805301	L	418.266010	209.636643	401.239461	201.123368	400.255445	200.631360	4
10	1099.651006	550.329141	1082.624457	541.815866	1081.640441	541.323858	A	305.181946	153.094611	288.155397	144.581337	287.171381	144.089329	3
11	1186.683034	593.845155	1169.656485	585.331881	1168.672469	584.839872	S	***234.144832***	117.576054	217.118283	109.062780	216.134267	108.570772	2
12							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
62.9	1331.781250	0.006538	NFLLLINSLASK
32.2	1331.781265	0.006523	FKTQLNLLLDK
5.6	1331.781281	0.006507	LIVVLSDAFLSR
4.5	1331.781265	0.006523	QKLLQSLFLDK

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

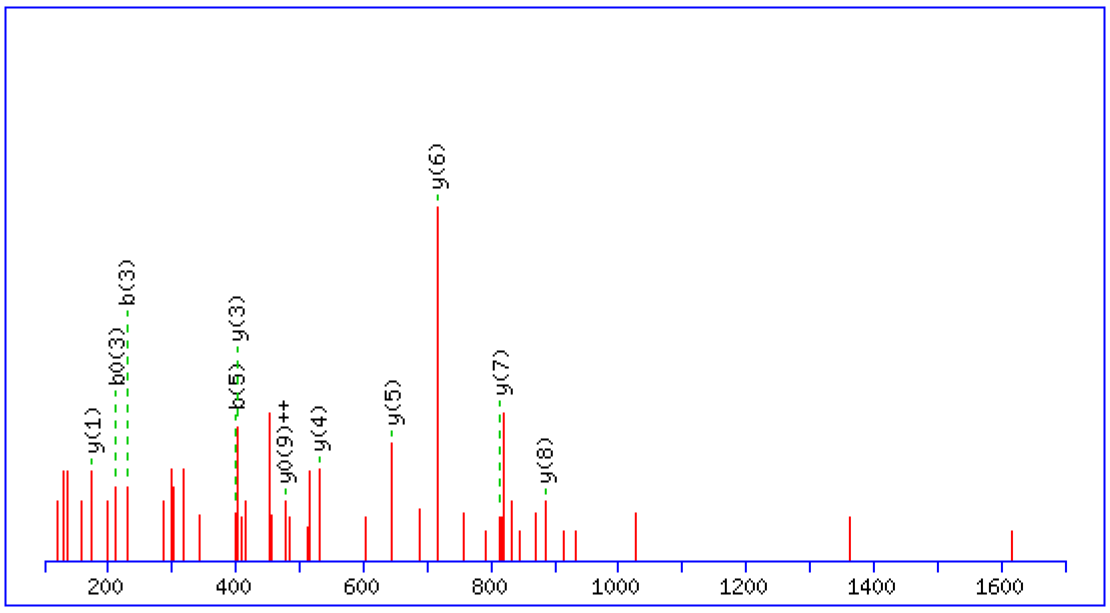
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ASAVALEVQR**
Found in **EF2K_HUMAN**, Eukaryotic elongation factor 2 kinase OS=Homo sapiens GN=EEF2K PE=1 SV=2

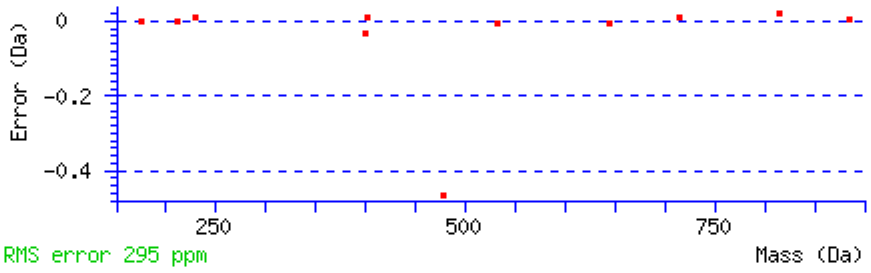
Match to Query 19702: 1042.576568 from(522.295560,2+) rtinseconds(1654) index(15239)
Title: Locus:1.1.1.2124.29
Data file 2011-11-10 - TFD - EP 4-2.mgf

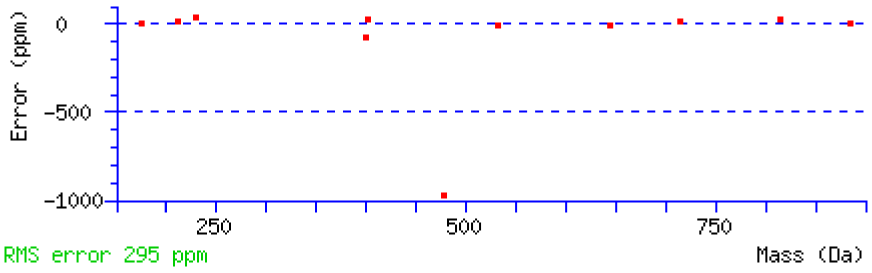
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1042.577087
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 35 **Expect:** 0.0029
Matches : 11/84 fragment ions using 31 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.044390	36.525833					A							10
2	159.076418	80.041847			141.065853	71.036564	S	972.547271	486.777274	955.520722	478.263999	954.536706	477.771991	9
3	**230.113532**	115.560404			212.102967	106.555121	A	***885.515243***	443.261260	868.488694	434.747985	867.504678	434.255977	8
4	329.181946	165.094611			311.171381	156.089328	V	***814.478129***	407.742703	797.451580	399.229428	796.467564	398.737420	7
5	**400.219060**	200.613168			382.208495	191.607885	A	***715.409715***	358.208496	698.383166	349.695221	697.399150	349.203213	6
6	513.303124	257.155200			495.292559	248.149918	L	***644.372601***	322.689939	627.346052	314.176664	626.362036	313.684656	5
7	642.345717	321.676497			624.335152	312.671214	E	***531.288537***	266.147907	514.261988	257.634632	513.277972	257.142624	4
8	741.414131	371.210704			723.403566	362.205421	V	***402.245944***	201.626610	385.219395	193.113336			3
9	869.472709	435.239993	852.446160	426.726718	851.462144	426.234710	Q	303.177530	152.092403	286.150981	143.579129			2
10							R	***175.118952***	88.063114	158.092403	79.549840			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.4	1042.577087	-0.000519	ASAVALEVQR

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

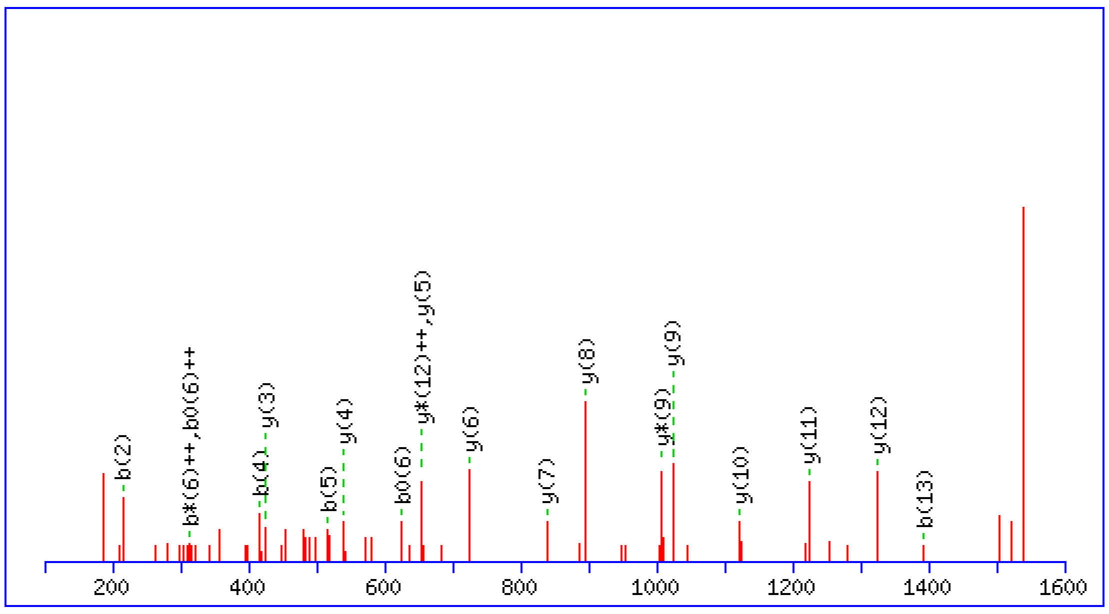
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLTTVQGIADDYDK**
Found in **EIF1B_HUMAN**, Eukaryotic translation initiation factor 1b OS=Homo sapiens GN=EIF1B PE=1 SV=2

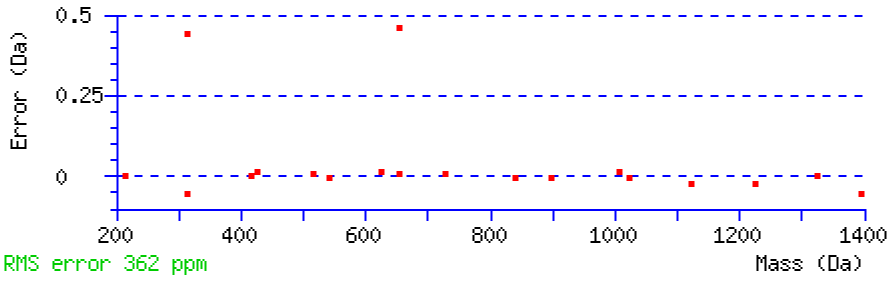
Match to Query 39734: 1538.740668 from(770.377610,2+) rtinseconds(2562) index(24981)
Title: Locus:1.1.1.2433.47
Data file 2011-11-10 - TFD - EP 4-7.mgf

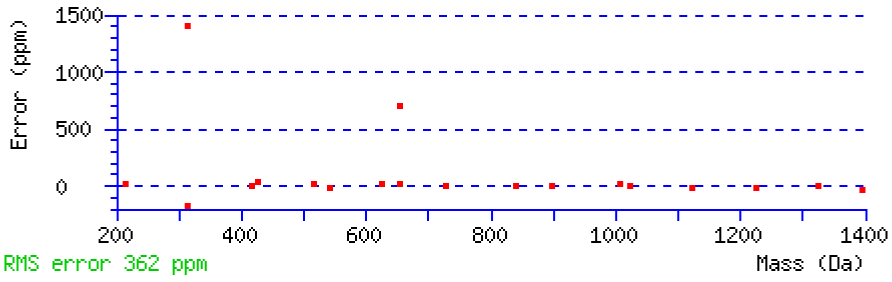
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1538.746429
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 87 **Expect:** 1.8e-008
Matches : 19/144 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							14
2	**215.139019**	108.073147			197.128454	99.067865	L	1438.706018	719.856647	1421.679469	711.343373	1420.695453	710.851365	13
3	316.186698	158.596987			298.176133	149.591704	T	***1325.621954***	663.314615	1308.595405	654.801341	1307.611389	654.309333	12
4	**417.234377**	209.120826			399.223812	200.115544	T	***1224.574275***	612.790776	1207.547726	604.277501	1206.563710	603.785493	11
5	**516.302791**	258.655034			498.292226	249.649751	V	***1123.526596***	562.266936	1106.500047	553.753662	1105.516031	553.261654	10
6	644.361369	322.684323	627.334820	314.171048	626.350804	313.679040	Q	***1024.458182***	512.732729	1007.431633	504.219455	1006.447617	503.727447	9
7	701.382833	351.195055	684.356284	342.681780	683.372268	342.189772	G	***896.399604***	448.703440	879.373055	440.190166	878.389039	439.698158	8
8	814.466897	407.737087	797.440348	399.223812	796.456332	398.731804	I	***839.378140***	420.192708	822.351591	411.679434	821.367575	411.187426	7
9	885.504011	443.255644	868.477462	434.742369	867.493446	434.250361	A	***726.294076***	363.650676	709.267527	355.137402	708.283511	354.645394	6
10	1000.530954	500.769115	983.504405	492.255841	982.520389	491.763833	D	***655.256962***	328.132119	638.230413	319.618845	637.246397	319.126837	5
11	1115.557897	558.282587	1098.531348	549.769312	1097.547332	549.277304	D	***540.230019***	270.618648	523.203470	262.105373	522.219454	261.613365	4
12	1278.621226	639.814251	1261.594677	631.300977	1260.610661	630.808969	Y	***425.203076***	213.105176	408.176527	204.591902	407.192511	204.099894	3
13	**1393.648169**	697.327723	1376.621620	688.814448	1375.637604	688.322440	D	262.139747	131.573512	245.113198	123.060237	244.129182	122.568229	2
14							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
87.5	1538.746429	-0.005761	TLTTVQGIADDYDK
4.7	1538.737183	0.003485	MEKHNAQGQGNGLR
3.7	1538.754929	-0.014261	DEARPGGAEAAPSRR
2.6	1538.754959	-0.014291	NQANPSRQPGSVPR

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

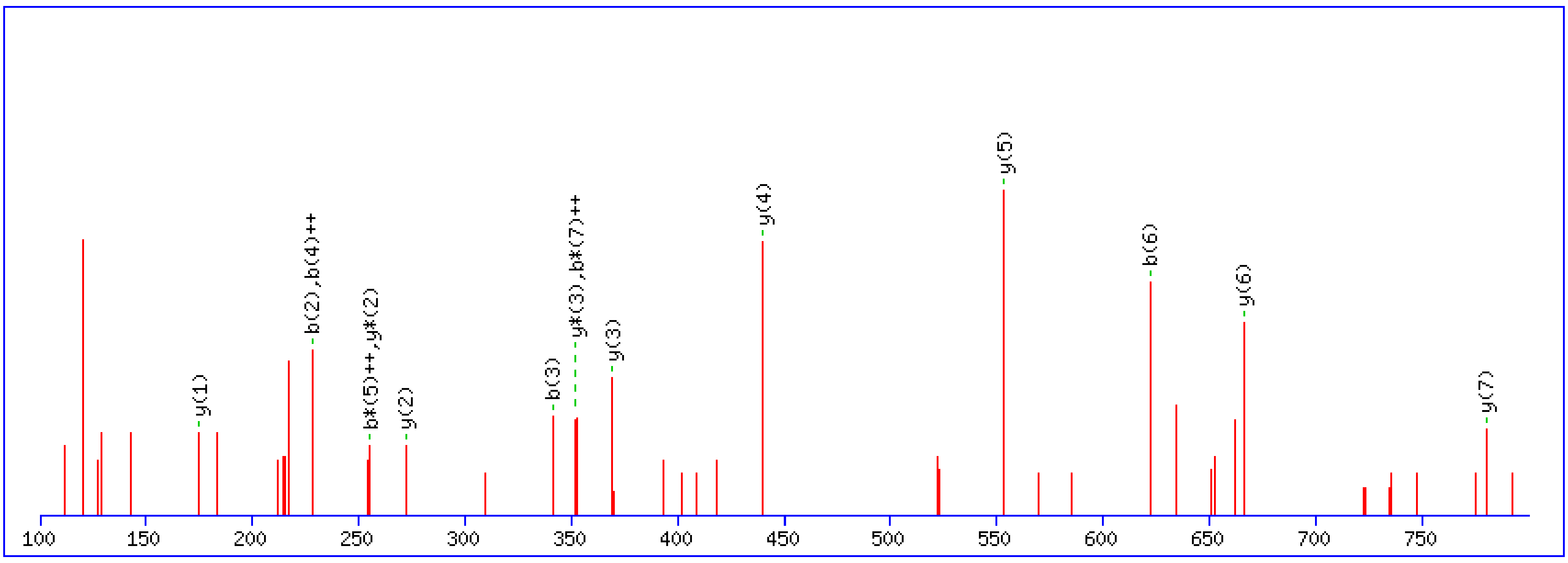
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **INLIAPPR**
Found in **IF2A_HUMAN**, Eukaryotic translation initiation factor 2 subunit 1 OS=Homo sapiens GN=EIF2S1 PE=1 SV=3

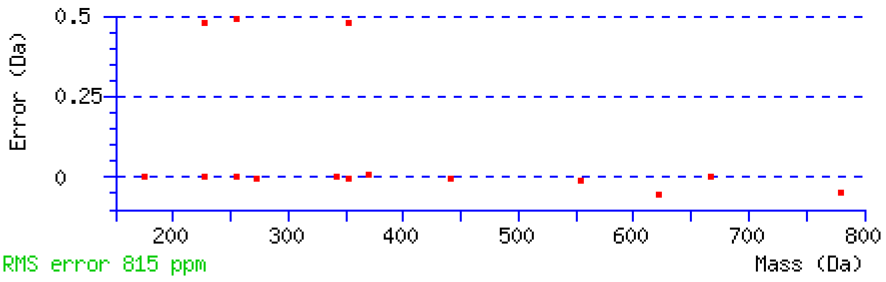
Match to Query 3731: 892.551008 from(447.282780,2+) rtinseconds(1974) index(22215)
Title: Locus:1.1.1.1134.6
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 2.mgf

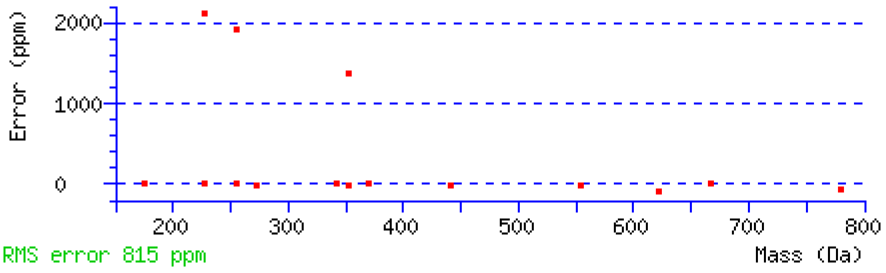
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [800] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 892.549408
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 44 **Expect:** 5.2e-005
Matches : 15/54 fragment ions using 26 most intense peaks (help)

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	114.091340	57.549308			I					8
2	**228.134267**	114.570771	211.107718	106.057497	N	***780.472649***	390.739963	763.446100	382.226688	7
3	**341.218331**	171.112803	324.191782	162.599529	L	***666.429722***	333.718499	649.403173	325.205225	6
4	454.302395	227.654835	437.275846	219.141561	I	***553.345658***	277.176467	536.319109	268.663193	5
5	525.339509	263.173393	508.312960	254.660118	A	***440.261594***	220.634435	423.235045	212.121161	4
6	**622.392273**	311.699775	605.365724	303.186500	P	***369.224480***	185.115878	352.197931	176.602604	3
7	719.445037	360.226157	702.418488	351.712882	P	***272.171716***	136.589496	255.145167	128.076222	2
8					R	***175.118952***	88.063114	158.092403	79.549840	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.3	892.549408	0.001600	INLIAPPR
7.3	892.549423	0.001585	RGPLPIPK
3.0	892.549423	0.001585	LQIGPIPR
1.2	892.549423	0.001585	LALAPVGPR

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

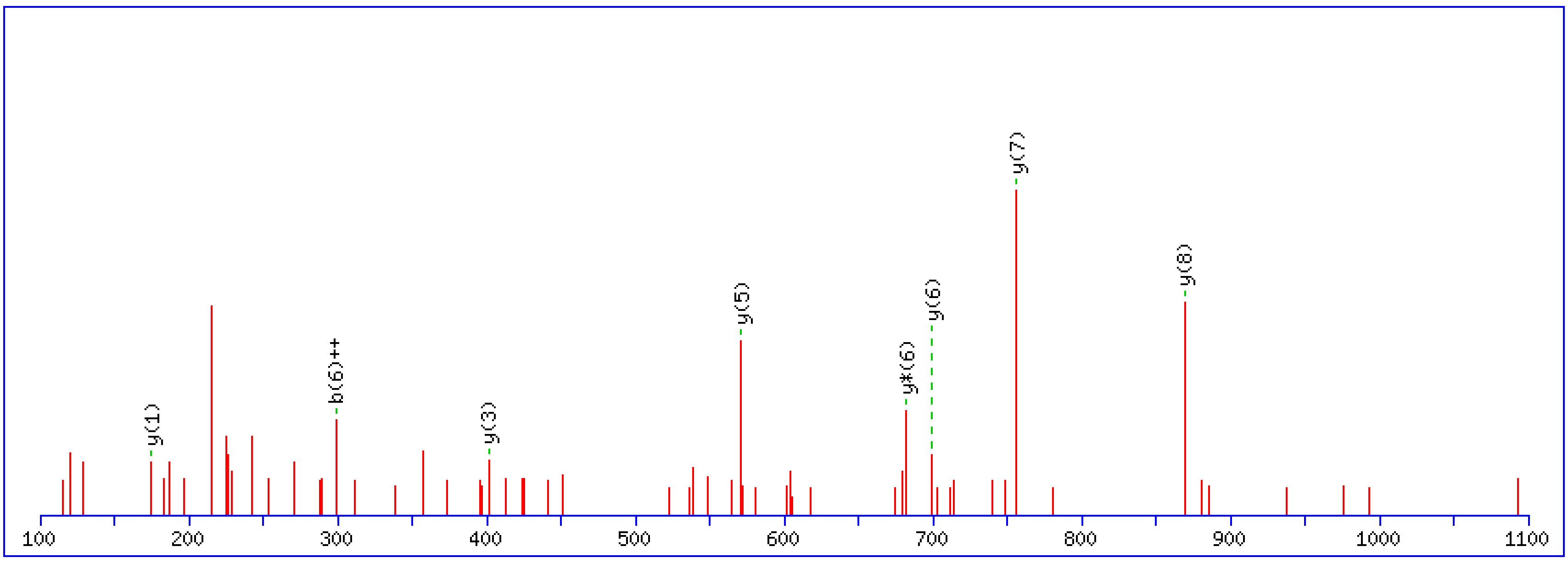
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELLGQGLLLR**
Found in **EIF3C_HUMAN**, Eukaryotic translation initiation factor 3 subunit C OS=Homo sapiens GN=EIF3C PE=1 SV=1

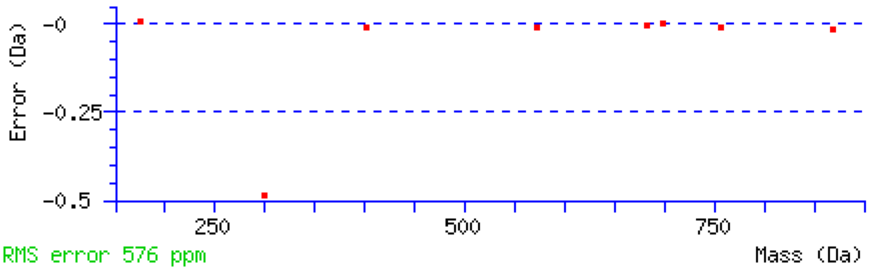
Match to Query 17218: 1110.666488 from(556.340520,2+) rtinseconds(3112) index(43526)
Title: Locus:1.1.1.1626.6
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 3.mgf

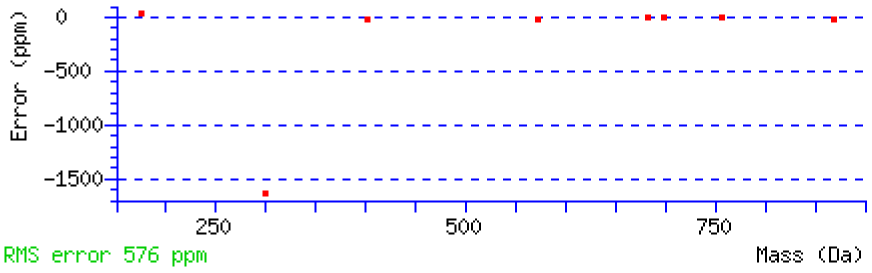
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1110.676071
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31  Expect: 0.0023
Matches : 8/82 fragment ions using 19 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	130.049869	65.528572			112.039304	56.523290	E					10
2	243.133933	122.070605			225.123368	113.065322	L	982.640778	491.824027	965.614229	483.310753	9
3	356.217997	178.612637			338.207432	169.607354	L	***869.556714***	435.281995	852.530165	426.768721	8
4	413.239461	207.123369			395.228896	198.118086	G	***756.472650***	378.739963	739.446101	370.226689	7
5	541.298039	271.152658	524.271490	262.639383	523.287474	262.147375	Q	***699.451186***	350.229231	682.424637	341.715957	6
6	598.319503	299.663390	581.292954	291.150115	580.308938	290.658107	G	***571.392608***	286.199942	554.366059	277.686668	5
7	711.403567	356.205422	694.377018	347.692147	693.393002	347.200139	L	514.371144	257.689210	497.344595	249.175936	4
8	824.487631	412.747454	807.461082	404.234179	806.477066	403.742171	L	***401.287080***	201.147178	384.260531	192.633903	3
9	937.571695	469.289486	920.545146	460.776211	919.561130	460.284203	L	288.203016	144.605146	271.176467	136.091871	2
10							R	***175.118952***	88.063114	158.092403	79.549839	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.8	1110.676071	-0.009583	ELLGQGLLLR
9.1	1110.676071	-0.009583	LLGNSLLPIR
4.1	1110.676071	-0.009583	ELLIIGGVAAR
2.4	1110.662125	0.004363	AARGAAAAALLR

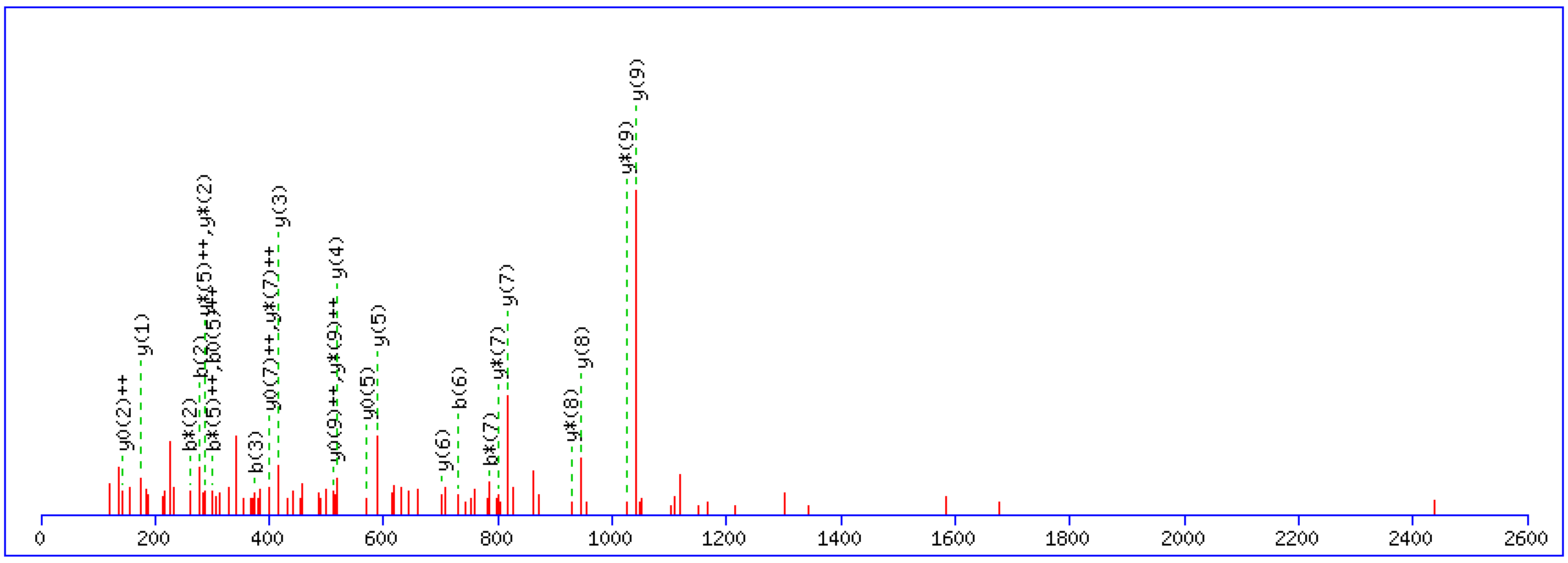
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YNPENLATLER**
Found in **EIF3K_HUMAN**, Eukaryotic translation initiation factor 3 subunit K OS=Homo sapiens GN=EIF3K PE=1 SV=1

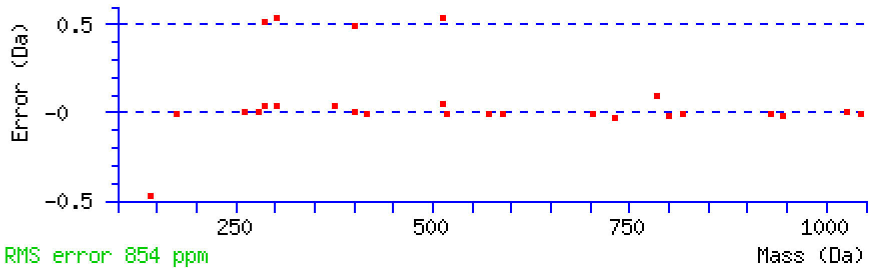
Match to Query 32756: 1318.647128 from(660.330840,2+) rtinseconds(2244) index(27203)
Title: Locus:1.1.1.1299.33
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 3.mgf

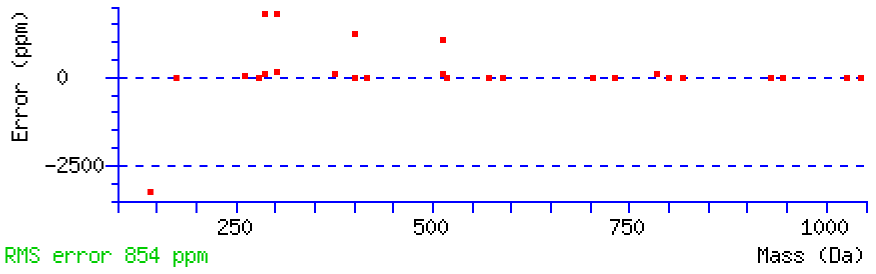
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1318.651688
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 34 **Expect:** 0.0054
Matches : 27/110 fragment ions using 61 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	164.070605	82.538940					Y							11
2	**278.113532**	139.560404	261.086983	131.047130			N	1156.595677	578.801477	1139.569128	570.288202	1138.585112	569.796194	10
3	**375.166296**	188.086786	358.139747	179.573512			P	***1042.552750***	521.780013	1025.526201	513.266739	1024.542185	512.774731	9
4	504.208889	252.608083	487.182340	244.094808	486.198324	243.602800	E	***945.499986***	473.253631	928.473437	464.740357	927.489421	464.248349	8
5	618.251816	309.629546	601.225267	301.116272	600.241251	300.624264	N	***816.457393***	408.732335	799.430844	400.219060	798.446828	399.727052	7
6	**731.335880**	366.171578	714.309331	357.658304	713.325315	357.166296	L	***702.414466***	351.710871	685.387917	343.197597	684.403901	342.705589	6
7	802.372994	401.690135	785.346445	393.176861	784.362429	392.684853	A	***589.330402***	295.168839	572.303853	286.655565	571.319837	286.163557	5
8	903.420673	452.213975	886.394124	443.700700	885.410108	443.208692	T	***518.293288***	259.650282	501.266739	251.137008	500.282723	250.645000	4
9	1016.504737	508.756007	999.478188	500.242732	998.494172	499.750724	L	***417.245609***	209.126442	400.219060	200.613168	399.235044	200.121160	3
10	1145.547330	573.277303	1128.520781	564.764029	1127.536765	564.272021	E	304.161545	152.584410	287.134996	144.071136	286.150980	143.579128	2
11							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of YNPENLATLER
(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	1318.651688	-0.004560	YNPENLATLER
3.2	1318.637970	0.009158	SLYWLHELQM
2.9	1318.645218	0.001910	GPPPPGMRPPRP
2.5	1318.655090	-0.007962	GVIDMGNSLIER

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

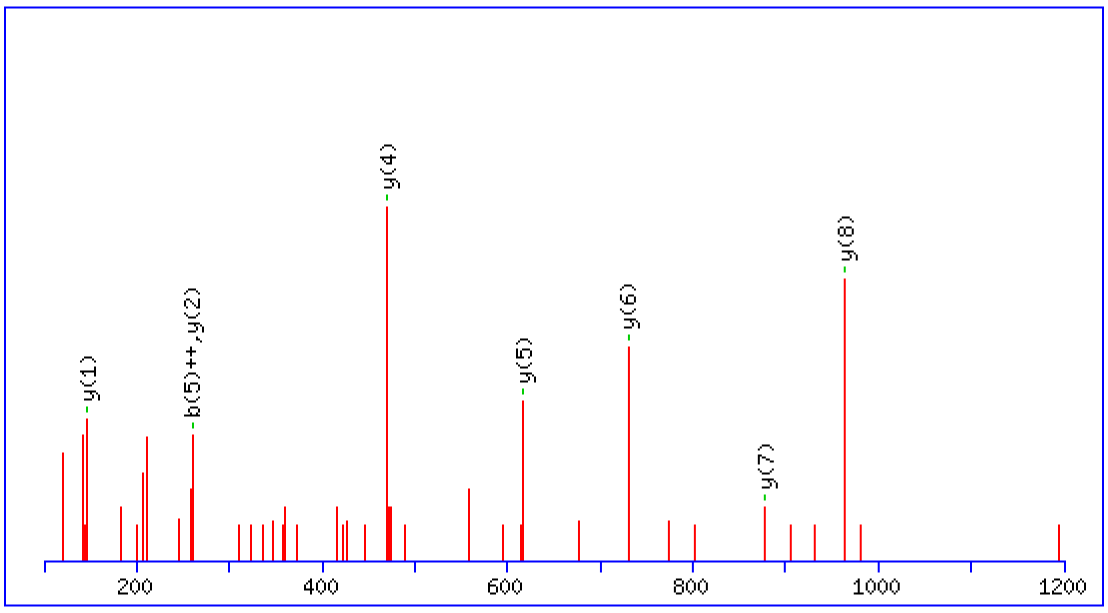
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLSFLFPLLK**
Found in **IF4G2_HUMAN**, Eukaryotic translation initiation factor 4 gamma 2 OS=Homo sapiens GN=EIF4G2 PE=1 SV=1

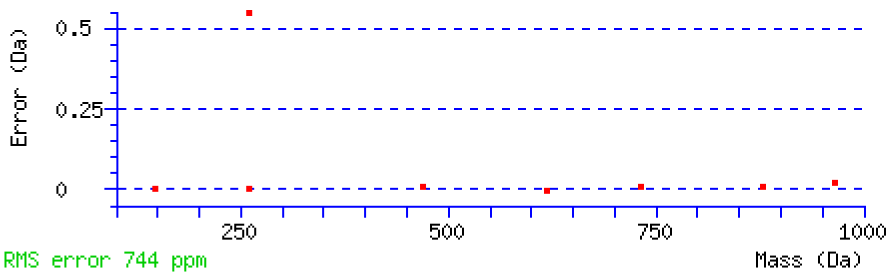
Match to Query 26841: 1133.688228 from(567.851390,2+) rtinseconds(4428) index(67291)
Title: Locus:1.1.1.3060.13
Data file 2011-11-14 - TFD - EP 8-4.mgf

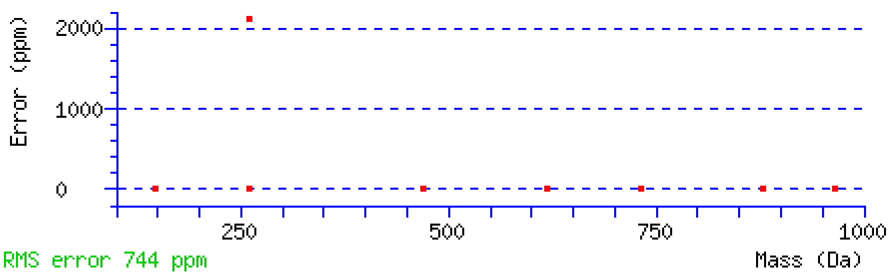
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1200] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1133.684860
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 64  Expect: 6.7e-007
Matches : 8/72 fragment ions using 9 most intense peaks   (help)
```

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	58.028740	29.518008			G							10
2	171.112804	86.060040			L	1077.670680	539.338978	1060.644131	530.825704	1059.660115	530.333696	9
3	258.144832	129.576054	240.134267	120.570772	S	***964.586616***	482.796946	947.560067	474.283672	946.576051	473.791664	8
4	405.213246	203.110261	387.202681	194.104978	F	***877.554588***	439.280932	860.528039	430.767658			7
5	518.297310	259.652293	500.286745	250.647011	L	***730.486174***	365.746725	713.459625	357.233451			6
6	665.365724	333.186500	647.355159	324.181218	F	***617.402110***	309.204693	600.375561	300.691419			5
7	762.418488	381.712882	744.407923	372.707600	P	***470.333696***	235.670486	453.307147	227.157212			4
8	875.502552	438.254914	857.491987	429.249632	L	373.280932	187.144104	356.254383	178.630830			3
9	988.586616	494.796946	970.576051	485.791664	L	***260.196868***	130.602072	243.170319	122.088798			2
10					K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
63.5	1133.684860	0.003368	GLSFLFPLLK
4.1	1133.680817	0.007411	KTNLFSALIK
1.3	1133.680847	0.007381	QIFVKTLTGK

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

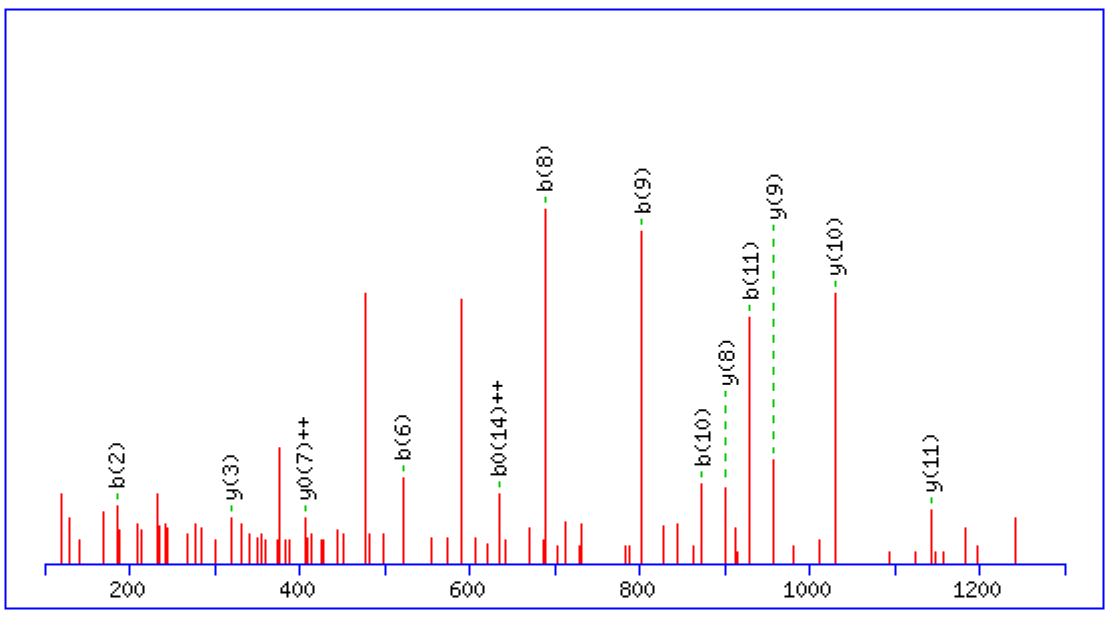
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALPPAAAPPAGAREPPGSR**
Found in **IF4E3_HUMAN**, Eukaryotic translation initiation factor 4E type 3 OS=Homo sapiens GN=EIF4E3 PE=2 SV=4

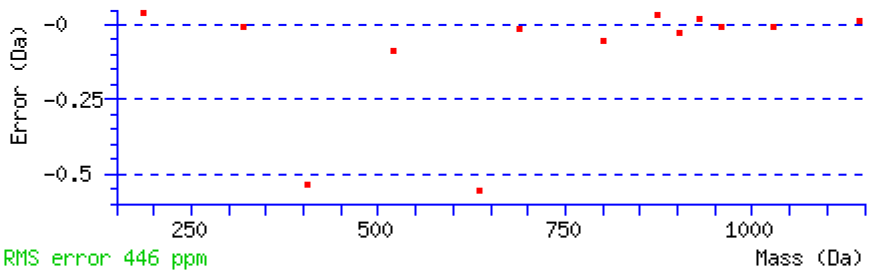
Match to Query 55023: 1829.944662 from(610.988830,3+) rtinseconds(3212) index(43852)
Title: Locus:1.1.1.2544.21
Data file 2011-11-14 - TFD - EP 8-5.mgf

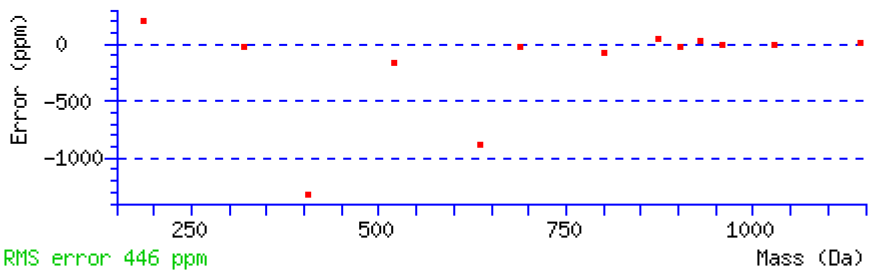
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1829.938385
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P9      : Oxidation (P)
P15     : Oxidation (P)
P16     : Oxidation (P)
Ions Score: 31  Expect: 0.0074
Matches : 13/164 fragment ions using 23 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							19
2	***185.128454***	93.067865					L	1759.908575	880.457925	1742.882026	871.944651	1741.898010	871.452643	18
3	282.181218	141.594247					P	1646.824511	823.915894	1629.797962	815.402619	1628.813946	814.910611	17
4	379.233982	190.120629					P	1549.771747	775.389512	1532.745198	766.876237	1531.761182	766.384229	16
5	450.271096	225.639186					A	1452.718983	726.863130	1435.692434	718.349855	1434.708418	717.857847	15
6	***521.308210***	261.157743					A	1381.681869	691.344572	1364.655320	682.831298	1363.671304	682.339290	14
7	592.345324	296.676300					A	1310.644755	655.826016	1293.618206	647.312741	1292.634190	646.820733	13
8	***689.398088***	345.202682					P	1239.607641	620.307458	1222.581092	611.794184	1221.597076	611.302176	12
9	***802.445767***	401.726522					P	***1142.554877***	571.781076	1125.528328	563.267802	1124.544312	562.775794	11
10	***873.482881***	437.245079					A	***1029.507198***	515.257237	1012.480649	506.743963	1011.496633	506.251955	10
11	***930.504345***	465.755811					G	***958.470084***	479.738680	941.443535	471.225405	940.459519	470.733397	9
12	1001.541459	501.274368					A	***901.448620***	451.227948	884.422071	442.714673	883.438055	442.222665	8
13	1157.642570	579.324923	1140.616021	570.811649			R	830.411506	415.709391	813.384957	407.196116	812.400941	406.704108	7
14	1286.685163	643.846219	1269.658614	635.332945	1268.674598	634.840937	E	674.310395	337.658836	657.283846	329.145561	656.299830	328.653553	6
15	1399.732842	700.370059	1382.706293	691.856785	1381.722277	691.364776	P	545.267802	273.137539	528.241253	264.624265	527.257237	264.132257	5
16	1512.780521	756.893898	1495.753972	748.380624	1494.769956	747.888616	P	432.220123	216.613699	415.193574	208.100425	414.209558	207.608417	4
17	1569.801985	785.404630	1552.775436	776.891356	1551.791420	776.399348	G	***319.172444***	160.089860	302.145895	151.576585	301.161879	151.084577	3
18	1656.834013	828.920644	1639.807464	820.407370	1638.823448	819.915362	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
19							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.0	1829.938385	0.006277	ALPPAAAPPAGAREPPGSR
13.6	1829.938385	0.006277	ALPPAAAPPAGAREPPGSR
7.8	1829.931183	0.013479	EPAPLDKYQPPPPPPR
5.0	1829.957672	-0.013010	GFVYSSFLKPYNPRR
4.3	1829.941116	0.003546	DITFPPGSVEATQPVLK
3.2	1829.949173	-0.004511	TMCLQRLQPVQPTTK
3.2	1829.931183	0.013479	EPAPLDKYQPPPPPPR
0.3	1829.931183	0.013479	EPAPLDKYQPPPPPPR
0.3	1829.942429	0.002233	THPIEVFEPGAEHIVR

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

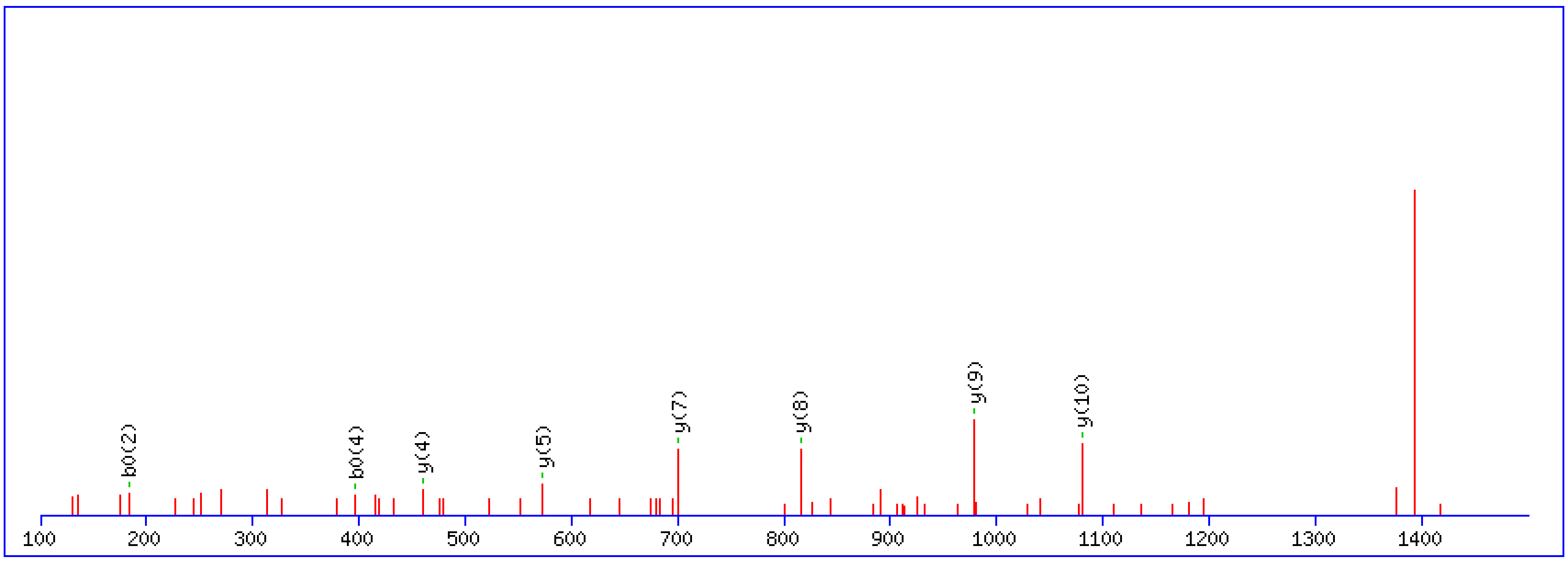
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EALTYDGALLGDR**
Found in **IF4H_HUMAN**, Eukaryotic translation initiation factor 4H OS=Homo sapiens GN=EIF4H PE=1 SV=5

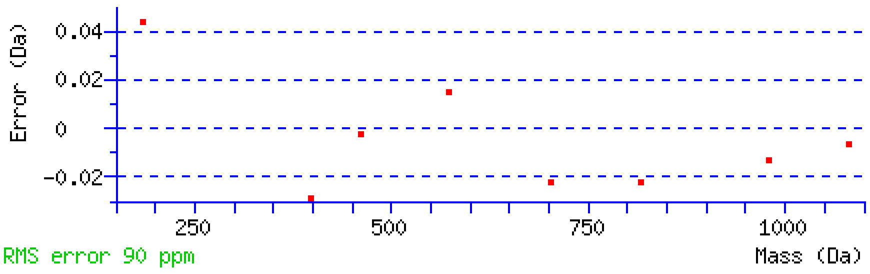
Match to Query 46529: 1392.685788 from(697.350170,2+) rtinseconds(2657) index(35719)
Title: Locus:1.1.1.1401.32
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 1.mgf

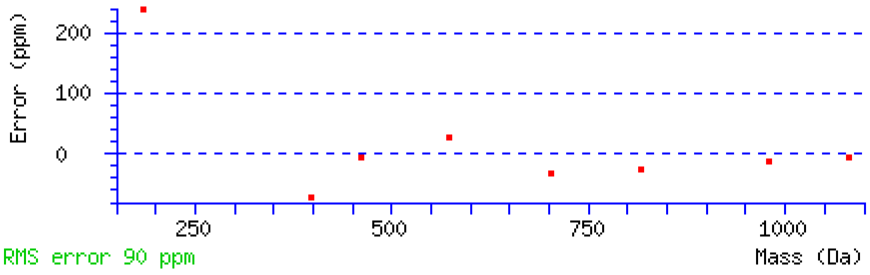
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1392.688492
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 39  Expect: 0.002
Matches : 8/118 fragment ions using 12 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572	112.039304	56.523290	E							13
2	201.086983	101.047130	183.076418	92.041847	A	1264.653194	632.830235	1247.626645	624.316961	1246.642629	623.824953	12
3	314.171047	157.589161	296.160482	148.583879	L	1193.616080	597.311678	1176.589531	588.798404	1175.605515	588.306396	11
4	415.218726	208.113001	397.208161	199.107719	T	***1080.532016***	540.769646	1063.505467	532.256372	1062.521451	531.764364	10
5	578.282055	289.644666	560.271490	280.639383	Y	***979.484337***	490.245807	962.457788	481.732532	961.473772	481.240524	9
6	693.308998	347.158137	675.298433	338.152855	D	***816.421008***	408.714142	799.394459	400.200868	798.410443	399.708860	8
7	750.330462	375.668869	732.319897	366.663587	G	***701.394065***	351.200671	684.367516	342.687396	683.383500	342.195388	7
8	821.367576	411.187426	803.357011	402.182144	A	644.372601	322.689939	627.346052	314.176664	626.362036	313.684656	6
9	934.451640	467.729458	916.441075	458.724176	L	***573.335487***	287.171382	556.308938	278.658107	555.324922	278.166099	5
10	1047.535704	524.271490	1029.525139	515.266208	L	***460.251423***	230.629349	443.224874	222.116075	442.240858	221.624067	4
11	1104.557168	552.782222	1086.546603	543.776940	G	347.167359	174.087317	330.140810	165.574043	329.156794	165.082035	3
12	1219.584111	610.295694	1201.573546	601.290411	D	290.145895	145.576585	273.119346	137.063311	272.135330	136.571303	2
13					R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.9	1392.688492	-0.002704	EALTYDGALLGDR

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

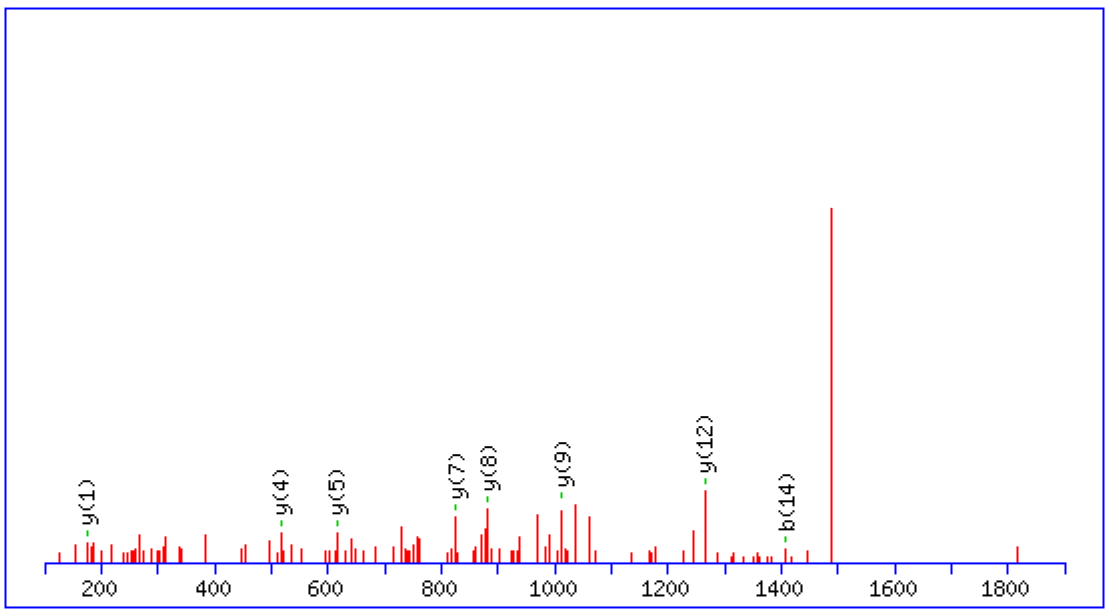
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LKEGDTIIVPGVEGPIVTQIR**
Found in **IF2P_HUMAN**, Eukaryotic translation initiation factor 5B OS=Homo sapiens GN=EIF5B PE=1 SV=4

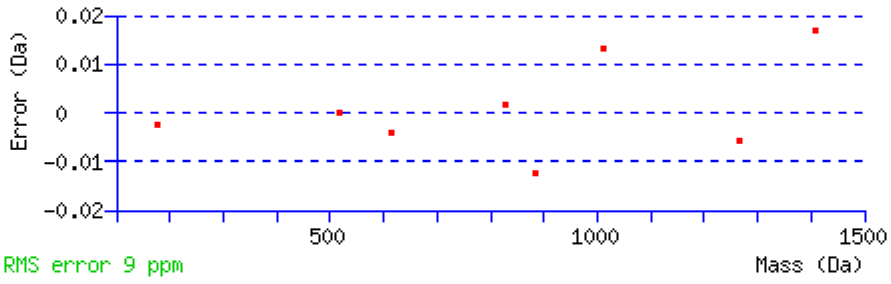
Match to Query 63438: 2233.265382 from(745.429070,3+) rtinseconds(3166) index(41156)
Title: Locus:1.1.1.2752.33
Data file 2011-11-12 - TFD - EP 5-1.mgf

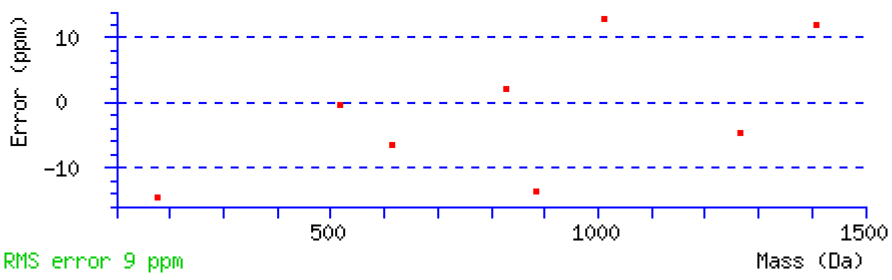
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2233.268188
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.0018
Matches : 8/228 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							21
2	242.186303	121.596790	225.159754	113.083515			K	2121.191398	1061.099337	2104.164849	1052.586062	2103.180833	1052.094054	20
3	371.228896	186.118086	354.202347	177.604812	353.218331	177.112804	E	1993.096435	997.051855	1976.069886	988.538581	1975.085870	988.046573	19
4	428.250360	214.628818	411.223811	206.115544	410.239795	205.623536	G	1864.053842	932.530559	1847.027293	924.017284	1846.043277	923.525276	18
5	543.277303	272.142290	526.250754	263.629015	525.266738	263.137007	D	1807.032378	904.019827	1790.005829	895.506553	1789.021813	895.014544	17
6	644.324982	322.666129	627.298433	314.152855	626.314417	313.660847	T	1692.005435	846.506355	1674.978886	837.993081	1673.994870	837.501073	16
7	757.409046	379.208161	740.382497	370.694887	739.398481	370.202879	I	1590.957756	795.982516	1573.931207	787.469241	1572.947191	786.977233	15
8	870.493110	435.750193	853.466561	427.236919	852.482545	426.744911	I	1477.873692	739.440484	1460.847143	730.927210	1459.863127	730.435201	14
9	969.561524	485.284400	952.534975	476.771126	951.550959	476.279118	V	1364.789628	682.898452	1347.763079	674.385177	1346.779063	673.893169	13
10	1066.614288	533.810782	1049.587739	525.297508	1048.603723	524.805500	P	***1265.721214***	633.364245	1248.694665	624.850971	1247.710649	624.358962	12
11	1123.635752	562.321514	1106.609203	553.808240	1105.625187	553.316231	G	1168.668450	584.837863	1151.641901	576.324589	1150.657885	575.832580	11
12	1222.704166	611.855721	1205.677617	603.342447	1204.693601	602.850439	V	1111.646986	556.327131	1094.620437	547.813857	1093.636421	547.321848	10
13	1351.746759	676.377017	1334.720210	667.863743	1333.736194	667.371735	E	***1012.578572***	506.792924	995.552023	498.279649	994.568007	497.787641	9
14	1408.768223	704.887749	1391.741674	696.374475	1390.757658	695.882467	G	***883.535979***	442.271628	866.509430	433.758353	865.525414	433.266345	8
15	1505.820987	753.414131	1488.794438	744.900857	1487.810422	744.408849	P	***826.514515***	413.760896	809.487966	405.247621	808.503950	404.755613	7
16	1618.905051	809.956163	1601.878502	801.442889	1600.894486	800.950881	I	729.461751	365.234514	712.435202	356.721239	711.451186	356.229231	6
17	1717.973465	859.490370	1700.946916	850.977096	1699.962900	850.485088	V	***616.377687***	308.692482	599.351138	300.179207	598.367122	299.687199	5
18	1819.021144	910.014210	1801.994595	901.500935	1801.010579	901.008927	T	***517.309273***	259.158275	500.282724	250.645000	499.298708	250.152992	4
19	1947.079722	974.043499	1930.053173	965.530224	1929.069157	965.038216	Q	416.261594	208.634435	399.235045	200.121160			3
20	2060.163786	1030.585531	2043.137237	1022.072256	2042.153221	1021.580248	I	288.203016	144.605146	271.176467	136.091872			2
21							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.8	2233.268188	-0.002806	LKEGDTIIVPGVEGPIVTQIR

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

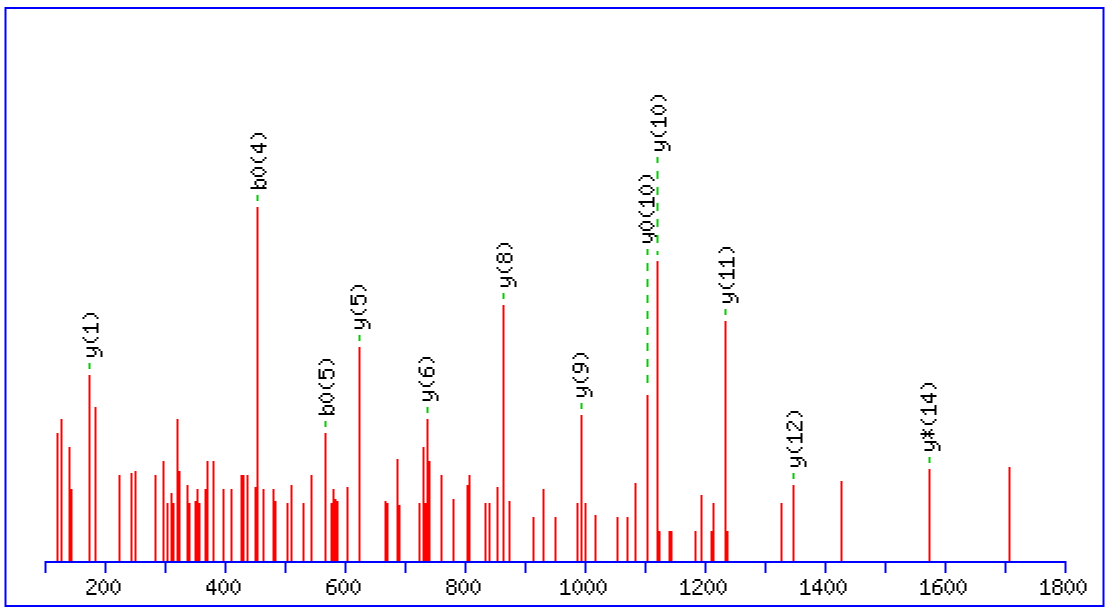
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ETQDLIEQGALLQAHR**
Found in **EXOC3_HUMAN**, Exocyst complex component 3 OS=Homo sapiens GN=EXOC3 PE=1 SV=2

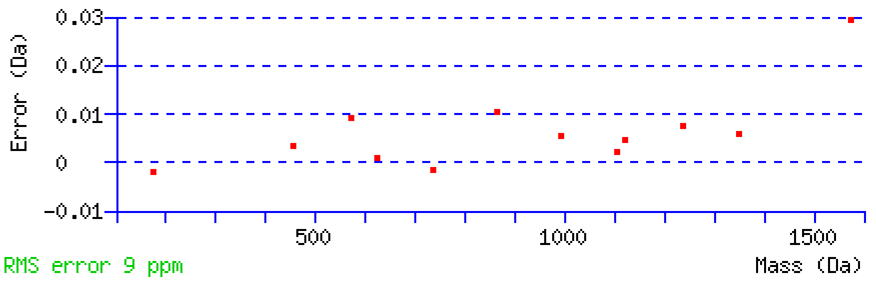
Match to Query 56685: 1820.933892 from(607.985240,3+) rtinseconds(2567) index(29723)
Title: Locus:1.1.1.2617.26
Data file 2011-11-12 - TFD - EP 5-2.mgf

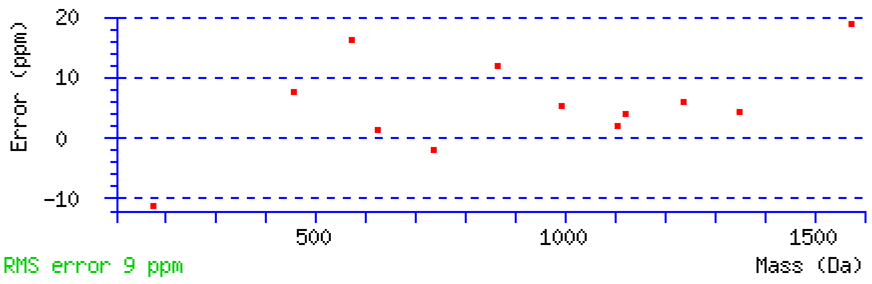
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1820.938049
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 52 **Expect:** 6.4e-005
Matches : 12/158 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	**E**							**16**
2	231.097548	116.052412			213.086983	107.047130	**T**	1692.902761	846.955019	1675.876212	838.441744	1674.892196	837.949736	**15**
3	359.156126	180.081701	342.129577	171.568427	341.145561	171.076419	**Q**	1591.855082	796.431179	1574.828533	787.917904	1573.844517	787.425896	**14**
4	474.183069	237.595173	457.156520	229.081898	456.172504	228.589890	**D**	1463.796504	732.401890	1446.769955	723.888616	1445.785939	723.396607	**13**
5	587.267133	294.137205	570.240584	285.623930	569.256568	285.131922	**L**	***1348.769561***	674.888418	1331.743012	666.375144	1330.758996	665.883136	**12**
6	700.351197	350.679237	683.324648	342.165962	682.340632	341.673954	**I**	***1235.685497***	618.346386	1218.658948	609.833112	1217.674932	609.341104	**11**
7	829.393790	415.200533	812.367241	406.687259	811.383225	406.195251	**E**	***1122.601433***	561.804355	1105.574884	553.291080	1104.590868	552.799072	**10**
8	957.452368	479.229822	940.425819	470.716548	939.441803	470.224540	**Q**	***993.558840***	497.283058	976.532291	488.769783			**9**
9	1014.473832	507.740554	997.447283	499.227280	996.463267	498.735272	**G**	***865.500262***	433.253769	848.473713	424.740494			**8**
10	1085.510946	543.259111	1068.484397	534.745837	1067.500381	534.253829	**A**	808.478798	404.743037	791.452249	396.229762			**7**
11	1198.595010	599.801143	1181.568461	591.287869	1180.584445	590.795861	**L**	***737.441684***	369.224480	720.415135	360.711205			**6**
12	1311.679074	656.343175	1294.652525	647.829901	1293.668509	647.337892	**L**	***624.357620***	312.682448	607.331071	304.169174			**5**
13	1439.737652	720.372464	1422.711103	711.859190	1421.727087	711.367182	**Q**	511.273556	256.140416	494.247007	247.627141			**4**
14	1510.774766	755.891021	1493.748217	747.377747	1492.764201	746.885739	**A**	383.214978	192.111127	366.188429	183.597852			**3**
15	1647.833678	824.420477	1630.807129	815.907203	1629.823113	815.415194	**H**	312.177864	156.592570	295.151315	148.079295			**2**
16							**R**	***175.118952***	88.063114	158.092403	79.549839			**1**





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.8	1820.938049	-0.004157	ETQDLIEQGALLQAHR
6.7	1820.920288	0.013604	HSGKLEPMEATAHLLR
1.9	1820.920303	0.013589	LSVLSSGCRYQEGPVR

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

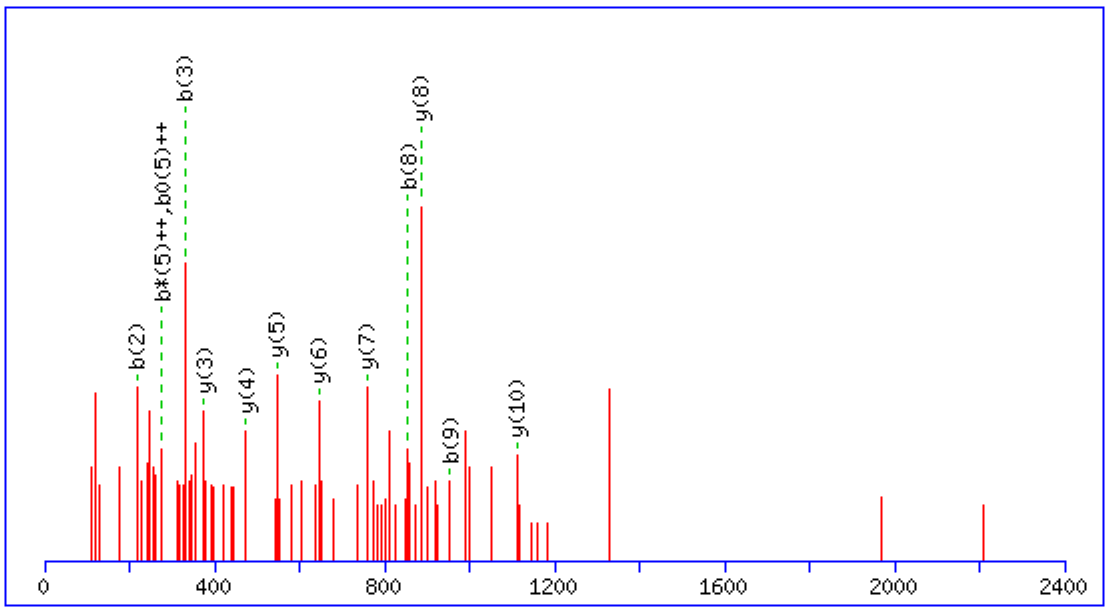
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SELIQLVAVTQK**
Found in **EXOC7_HUMAN**, Exocyst complex component 7 OS=Homo sapiens GN=EXOC7 PE=1 SV=3

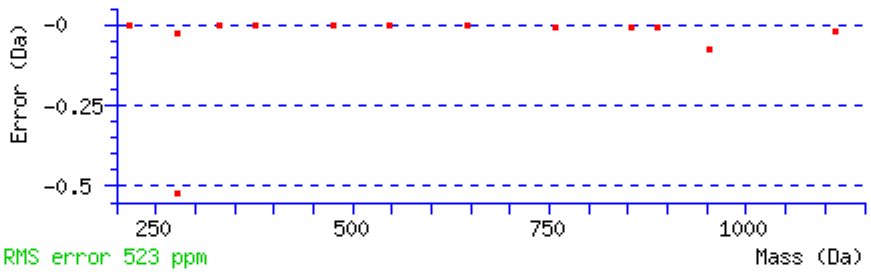
Match to Query 35730: 1327.778528 from(664.896540,2+) rtinseconds(2961) index(37073)
Title: Locus:1.1.1.2764.26
Data file 2011-11-12 - TFD - EP 5-2.mgf

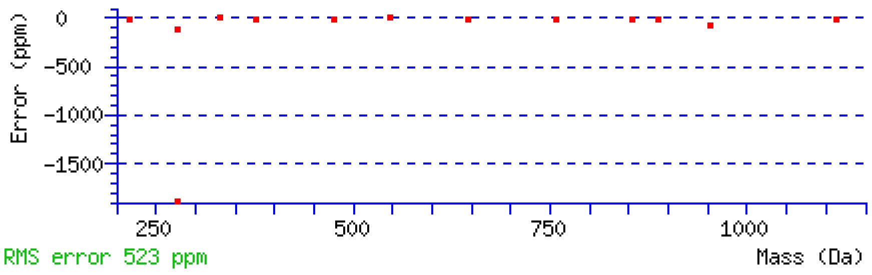
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1327.771103
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.0017
Matches : 13/120 fragment ions using 31 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	88.039304	44.523290			70.028739	35.518008	S							12
2	**217.081897**	109.044586			199.071332	100.039304	E	1241.746366	621.376821	1224.719817	612.863547	1223.735801	612.371539	11
3	**330.165961**	165.586618			312.155396	156.581336	L	***1112.703773***	556.855525	1095.677224	548.342250	1094.693208	547.850242	10
4	443.250025	222.128650			425.239460	213.123368	I	999.619709	500.313493	982.593160	491.800218	981.609144	491.308210	9
5	571.308603	286.157940	554.282054	277.644665	553.298038	277.152657	Q	***886.535645***	443.771461	869.509096	435.258186	868.525080	434.766178	8
6	684.392667	342.699972	667.366118	334.186697	666.382102	333.694689	L	***758.477067***	379.742172	741.450518	371.228897	740.466502	370.736889	7
7	783.461081	392.234179	766.434532	383.720904	765.450516	383.228896	V	***645.393003***	323.200140	628.366454	314.686865	627.382438	314.194857	6
8	**854.498195**	427.752736	837.471646	419.239461	836.487630	418.747453	A	***546.324589***	273.665933	529.298040	265.152658	528.314024	264.660650	5
9	**953.566609**	477.286943	936.540060	468.773668	935.556044	468.281660	V	***475.287475***	238.147376	458.260926	229.634101	457.276910	229.142093	4
10	1054.614288	527.810782	1037.587739	519.297508	1036.603723	518.805500	T	***376.219061***	188.613169	359.192512	180.099894	358.208496	179.607886	3
11	1182.672866	591.840071	1165.646317	583.326797	1164.662301	582.834789	Q	275.171382	138.089329	258.144833	129.576055			2
12							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.2	1327.771103	0.007425	SELIQLVAVTQK

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

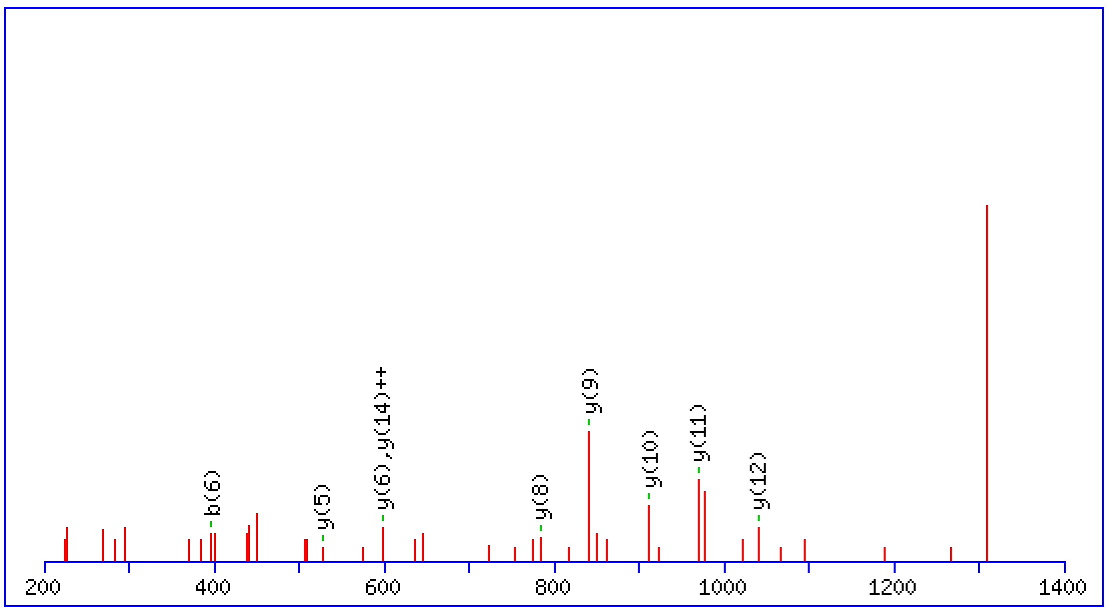
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GGGPAGAGGEAPAALR**
Found in **EXOS6_HUMAN**, Exosome complex component MTR3 OS=Homo sapiens GN=EXOSC6 PE=1 SV=1

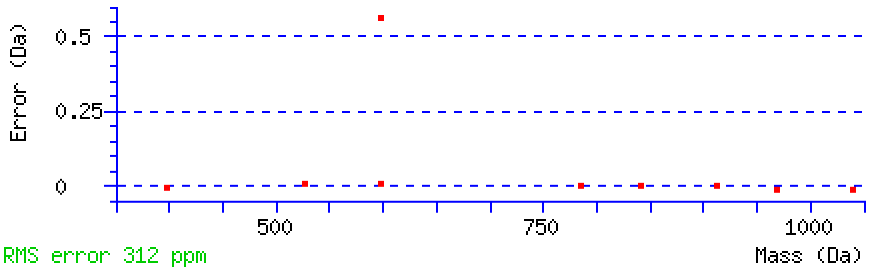
Match to Query 648753: 1307.658048 from(654.836300,2+) rtinseconds(1545) index(254008)
Title: Locus:1.1.1.1034.31
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

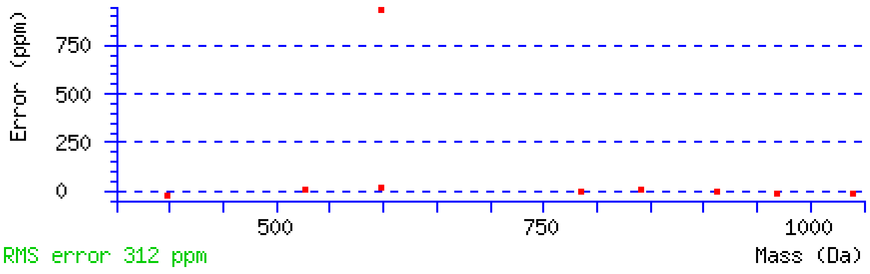
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1307.658203
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.0025
Matches : 9/120 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008			G							16
2	115.050204	58.028740			G	1251.644027	626.325652	1234.617478	617.812377	1233.633462	617.320369	15
3	172.071668	86.539472			G	1194.622563	597.814919	1177.596014	589.301645	1176.611998	588.809637	14
4	269.124432	135.065854			P	1137.601099	569.304188	1120.574550	560.790913	1119.590534	560.298905	13
5	340.161546	170.584411			A	***1040.548335***	520.777806	1023.521786	512.264531	1022.537770	511.772523	12
6	397.183010	199.095143			G	***969.511221***	485.259249	952.484672	476.745974	951.500656	476.253966	11
7	468.220124	234.613700			A	***912.489757***	456.748517	895.463208	448.235242	894.479192	447.743234	10
8	525.241588	263.124432			G	***841.452643***	421.229960	824.426094	412.716685	823.442078	412.224677	9
9	582.263052	291.635164			G	***784.431179***	392.719227	767.404630	384.205953	766.420614	383.713945	8
10	711.305645	356.156461	693.295080	347.151178	E	727.409715	364.208495	710.383166	355.695221	709.399150	355.203213	7
11	782.342759	391.675018	764.332194	382.669735	A	***598.367122***	299.687199	581.340573	291.173924			6
12	879.395523	440.201400	861.384958	431.196117	P	***527.330008***	264.168642	510.303459	255.655367			5
13	950.432637	475.719957	932.422072	466.714674	A	430.277244	215.642260	413.250695	207.128985			4
14	1021.469751	511.238514	1003.459186	502.233231	A	359.240130	180.123703	342.213581	171.610428			3
15	1134.553815	567.780546	1116.543250	558.775263	L	288.203016	144.605146	271.176467	136.091871			2
16					R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.7	1307.658203	-0.000155	GGGPAGAGGEAPAALR

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

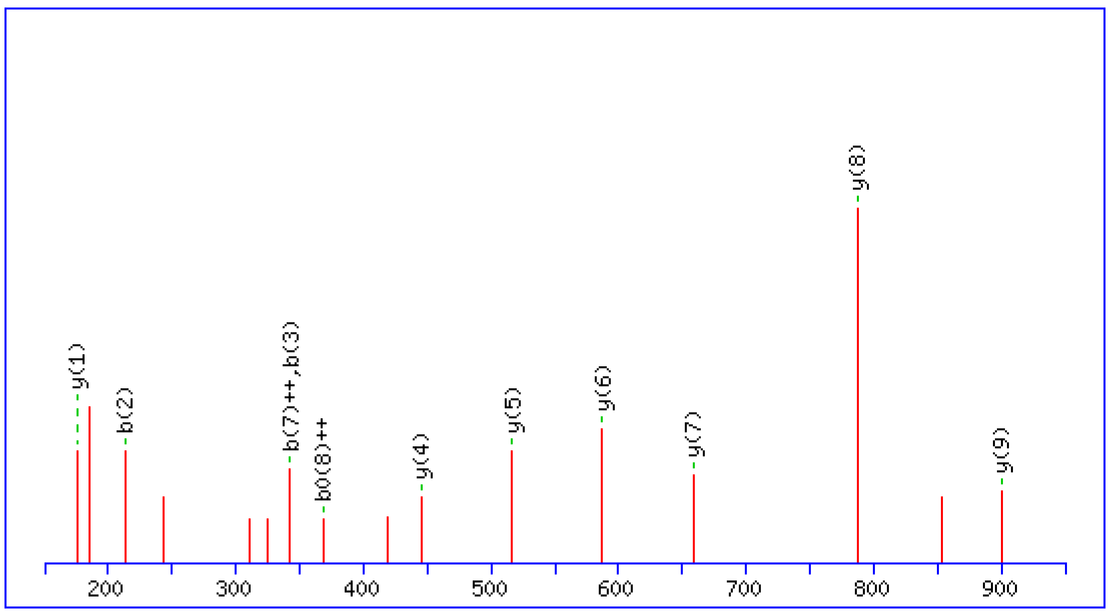
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLEAAAQAAR**
Found in **EXOS4_HUMAN**, Exosome complex component RRP41 OS=Homo sapiens GN=EXOSC4 PE=1 SV=3

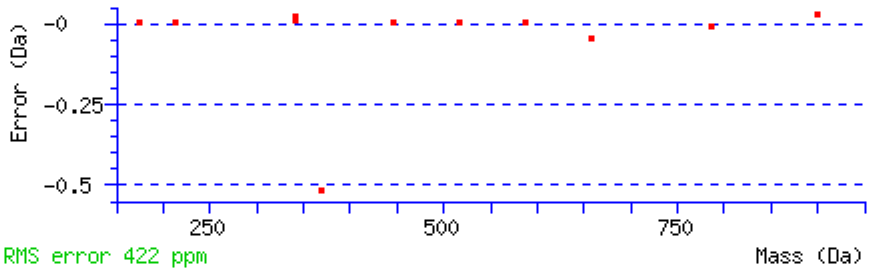
Match to Query 16087: 998.548968 from(500.281760,2+) rtinseconds(1256) index(6820)
Title: Locus:1.1.1.1793.25
Data file 2011-11-10 - TFD - EP 4-5.mgf

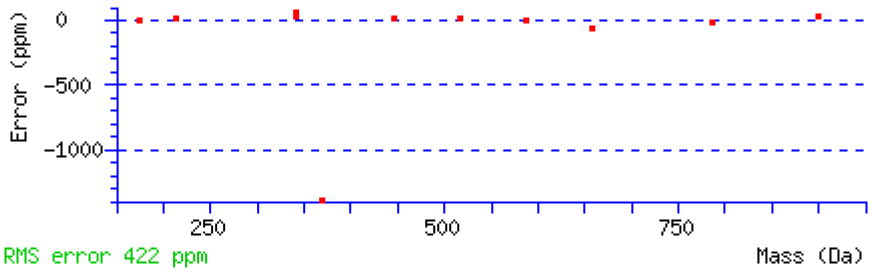
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 998.550858
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 59  Expect: 1.5e-005
Matches : 11/78 fragment ions using 15 most intense peaks  (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							10
2	**213.159754**	107.083515					L	***900.489757***	450.748516	883.463208	442.235242	882.479192	441.743234	9
3	**342.202347**	171.604811			324.191782	162.599529	E	***787.405693***	394.206484	770.379144	385.693210	769.395128	385.201202	8
4	413.239461	207.123368			395.228896	198.118086	A	***658.363100***	329.685188	641.336551	321.171913			7
5	484.276575	242.641925			466.266010	233.636643	A	***587.325986***	294.166631	570.299437	285.653356			6
6	555.313689	278.160483			537.303124	269.155200	A	***516.288872***	258.648074	499.262323	250.134799			5
7	683.372267	342.189772	666.345718	333.676497	665.361702	333.184489	Q	***445.251758***	223.129517	428.225209	214.616242			4
8	754.409381	377.708328	737.382832	369.195054	736.398816	368.703046	A	317.193180	159.100228	300.166631	150.586953			3
9	825.446495	413.226885	808.419946	404.713611	807.435930	404.221603	A	246.156066	123.581671	229.129517	115.068396			2
10							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.8	998.550858	-0.001890	VLEAAAQAAR
29.7	998.539642	0.009326	VPEAVALER
10.2	998.539642	0.009326	GLPEAAGKPK
9.5	998.539673	0.009295	VPVPIGTER
7.2	998.540970	0.007998	KHIHEHAK
7.0	998.547043	0.001925	VLMPPDAIK
5.9	998.550873	-0.001905	VPGNEARLK
5.1	998.550873	-0.001905	QNVEALVAR
4.8	998.547043	0.001925	VLMPPDAIK
4.8	998.547043	0.001925	VLMPPDAIK

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

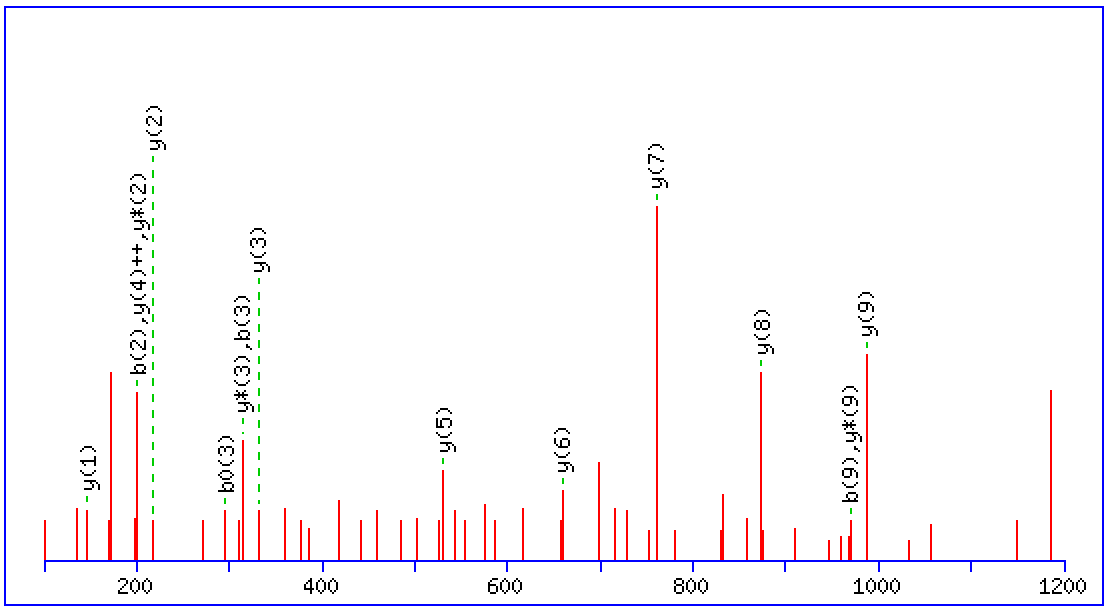
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SILLTEQALAK**
Found in **LACRT_HUMAN**, Extracellular glycoprotein lacritin OS=Homo sapiens GN=LACRT PE=1 SV=1

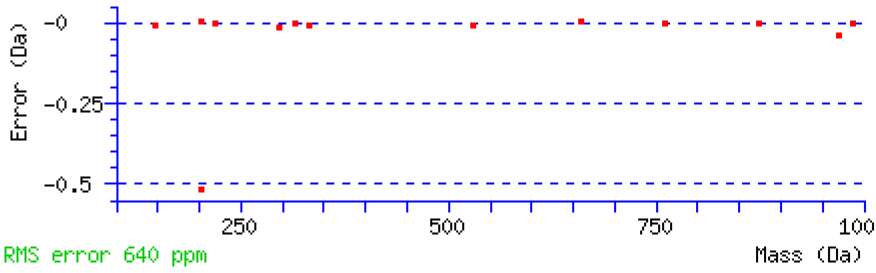
Match to Query 29262: 1185.694548 from(593.854550,2+) rtinseconds(2550) index(31462)
Title: Locus:1.1.1.2286.30
Data file 2011-11-10 - TFD - EP 4-5.mgf

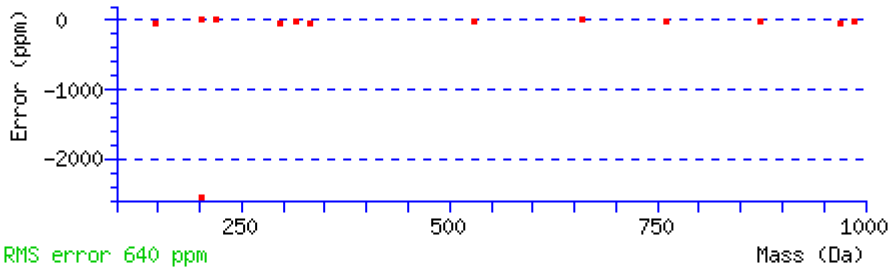
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1200] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1185.696854
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 47 **Expect:** 8.4e-005
Matches : 16/98 fragment ions using 30 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							11
2	**201.123368**	101.065322			183.112803	92.060039	I	1099.672138	550.339707	1082.645589	541.826433	1081.661573	541.334425	10
3	**314.207432**	157.607354			296.196867	148.602071	L	***986.588074***	493.797675	969.561525	485.284401	968.577509	484.792393	9
4	427.291496	214.149386			409.280931	205.144104	L	***873.504010***	437.255643	856.477461	428.742369	855.493445	428.250361	8
5	528.339175	264.673226			510.328610	255.667943	T	***760.419946***	380.713611	743.393397	372.200337	742.409381	371.708329	7
6	657.381768	329.194522			639.371203	320.189240	E	***659.372267***	330.189772	642.345718	321.676497	641.361702	321.184489	6
7	785.440346	393.223811	768.413797	384.710537	767.429781	384.218529	Q	***530.329674***	265.668475	513.303125	257.155201			5
8	856.477460	428.742368	839.450911	420.229094	838.466895	419.737086	A	402.271096	201.639186	385.244547	193.125912			4
9	**969.561524**	485.284400	952.534975	476.771126	951.550959	476.279118	L	***331.233982***	166.120629	314.207433	157.607355			3
10	1040.598638	520.802957	1023.572089	512.289683	1022.588073	511.797675	A	***218.149918***	109.578597	201.123369	101.065323			2
11							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.9	1185.696854	-0.002306	SILLTEQALAK
9.5	1185.690338	0.004210	LSLCGLLLQR
2.8	1185.682968	0.011580	TVLGIVSRGER

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

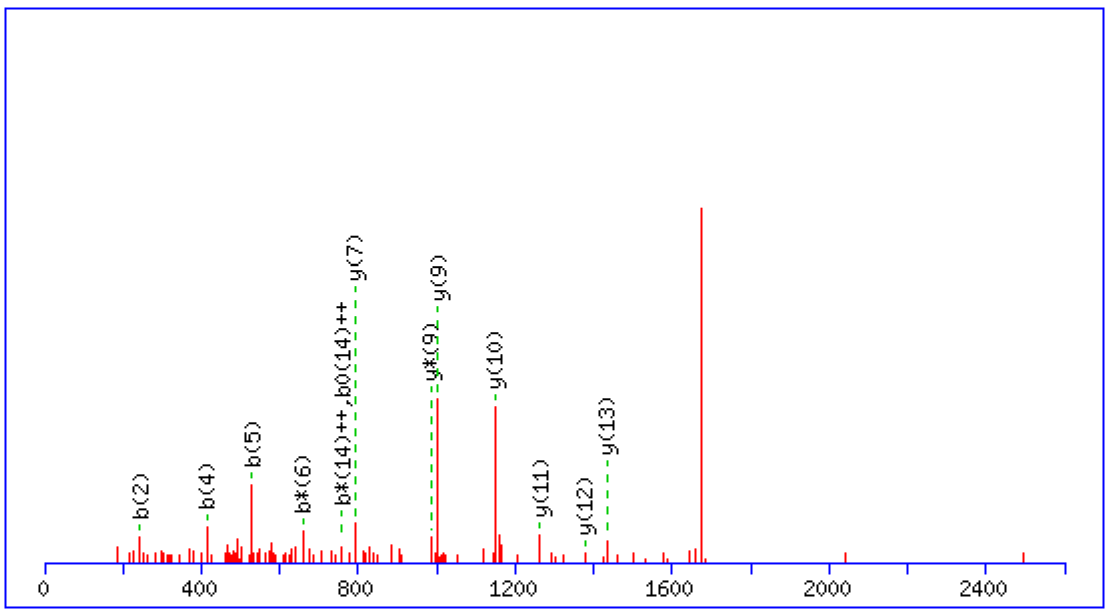
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NEGNIFPNPEATFVK**
Found in **SP16H_HUMAN**, FACT complex subunit SPT16 OS=Homo sapiens GN=SUPT16H PE=1 SV=1

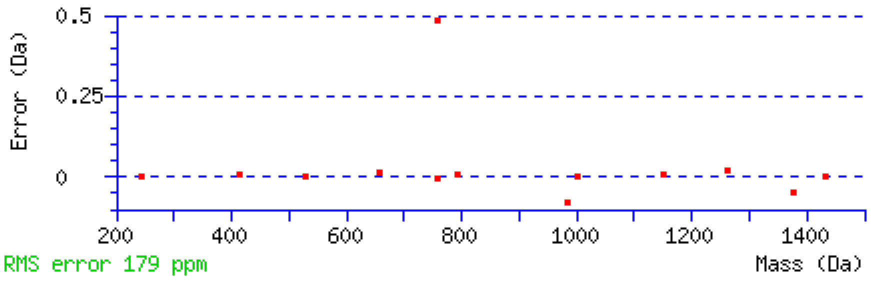
Match to Query 49354: 1675.830828 from(838.922690,2+) rtinseconds(3045) index(38921)
Title: Locus:1.1.1.2707.48
Data file 2011-11-12 - TFD - EP 5-1.mgf

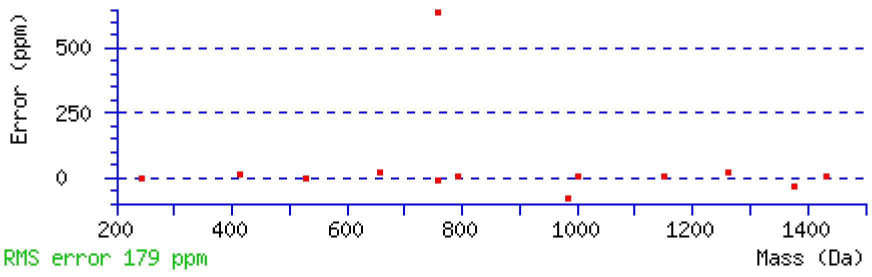
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1675.820572
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 47 **Expect:** 0.00026
Matches : 13/160 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			N							15
2	**244.092796**	122.550036	227.066247	114.036762	226.082231	113.544754	E	1562.784935	781.896106	1545.758386	773.382831	1544.774370	772.890823	14
3	301.114260	151.060768	284.087711	142.547494	283.103695	142.055486	G	***1433.742342***	717.374809	1416.715793	708.861535	1415.731777	708.369527	13
4	**415.157187**	208.082232	398.130638	199.568957	397.146622	199.076949	N	***1376.720878***	688.864077	1359.694329	680.350803	1358.710313	679.858795	12
5	**528.241251**	264.624264	511.214702	256.110989	510.230686	255.618981	I	***1262.677951***	631.842614	1245.651402	623.329339	1244.667386	622.837331	11
6	675.309665	338.158471	658.283116	329.645196	657.299100	329.153188	F	***1149.593887***	575.300582	1132.567338	566.787307	1131.583322	566.295299	10
7	772.362429	386.684853	755.335880	378.171578	754.351864	377.679570	P	***1002.525473***	501.766375	985.498924	493.253100	984.514908	492.761092	9
8	886.405356	443.706316	869.378807	435.193041	868.394791	434.701033	N	905.472709	453.239993	888.446160	444.726718	887.462144	444.234710	8
9	983.458120	492.232698	966.431571	483.719424	965.447555	483.227416	P	***791.429782***	396.218529	774.403233	387.705255	773.419217	387.213247	7
10	1112.500713	556.753995	1095.474164	548.240720	1094.490148	547.748712	E	694.377018	347.692147	677.350469	339.178873	676.366453	338.686865	6
11	1183.537827	592.272552	1166.511278	583.759277	1165.527262	583.267269	A	565.334425	283.170851	548.307876	274.657576	547.323860	274.165568	5
12	1284.585506	642.796391	1267.558957	634.283117	1266.574941	633.791109	T	494.297311	247.652294	477.270762	239.139019	476.286746	238.647011	4
13	1431.653920	716.330598	1414.627371	707.817324	1413.643355	707.325316	F	393.249632	197.128454	376.223083	188.615180			3
14	1530.722334	765.864805	1513.695785	757.351531	1512.711769	756.859523	V	246.181218	123.594247	229.154669	115.080973			2
15							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.8	1675.820572	0.010256	NEGNIFPNPEATFVK
10.9	1675.826447	0.004381	DLADLQGSDSVTKAEK
9.3	1675.838516	-0.007688	ISMAMQEGAASLSRPK
3.4	1675.845062	-0.014234	EEAVVMVEVNQSAKK
2.6	1675.816574	0.014254	DPPASAFQSAGITGVSR

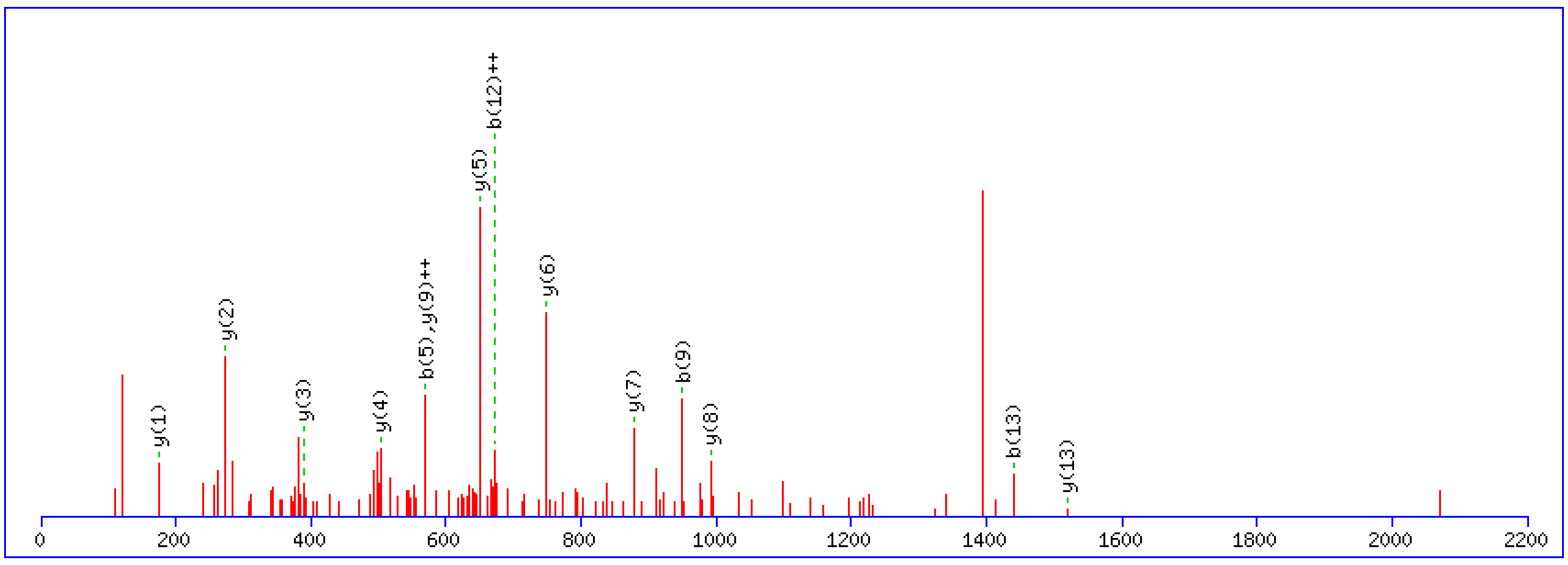
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FITHAPPGEFNEVFNDVR**
Found in **CAZA1_HUMAN**, F-actin-capping protein subunit alpha-1 OS=Homo sapiens GN=CAPZA1 PE=1 SV=3

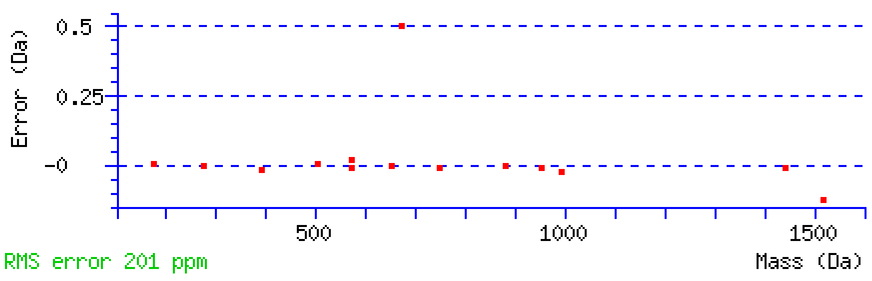
Match to Query 74267: 2087.991912 from(697.004580,3+) rtinseconds(2898) index(39491)
Title: Locus:1.1.1.1545.21
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 3.mgf

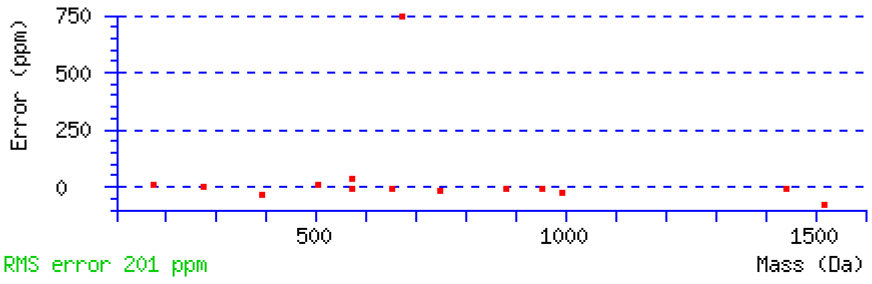
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2088.006500
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 43 **Expect:** 0.00021
Matches : 14/176 fragment ions using 30 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.075690	74.541483					F							18
2	261.159754	131.083515					I	1941.945352	971.476314	1924.918803	962.963040	1923.934787	962.471032	17
3	362.207433	181.607354			344.196868	172.602072	T	1828.861288	914.934282	1811.834739	906.421008	1810.850723	905.929000	16
4	499.266345	250.136810			481.255780	241.131528	H	1727.813609	864.410443	1710.787060	855.897168	1709.803044	855.405160	15
5	**570.303459**	285.655368			552.292894	276.650085	A	1590.754697	795.880987	1573.728148	787.367712	1572.744132	786.875704	14
6	667.356223	334.181750			649.345658	325.176467	P	***1519.717583***	760.362430	1502.691034	751.849155	1501.707018	751.357147	13
7	764.408987	382.708132			746.398422	373.702849	P	1422.664819	711.836048	1405.638270	703.322773	1404.654254	702.830765	12
8	821.430451	411.218864			803.419886	402.213581	G	1325.612055	663.309666	1308.585506	654.796391	1307.601490	654.304383	11
9	**950.473044**	475.740160			932.462479	466.734878	E	1268.590591	634.798934	1251.564042	626.285659	1250.580026	625.793651	10
10	1097.541458	549.274367			1079.530893	540.269085	F	1139.547998	570.277637	1122.521449	561.764363	1121.537433	561.272355	9
11	1211.584385	606.295831	1194.557836	597.782556	1193.573820	597.290548	N	***992.479584***	496.743430	975.453035	488.230156	974.469019	487.738148	8
12	1340.626978	670.817127	1323.600429	662.303853	1322.616413	661.811845	E	***878.436657***	439.721967	861.410108	431.208692	860.426092	430.716684	7
13	**1439.695392**	720.351334	1422.668843	711.838060	1421.684827	711.346052	V	***749.394064***	375.200670	732.367515	366.687396	731.383499	366.195388	6
14	1586.763806	793.885541	1569.737257	785.372267	1568.753241	784.880259	F	***650.325650***	325.666463	633.299101	317.153189	632.315085	316.661181	5
15	1700.806733	850.907005	1683.780184	842.393730	1682.796168	841.901722	N	***503.257236***	252.132256	486.230687	243.618982	485.246671	243.126974	4
16	1815.833676	908.420476	1798.807127	899.907202	1797.823111	899.415194	D	***389.214309***	195.110793	372.187760	186.597518	371.203744	186.105510	3
17	1914.902090	957.954683	1897.875541	949.441409	1896.891525	948.949401	V	***274.187366***	137.597321	257.160817	129.084047			2
18							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.8	2088.006500	-0.014588	FITHAPPGEFNEVFNDVR
3.6	2088.012360	-0.020448	TYVARNGEPEPTPVVNGEK
3.6	2088.012360	-0.020448	TYVARNGEPEPTPVVNGEK

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

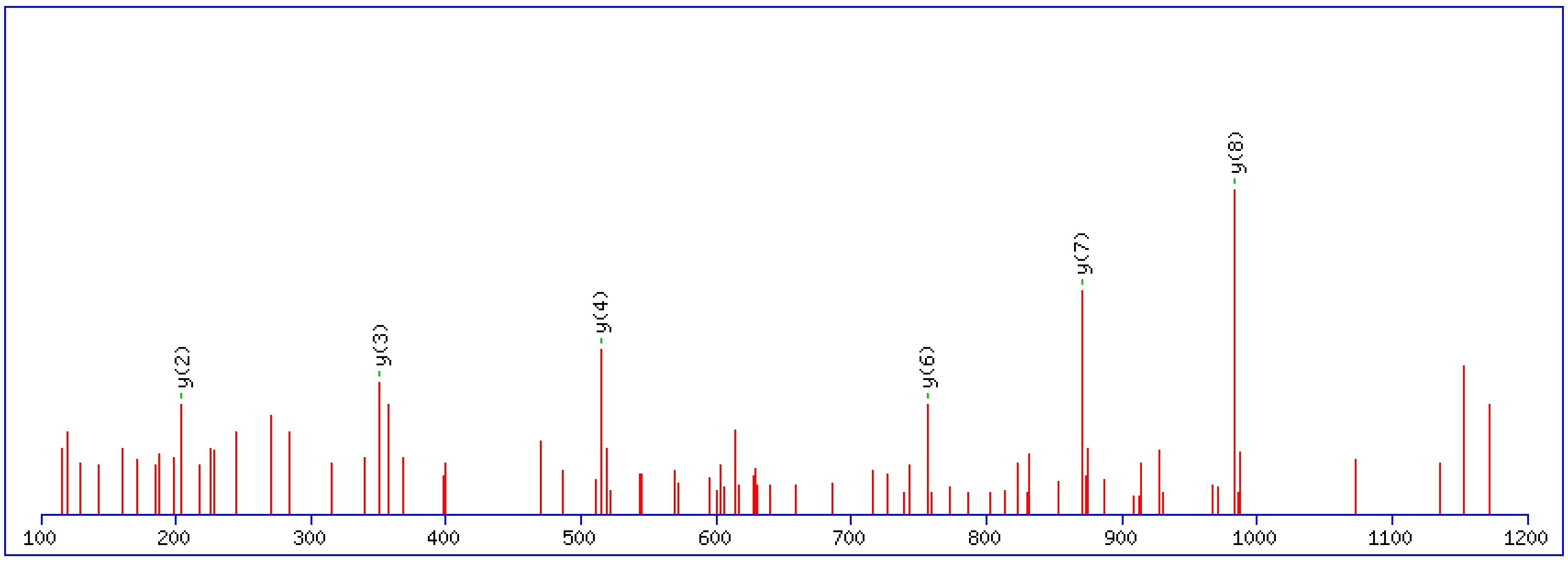
Mascot Search Results

Peptide View

MS/MS Fragmentation of **STLNEIYFGK**
Found in **CAPZB_HUMAN**, F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=4

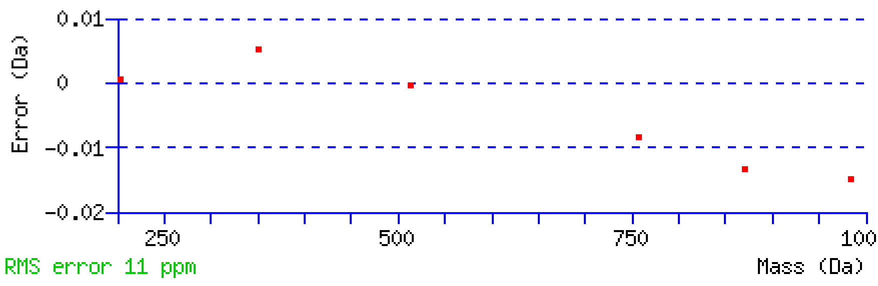
Match to Query 21374: 1170.592928 from(586.303740,2+) rtinseconds(2459) index(31240)
Title: Locus:1.1.1.1380.20
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 3.mgf

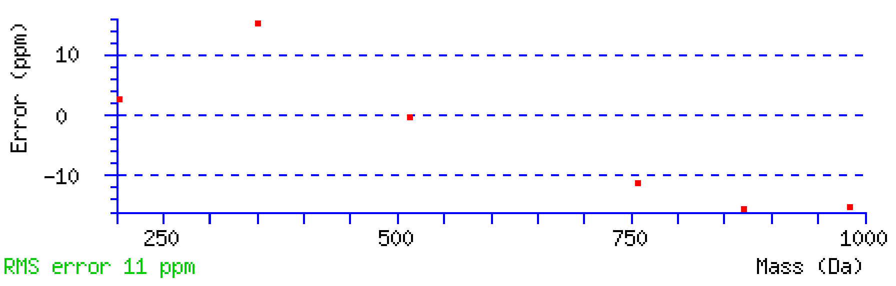
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1170.592072
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 42  Expect: 0.00046
Matches : 6/92 fragment ions using 11 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							10
2	189.086983	95.047129			171.076418	86.041847	T	1084.567338	542.787307	1067.540789	534.274033	1066.556773	533.782025	9
3	302.171047	151.589161			284.160482	142.583879	L	***983.519659***	492.263468	966.493110	483.750193	965.509094	483.258185	8
4	416.213974	208.610625	399.187425	200.097351	398.203409	199.605343	N	***870.435595***	435.721436	853.409046	427.208161	852.425030	426.716153	7
5	545.256567	273.131922	528.230018	264.618647	527.246002	264.126639	E	***756.392668***	378.699972	739.366119	370.186698	738.382103	369.694690	6
6	658.340631	329.673954	641.314082	321.160679	640.330066	320.668671	I	627.350075	314.178676	610.323526	305.665401			5
7	821.403960	411.205618	804.377411	402.692344	803.393395	402.200336	Y	***514.266011***	257.636644	497.239462	249.123369			4
8	968.472374	484.739825	951.445825	476.226551	950.461809	475.734543	F	***351.202682***	176.104979	334.176133	167.591704			3
9	1025.493838	513.250557	1008.467289	504.737283	1007.483273	504.245275	G	***204.134268***	102.570772	187.107719	94.057498			2
10							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.5	1170.592072	0.000856	STLNEIYFGK
6.7	1170.588058	0.004870	DQDGEILLPR
5.9	1170.599289	-0.006361	TAAPASPQQIR
4.7	1170.588074	0.004854	GIPGDASGPLSGK

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

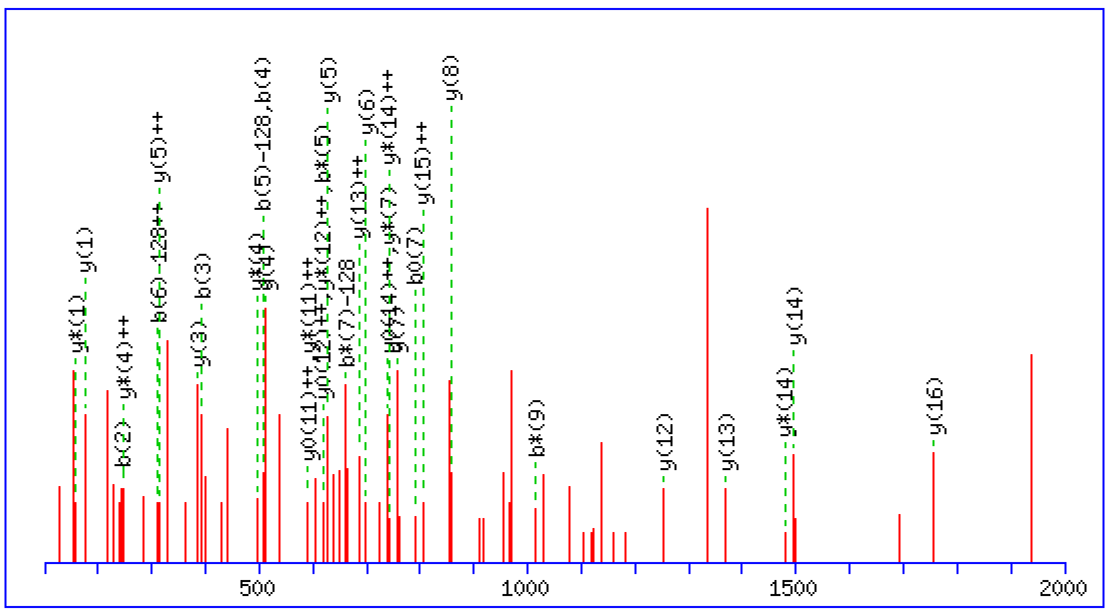
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVMIQDGPLPTGADKPLR**
Found in **FUBP3_HUMAN**, Far upstream element-binding protein 3 OS=Homo sapiens GN=FUBP3 PE=1 SV=2

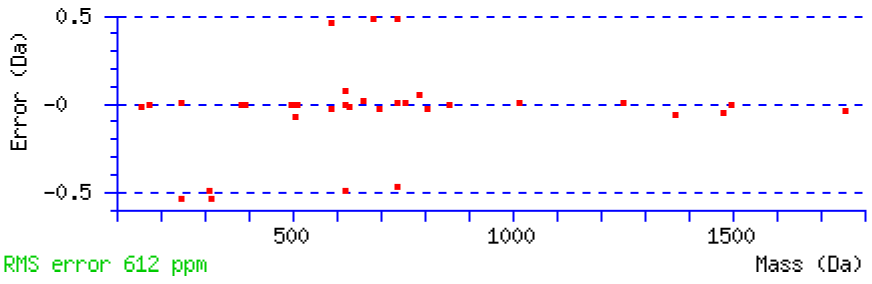
Match to Query 37807: 2001.992232 from(668.338020,3+) rtinseconds(1644) index(15057)
Title: Locus:1.1.1.2120.47
Data file 2011-11-10 - TFD - EP 4-2.mgf

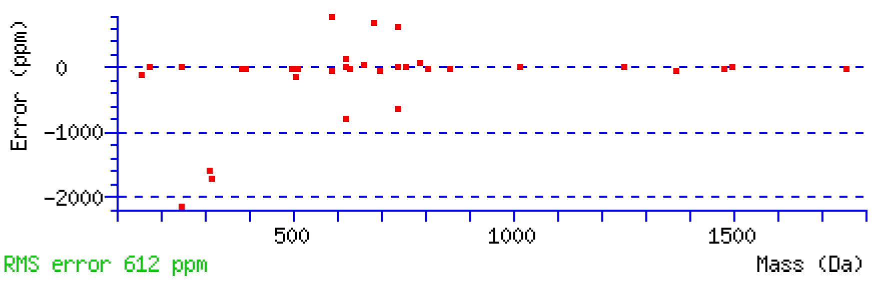
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2001.986359
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M1      : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
M3      : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
P8      : Oxidation (P)
P10     : Oxidation (P)
Ions Score: 44  Expect: 0.00014
Matches : 34/274 fragment ions using 70 most intense peaks   (help)
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	148.042676	74.524976					M							18
2	**247.111090**	124.059183					V	1855.958228	928.482752	1838.931679	919.969478	1837.947663	919.477469	17
3	**394.146490**	197.576883					M	***1756.889814***	878.948545	1739.863265	870.435271	1738.879249	869.943262	16
4	**507.230554**	254.118915					I	1609.854414	805.430845	1592.827865	796.917571	1591.843849	796.425562	15
5	635.289132	318.148204	618.262583	309.634930			Q	***1496.770350***	748.888813	1479.743801	740.375539	1478.759785	739.883531	14
6	750.316075	375.661676	733.289526	367.148401	732.305510	366.656393	D	***1368.711772***	684.859524	1351.685223	676.346250	1350.701207	675.854241	13
7	807.337539	404.172408	790.310990	395.659133	789.326974	395.167125	G	***1253.684829***	627.346053	1236.658280	618.832778	1235.674264	618.340770	12
8	920.385218	460.696247	903.358669	452.182973	902.374653	451.690965	P	1196.663365	598.835320	1179.636816	590.322046	1178.652800	589.830038	11
9	1033.469282	517.238279	1016.442733	508.725005	1015.458717	508.232997	L	1083.615686	542.311481	1066.589137	533.798206	1065.605121	533.306198	10
10	1146.516961	573.762119	1129.490412	565.248844	1128.506396	564.756836	P	970.531622	485.769449	953.505073	477.256174	952.521057	476.764166	9
11	1247.564640	624.285958	1230.538091	615.772684	1229.554075	615.280676	T	***857.483943***	429.245610	840.457394	420.732335	839.473378	420.240327	8
12	1304.586104	652.796690	1287.559555	644.283416	1286.575539	643.791407	G	***756.436264***	378.721770	739.409715	370.208495	738.425699	369.716487	7
13	1375.623218	688.315247	1358.596669	679.801973	1357.612653	679.309964	A	***699.414800***	350.211038	682.388251	341.697764	681.404235	341.205756	6
14	1490.650161	745.828719	1473.623612	737.315444	1472.639596	736.823436	D	***628.377686***	314.692481	611.351137	306.179207	610.367121	305.687199	5
15	1618.745124	809.876200	1601.718575	801.362926	1600.734559	800.870918	K	***513.350743***	257.179010	496.324194	248.665735			4
16	1715.797888	858.402582	1698.771339	849.889308	1697.787323	849.397300	P	***385.255780***	193.131528	368.229231	184.618253			3
17	1828.881952	914.944614	1811.855403	906.431340	1810.871387	905.939331	L	288.203016	144.605146	271.176467	136.091871			2
18							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.4	2001.986359	0.005873	MVMIQDGPLPTGADKPLR
3.4	2001.986359	0.005873	MVMIQDGPLPTGADKPLR
2.9	2001.986359	0.005873	MVMIQDGPLPTGADKPLR
1.0	2001.986313	0.005919	MLAMPIDLDTLSPEERR

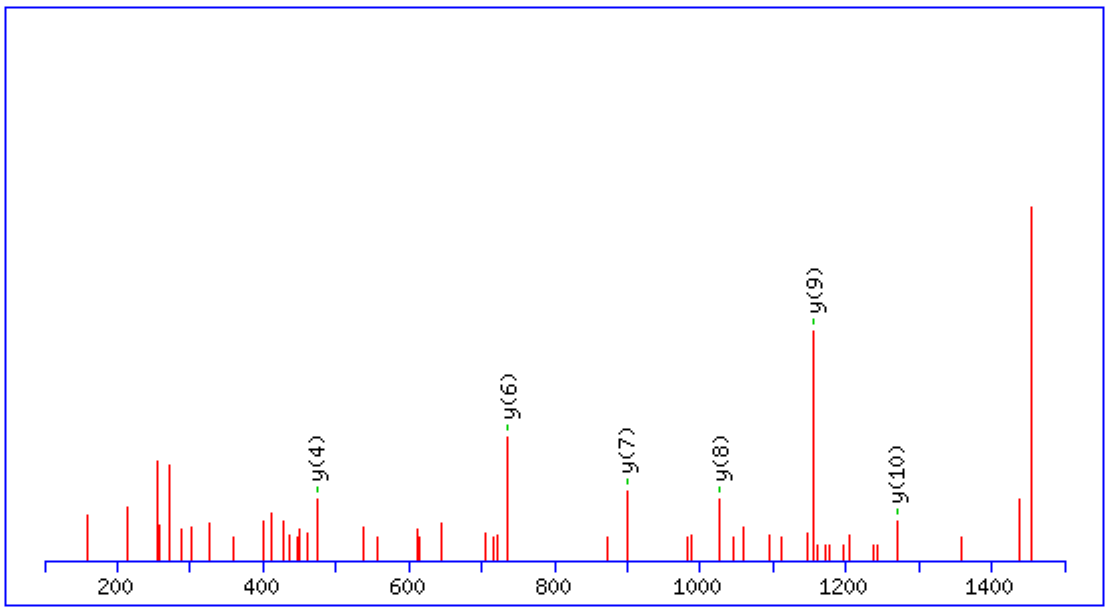
Mascot Search Results

Peptide View

MS/MS Fragmentation of **WLEQYYVGELR**
Found in **FA2H_HUMAN**, Fatty acid 2-hydroxylase OS=Homo sapiens GN=FA2H PE=1 SV=1

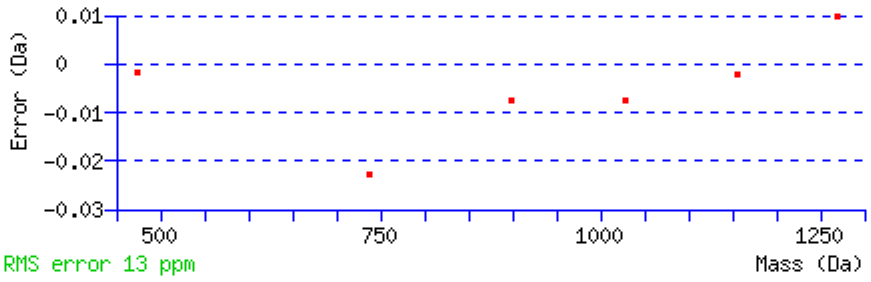
Match to Query 44788: 1454.709928 from(728.362240,2+) rtinseconds(3214) index(45554)
Title: Locus:1.1.1.2564.35
Data file 2011-11-10 - TFD - EP 3-4.mgf

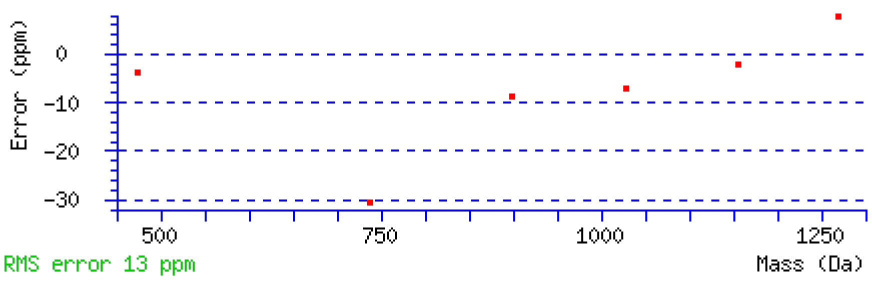
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1454.719391
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 37 **Expect:** 0.0034
Matches : 6/106 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	187.086589	94.046932					W							11
2	300.170653	150.588965					L	*1269.647380*	635.327328	1252.620831	626.814054	1251.636815	626.322046	10
3	429.213246	215.110261			411.202681	206.104979	E	*1156.563316*	578.785296	1139.536767	570.272022	1138.552751	569.780014	9
4	557.271824	279.139550	540.245275	270.626276	539.261259	270.134268	Q	*1027.520723*	514.264000	1010.494174	505.750725	1009.510158	505.258717	8
5	720.335153	360.671215	703.308604	352.157940	702.324588	351.665932	Y	*899.462145*	450.234711	882.435596	441.721436	881.451580	441.229428	7
6	883.398482	442.202879	866.371933	433.689605	865.387917	433.197597	Y	*736.398816*	368.703046	719.372267	360.189771	718.388251	359.697763	6
7	982.466896	491.737086	965.440347	483.223812	964.456331	482.731804	V	573.335487	287.171381	556.308938	278.658107	555.324922	278.166099	5
8	1039.488360	520.247818	1022.461811	511.734544	1021.477795	511.242536	G	*474.267073*	237.637174	457.240524	229.123900	456.256508	228.631892	4
9	1168.530953	584.769115	1151.504404	576.255840	1150.520388	575.763832	E	417.245609	209.126442	400.219060	200.613168	399.235044	200.121160	3
10	1281.615017	641.311147	1264.588468	632.797872	1263.604452	632.305864	L	288.203016	144.605146	271.176467	136.091871			2
11							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.1	1454.719391	-0.009463	WLEQYYVGELR
8.0	1454.711365	-0.001437	DAPSLRSSPGPAPR

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

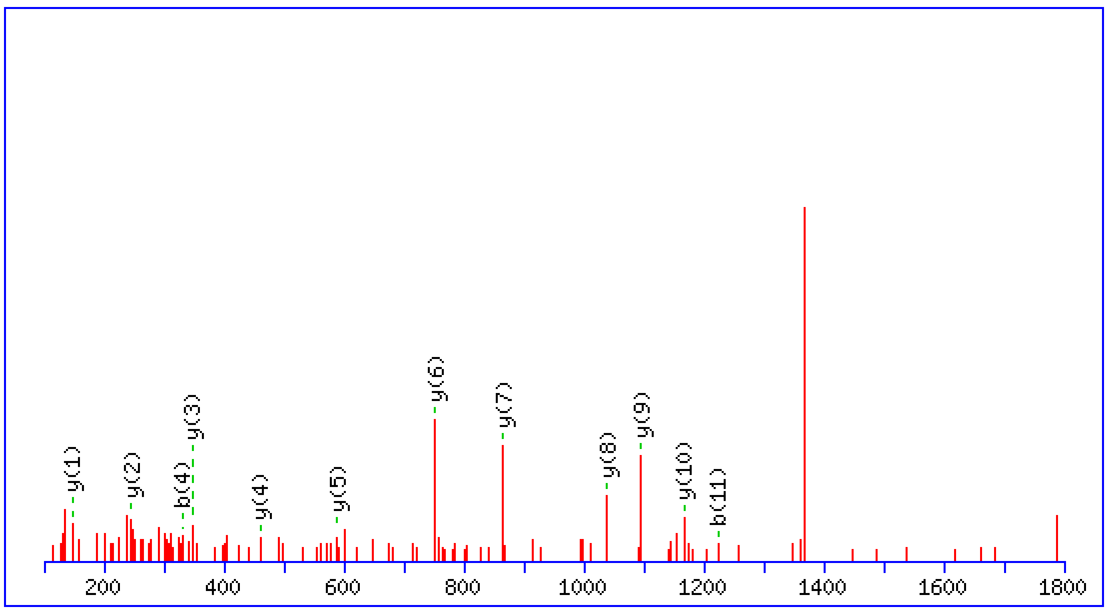
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SDAGCLYELTVK**
Found in **FBX2_HUMAN**, F-box only protein 2 OS=Homo sapiens GN=FBXO2 PE=1 SV=2

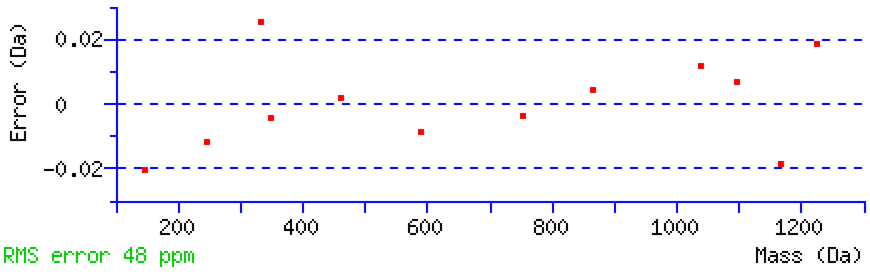
Match to Query 40022: 1368.662588 from(685.338570,2+) rtinseconds(2643) index(34215)
Title: Locus:1.1.1.2422.29
Data file 2011-11-12 - TFD - EP 5-4.mgf

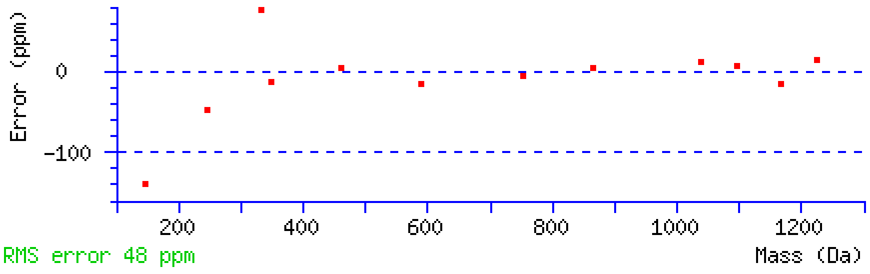
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1368.659500
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 69 **Expect:** 7e-007
Matches : 12/106 fragment ions using 26 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	S							12
2	203.066247	102.036761	185.055682	93.031479	D	1282.634767	641.821022	1265.608218	633.307747	1264.624202	632.815739	11
3	274.103361	137.555319	256.092796	128.550036	A	***1167.607824***	584.307550	1150.581275	575.794276	1149.597259	575.302268	10
4	**331.124825**	166.066050	313.114260	157.060768	G	***1096.570710***	548.788993	1079.544161	540.275719	1078.560145	539.783711	9
5	505.171124	253.089200	487.160559	244.083918	C	***1039.549246***	520.278261	1022.522697	511.764987	1021.538681	511.272979	8
6	618.255188	309.631232	600.244623	300.625950	L	***865.502947***	433.255112	848.476398	424.741837	847.492382	424.249829	7
7	781.318517	391.162897	763.307952	382.157614	Y	***752.418883***	376.713080	735.392334	368.199805	734.408318	367.707797	6
8	910.361110	455.684193	892.350545	446.678911	E	***589.355554***	295.181415	572.329005	286.668141	571.344989	286.176133	5
9	1023.445174	512.226225	1005.434609	503.220943	L	***460.312961***	230.660119	443.286412	222.146844	442.302396	221.654836	4
10	1124.492853	562.750065	1106.482288	553.744782	T	***347.228897***	174.118087	330.202348	165.604812	329.218332	165.112804	3
11	**1223.561267**	612.284272	1205.550702	603.278989	V	***246.181218***	123.594247	229.154669	115.080973			2
12					K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
69.0	1368.659500	0.003088	SDAGCLYELTVK
3.3	1368.652985	0.009603	GGDEVMFMRIAK
2.8	1368.667374	-0.004786	DLNFKGFSGAGEK
2.1	1368.674774	-0.012186	QIEAMGFPAFVK

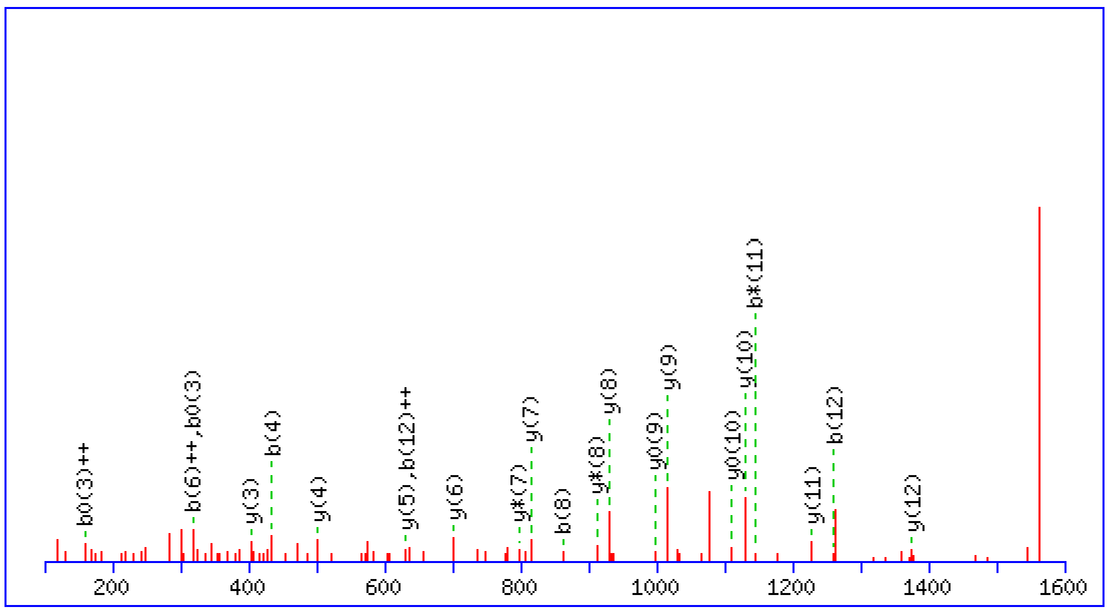
Mascot Search Results

Peptide View

MS/MS Fragmentation of **STFVLSNLAEVVER**
Found in **FBX22_HUMAN**, F-box only protein 22 OS=Homo sapiens GN=FBXO22 PE=1 SV=1

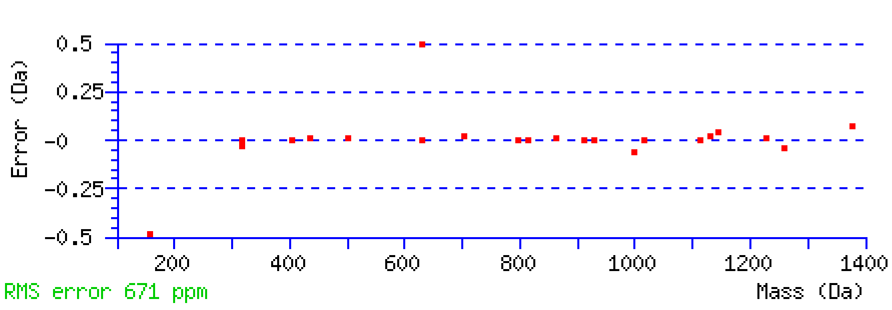
Match to Query 49976: 1562.819948 from(782.417250,2+) rtinseconds(3775) index(55467)
Title: Locus:1.1.1.2847.31
Data file 2011-11-12 - TFD - EP 5-4.mgf

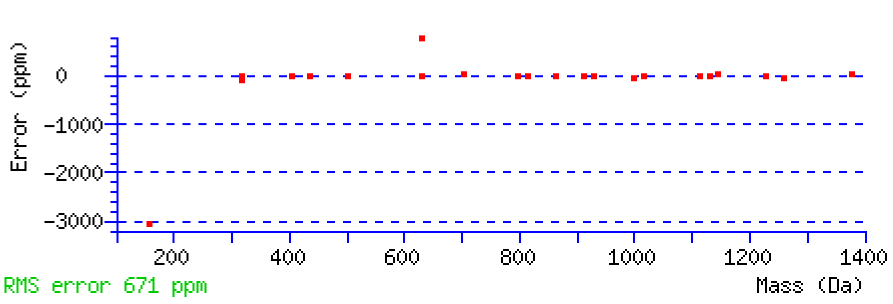
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from [100] to [1600] Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1562.830414
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 59 **Expect:** 2.7e-005
Matches : 22/142 fragment ions using 41 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	88.039304	44.523290			70.028739	35.518008	S							14
2	189.086983	95.047129			171.076418	86.041847	T	1476.805670	738.906473	1459.779121	730.393199	1458.795105	729.901190	13
3	336.155397	168.581336			318.144832	159.576054	F	***1375.757991***	688.382634	1358.731442	679.869359	1357.747426	679.377351	12
4	**435.223811**	218.115543			417.213246	209.110261	V	***1228.689577***	614.848427	1211.663028	606.335152	1210.679012	605.843144	11
5	548.307875	274.657576			530.297310	265.652293	L	***1129.621163***	565.314220	1112.594614	556.800945	1111.610598	556.308937	10
6	635.339903	318.173589			617.329338	309.168307	S	***1016.537099***	508.772188	999.510550	500.258913	998.526534	499.766905	9
7	749.382830	375.195053	732.356281	366.681778	731.372265	366.189770	N	***929.505071***	465.256174	912.478522	456.742899	911.494506	456.250891	8
8	**862.466894**	431.737085	845.440345	423.223810	844.456329	422.731802	L	***815.462144***	408.234710	798.435595	399.721436	797.451579	399.229428	7
9	933.504008	467.255642	916.477459	458.742367	915.493443	458.250359	A	***702.378080***	351.692678	685.351531	343.179404	684.367515	342.687396	6
10	1062.546601	531.776938	1045.520052	523.263664	1044.536036	522.771656	E	***631.340966***	316.174121	614.314417	307.660847	613.330401	307.168839	5
11	1161.615015	581.311145	1144.588466	572.797871	1143.604450	572.305863	V	***502.298373***	251.652825	485.271824	243.139550	484.287808	242.647542	4
12	**1260.683429**	630.845352	1243.656880	622.332078	1242.672864	621.840070	V	***403.229959***	202.118618	386.203410	193.605343	385.219394	193.113335	3
13	1389.726022	695.366649	1372.699473	686.853375	1371.715457	686.361367	E	304.161545	152.584411	287.134996	144.071136	286.150980	143.579128	2
14							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
59.4	1562.830414	-0.010466	STFVLSNLAEVVER
18.2	1562.809311	0.010637	WNSVFDQLTQVVK
3.3	1562.812683	0.007265	IMPPSKPHPPVVGK
3.3	1562.812683	0.007265	IMPPSKPHPPVVGK

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

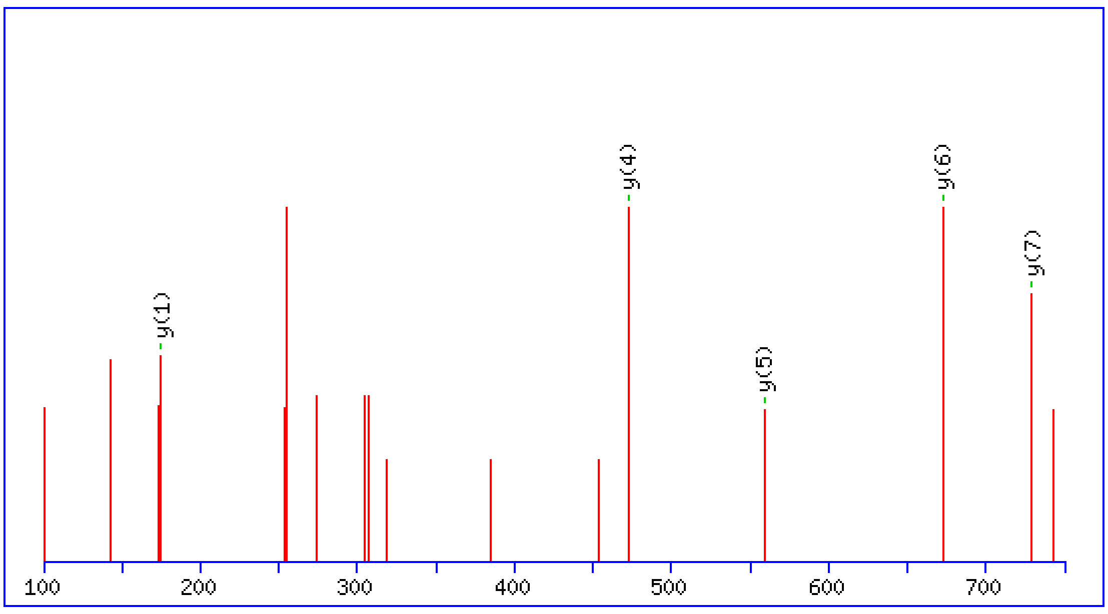
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IGLSLAPR**
Found in **FBX42_HUMAN**, F-box only protein 42 OS=Homo sapiens GN=FBXO42 PE=1 SV=1

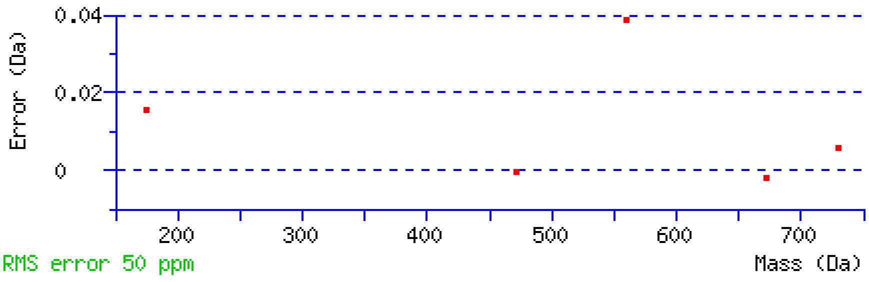
Match to Query 3493: 841.503568 from(421.759060,2+) rtinseconds(1915) index(19574)
Title: Locus:1.1.1.2189.6
Data file 2011-11-14 - TFD - EP 7-2.mgf

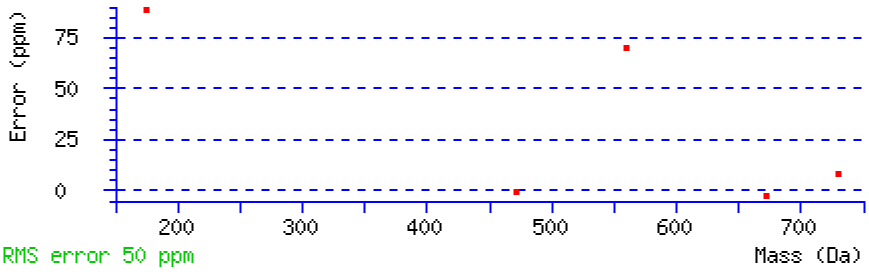
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 841.502136
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P7      : Oxidation (P)
Ions Score: 42  Expect: 0.00043
Matches : 5/56 fragment ions using 7 most intense peaks   (help)
```

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308			I							8
2	171.112804	86.060040			G	*729.425365*	365.216321	712.398816	356.703046	711.414800	356.211038	7
3	284.196868	142.602072			L	*672.403901*	336.705589	655.377352	328.192314	654.393336	327.700306	6
4	371.228896	186.118086	353.218331	177.112804	S	*559.319837*	280.163557	542.293288	271.650282	541.309272	271.158274	5
5	484.312960	242.660118	466.302395	233.654836	L	*472.287809*	236.647543	455.261260	228.134268			4
6	555.350074	278.178675	537.339509	269.173393	A	359.203745	180.105511	342.177196	171.592236			3
7	668.397753	334.702515	650.387188	325.697232	P	288.166631	144.586954	271.140082	136.073679			2
8					R	*175.118952*	88.063114	158.092403	79.549840			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.3	841.502136	0.001432	IGLSLAPR
16.7	841.502136	0.001432	LEKTVPR
12.6	841.502151	0.001417	ISGLPVTR
11.4	841.502136	0.001432	ILGLAPSR
11.4	841.502121	0.001447	IVAEAIAR
8.4	841.502167	0.001401	VVATVPTR
8.3	841.502136	0.001432	LPKTEVR
7.5	841.502121	0.001447	ELKSIPR
5.6	841.502151	0.001417	ITQLPVR
4.0	841.502136	0.001432	LTPIDKR

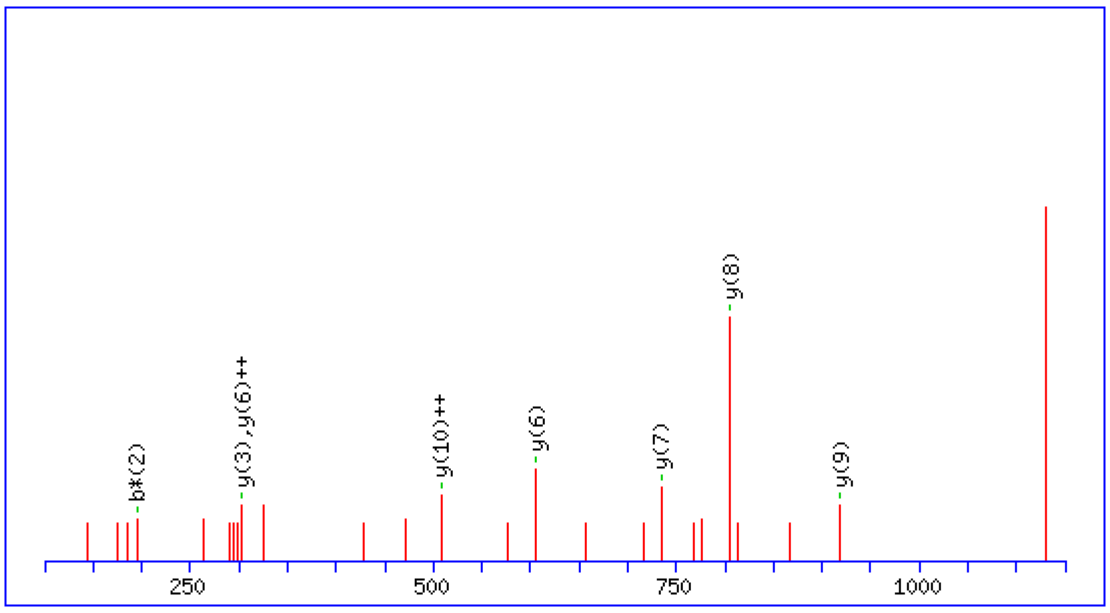
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NPIAQSTDGAR**
Found in **FBSP1_HUMAN**, F-box/SPRY domain-containing protein 1 OS=Homo sapiens GN=FBXO45 PE=1 SV=1

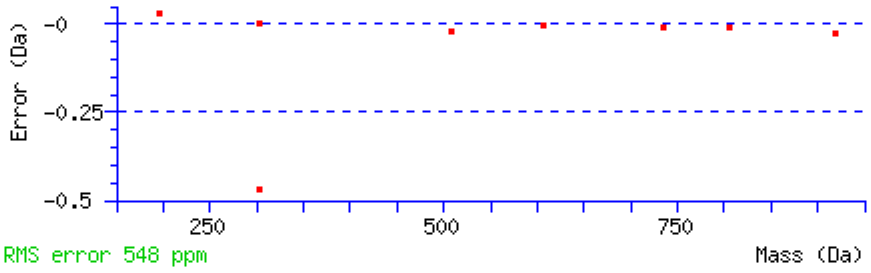
Match to Query 25322: 1128.545088 from(565.279820,2+) rtinseconds(1041) index(3087)
Title: Locus:1.1.1.1710.38
Data file 2011-11-10 - TFD - EP 4-5.mgf

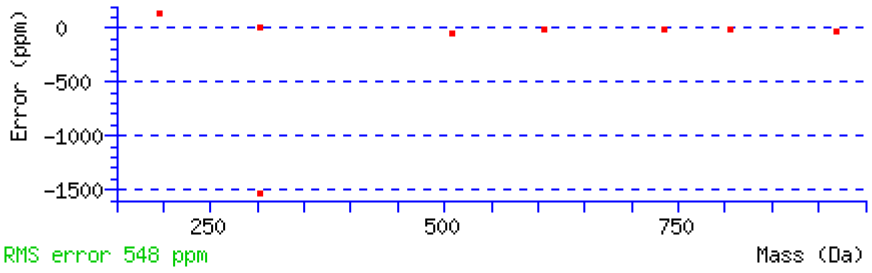
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1128.552338
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.00026
Matches : 8/104 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			N							11
2	212.102967	106.555121	195.076418	98.041847			P	1015.516700	508.261988	998.490151	499.748714	997.506135	499.256706	10
3	325.187031	163.097153	308.160482	154.583879			I	***918.463936***	459.735606	901.437387	451.222332	900.453371	450.730324	9
4	396.224145	198.615710	379.197596	190.102436			A	***805.379872***	403.193574	788.353323	394.680300	787.369307	394.188292	8
5	524.282723	262.645000	507.256174	254.131725			Q	***734.342758***	367.675017	717.316209	359.161743	716.332193	358.669735	7
6	611.314751	306.161014	594.288202	297.647739	593.304186	297.155731	S	***606.284180***	303.645728	589.257631	295.132454	588.273615	294.640446	6
7	712.362430	356.684853	695.335881	348.171579	694.351865	347.679571	T	519.252152	260.129714	502.225603	251.616440	501.241587	251.124432	5
8	827.389373	414.198325	810.362824	405.685050	809.378808	405.193042	D	418.204473	209.605875	401.177924	201.092600	400.193908	200.600592	4
9	884.410837	442.709057	867.384288	434.195782	866.400272	433.703774	G	***303.177530***	152.092403	286.150981	143.579129			3
10	955.447951	478.227614	938.421402	469.714339	937.437386	469.222331	A	246.156066	123.581671	229.129517	115.068397			2
11							R	175.118952	88.063114	158.092403	79.549840			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.0	1128.552338	-0.007250	NPIAQSTDGAR
0.8	1128.552338	-0.007250	NPSSAAPVQSR
0.4	1128.552338	-0.007250	NPSSAAPVQSR

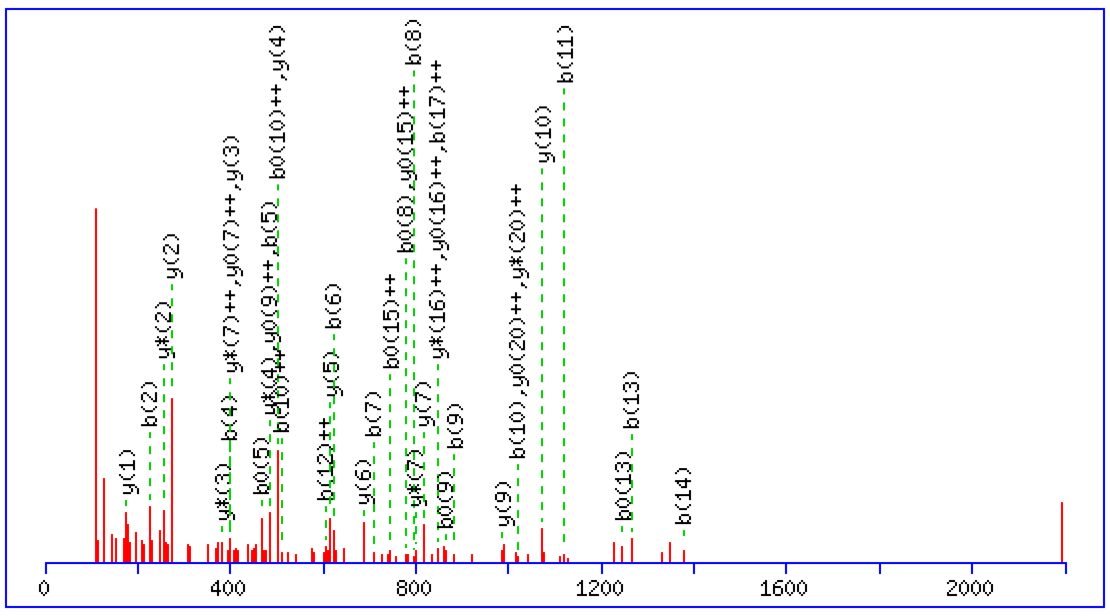
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **HSTASHSSSHTSGIEADTKPR**
Found in **FRMD6_HUMAN**, FERM domain-containing protein 6 OS=Homo sapiens GN=FRMD6 PE=1 SV=1

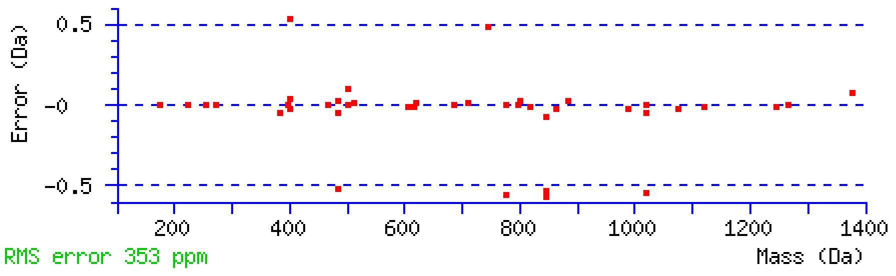
Match to Query 1032532: 2192.013970 from(439.410070,5+) rtinseconds(701) index(817119)
Title: Locus:1.1.1.803.3
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

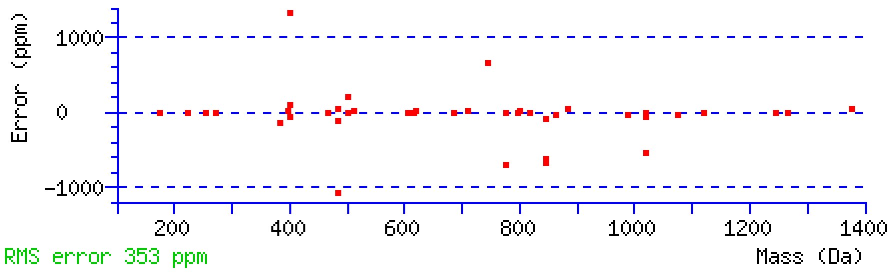
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2192.020630
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 63 **Expect:** 2.7e-006
Matches : 41/196 fragment ions using 80 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	138.066188	69.536732					H							21
2	***225.098216***	113.052746			207.087651	104.047463	S	2055.969000	1028.488138	2038.942451	1019.974863	2037.958435	1019.482855	20
3	326.145895	163.576585			308.135330	154.571303	T	1968.936972	984.972124	1951.910423	976.458850	1950.926407	975.966842	19
4	***397.183009***	199.095143			379.172444	190.089860	A	1867.889293	934.448285	1850.862744	925.935010	1849.878728	925.443002	18
5	***484.215037***	242.611156			466.204472	233.605874	S	1796.852179	898.929728	1779.825630	890.416453	1778.841614	889.924445	17
6	***621.273949***	311.140613			603.263384	302.135330	H	1709.820151	855.413714	1692.793602	846.900439	1691.809586	846.408431	16
7	***708.305977***	354.656627			690.295412	345.651344	S	1572.761239	786.884258	1555.734690	778.370983	1554.750674	777.878975	15
8	***795.338005***	398.172641			777.327440	389.167358	S	1485.729211	743.368244	1468.702662	734.854969	1467.718646	734.362961	14
9	***882.370033***	441.688654			864.359468	432.683372	S	1398.697183	699.852230	1381.670634	691.338955	1380.686618	690.846947	13
10	***1019.428945***	**510.218110**			1001.418380	501.212828	H	1311.665155	656.336216	1294.638606	647.822941	1293.654590	647.330933	12
11	***1120.476624***	560.741950			1102.466059	551.736667	T	1174.606243	587.806760	1157.579694	579.293485	1156.595678	578.801477	11
12	1207.508652	**604.257964**			1189.498087	595.252681	S	***1073.558564***	537.282920	1056.532015	528.769646	1055.547999	528.277638	10
13	***1264.530116***	632.768696			1246.519551	623.763413	G	***986.526536***	493.766906	969.499987	485.253632	968.515971	484.761624	9
14	***1377.614180***	689.310728			1359.603615	680.305445	I	929.505072	465.256174	912.478523	456.742900	911.494507	456.250892	8
15	1506.656773	753.832024			1488.646208	744.826742	E	***816.421008***	408.714142	799.394459	400.200868	798.410443	399.708860	7
16	1577.693887	789.350581			1559.683322	780.345299	A	***687.378415***	344.192846	670.351866	335.679571	669.367850	335.187563	6
17	1692.720830	**846.864053**			1674.710265	837.858770	D	***616.341301***	308.674289	599.314752	300.161014	598.330736	299.669006	5
18	1793.768509	897.387893			1775.757944	888.382610	T	***501.314358***	251.160817	484.287809	242.647543	483.303793	242.155535	4
19	1921.863472	961.435374	1904.836923	952.922100	1903.852907	952.430092	K	***400.266679***	200.636978	383.240130	192.123703			3
20	2018.916236	1009.961756	2001.889687	1001.448482	2000.905671	1000.956474	P	***272.171716***	136.589496	255.145167	128.076222			2
21							R	***175.118952***	88.063114	158.092403	79.549840			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
63.4	2192.020630	-0.006660	HSTASHSSSHTSGIEADTKPR
3.8	2192.031555	-0.017585	MAEAVAAPISPWTMAATIQAM
0.9	2192.031555	-0.017585	MAEAVAAPISPWTMAATIQAM
0.9	2192.031555	-0.017585	MAEAVAAPISPWTMAATIQAM
0.3	2192.015472	-0.001502	SPVLSNTTTEPASTMSPPPAK
0.3	2192.015472	-0.001502	SPVLSNTTTEPASTMSPPPAK
0.3	2192.015472	-0.001502	SPVLSNTTTEPASTMSPPPAK

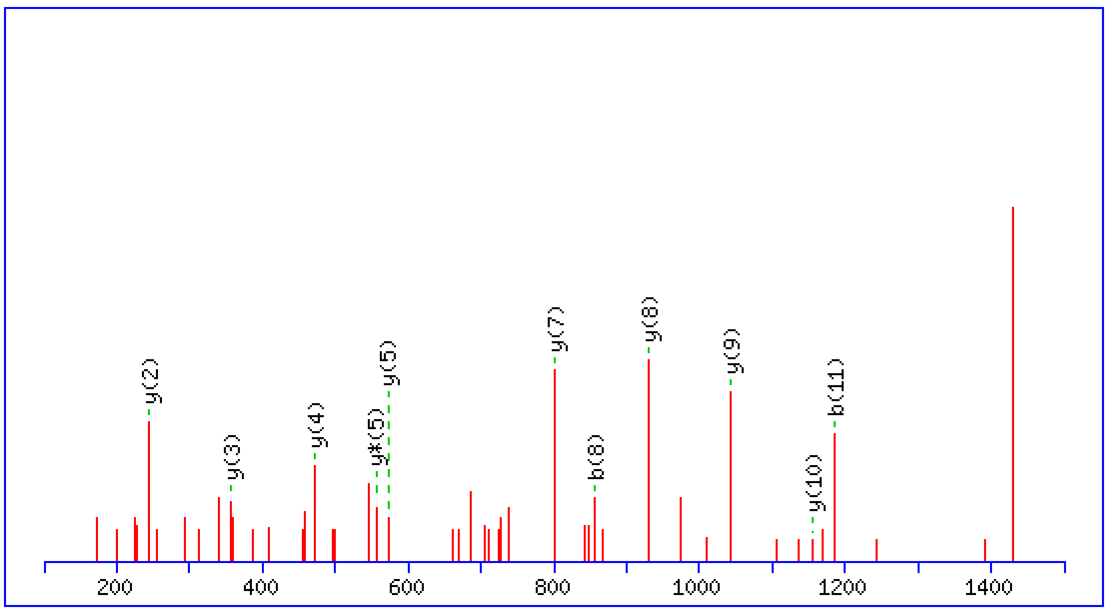
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ADSLLEDITDIPK**
Found in **FERM1_HUMAN**, Fermitin family homolog 1 OS=Homo sapiens GN=FERMT1 PE=1 SV=1

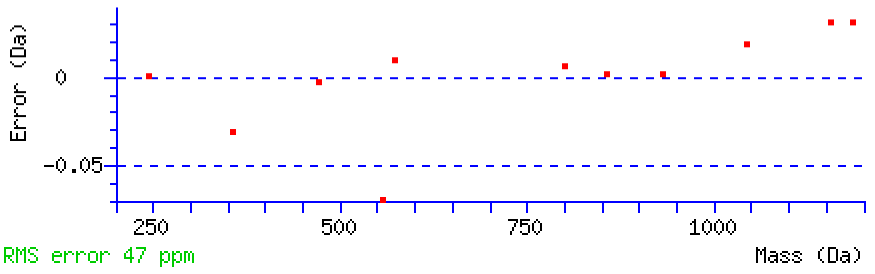
Match to Query 44088: 1428.742848 from(715.378700,2+) rtinseconds(3667) index(53512)
Title: Locus:1.1.1.2826.26
Data file 2011-11-10 - TFD - EP 3-2.mgf

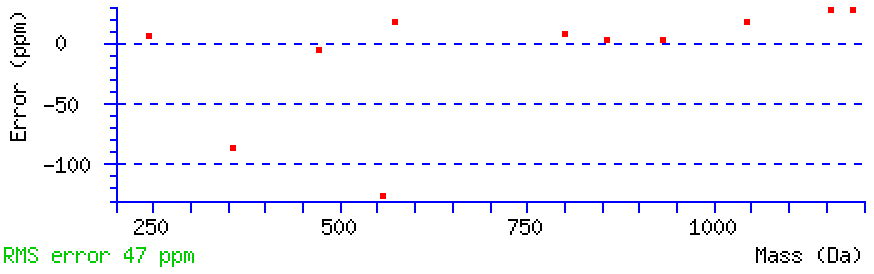
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1428.734772
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 50 **Expect:** 0.0001
Matches : 11/112 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			A							13
2	187.071333	94.039304	169.060768	85.034022	D	1358.704953	679.856115	1341.678404	671.342840	1340.694388	670.850832	12
3	274.103361	137.555319	256.092796	128.550036	S	1243.678010	622.342643	1226.651461	613.829369	1225.667445	613.337361	11
4	387.187425	194.097351	369.176860	185.092068	L	***1156.645982***	578.826629	1139.619433	570.313355	1138.635417	569.821347	10
5	500.271489	250.639383	482.260924	241.634100	L	***1043.561918***	522.284597	1026.535369	513.771323	1025.551353	513.279315	9
6	629.314082	315.160679	611.303517	306.155397	E	***930.477854***	465.742565	913.451305	457.229291	912.467289	456.737283	8
7	744.341025	372.674151	726.330460	363.668868	D	***801.435261***	401.221269	784.408712	392.707994	783.424696	392.215986	7
8	**857.425089**	429.216183	839.414524	420.210900	I	686.408318	343.707797	669.381769	335.194523	668.397753	334.702515	6
9	958.472768	479.740022	940.462203	470.734740	T	***573.324254***	287.165765	556.297705	278.652491	555.313689	278.160483	5
10	1073.499711	537.253494	1055.489146	528.248211	D	***472.276575***	236.641925	455.250026	228.128651	454.266010	227.636643	4
11	**1186.583775**	593.795526	1168.573210	584.790243	I	***357.249632***	179.128454	340.223083	170.615179			3
12	1283.636539	642.321908	1265.625974	633.316625	P	***244.165568***	122.586422	227.139019	114.073148			2
13					K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
50.4	1428.734772	0.008076	ADSLLEDITDIPK
7.4	1428.736084	0.006764	ENLYPKANIPDR
3.1	1428.747345	-0.004497	RSPNVELSFPQR
1.6	1428.739502	0.003346	ASCPGKISVPPVR

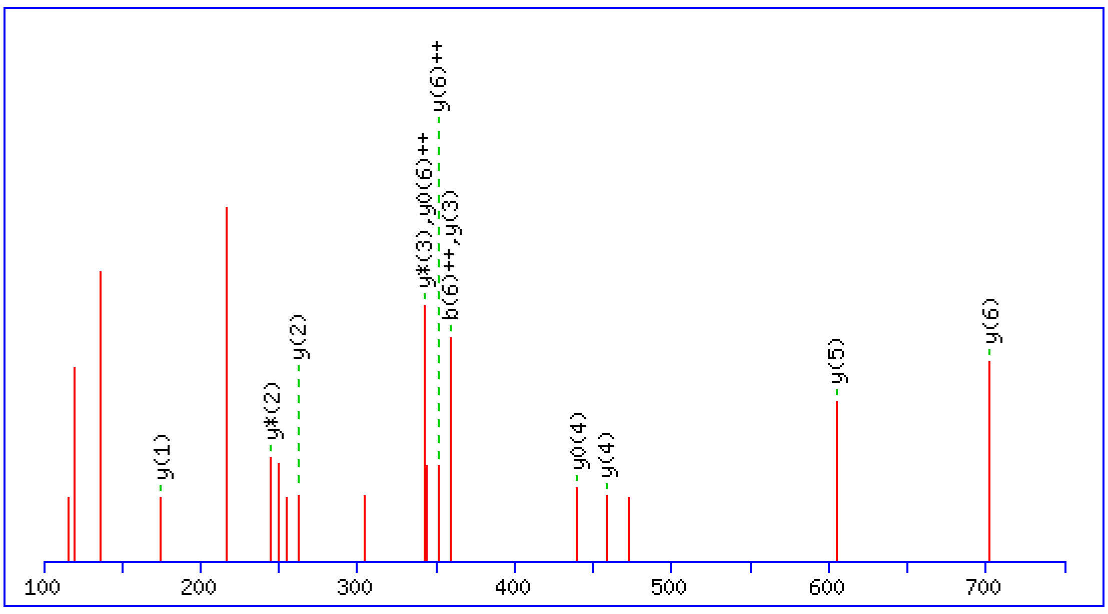
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YLPFVPSR**
Found in **FMOD_HUMAN**, Fibromodulin OS=Homo sapiens GN=FMOD PE=1 SV=2

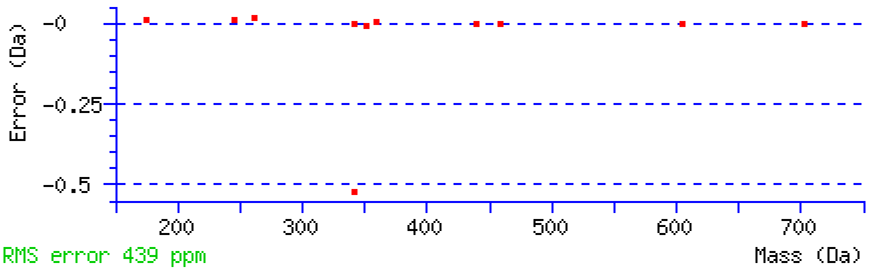
Match to Query 231696: 977.536448 from(489.775500,2+) rtinseconds(2731) index(689664)
Title: Locus:1.1.1.1711.12
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

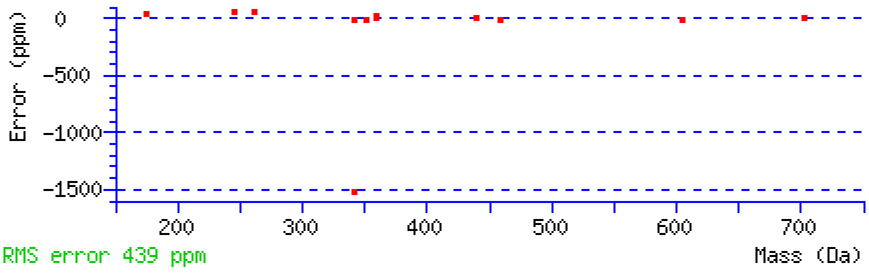
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 977.533447
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 41  Expect: 0.00077
Matches : 12/56 fragment ions using 17 most intense peaks   (help)
```

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	164.070605	82.538940			Y							8
2	277.154669	139.080973			L	815.477400	408.242338	798.450851	399.729064	797.466835	399.237056	7
3	374.207433	187.607354			P	*702.393336*	351.700306	685.366787	343.187032	684.382771	342.695024	6
4	521.275847	261.141562			F	*605.340572*	303.173924	588.314023	294.660650	587.330007	294.168642	5
5	620.344261	310.675769			V	*458.272158*	229.639717	441.245609	221.126443	440.261593	220.634435	4
6	717.397025	359.202151			P	*359.203744*	180.105510	342.177195	171.592236	341.193179	171.100228	3
7	804.429053	402.718165	786.418488	393.712882	S	*262.150980*	131.579128	245.124431	123.065854	244.140415	122.573846	2
8					R	*175.118952*	88.063114	158.092403	79.549840			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.8	977.533447	0.003001	YLPFVPSR
13.2	977.529419	0.007029	VGNYLIGSR
12.1	977.544678	-0.008230	VGIYGWRK
9.3	977.529404	0.007044	IYPSKTNR
9.1	977.529419	0.007029	IYNGIGVSR
7.6	977.529404	0.007044	YIQAKPSR
7.6	977.529404	0.007044	YLQPAKSR
4.3	977.540649	-0.004201	LQGALHPAR
1.4	977.544662	-0.008214	IRYYVHK
0.5	977.529419	0.007029	ISWTTKSR

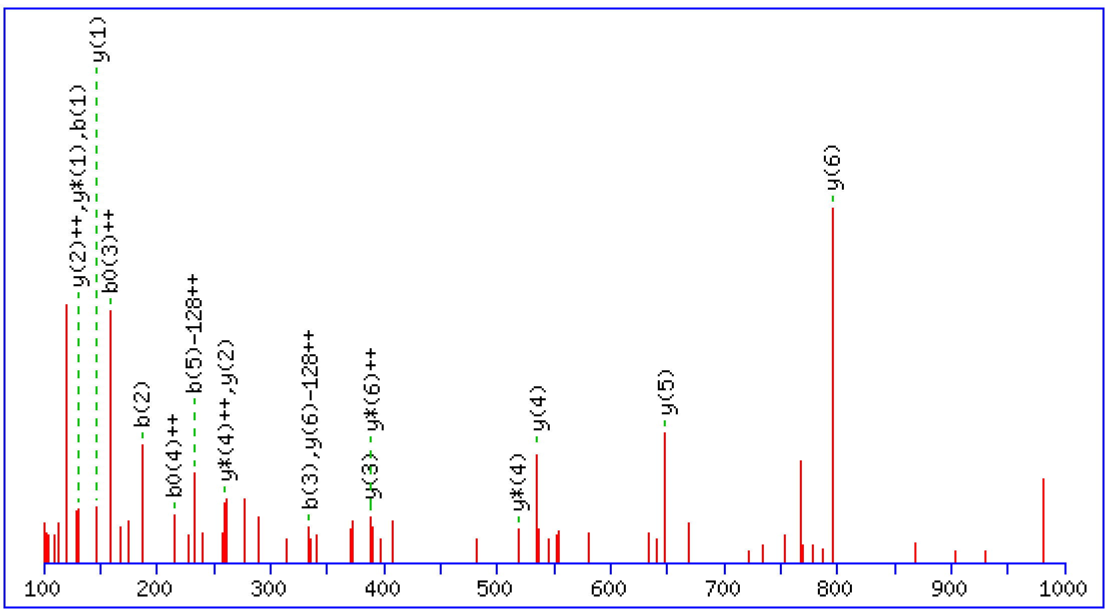
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EGMLMKIK**
Found in **FSD1_HUMAN**, Fibronectin type III and SPRY domain-containing protein 1 OS=Homo sapiens GN=FSD1 PE=1 SV=1

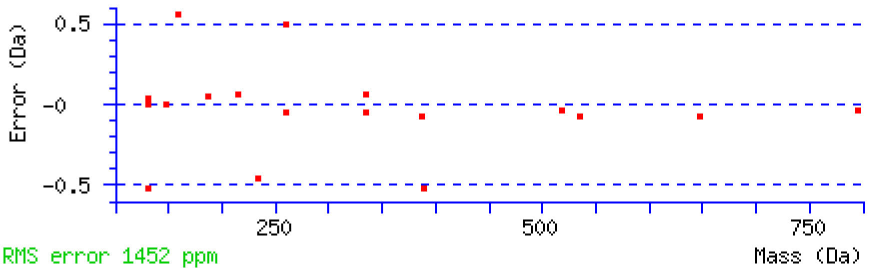
Match to Query 13745: 980.503788 from(491.259170,2+) rtinseconds(2274) index(28193)
Title: Locus:1.1.1.2193.14
Data file 2011-11-10 - TFD - EP 4-4.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●

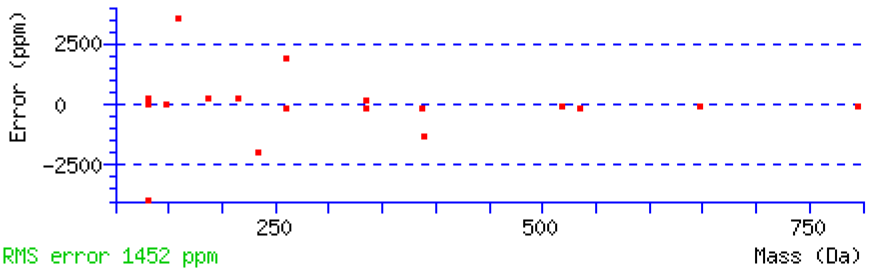


```
Monoisotopic mass of neutral peptide Mr(calc): 980.503448
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M3      : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
M5      : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 31  Expect: 0.0084
Matches : 18/100 fragment ions using 34 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	#
1	**130.049869**	65.528572			112.039304	56.523290	E					8
2	**187.071333**	94.039305			169.060768	85.034022	G	852.468159	426.737718	835.441610	418.224443	7
3	**334.106733**	167.557005			316.096168	158.551722	M	***795.446695***	398.226986	778.420146	389.713711	6
4	447.190797	224.099037			429.180232	215.093754	L	***648.411295***	324.709286	631.384746	316.196011	5
5	594.226197	297.616737			576.215632	288.611454	M	***535.327231***	268.167254	518.300682	259.653979	4
6	722.321160	361.664218	705.294611	353.150944	704.310595	352.658936	K	***388.291831***	194.649554	371.265282	186.136279	3
7	835.405224	418.206250	818.378675	409.692976	817.394659	409.200968	I	***260.196868***	130.602072	243.170319	122.088798	2
8							K	***147.112804***	74.060040	130.086255	65.546765	1



RMS error 1452 ppm



RMS error 1452 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.9	980.503448	0.000340	EGMLMKIK
22.2	980.500092	0.003696	SVFLEQMK
10.5	980.500076	0.003712	LSIFMENK
7.6	980.500092	0.003696	DPMSFKLK
6.4	980.511978	-0.008190	WKYPFPK
3.5	980.503464	0.000324	LTVLNMMK
3.0	980.511307	-0.007519	LMEKFAAR
2.4	980.500092	0.003696	ISPFSCLK
1.0	980.500092	0.003696	DPMSFKLK
0.8	980.511322	-0.007534	ILSFNTMR

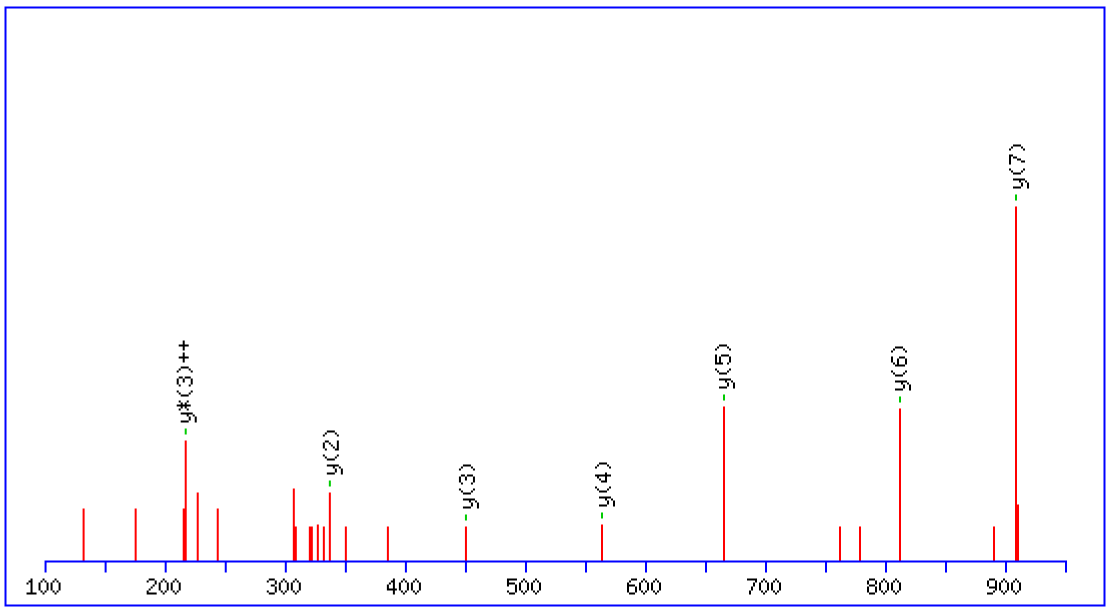
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DQPFTILYR**
Found in **FBLN5_HUMAN**, Fibulin-5 OS=Homo sapiens GN=FBLN5 PE=1 SV=1

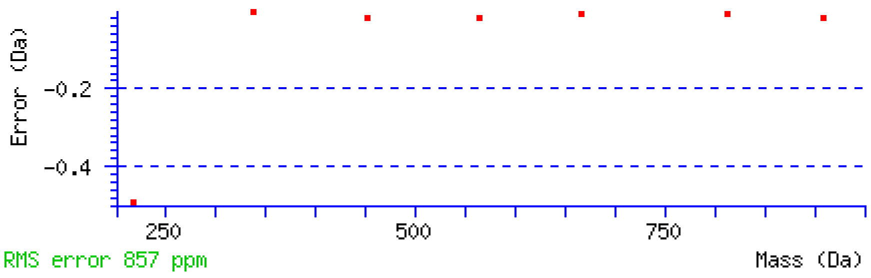
Match to Query 460860: 1151.596688 from(576.805620,2+) rtinseconds(3071) index(935232)
Title: Locus:1.1.1.1573.23
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

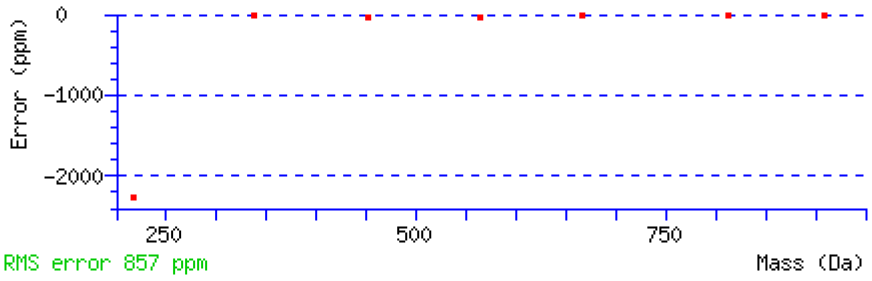
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1151.597504
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 56 **Expect:** 9e-006
Matches : 7/86 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.034219	58.520748			98.023654	49.515465	D							9
2	244.092797	122.550037	227.066248	114.036762	226.082232	113.544754	Q	1037.577844	519.292560	1020.551295	510.779286	1019.567279	510.287278	8
3	341.145561	171.076418	324.119012	162.563144	323.134996	162.071136	P	***909.519266***	455.263271	892.492717	446.749997	891.508701	446.257989	7
4	488.213975	244.610625	471.187426	236.097351	470.203410	235.605343	F	***812.466502***	406.736889	795.439953	398.223615	794.455937	397.731607	6
5	589.261654	295.134465	572.235105	286.621191	571.251089	286.129183	T	***665.398088***	333.202682	648.371539	324.689408	647.387523	324.197400	5
6	702.345718	351.676497	685.319169	343.163223	684.335153	342.671215	I	***564.350409***	282.678843	547.323860	274.165568			4
7	815.429782	408.218529	798.403233	399.705255	797.419217	399.213247	L	***451.266345***	226.136810	434.239796	217.623536			3
8	978.493111	489.750194	961.466562	481.236919	960.482546	480.744911	Y	***338.182281***	169.594778	321.155732	161.081504			2
9							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.4	1151.597504	-0.000816	DQPFTILYR
2.6	1151.604706	-0.008018	RSSLHSQPPK

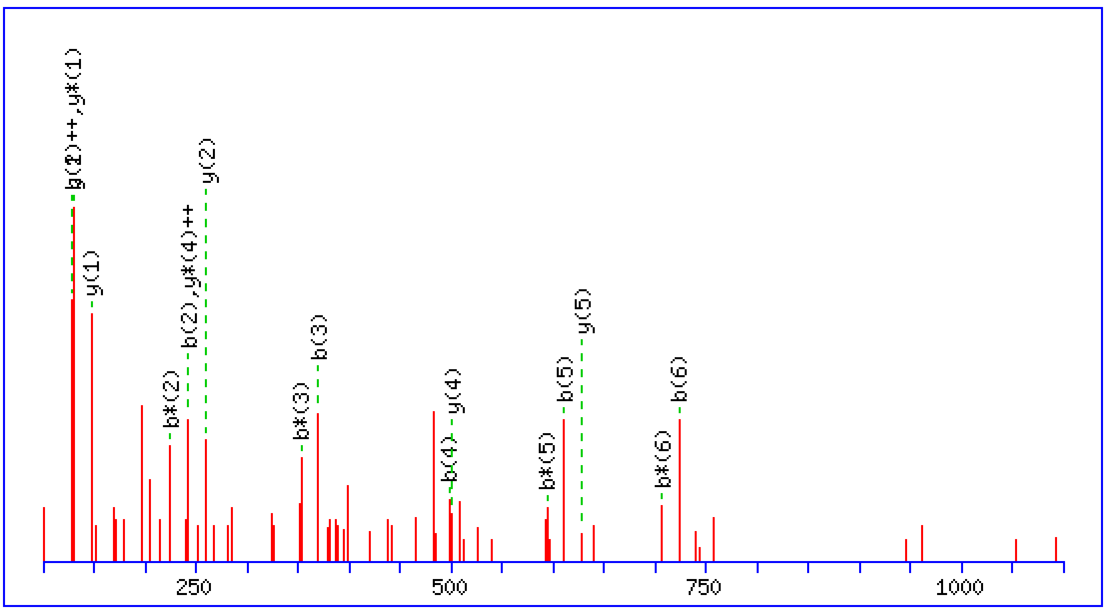
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QLQQLLK**
Found in **FBLN7_HUMAN**, Fibulin-7 OS=Homo sapiens GN=FBLN7 PE=2 SV=1

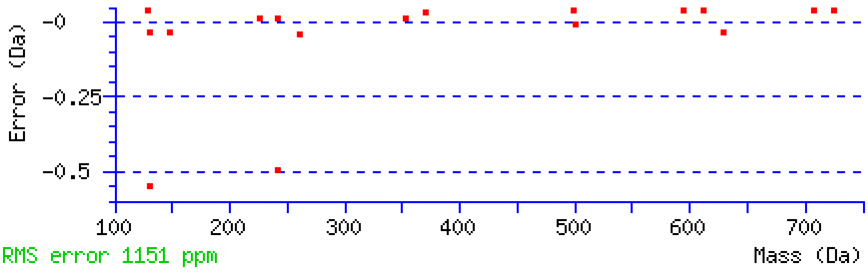
Match to Query 4558: 869.539308 from(435.776930,2+) rtinseconds(1635) index(4252)
Title: Locus:1.1.1.2279.5
Data file 2011-11-13 - TFD - EP 7-8.mgf

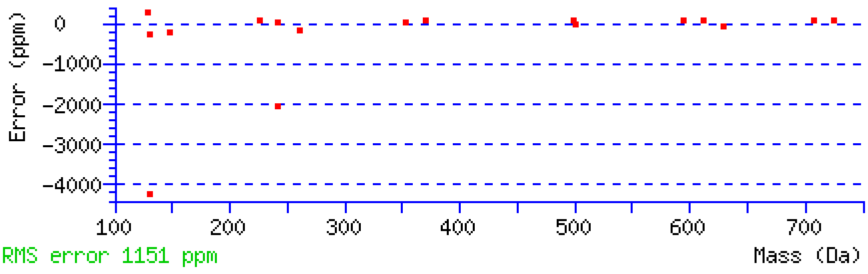
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 869.533432
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 49  Expect: 9.6e-005
Matches : 17/48 fragment ions using 21 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	***129.065854***	65.036565	112.039305	56.523291	**Q**					7
2	***242.149918***	121.578597	225.123369	113.065323	**L**	742.482152	371.744714	725.455603	363.231440	6
3	***370.208496***	185.607886	353.181947	177.094612	**Q**	**629.398088**	315.202682	612.371539	306.689408	5
4	***498.267074***	249.637175	481.240525	241.123901	**Q**	**501.339510**	251.173393	484.312961	242.660119	4
5	***611.351138***	306.179207	594.324589	297.665933	**L**	373.280932	187.144104	356.254383	178.630830	3
6	***724.435202***	362.721239	707.408653	354.207965	**L**	**260.196868**	130.602072	243.170319	122.088798	2
7					**K**	**147.112804**	74.060040	130.086255	65.546765	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.3	869.533432	0.005876	KPKPKPK
49.3	869.533432	0.005876	QPQLKLK
49.1	869.533432	0.005876	QLQQLLK
41.3	869.533432	0.005876	LKQIGALQ
34.0	869.533432	0.005876	KAAVPQIK
33.7	869.533432	0.005876	QQLQLLK
31.5	869.533432	0.005876	KPLKQPK
31.4	869.533432	0.005876	KLQPIQK
21.4	869.544662	-0.005354	QRPTKLK
20.9	869.533432	0.005876	QKLLGPSK

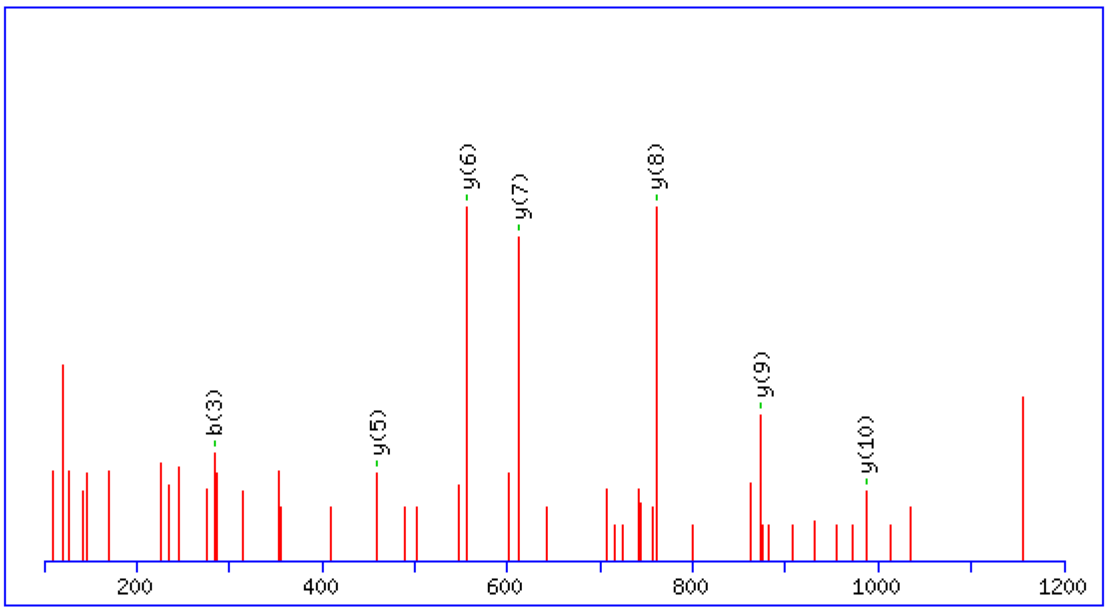
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GILLFGPPGTGK**
Found in **FIGL1_HUMAN**, Fidgetin-like protein 1 OS=Homo sapiens GN=FIGNL1 PE=1 SV=2

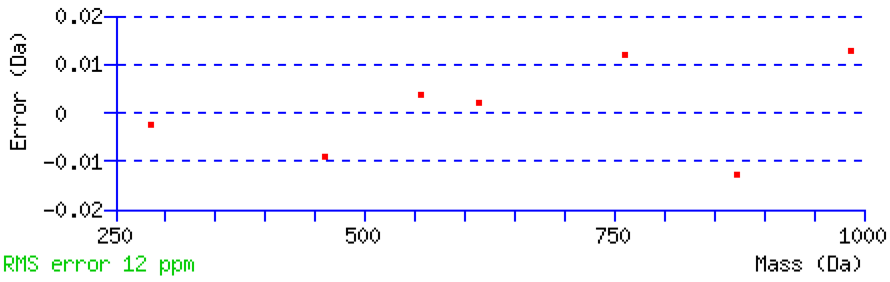
Match to Query 25864: 1155.666708 from(578.840630,2+) rtinseconds(3085) index(42860)
Title: Locus:1.1.1.2602.14
Data file 2011-11-13 - TFD - EP 7-4.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●

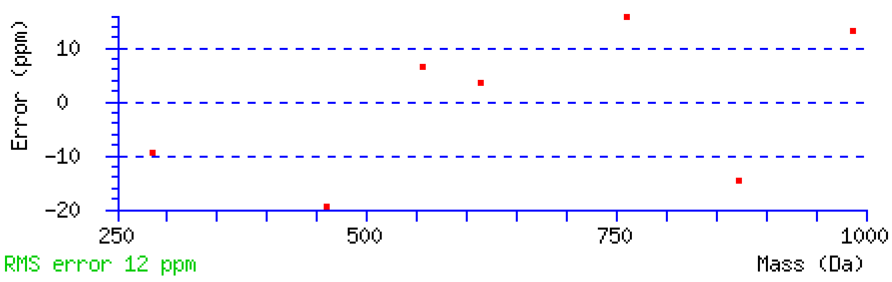


Monoisotopic mass of neutral peptide Mr(calc): 1155.665207
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 42 **Expect:** 0.0002
Matches : 7/88 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	58.028740	29.518008			G							12
2	171.112804	86.060040			I	1099.651009	550.329143	1082.624460	541.815868	1081.640444	541.323860	11
3	284.196868	142.602072			L	***986.566945***	493.787111	969.540396	485.273836	968.556380	484.781828	10
4	397.280932	199.144104			L	***873.482881***	437.245079	856.456332	428.731804	855.472316	428.239796	9
5	544.349346	272.678311			F	***760.398817***	380.703047	743.372268	372.189772	742.388252	371.697764	8
6	601.370810	301.189043			G	***613.330403***	307.168840	596.303854	298.655565	595.319838	298.163557	7
7	698.423574	349.715425			P	***556.308939***	278.658108	539.282390	270.144833	538.298374	269.652825	6
8	795.476338	398.241807			P	***459.256175***	230.131726	442.229626	221.618451	441.245610	221.126443	5
9	852.497802	426.752539			G	362.203411	181.605344	345.176862	173.092069	344.192846	172.600061	4
10	953.545481	477.276379	935.534916	468.271096	T	305.181947	153.094612	288.155398	144.581337	287.171382	144.089329	3
11	1010.566945	505.787111	992.556380	496.781828	G	204.134268	102.570772	187.107719	94.057498			2
12					K	147.112804	74.060040	130.086255	65.546765			1



RMS error 12 ppm



RMS error 12 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.6	1155.665207	0.001501	GILLFGPPGTGK
2.3	1155.661148	0.005560	GLIGPEKLASR

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

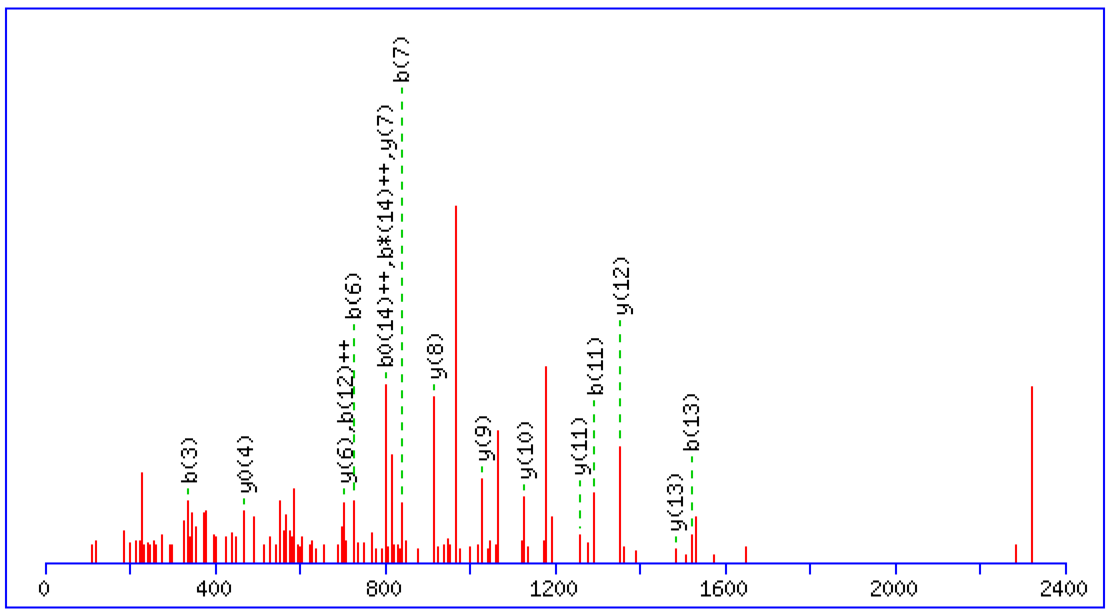
Mascot Search Results

Peptide View

MS/MS Fragmentation of EAHQLFLEPEVLDPESVELK
Found in FEN1_HUMAN, Flap endonuclease 1 OS=Homo sapiens GN=FEN1 PE=1 SV=1

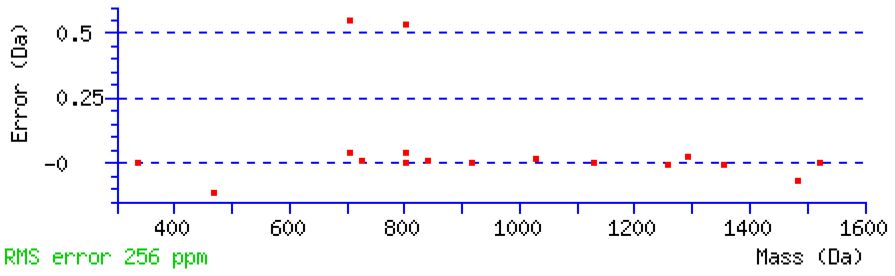
Match to Query 73332: 2321.175642 from(774.732490,3+) rtinseconds(3486) index(50070)
Title: Locus:1.1.1.2739.34
Data file 2011-11-12 - TFD - EP 5-4.mgf

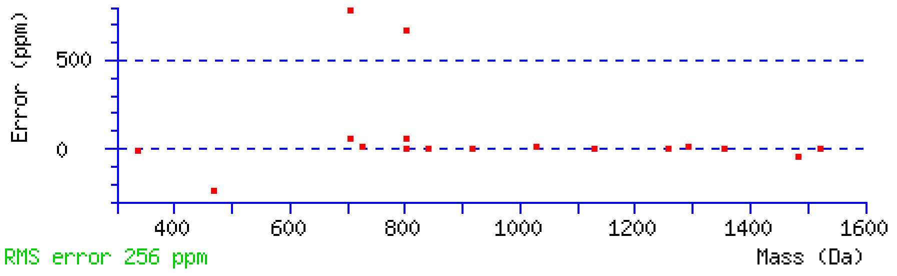
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2321.179062
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.0017
Matches : 17/218 fragment ions using 32 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	E							20
2	201.086983	101.047130			183.076418	92.041847	A	2193.143777	1097.075526	2176.117228	1088.562252	2175.133212	1088.070244	19
3	*338.145895*	169.576585			320.135330	160.571303	H	2122.106663	1061.556969	2105.080114	1053.043695	2104.096098	1052.551687	18
4	466.204473	233.605875	449.177924	225.092600	448.193908	224.600592	Q	1985.047751	993.027514	1968.021202	984.514239	1967.037186	984.022231	17
5	579.288537	290.147907	562.261988	281.634632	561.277972	281.142624	L	1856.989173	928.998225	1839.962624	920.484950	1838.978608	919.992942	16
6	*726.356951*	363.682114	709.330402	355.168839	708.346386	354.676831	F	1743.905109	872.456193	1726.878560	863.942918	1725.894544	863.450910	15
7	*839.441015*	420.224146	822.414466	411.710871	821.430450	411.218863	L	1596.836695	798.921986	1579.810146	790.408711	1578.826130	789.916703	14
8	968.483608	484.745442	951.457059	476.232168	950.473043	475.740160	E	*1483.752631*	742.379954	1466.726082	733.866679	1465.742066	733.374671	13
9	1065.536372	533.271824	1048.509823	524.758550	1047.525807	524.266542	P	*1354.710038*	677.858657	1337.683489	669.345383	1336.699473	668.853375	12
10	1194.578965	597.793120	1177.552416	589.279846	1176.568400	588.787838	E	*1257.657274*	629.332275	1240.630725	620.819001	1239.646709	620.326993	11
11	*1293.647379*	647.327328	1276.620830	638.814053	1275.636814	638.322045	V	*1128.614681*	564.810979	1111.588132	556.297704	1110.604116	555.805696	10
12	1406.731443	703.869359	1389.704894	695.356085	1388.720878	694.864077	L	*1029.546267*	515.276772	1012.519718	506.763497	1011.535702	506.271489	9
13	*1521.758386*	761.382831	1504.731837	752.869557	1503.747821	752.377548	D	*916.462203*	458.734740	899.435654	450.221465	898.451638	449.729457	8
14	1618.811150	809.909213	1601.784601	801.395939	1600.800585	800.903931	P	*801.435260*	401.221268	784.408711	392.707994	783.424695	392.215986	7
15	1747.853743	874.430509	1730.827194	865.917235	1729.843178	865.425227	E	*704.382496*	352.694886	687.355947	344.181612	686.371931	343.689604	6
16	1834.885771	917.946524	1817.859222	909.433249	1816.875206	908.941241	S	575.339903	288.173590	558.313354	279.660315	557.329338	279.168307	5
17	1933.954185	967.480731	1916.927636	958.967456	1915.943620	958.475448	V	488.307875	244.657576	471.281326	236.144301	470.297310	235.652293	4
18	2062.996778	1032.002027	2045.970229	1023.488752	2044.986213	1022.996744	E	389.239461	195.123369	372.212912	186.610094	371.228896	186.118086	3
19	2176.080842	1088.544059	2159.054293	1080.030784	2158.070277	1079.538776	L	260.196868	130.602072	243.170319	122.088798			2
20							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.7	2321.179062	-0.003420	EAHQLFLEPEVLDPESVELK
2.2	2321.157288	0.018354	ALGDVPEPGAAREALMPPLEQL
0.1	2321.157288	0.018354	ALGDVPEPGAAREALMPPLEQL

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

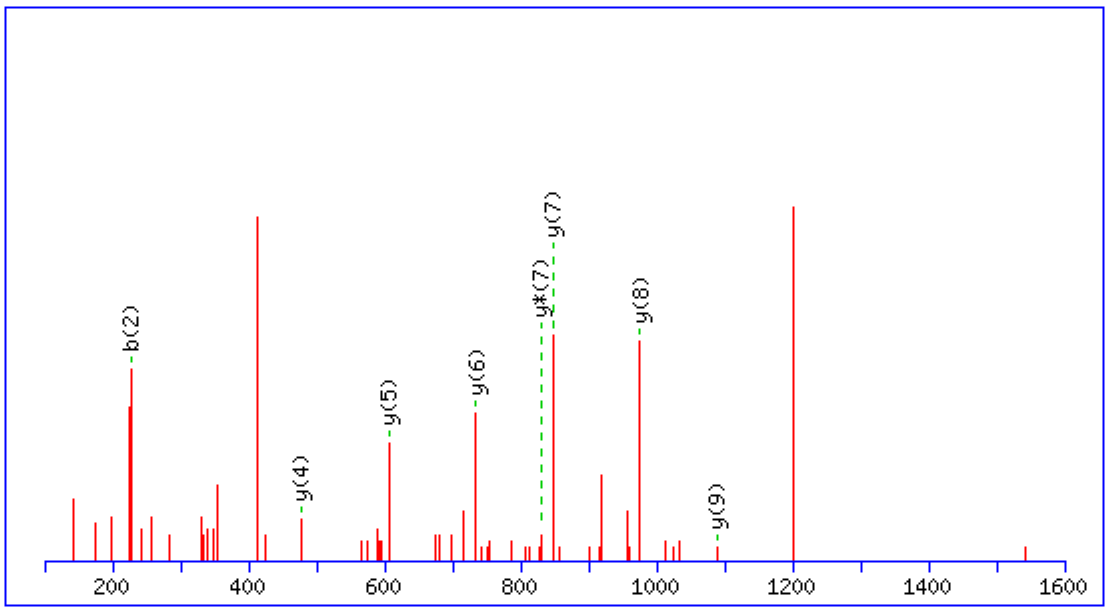
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLQLQEMGNR**
Found in **FHAD1_HUMAN**, Forkhead-associated domain-containing protein 1 OS=Homo sapiens GN=FHAD1 PE=2 SV=2

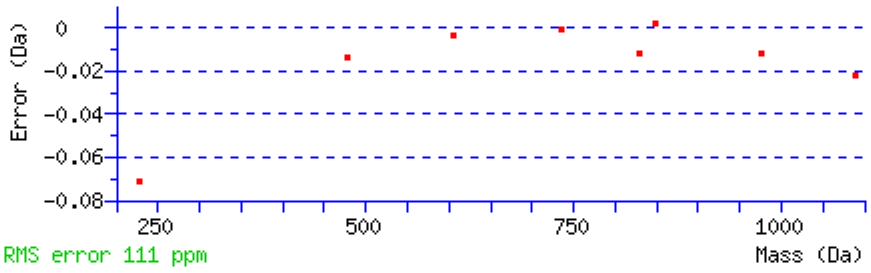
Match to Query 522879: 1200.619388 from(601.316970,2+) rtinseconds(1906) index(593041)
Title: Locus:1.1.1.1049.23
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

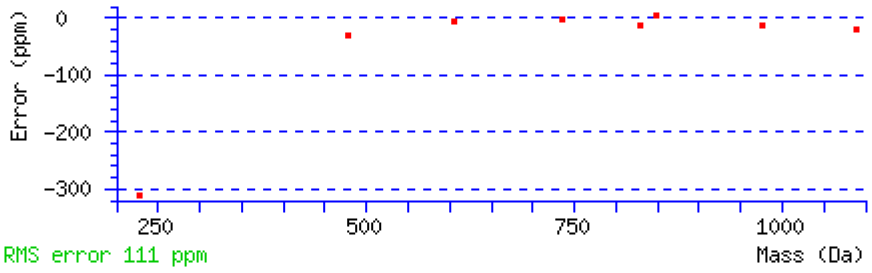
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1200.628464
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 46 **Expect:** 0.00034
Matches : 8/86 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					L							10
2	227.175404	114.091340					L	*1088.551705*	544.779491	1071.525156	536.266216	1070.541140	535.774208	9
3	355.233982	178.120629	338.207433	169.607355			Q	*975.467641*	488.237459	958.441092	479.724184	957.457076	479.232176	8
4	468.318046	234.662661	451.291497	226.149387			L	*847.409063*	424.208170	830.382514	415.694895	829.398498	415.202887	7
5	596.376624	298.691950	579.350075	290.178676			Q	*734.324999*	367.666138	717.298450	359.152863	716.314434	358.660855	6
6	725.419217	363.213247	708.392668	354.699972	707.408652	354.207964	E	*606.266421*	303.636849	589.239872	295.123574	588.255856	294.631566	5
7	856.459702	428.733489	839.433153	420.220215	838.449137	419.728207	M	*477.223828*	239.115552	460.197279	230.602278			4
8	913.481166	457.244221	896.454617	448.730947	895.470601	448.238939	G	346.183343	173.595310	329.156794	165.082035			3
9	1027.524093	514.265685	1010.497544	505.752410	1009.513528	505.260402	N	289.161879	145.084577	272.135330	136.571303			2
10							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.3	1200.628464	-0.009076	LLQLQEMGNR
8.8	1200.609818	0.009570	LLQEEEERR
3.9	1200.609848	0.009540	LPANTADISQR
0.7	1200.625092	-0.005704	KDQLEYHIR

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

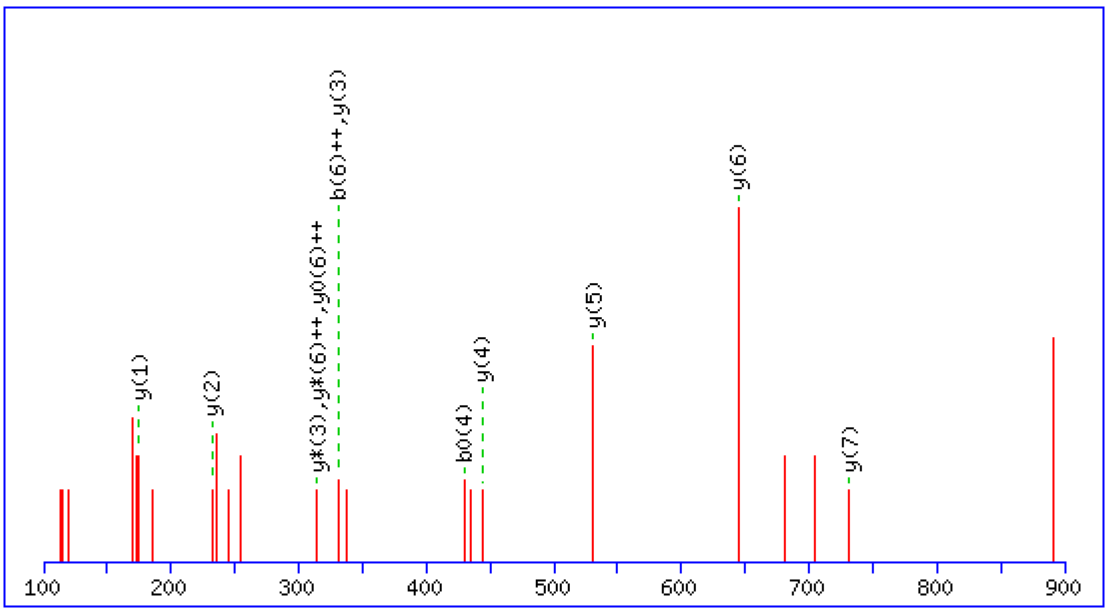
Mascot Search Results

Peptide View

MS/MS Fragmentation of **CSLSLVGR**
Found in **FHL2_HUMAN**, Four and a half LIM domains protein 2 OS=Homo sapiens GN=FHL2 PE=1 SV=3

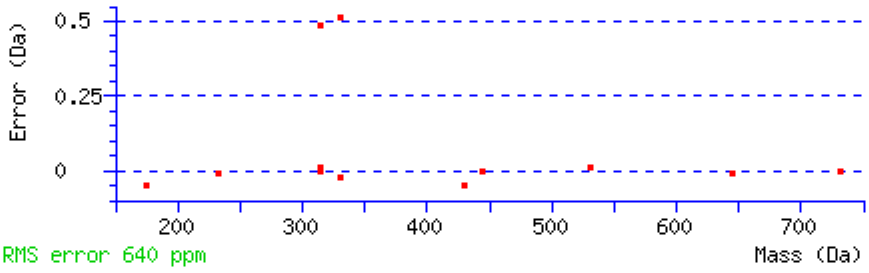
Match to Query 116286: 890.471188 from(446.242870,2+) rtinseconds(1906) index(674367)
Title: Locus:1.1.1.1395.9
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

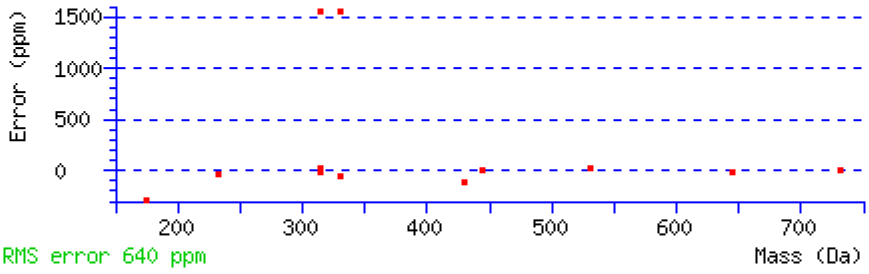
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 890.464386
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 49  Expect: 0.00013
Matches : 12/60 fragment ions using 17 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	161.037925	81.022600			C							8
2	248.069953	124.538614	230.059388	115.533332	S	*731.441014*	366.224145	714.414465	357.710871	713.430449	357.218863	7
3	361.154017	181.080647	343.143452	172.075364	L	*644.408986*	322.708131	627.382437	314.194857	626.398421	313.702849	6
4	448.186045	224.596660	430.175480	215.591378	S	*531.324922*	266.166099	514.298373	257.652825	513.314357	257.160817	5
5	561.270109	281.138693	543.259544	272.133410	L	*444.292894*	222.650085	427.266345	214.136810			4
6	660.338523	330.672900	642.327958	321.667617	V	*331.208830*	166.108053	314.182281	157.594778			3
7	717.359987	359.183632	699.349422	350.178349	G	*232.140416*	116.573846	215.113867	108.060571			2
8					R	*175.118952*	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.9	890.464386	0.006802	CSLSLVGR
5.7	890.475601	-0.004413	SCLRSLR

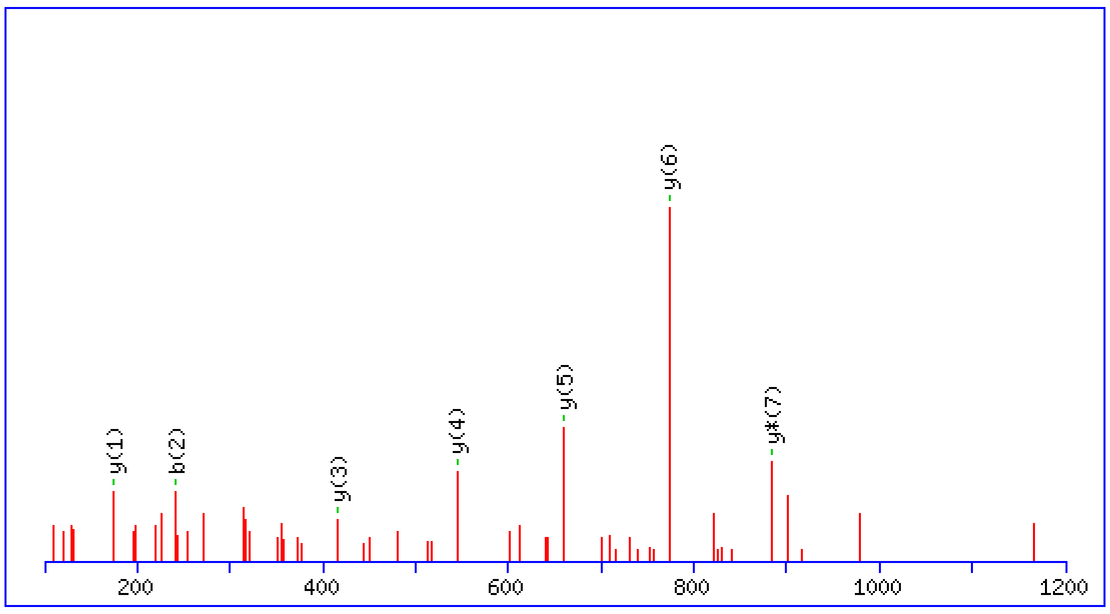
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LQIDEQLR**
Found in **FMR1_HUMAN**, Fragile X mental retardation 1 protein OS=Homo sapiens GN=FMR1 PE=1 SV=1

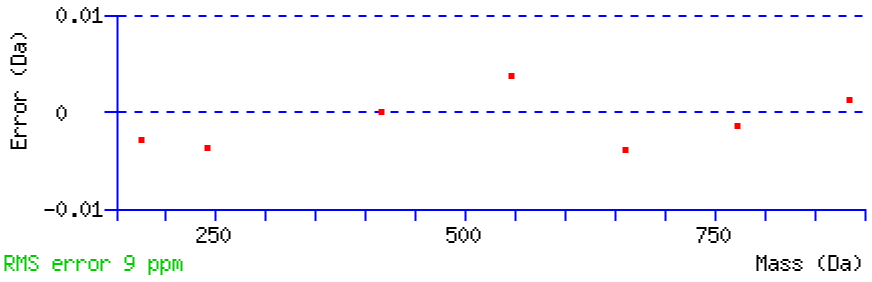
Match to Query 17417: 1013.551248 from(507.782900,2+) rtinseconds(2021) index(22276)
Title: Locus:1.1.1.2163.24
Data file 2011-11-12 - TFD - EP 6-2.mgf

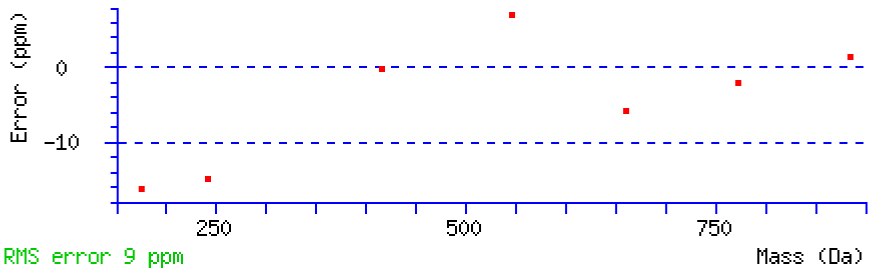
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1013.550537
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 37 **Expect:** 0.0027
Matches : 7/70 fragment ions using 9 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.091340	57.549308					L							8
2	242.149918	121.578597	225.123369	113.065323			Q	901.473772	451.240524	884.447223	442.727250	883.463207	442.235242	7
3	355.233982	178.120629	338.207433	169.607355			I	***773.415194***	387.211235	756.388645	378.697961	755.404629	378.205953	6
4	470.260925	235.634101	453.234376	227.120826	452.250360	226.628818	D	***660.331130***	330.669203	643.304581	322.155929	642.320565	321.663921	5
5	599.303518	300.155397	582.276969	291.642123	581.292953	291.150115	E	***545.304187***	273.155732	528.277638	264.642457	527.293622	264.150449	4
6	727.362096	364.184686	710.335547	355.671412	709.351531	355.179404	Q	***416.261594***	208.634435	399.235045	200.121160			3
7	840.446160	420.726718	823.419611	412.213444	822.435595	411.721436	L	288.203016	144.605146	271.176467	136.091871			2
8							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.0	1013.550537	0.000711	LQIDEQLR
8.2	1013.550537	0.000711	IKAAVEDPR
4.2	1013.550568	0.000680	LLQGDTPVR
3.6	1013.550537	0.000711	QLVQEELR
2.9	1013.550537	0.000711	KEVLASPDR
2.7	1013.550537	0.000711	LEEVQQLR
2.6	1013.550552	0.000696	QPASLLDVR
0.0	1013.550552	0.000696	SPGTSPLLSR

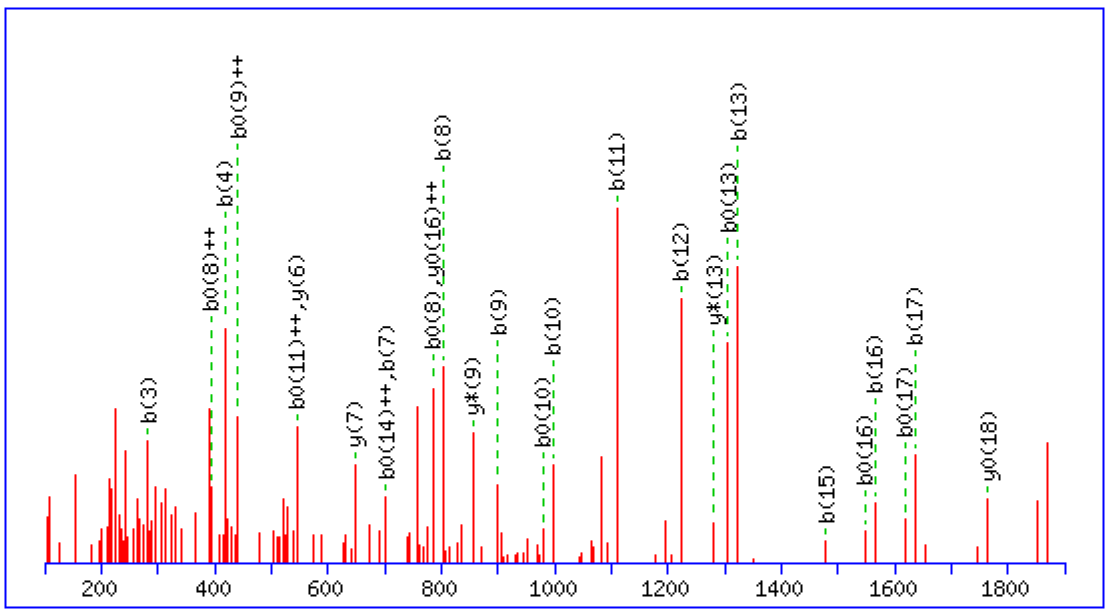
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SGHHPGETPPLITPGSAQS**
Found in **FXYD3_HUMAN**, FXYD domain-containing ion transport regulator 3 OS=Homo sapiens GN=FXYD3 PE=2 SV=1

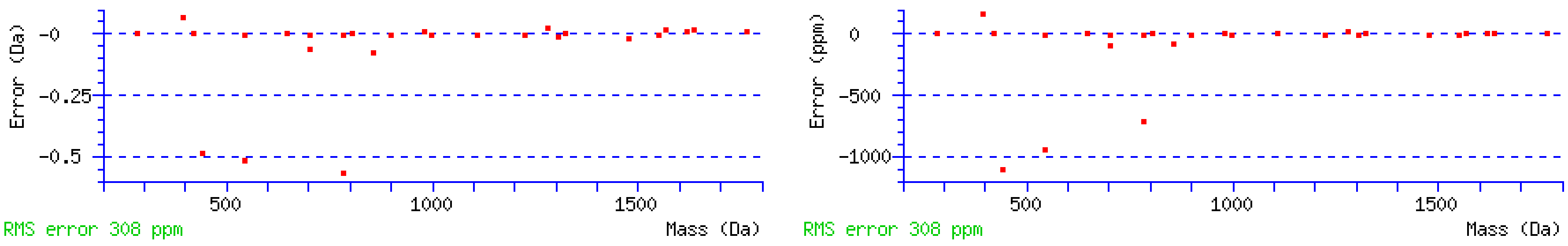
Match to Query 46804: 1868.898222 from(623.973350,3+) rtinseconds(1744) index(12573)
Title: Locus:1.1.1.1994.32
Data file 2011-11-12 - TFD - EP 6-7.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1868.901703
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 108 **Expect:** 2.2e-010
Matches : 28/180 fragment ions using 34 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	88.039304	44.523290			70.028739	35.518008	S							19
2	145.060768	73.034022			127.050203	64.028740	G	1782.876940	891.942108	1765.850391	883.428834	1764.866375	882.936825	18
3	***282.119680***	141.563478			264.109115	132.558195	H	1725.855476	863.431376	1708.828927	854.918102	1707.844911	854.426093	17
4	***419.178592***	210.092934			401.168027	201.087651	H	1588.796564	794.901920	1571.770015	786.388646	1570.785999	785.896638	16
5	516.231356	258.619316			498.220791	249.614034	P	1451.737652	726.372464	1434.711103	717.859190	1433.727087	717.367182	15
6	573.252820	287.130048			555.242255	278.124766	G	1354.684888	677.846082	1337.658339	669.332808	1336.674323	668.840800	14
7	***702.295413***	351.651345			684.284848	342.646062	E	1297.663424	649.335350	1280.636875	640.822076	1279.652859	640.330068	13
8	***803.343092***	402.175184			785.332527	393.169902	T	1168.620831	584.814054	1151.594282	576.300779	1150.610266	575.808771	12
9	***900.395856***	450.701566			882.385291	441.696284	P	1067.573152	534.290214	1050.546603	525.776940	1049.562587	525.284931	11
10	***997.448620***	499.227948			979.438055	490.222666	P	970.520388	485.763832	953.493839	477.250557	952.509823	476.758549	10
11	***1110.532684***	555.769980			1092.522119	546.764698	L	873.467624	437.237450	856.441075	428.724175	855.457059	428.232167	9
12	***1223.616748***	612.312012			1205.606183	603.306729	I	760.383560	380.695418	743.357011	372.182144	742.372995	371.690136	8
13	***1324.664427***	662.835851			1306.653862	653.830569	T	**647.299496**	324.153386	630.272947	315.640112	629.288931	315.148104	7
14	1421.717191	711.362234			1403.706626	702.356951	P	**546.251817**	273.629547	529.225268	265.116272	528.241252	264.624264	6
15	***1478.738655***	739.872965			1460.728090	730.867683	G	449.199053	225.103164	432.172504	216.589890	431.188488	216.097882	5
16	***1565.770683***	783.388980			1547.760118	774.383697	S	392.177589	196.592433	375.151040	188.079158	374.167024	187.587150	4
17	***1636.807797***	818.907536			1618.797232	809.902254	A	305.145561	153.076418	288.119012	144.563144	287.134996	144.071136	3
18	***1764.866375***	882.936825	1747.839826	874.423551	1746.855810	873.931543	Q	234.108447	117.557861	217.081898	109.044587	216.097882	108.552579	2
19							S	106.049869	53.528573			88.039304	44.523290	1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
107.6	1868.901703	-0.003481	SGHHPGETPPLITPGSAQS

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

{MATRIX}
{SCIENCE}

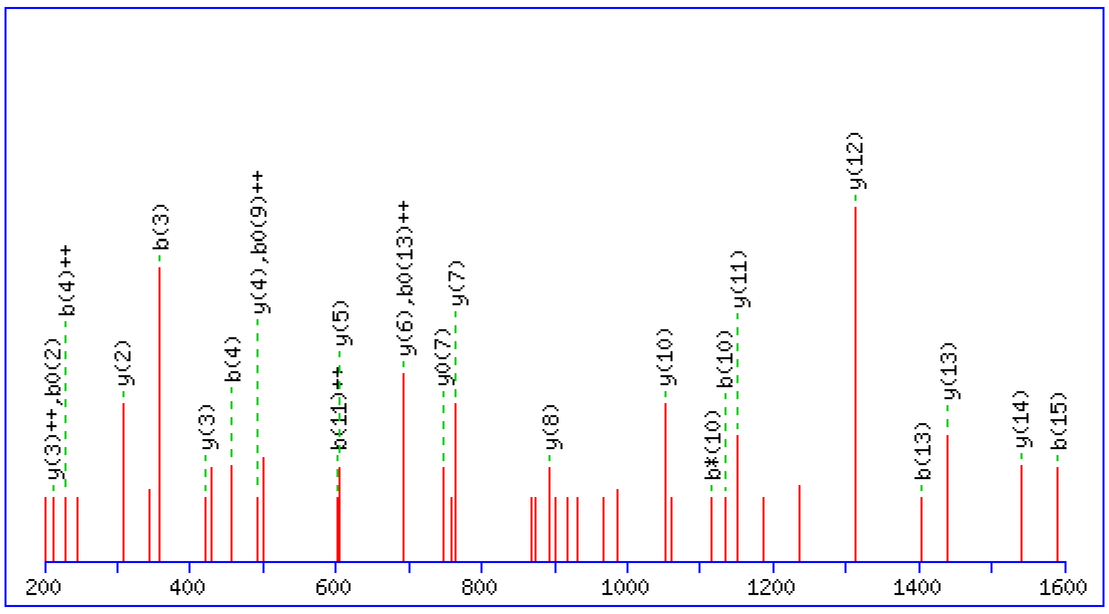
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LDEVQCTGTEASLADCK**
Found in **LG3BP_HUMAN**, Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1

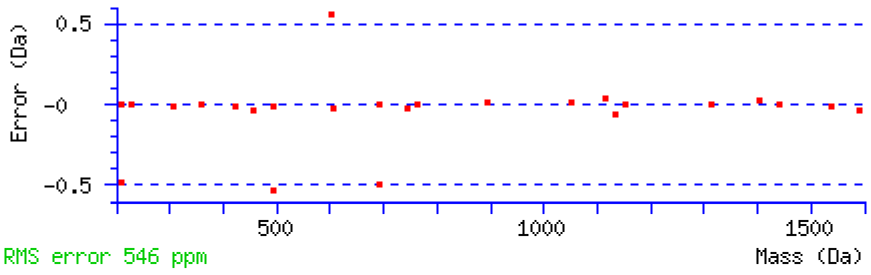
Match to Query 1005914: 1895.833548 from(948.924050,2+) rtinseconds(1964) index(261867)
Title: Locus:1.1.1.1196.50
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

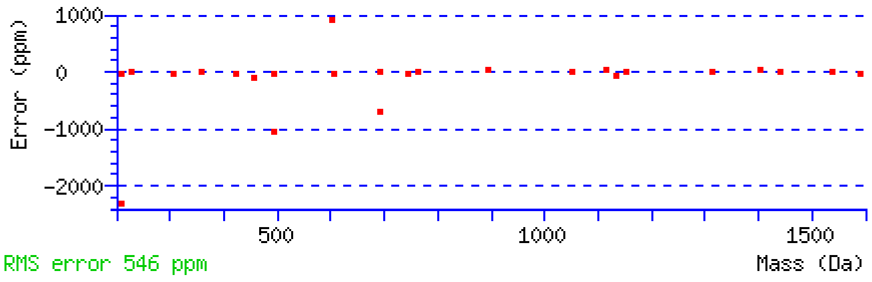
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1895.824097
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 84 **Expect:** 2.9e-008
Matches : 26/178 fragment ions using 38 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					L							17
2	**229.118283**	115.062779			211.107718	106.057497	D	1783.747308	892.377292	1766.720759	883.864018	1765.736743	883.372010	16
3	**358.160876**	179.584076			340.150311	170.578793	E	1668.720365	834.863821	1651.693816	826.350546	1650.709800	825.858538	15
4	**457.229290**	229.118283			439.218725	220.113001	V	***1539.677772***	770.342524	1522.651223	761.829250	1521.667207	761.337242	14
5	585.287868	293.147572	568.261319	284.634298	567.277303	284.142290	Q	***1440.609358***	720.808317	1423.582809	712.295043	1422.598793	711.803035	13
6	745.318517	373.162897	728.291968	364.649622	727.307952	364.157614	C	***1312.550780***	656.779028	1295.524231	648.265754	1294.540215	647.773746	12
7	846.366196	423.686736	829.339647	415.173462	828.355631	414.681454	T	***1152.520131***	576.763704	1135.493582	568.250429	1134.509566	567.758421	11
8	903.387660	452.197468	886.361111	443.684194	885.377095	443.192186	G	***1051.472452***	526.239864	1034.445903	517.726590	1033.461887	517.234582	10
9	1004.435339	502.721308	987.408790	494.208033	986.424774	493.716025	T	994.450988	497.729132	977.424439	489.215858	976.440423	488.723850	9
10	**1133.477932**	567.242604	1116.451383	558.729330	1115.467367	558.237322	E	***893.403309***	447.205293	876.376760	438.692018	875.392744	438.200010	8
11	1204.515046	602.761161	1187.488497	594.247887	1186.504481	593.755879	A	***764.360716***	382.683996	747.334167	374.170722	746.350151	373.678714	7
12	1291.547074	646.277175	1274.520525	637.763901	1273.536509	637.271893	S	***693.323602***	347.165439	676.297053	338.652165	675.313037	338.160157	6
13	**1404.631138**	702.819207	1387.604589	694.305933	1386.620573	693.813925	L	***606.291574***	303.649425	589.265025	295.136151	588.281009	294.644143	5
14	1475.668252	738.337764	1458.641703	729.824490	1457.657687	729.332482	A	***493.207510***	247.107393	476.180961	238.594119	475.196945	238.102111	4
15	**1590.695195**	795.851236	1573.668646	787.337961	1572.684630	786.845953	D	***422.170396***	211.588836	405.143847	203.075562	404.159831	202.583554	3
16	1750.725844	875.866560	1733.699295	867.353286	1732.715279	866.861278	C	***307.143453***	154.075365	290.116904	145.562090			2
17							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
83.5	1895.824097	0.009451	LDEVQCTGTEASLADCK

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

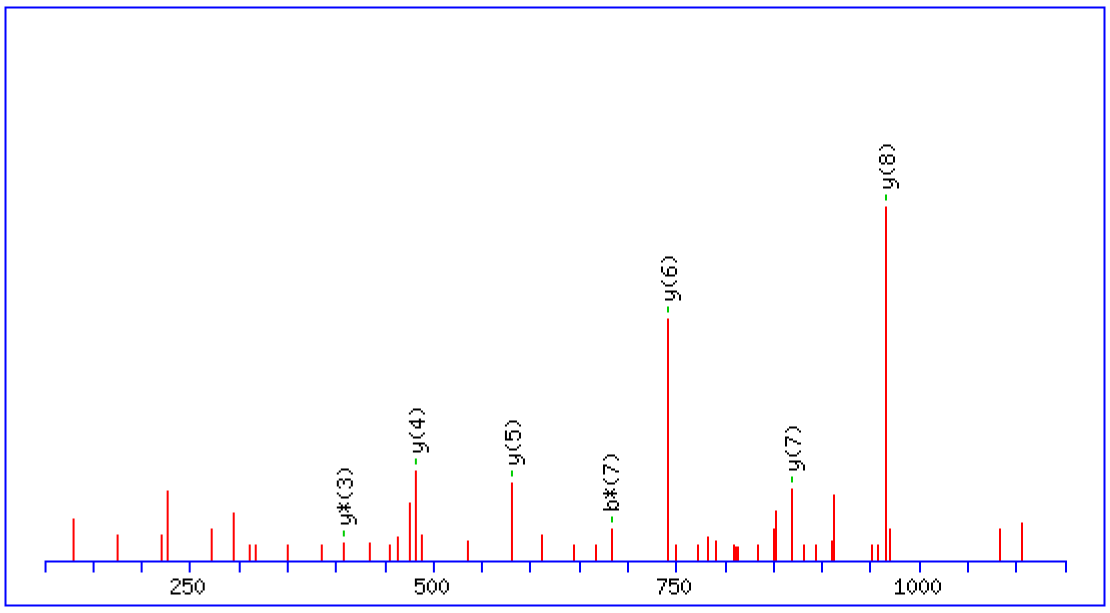
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ASPQCVGYSR**
Found in **OFUT1_HUMAN**, GDP-fucose protein O-fucosyltransferase 1 OS=Homo sapiens GN=POFUT1 PE=1 SV=1

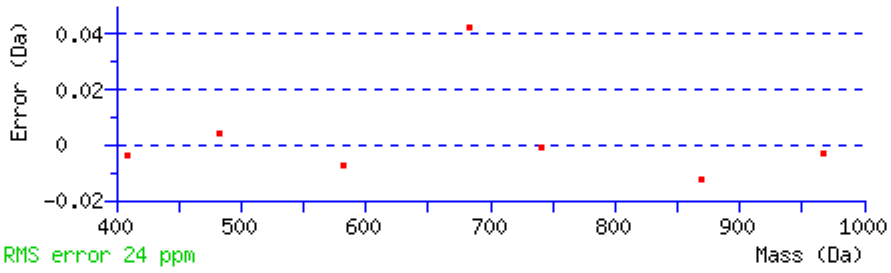
Match to Query 423680: 1123.509308 from(562.761930,2+) rtinseconds(1095) index(330430)
Title: Locus:1.1.1.750.31
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

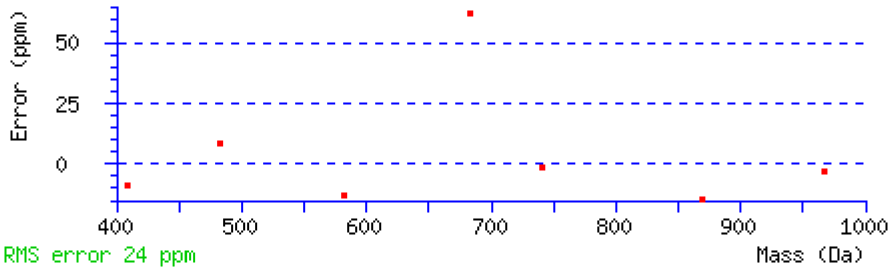
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1123.508041
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 37 **Expect:** 0.001
Matches : 7/98 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.044390	36.525833					A							10
2	159.076418	80.041847			141.065853	71.036564	S	1053.478206	527.242741	1036.451657	518.729467	1035.467641	518.237459	9
3	256.129182	128.568229			238.118617	119.562947	P	***966.446178***	483.726727	949.419629	475.213453	948.435613	474.721445	8
4	384.187760	192.597518	367.161211	184.084243	366.177195	183.592235	Q	***869.393414***	435.200345	852.366865	426.687071	851.382849	426.195063	7
5	544.218409	272.612843	527.191860	264.099568	526.207844	263.607560	C	***741.334836***	371.171056	724.308287	362.657782	723.324271	362.165774	6
6	643.286823	322.147050	626.260274	313.633775	625.276258	313.141767	V	***581.304187***	291.155732	564.277638	282.642457	563.293622	282.150449	5
7	700.308287	350.657782	683.281738	342.144507	682.297722	341.652499	G	***482.235773***	241.621525	465.209224	233.108250	464.225208	232.616242	4
8	863.371616	432.189446	846.345067	423.676172	845.361051	423.184164	Y	425.214309	213.110793	408.187760	204.597518	407.203744	204.105510	3
9	950.403644	475.705460	933.377095	467.192186	932.393079	466.700178	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
10							R	175.118952	88.063114	158.092403	79.549840			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.6	1123.508041	0.001267	ASPQCVGYSR

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

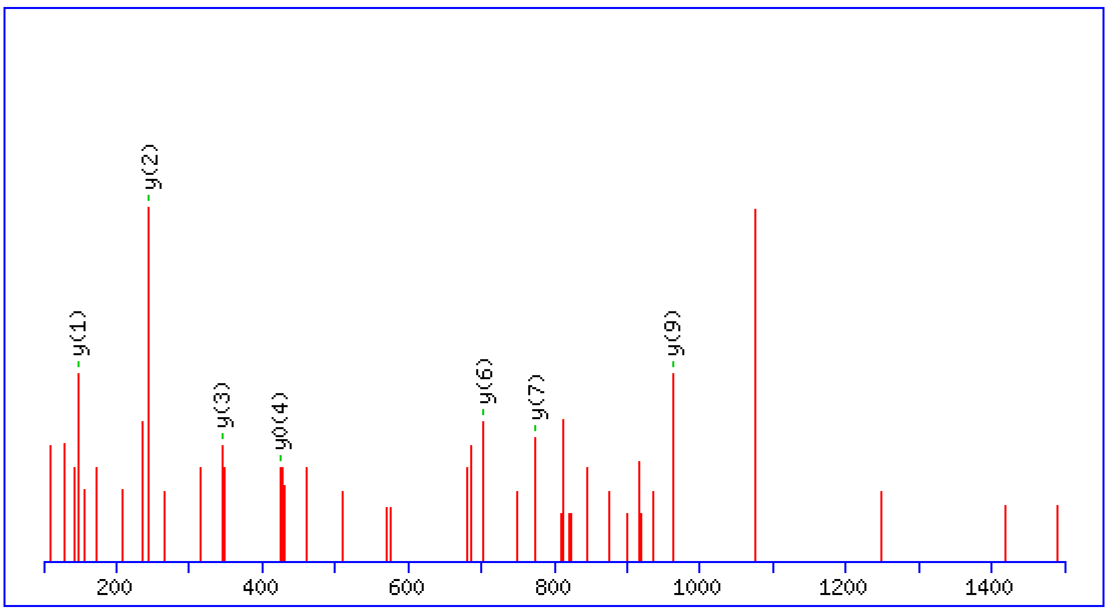
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSTASCPTPK**
Found in **GEPH_HUMAN**, Gephyrin OS=Homo sapiens GN=GPHN PE=1 SV=1

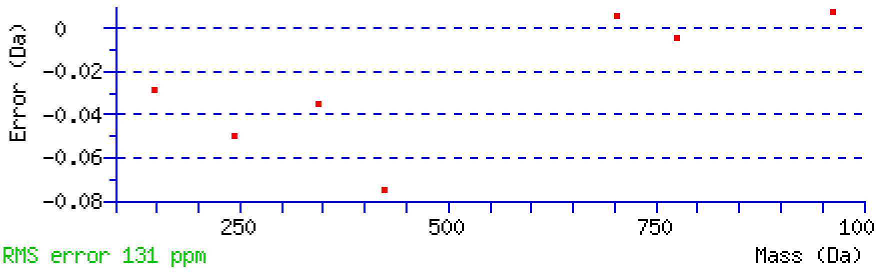
Match to Query 21980: 1074.532328 from(538.273440,2+) rtinseconds(1058) index(4090)
Title: Locus:1.1.1.1799.38
Data file 2011-11-12 - TFD - EP 6-2.mgf

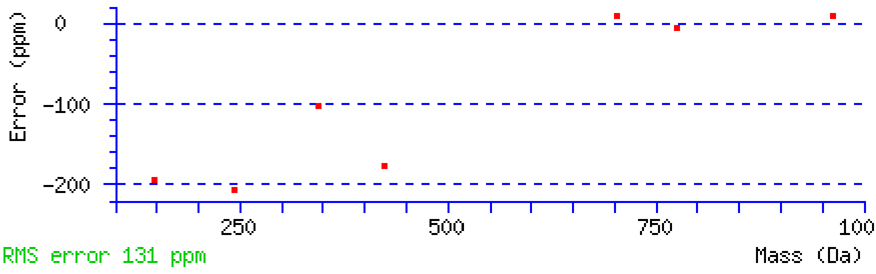
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1074.537933
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 51  Expect: 9.7e-005
Matches : 7/84 fragment ions using 9 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							10
2	201.123368	101.065322	183.112803	92.060039	S	*962.461159*	481.734218	945.434610	473.220943	944.450594	472.728935	9
3	302.171047	151.589161	284.160482	142.583879	T	875.429131	438.218204	858.402582	429.704929	857.418566	429.212921	8
4	373.208161	187.107718	355.197596	178.102436	A	*774.381452*	387.694364	757.354903	379.181090	756.370887	378.689082	7
5	460.240189	230.623732	442.229624	221.618450	S	*703.344338*	352.175807	686.317789	343.662533	685.333773	343.170525	6
6	634.286488	317.646882	616.275923	308.641599	C	616.312310	308.659793	599.285761	300.146519	598.301745	299.654511	5
7	731.339252	366.173264	713.328687	357.167982	P	442.266011	221.636644	425.239462	213.123369	424.255446	212.631361	4
8	832.386931	416.697104	814.376366	407.691821	T	*345.213247*	173.110262	328.186698	164.596987	327.202682	164.104979	3
9	929.439695	465.223486	911.429130	456.218203	P	*244.165568*	122.586422	227.139019	114.073148			2
10					K	*147.112804*	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.1	1074.537933	-0.005605	LSTASCPTPK
13.5	1074.541763	-0.009435	EATSADARVR
6.7	1074.534576	-0.002248	QDQLPSFPK
5.5	1074.534561	-0.002233	SLFPEGNPAK
5.4	1074.526703	0.005625	DMPLEEVVK
2.7	1074.530548	0.001780	TEGTPNQGKK
2.2	1074.528046	0.004282	IDMPHRFK

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

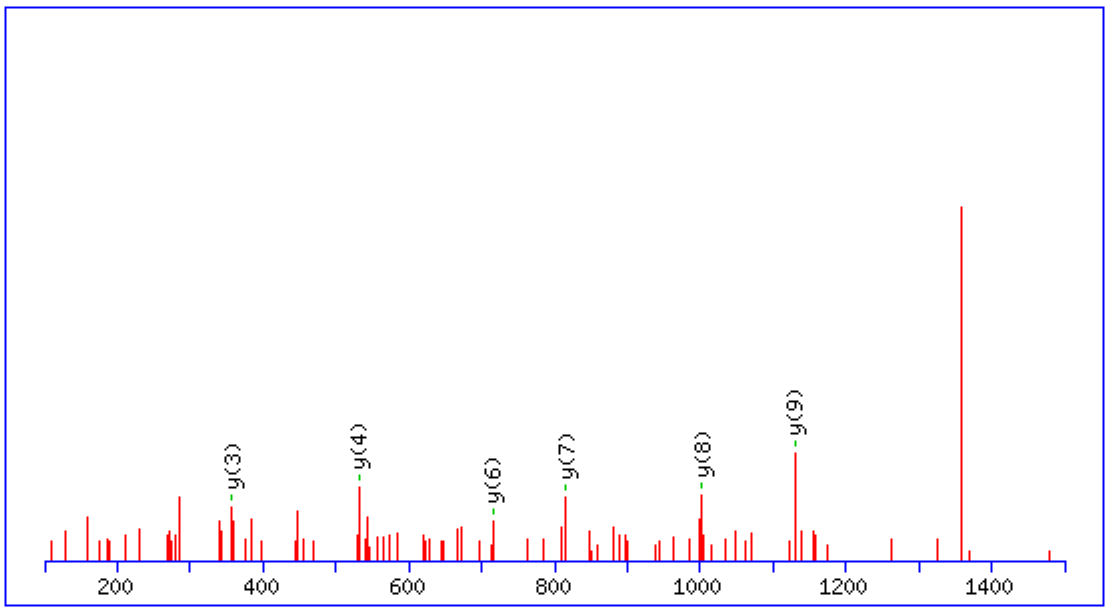
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TQQWTAICPLK**
Found in **GAN_HUMAN**, Gigaxonin OS=Homo sapiens GN=GAN PE=1 SV=1

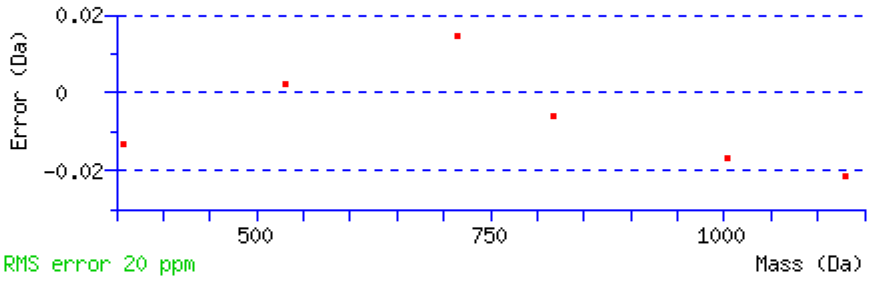
Match to Query 37112: 1358.700068 from(680.357310,2+) rtinseconds(2662) index(35885)
Title: Locus:1.1.1.2432.40
Data file 2011-11-10 - TFD - EP 3-3.mgf

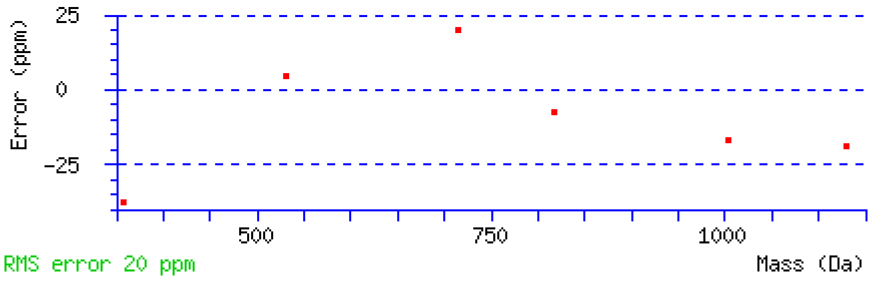
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1358.701645
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 34  Expect: 0.0043
Matches : 6/106 fragment ions using 13 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							11
2	230.113533	115.560405	213.086984	107.047130	212.102968	106.555122	Q	1258.661257	629.834267	1241.634708	621.320992	1240.650692	620.828984	10
3	358.172111	179.589694	341.145562	171.076419	340.161546	170.584411	Q	***1130.602679***	565.804977	1113.576130	557.291703	1112.592114	556.799695	9
4	544.251424	272.629350	527.224875	264.116076	526.240859	263.624068	W	***1002.544101***	501.775689	985.517552	493.262414	984.533536	492.770406	8
5	645.299103	323.153190	628.272554	314.639915	627.288538	314.147907	T	***816.464788***	408.736032	799.438239	400.222758	798.454223	399.730750	7
6	716.336217	358.671747	699.309668	350.158472	698.325652	349.666464	A	***715.417109***	358.212193	698.390560	349.698918			6
7	829.420281	415.213779	812.393732	406.700504	811.409716	406.208496	I	644.379995	322.693636	627.353446	314.180361			5
8	1003.466580	502.236928	986.440031	493.723654	985.456015	493.231646	C	***531.295931***	266.151604	514.269382	257.638329			4
9	1100.519344	550.763310	1083.492795	542.250036	1082.508779	541.758028	P	***357.249632***	179.128454	340.223083	170.615179			3
10	1213.603408	607.305342	1196.576859	598.792068	1195.592843	598.300059	L	260.196868	130.602072	243.170319	122.088797			2
11							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.5	1358.701645	-0.001577	TQQWTAICPLK

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

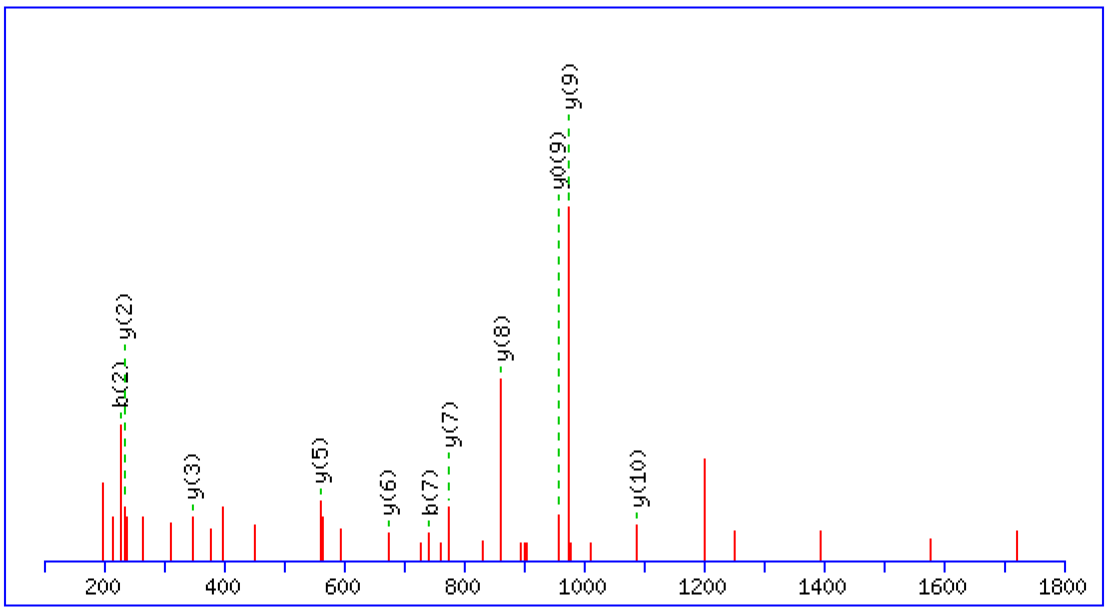
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLLSTLTLLSK**
Found in **GNA1_HUMAN**, Glucosamine 6-phosphate N-acetyltransferase OS=Homo sapiens GN=GNPNAT1 PE=1 SV=1

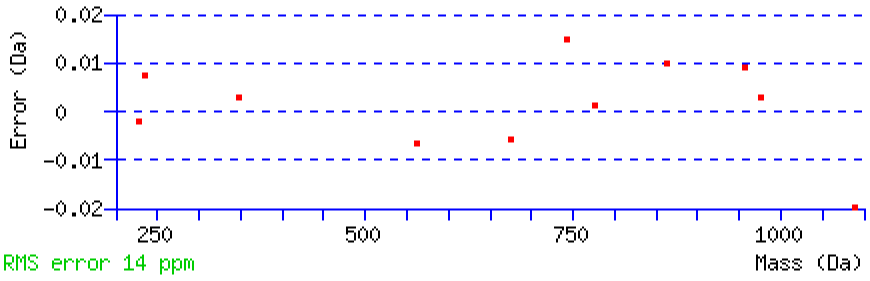
Match to Query 30381: 1200.772008 from(601.393280,2+) rtinseconds(3729) index(51331)
Title: Locus:1.1.1.2569.10
Data file 2011-11-12 - TFD - EP 6-6.mgf

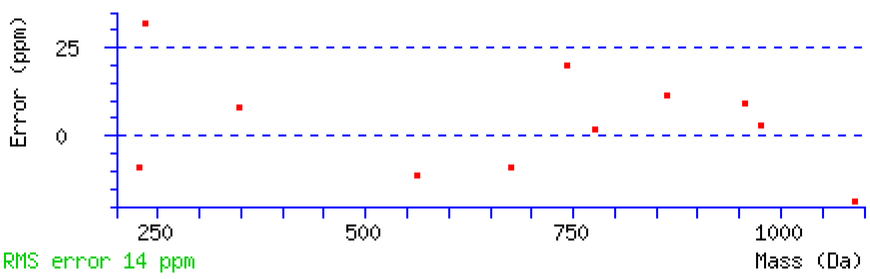
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1200.769302
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 58 **Expect:** 1.4e-006
Matches : 11/92 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							11
2	**227.175404**	114.091340			L	***1088.692538***	544.849907	1071.665989	536.336633	1070.681973	535.844625	10
3	340.259468	170.633372			L	***975.608474***	488.307875	958.581925	479.794601	957.597909	479.302593	9
4	427.291496	214.149386	409.280931	205.144104	S	***862.524410***	431.765843	845.497861	423.252569	844.513845	422.760561	8
5	528.339175	264.673226	510.328610	255.667943	T	***775.492382***	388.249829	758.465833	379.736555	757.481817	379.244547	7
6	641.423239	321.215258	623.412674	312.209975	L	***674.444703***	337.725990	657.418154	329.212715	656.434138	328.720707	6
7	**742.470918**	371.739097	724.460353	362.733815	T	***561.360639***	281.183958	544.334090	272.670683	543.350074	272.178675	5
8	855.554982	428.281129	837.544417	419.275847	L	460.312960	230.660118	443.286411	222.146843	442.302395	221.654835	4
9	968.639046	484.823161	950.628481	475.817879	L	***347.228896***	174.118086	330.202347	165.604811	329.218331	165.112803	3
10	1055.671074	528.339175	1037.660509	519.333893	S	***234.144832***	117.576054	217.118283	109.062779	216.134267	108.570771	2
11					K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.4	1200.769302	0.002706	LLLSTLTLLSK

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

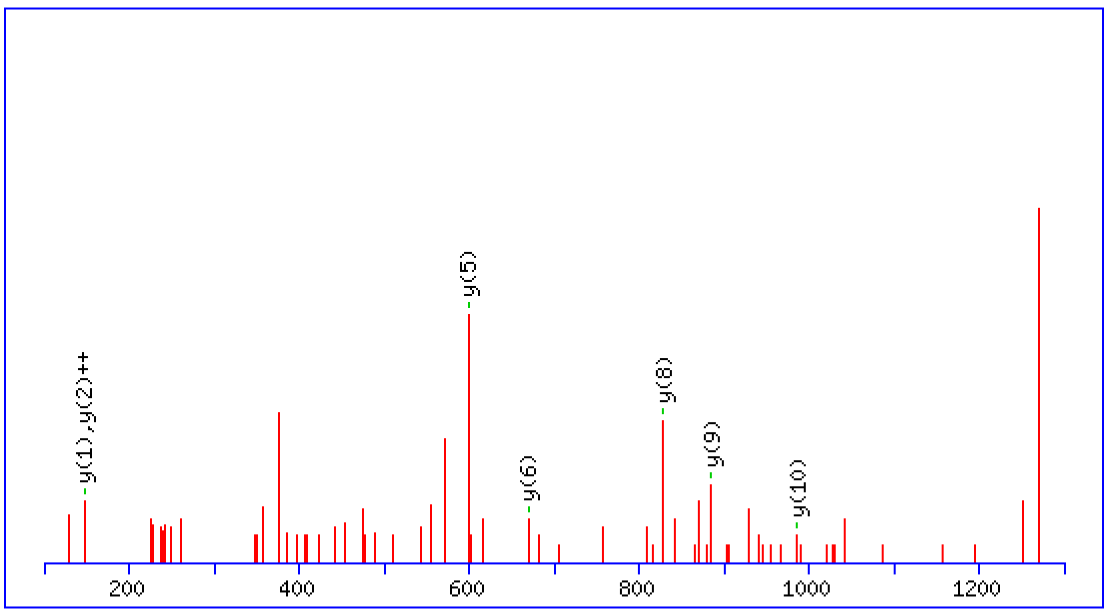
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IAVTGTGAHPAFK**
Found in **GPX7_HUMAN**, Glutathione peroxidase 7 OS=Homo sapiens GN=GPX7 PE=1 SV=1

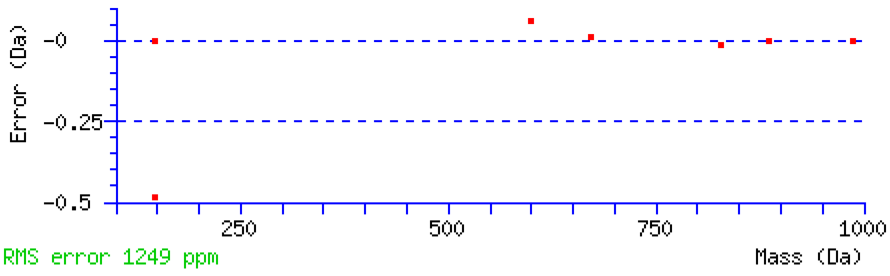
Match to Query 34039: 1268.675868 from(635.345210,2+) rtinseconds(1686) index(15853)
Title: Locus:1.1.1.2136.43
Data file 2011-11-10 - TFD - EP 4-2.mgf

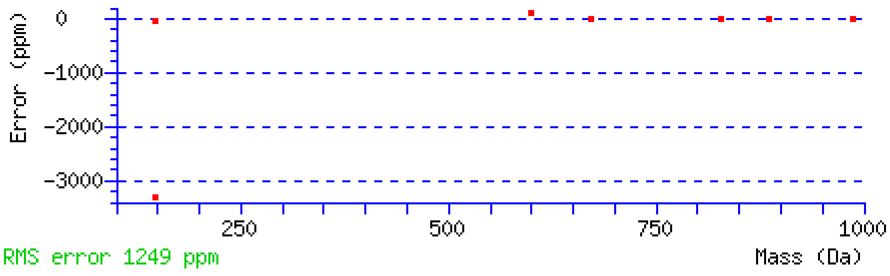
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1268.687729
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 37  Expect: 0.0043
Matches : 7/100 fragment ions using 12 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							13
2	185.128454	93.067865			A	1156.610936	578.809106	1139.584387	570.295832	1138.600371	569.803824	12
3	284.196868	142.602072			V	1085.573822	543.290549	1068.547273	534.777275	1067.563257	534.285267	11
4	385.244547	193.125912	367.233982	184.120629	T	***986.505408***	493.756342	969.478859	485.243068	968.494843	484.751060	10
5	442.266011	221.636643	424.255446	212.631361	G	***885.457729***	443.232503	868.431180	434.719228	867.447164	434.227220	9
6	543.313690	272.160483	525.303125	263.155201	T	***828.436265***	414.721771	811.409716	406.208496	810.425700	405.716488	8
7	600.335154	300.671215	582.324589	291.665933	G	727.388586	364.197931	710.362037	355.684657			7
8	671.372268	336.189772	653.361703	327.184490	A	***670.367122***	335.687199	653.340573	327.173925			6
9	808.431180	404.719228	790.420615	395.713946	H	***599.330008***	300.168642	582.303459	291.655368			5
10	905.483944	453.245610	887.473379	444.240328	P	462.271096	231.639186	445.244547	223.125912			4
11	976.521058	488.764167	958.510493	479.758885	A	365.218332	183.112804	348.191783	174.599530			3
12	1123.589472	562.298374	1105.578907	553.293092	F	294.181218	147.594247	277.154669	139.080973			2
13					K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.0	1268.687729	-0.011861	IAVTGTGAHPAFK
5.2	1268.665924	0.009944	LSAPVSQKMHR
3.8	1268.672440	0.003428	QLSLPQQEAQK
2.8	1268.679855	-0.003987	ASAQVVMPPIPK
2.8	1268.679855	-0.003987	ASAQVVMPPIPK
2.8	1268.679855	-0.003987	ASAQVVMPPIPK
1.5	1268.683685	-0.007817	KIPSQQDALGGR
1.4	1268.687698	-0.011830	ERIWPALQPK
1.2	1268.679855	-0.003987	ASAQVVMPPIPK
1.2	1268.683685	-0.007817	KPPSGSQAPRTK

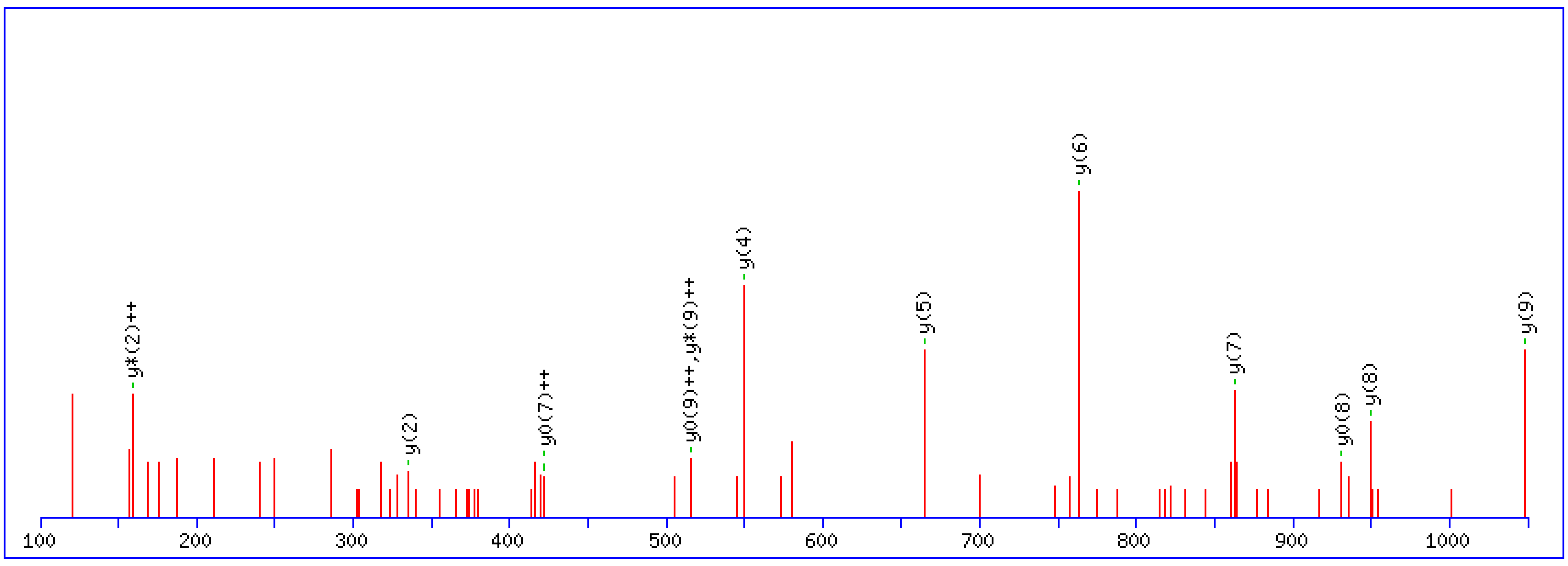
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VPTPDVSVVDLTCR**
Found in **G3PT_HUMAN**, Glyceraldehyde-3-phosphate dehydrogenase, testis-specific OS=Homo sapiens GN=GAPDHS PE=1 SV=2

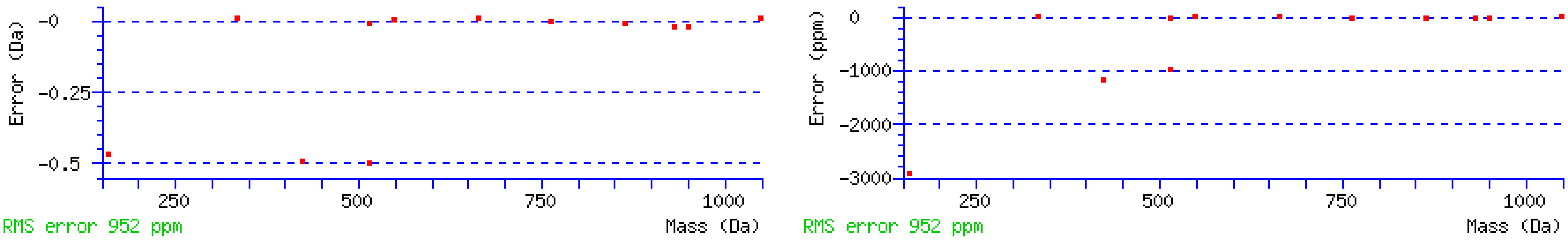
Match to Query 47315: 1572.786252 from(525.269360,3+) rtinseconds(2025) index(23178)
Title: Locus:1.1.1.1153.19
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 2.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1572.781799
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
P4      : Oxidation (P)
Ions Score: 43  Expect: 0.00016
Matches : 12/122 fragment ions using 19 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	100.075690	50.541483			V							14
2	197.128454	99.067865			P	1474.720622	737.863949	1457.694073	729.350674	1456.710057	728.858666	13
3	298.176133	149.591704	280.165568	140.586422	T	1377.667858	689.337567	1360.641309	680.824293	1359.657293	680.332285	12
4	411.223812	206.115544	393.213247	197.110262	P	1276.620179	638.813727	1259.593630	630.300453	1258.609614	629.808445	11
5	526.250755	263.629016	508.240190	254.623733	D	1163.572500	582.289888	1146.545951	573.776614	1145.561935	573.284606	10
6	625.319169	313.163223	607.308604	304.157940	V	***1048.545557***	524.776416	1031.519008	516.263142	1030.534992	515.771134	9
7	712.351197	356.679237	694.340632	347.673954	S	***949.477143***	475.242210	932.450594	466.728935	931.466578	466.236927	8
8	811.419611	406.213443	793.409046	397.208161	V	***862.445115***	431.726196	845.418566	423.212921	844.434550	422.720913	7
9	910.488025	455.747650	892.477460	446.742368	V	***763.376701***	382.191989	746.350152	373.678714	745.366136	373.186706	6
10	1025.514968	513.261122	1007.504403	504.255839	D	***664.308287***	332.657782	647.281738	324.144507	646.297722	323.652499	5
11	1138.599032	569.803154	1120.588467	560.797871	L	***549.281344***	275.144310	532.254795	266.631036	531.270779	266.139028	4
12	1239.646711	620.326993	1221.636146	611.321711	T	436.197280	218.602278	419.170731	210.089003	418.186715	209.596995	3
13	1399.677360	700.342318	1381.666795	691.337035	C	***335.149601***	168.078438	318.123052	159.565164			2
14					R	175.118952	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
43.0	1572.781799	0.004453	VPTPDVSVVDLTCR
43.0	1572.781799	0.004453	VPTPDVSVVDLTCR
2.5	1572.785782	0.000470	TSMASLFSFTSPAVK
2.0	1572.775223	0.011029	KPNAVPKACCAPTK

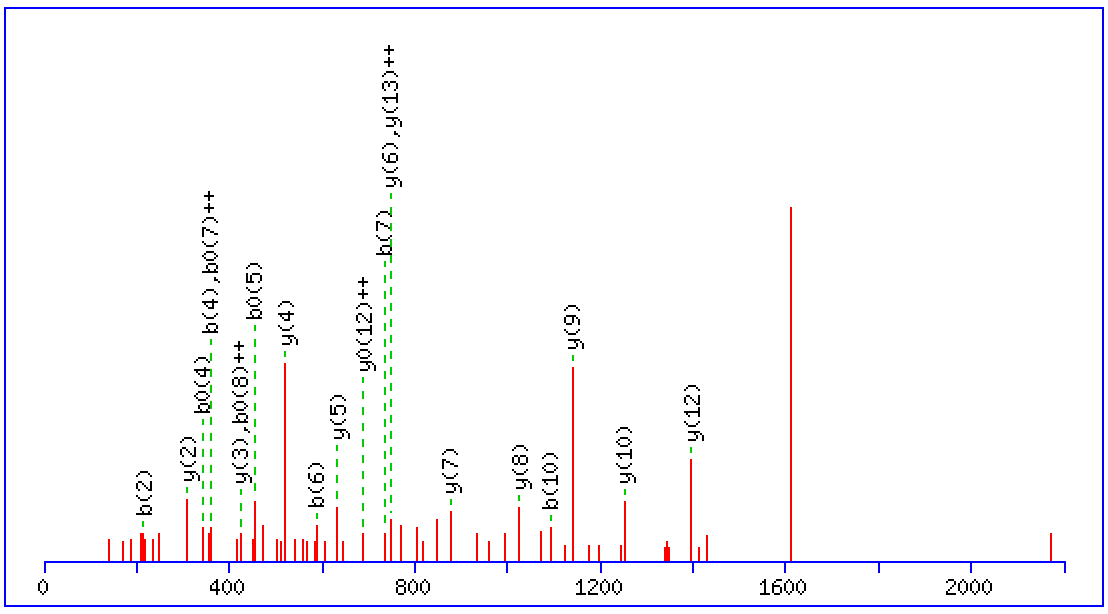
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DVGSLDFEDLPLYK**
Found in **GDPD3_HUMAN**, Glycerophosphodiester phosphodiesterase domain-containing protein 3 OS=Homo sapiens GN=GDPD3 PE=2 SV=3

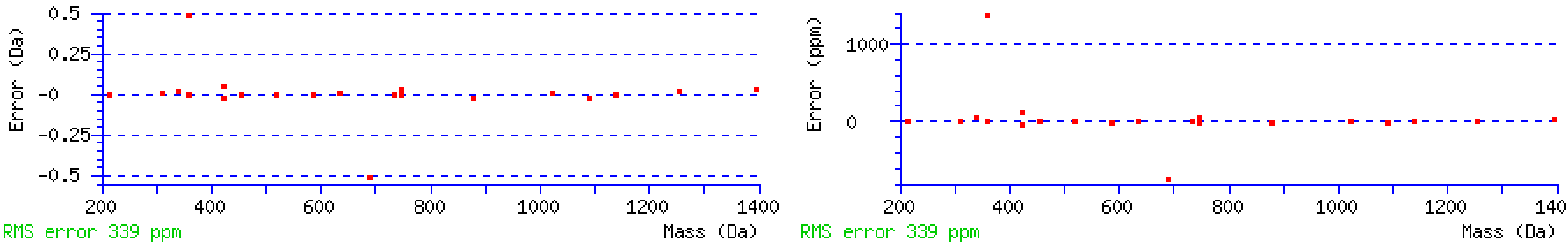
Match to Query 52476: 1609.791548 from(805.903050,2+) rtinseconds(3734) index(55359)
Title: Locus:1.1.1.2801.36
Data file 2011-11-14 - TFD - EP 8-4.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1609.787552
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 80 **Expect:** 1.3e-007
Matches : 21/120 fragment ions using 26 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	116.034219	58.520748	98.023654	49.515465	D							14
2	**215.102633**	108.054954	197.092068	99.049672	V	1495.767888	748.387582	1478.741339	739.874307	1477.757323	739.382299	13
3	272.124097	136.565687	254.113532	127.560404	G	***1396.699474***	698.853375	1379.672925	690.340101	1378.688909	689.848093	12
4	**359.156125**	180.081701	341.145560	171.076418	S	1339.678010	670.342643	1322.651461	661.829368	1321.667445	661.337360	11
5	472.240189	236.623733	454.229624	227.618450	L	***1252.645982***	626.826629	1235.619433	618.313354	1234.635417	617.821346	10
6	**587.267132**	294.137204	569.256567	285.131922	D	***1139.561918***	570.284597	1122.535369	561.771323	1121.551353	561.279314	9
7	**734.335546**	367.671411	716.324981	358.666129	F	***1024.534975***	512.771125	1007.508426	504.257851	1006.524410	503.765843	8
8	863.378139	432.192708	845.367574	423.187425	E	***877.466561***	439.236919	860.440012	430.723644	859.455996	430.231636	7
9	978.405082	489.706179	960.394517	480.700897	D	***748.423968***	374.715622	731.397419	366.202347	730.413403	365.710339	6
10	**1091.489146**	546.248211	1073.478581	537.242928	L	***633.397025***	317.202151	616.370476	308.688876			5
11	1188.541910	594.774593	1170.531345	585.769310	P	***520.312961***	260.660119	503.286412	252.146844			4
12	1301.625974	651.316625	1283.615409	642.311342	L	***423.260197***	212.133736	406.233648	203.620462			3
13	1464.689303	732.848289	1446.678738	723.843007	Y	***310.176133***	155.591705	293.149584	147.078430			2
14					K	147.112804	74.060040	130.086255	65.546765			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
79.6	1609.787552	0.003996	DVGSLDFEDLPLYK
8.9	1609.783569	0.007979	TPGPPGLTTTPAPPDK
6.3	1609.783569	0.007979	TPGPPGLTTTPAPPDK
1.7	1609.783569	0.007979	TPGPPGLTTTPAPPDK

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

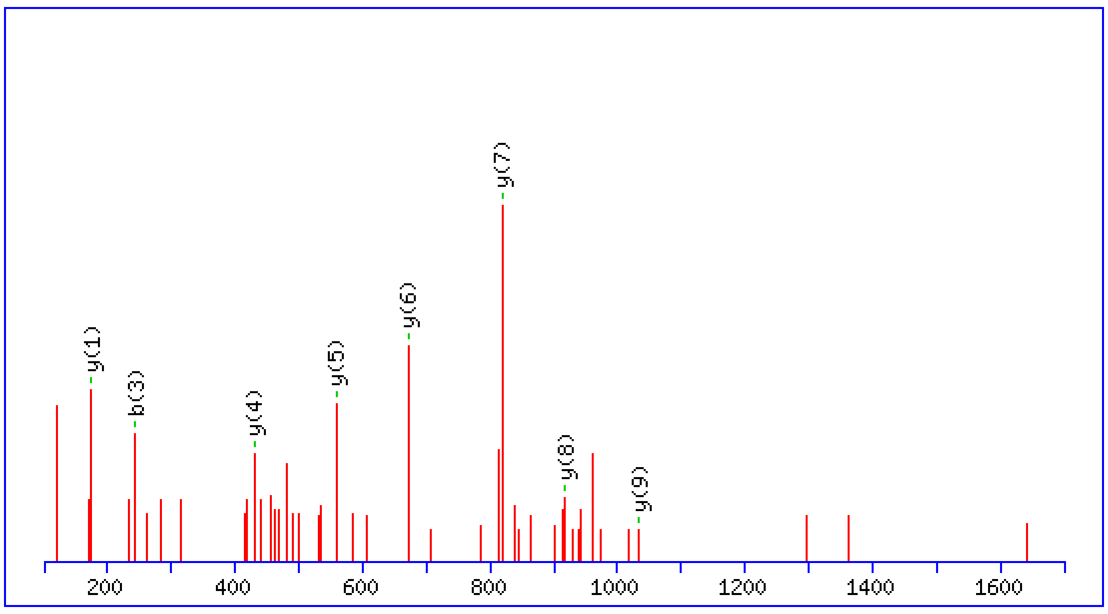
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GADVFLEALAR**
Found in **GYS1_HUMAN**, Glycogen [starch] synthase, muscle OS=Homo sapiens GN=GYS1 PE=1 SV=2

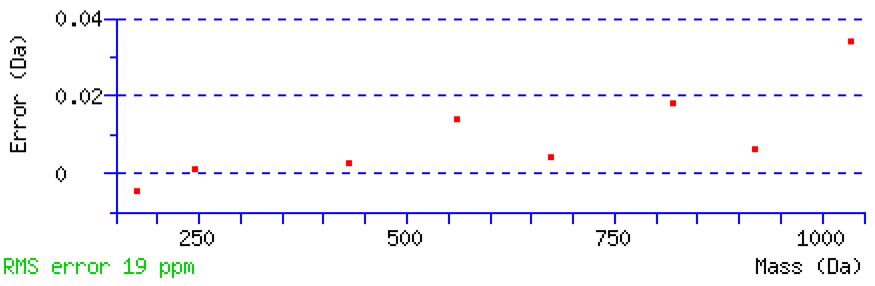
Match to Query 27240: 1160.618528 from(581.316540,2+) rtinseconds(3470) index(49312)
Title: Locus:1.1.1.2704.10
Data file 2011-11-12 - TFD - EP 6-2.mgf

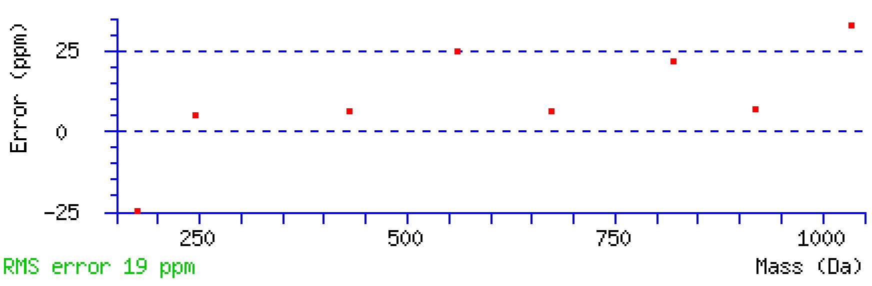
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1700] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1160.618958
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 59 **Expect:** 9e-006
Matches : 8/88 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008			G							11
2	129.065854	65.036565			A	1104.604786	552.806031	1087.578237	544.292757	1086.594221	543.800749	10
3	244.092797	122.550037	226.082232	113.544754	D	***1033.567672***	517.287474	1016.541123	508.774200	1015.557107	508.282192	9
4	343.161211	172.084244	325.150646	163.078961	V	***918.540729***	459.774003	901.514180	451.260728	900.530164	450.768720	8
5	490.229625	245.618450	472.219060	236.613168	F	***819.472315***	410.239796	802.445766	401.726521	801.461750	401.234513	7
6	603.313689	302.160483	585.303124	293.155200	L	***672.403901***	336.705589	655.377352	328.192314	654.393336	327.700306	6
7	732.356282	366.681779	714.345717	357.676497	E	***559.319837***	280.163557	542.293288	271.650282	541.309272	271.158274	5
8	803.393396	402.200336	785.382831	393.195054	A	***430.277244***	215.642260	413.250695	207.128985			4
9	916.477460	458.742368	898.466895	449.737086	L	359.240130	180.123703	342.213581	171.610428			3
10	987.514574	494.260925	969.504009	485.255643	A	246.156066	123.581671	229.129517	115.068396			2
11					R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.6	1160.618958	-0.000430	GADVFLEALAR
4.5	1160.618973	-0.000445	QSSFILTPPR
4.5	1160.618973	-0.000445	QSSFILTPPR
3.3	1160.618958	-0.000430	EIVNFSPIAR
3.1	1160.614914	0.003614	SRLEALSTER
0.7	1160.618973	-0.000445	VTFEGPLLNR

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

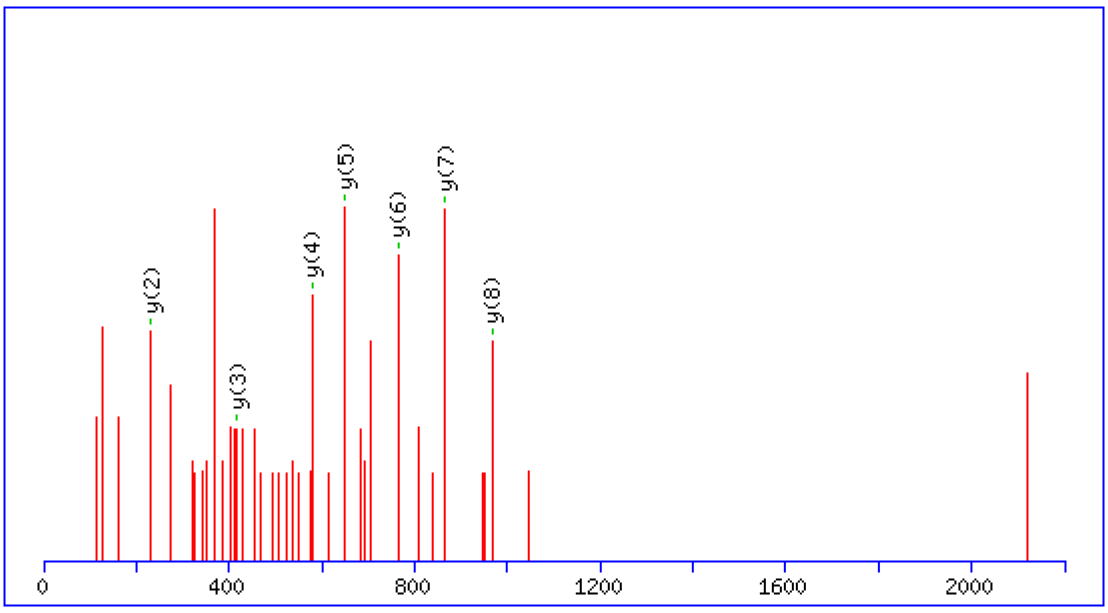
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ITTDACWGR**
Found in **GPHB5_HUMAN**, Glycoprotein hormone beta-5 OS=Homo sapiens GN=GPHB5 PE=1 SV=1

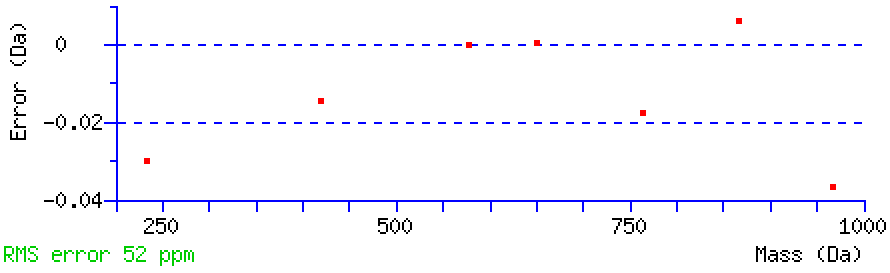
Match to Query 366552: 1078.489828 from(540.252190,2+) rtinseconds(1750) index(671712)
Title: Locus:1.1.1.1334.31
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●

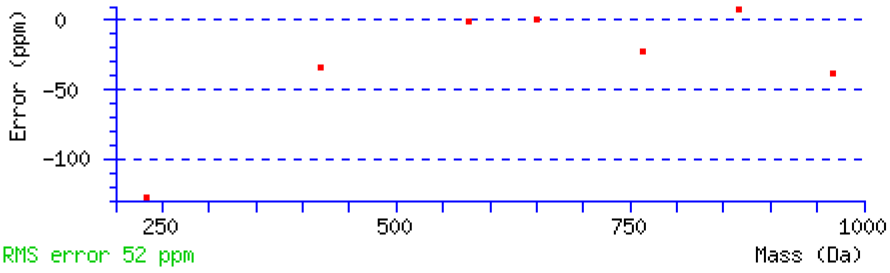


Monoisotopic mass of neutral peptide Mr(calc): 1078.486588
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 60 **Expect:** 5.9e-006
Matches : 7/68 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							9
2	215.139019	108.073147	197.128454	99.067865	T	***966.409793***	483.708535	949.383244	475.195260	948.399228	474.703252	8
3	316.186698	158.596987	298.176133	149.591704	T	***865.362114***	433.184695	848.335565	424.671421	847.351549	424.179413	7
4	431.213641	216.110458	413.203076	207.105176	D	***764.314435***	382.660856	747.287886	374.147581	746.303870	373.655573	6
5	502.250755	251.629015	484.240190	242.623733	A	***649.287492***	325.147384	632.260943	316.634110			5
6	662.281404	331.644340	644.270839	322.639058	C	***578.250378***	289.628827	561.223829	281.115553			4
7	848.360717	424.683997	830.350152	415.678714	W	***418.219729***	209.613503	401.193180	201.100228			3
8	905.382181	453.194729	887.371616	444.189446	G	***232.140416***	116.573846	215.113867	108.060572			2
9					R	175.118952	88.063114	158.092403	79.549840			1



RMS error 52 ppm



RMS error 52 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
60.0	1078.486588	0.003240	ITTDACWGR
4.2	1078.493118	-0.003290	DVGHLPSEPP
3.9	1078.493118	-0.003290	DVGHLPSEPP
0.9	1078.493118	-0.003290	DVGHLPSEPP

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

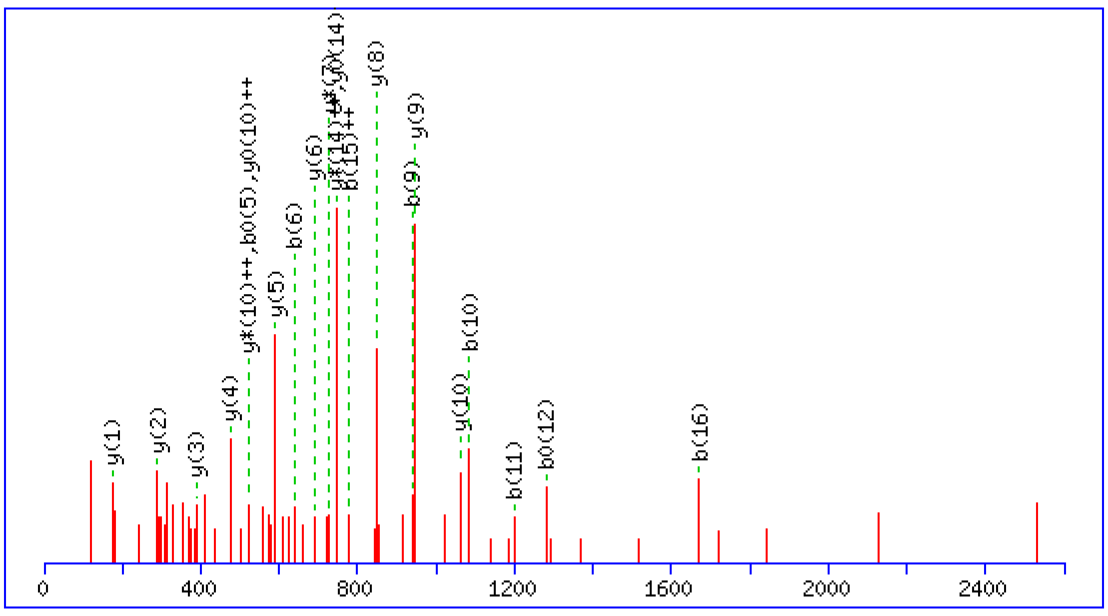
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EPPTDVTPTFLTTGVLSTLR**
Found in **GUAA_HUMAN**, GMP synthase [glutamine-hydrolyzing] OS=Homo sapiens GN=GMPS PE=1 SV=1

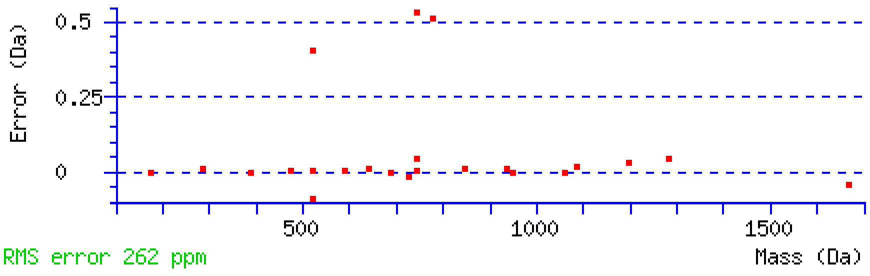
Match to Query 62782: 2144.135592 from(715.719140,3+) rtinseconds(4037) index(58831)
Title: Locus:1.1.1.2978.18
Data file 2011-11-14 - TFD - EP 7-2.mgf

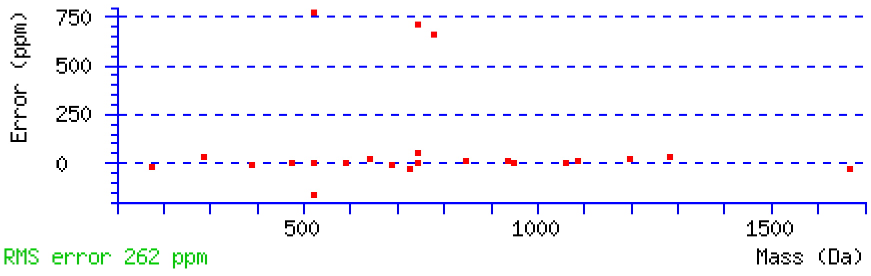
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2144.136536
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 48 **Expect:** 4.1e-005
Matches : 23/186 fragment ions using 41 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	130.049869	65.528572	112.039304	56.523290	E							20
2	227.102633	114.054954	209.092068	105.049672	P	2016.101187	1008.554232	1999.074638	1000.040957	1998.090622	999.548949	19
3	324.155397	162.581336	306.144832	153.576054	P	1919.048423	960.027850	1902.021874	951.514575	1901.037858	951.022567	18
4	425.203076	213.105176	407.192511	204.099894	T	1821.995659	911.501468	1804.969110	902.988193	1803.985094	902.496185	17
5	540.230019	270.618648	522.219454	261.613365	D	1720.947980	860.977628	1703.921431	852.464354	1702.937415	851.972346	16
6	**639.298433**	320.152855	621.287868	311.147572	V	1605.921037	803.464157	1588.894488	794.950882	1587.910472	794.458874	15
7	740.346112	370.676694	722.335547	361.671412	T	1506.852623	753.929950	1489.826074	745.416675	1488.842058	744.924667	14
8	837.398876	419.203076	819.388311	410.197794	P	1405.804944	703.406110	1388.778395	694.892836	1387.794379	694.400828	13
9	**938.446555**	469.726916	920.435990	460.721633	T	1308.752180	654.879728	1291.725631	646.366454	1290.741615	645.874446	12
10	**1085.514969**	543.261123	1067.504404	534.255840	F	1207.704501	604.355888	1190.677952	595.842614	1189.693936	595.350606	11
11	**1198.599033**	599.803155	1180.588468	590.797872	L	***1060.636087***	530.821682	1043.609538	522.308407	1042.625522	521.816399	10
12	1299.646712	650.326994	1281.636147	641.321711	T	***947.552023***	474.279650	930.525474	465.766375	929.541458	465.274367	9
13	1400.694391	700.850834	1382.683826	691.845551	T	***846.504344***	423.755810	829.477795	415.242536	828.493779	414.750528	8
14	1457.715855	729.361565	1439.705290	720.356283	G	***745.456665***	373.231971	728.430116	364.718696	727.446100	364.226688	7
15	1556.784269	778.895773	1538.773704	769.890490	V	***688.435201***	344.721239	671.408652	336.207964	670.424636	335.715956	6
16	**1669.868333**	835.437804	1651.857768	826.432522	L	***589.366787***	295.187032	572.340238	286.673757	571.356222	286.181749	5
17	1756.900361	878.953819	1738.889796	869.948536	S	***476.282723***	238.645000	459.256174	230.131725	458.272158	229.639717	4
18	1857.948040	929.477658	1839.937475	920.472376	T	***389.250695***	195.128986	372.224146	186.615711	371.240130	186.123703	3
19	1971.032104	986.019690	1953.021539	977.014407	L	***288.203016***	144.605146	271.176467	136.091872			2
20					R	***175.118952***	88.063114	158.092403	79.549840			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.0	2144.136536	-0.000944	EPPTDVTPTFLTTGVLSTLR
1.3	2144.127930	0.007662	LRLQQLPWSSPLHPWDR

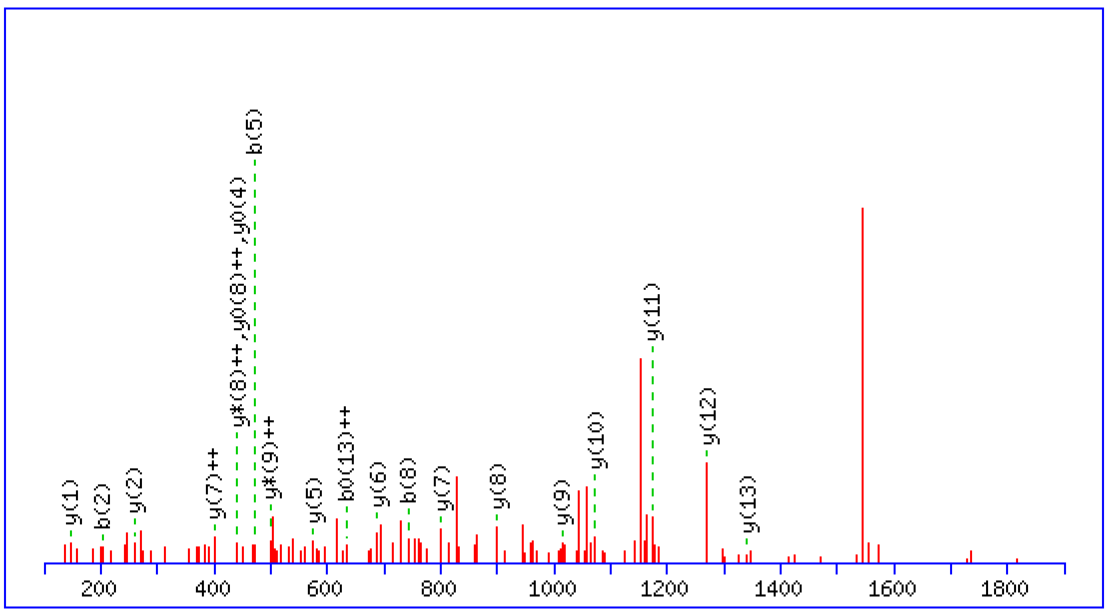
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SDAPTGDVLLDEALK**
Found in **GOLP3_HUMAN**, Golgi phosphoprotein 3 OS=Homo sapiens GN=GOLPH3 PE=1 SV=1

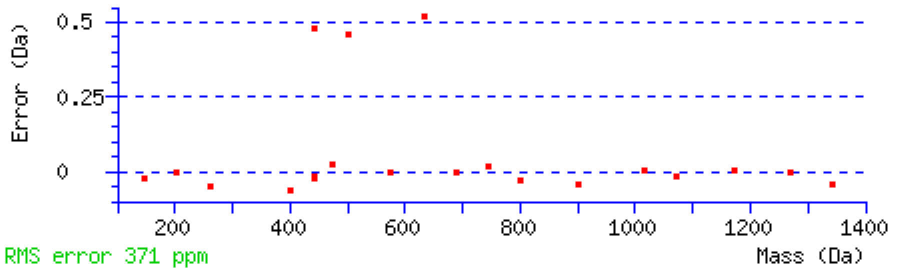
Match to Query 48069: 1542.784848 from(772.399700,2+) rtinseconds(3094) index(43667)
Title: Locus:1.1.1.2502.38
Data file 2011-11-10 - TFD - EP 4-4.mgf

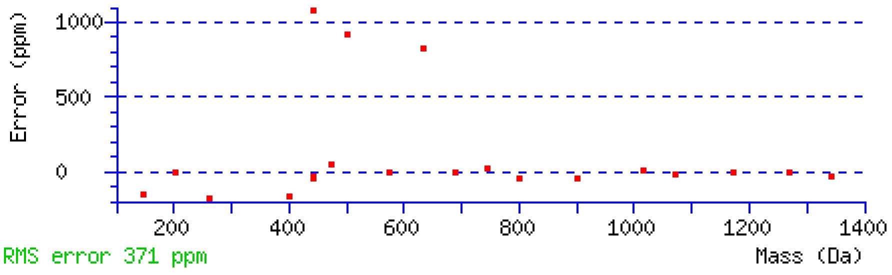
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1542.777710
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 40  Expect: 0.0012
Matches : 20/134 fragment ions using 64 most intense peaks   (help)
```

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	S							15
2	**203.066247**	102.036761	185.055682	93.031479	D	1456.752967	728.880122	1439.726418	720.366847	1438.742402	719.874839	14
3	274.103361	137.555319	256.092796	128.550036	A	***1341.726024***	671.366650	1324.699475	662.853376	1323.715459	662.361368	13
4	371.156125	186.081701	353.145560	177.076418	P	***1270.688910***	635.848093	1253.662361	627.334819	1252.678345	626.842811	12
5	**472.203804**	236.605540	454.193239	227.600258	T	***1173.636146***	587.321711	1156.609597	578.808437	1155.625581	578.316429	11
6	529.225268	265.116272	511.214703	256.110990	G	***1072.588467***	536.797872	1055.561918	528.284597	1054.577902	527.792589	10
7	644.252211	322.629744	626.241646	313.624461	D	***1015.567003***	508.287140	998.540454	499.773865	997.556438	499.281857	9
8	**743.320625**	372.163951	725.310060	363.158668	V	***900.540060***	450.773668	883.513511	442.260394	882.529495	441.768386	8
9	856.404689	428.705983	838.394124	419.700700	L	***801.471646***	401.239461	784.445097	392.726187	783.461081	392.234179	7
10	969.488753	485.248015	951.478188	476.242732	L	***688.387582***	344.697429	671.361033	336.184155	670.377017	335.692147	6
11	1084.515696	542.761486	1066.505131	533.756204	D	***575.303518***	288.155397	558.276969	279.642123	557.292953	279.150115	5
12	1213.558289	607.282783	1195.547724	598.277500	E	460.276575	230.641925	443.250026	222.128651	442.266010	221.636643	4
13	1284.595403	642.801340	1266.584838	633.796057	A	331.233982	166.120629	314.207433	157.607354			3
14	1397.679467	699.343372	1379.668902	690.338089	L	***260.196868***	130.602072	243.170319	122.088797			2
15					K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.3	1542.777710	0.007138	SDAPTGDVLLDEALK
10.0	1542.792938	-0.008090	ISEGLPALEFPNEK
5.8	1542.788940	-0.004092	NSSTIIQNPVETPK
3.6	1542.771179	0.013669	ATPTPVTPEMERAK
3.0	1542.771225	0.013623	VSSPVMVAQGGGPTPK
2.6	1542.788940	-0.004092	NSSTIIQNPVETPK
2.2	1542.771179	0.013669	ATPTPVTPEMERAK

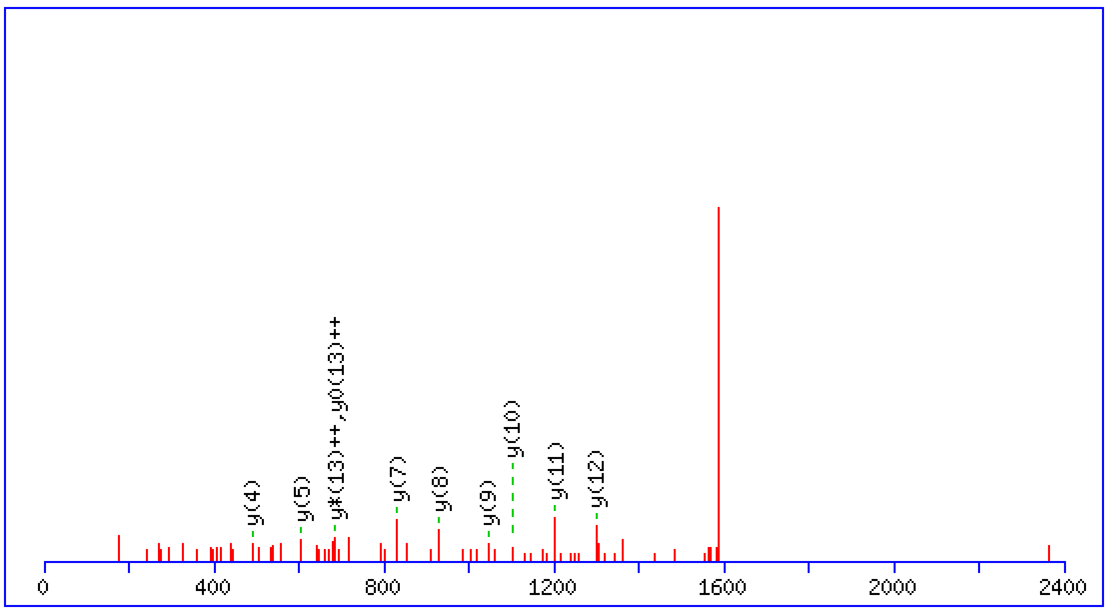
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SDSPTGDVLLDETLK**
Found in **GLP3L_HUMAN**, Golgi phosphoprotein 3-like OS=Homo sapiens GN=GOLPH3L PE=1 SV=1

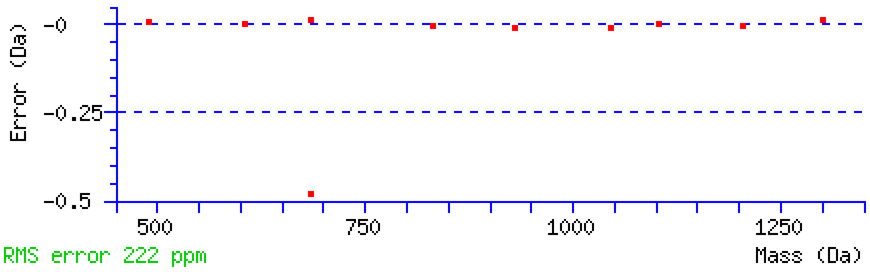
Match to Query 50552: 1588.791808 from(795.403180,2+) rtinseconds(2882) index(39263)
Title: Locus:1.1.1.2438.44
Data file 2011-11-10 - TFD - EP 3-4.mgf

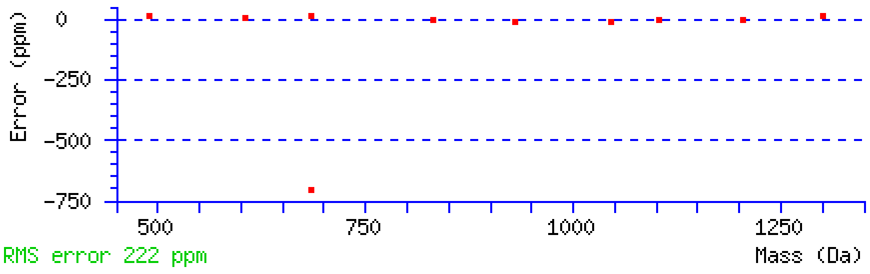
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1588.783203
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 58 **Expect:** 2.3e-005
Matches : 10/136 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	S							15
2	203.066247	102.036761	185.055682	93.031479	D	1502.758446	751.882861	1485.731897	743.369587	1484.747881	742.877579	14
3	290.098275	145.552776	272.087710	136.547493	S	1387.731503	694.369390	1370.704954	685.856115	1369.720938	685.364107	13
4	387.151039	194.079158	369.140474	185.073875	P	***1300.699475***	650.853376	1283.672926	642.340101	1282.688910	641.848093	12
5	488.198718	244.602997	470.188153	235.597715	T	***1203.646711***	602.326994	1186.620162	593.813719	1185.636146	593.321711	11
6	545.220182	273.113729	527.209617	264.108447	G	***1102.599032***	551.803154	1085.572483	543.289880	1084.588467	542.797872	10
7	660.247125	330.627201	642.236560	321.621918	D	***1045.577568***	523.292422	1028.551019	514.779148	1027.567003	514.287139	9
8	759.315539	380.161408	741.304974	371.156125	V	***930.550625***	465.778951	913.524076	457.265676	912.540060	456.773668	8
9	872.399603	436.703440	854.389038	427.698157	L	***831.482211***	416.244744	814.455662	407.731469	813.471646	407.239461	7
10	985.483667	493.245472	967.473102	484.240189	L	718.398147	359.702712	701.371598	351.189437	700.387582	350.697429	6
11	1100.510610	550.758943	1082.500045	541.753661	D	***605.314083***	303.160680	588.287534	294.647405	587.303518	294.155397	5
12	1229.553203	615.280240	1211.542638	606.274957	E	***490.287140***	245.647208	473.260591	237.133934	472.276575	236.641926	4
13	1330.600882	665.804079	1312.590317	656.798797	T	361.244547	181.125911	344.217998	172.612637	343.233982	172.120629	3
14	1443.684946	722.346111	1425.674381	713.340829	L	260.196868	130.602072	243.170319	122.088797			2
15					K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
57.9	1588.783203	0.008605	SDSPTGDVLLDETLK

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

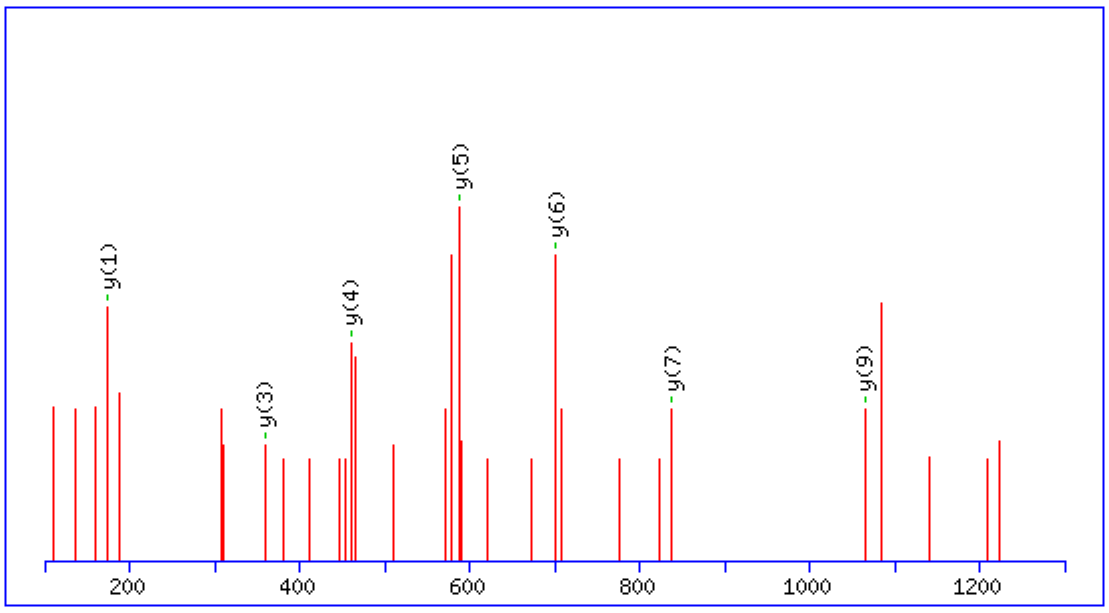
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YDVQHLQTALR**
Found in **GOSR2_HUMAN**, Golgi SNAP receptor complex member 2 OS=Homo sapiens GN=GOSR2 PE=1 SV=2

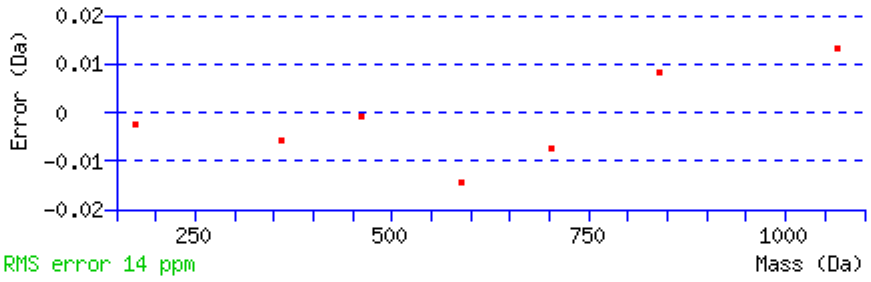
Match to Query 34047: 1342.698252 from(448.573360,3+) rtinseconds(2183) index(21242)
Title: Locus:1.1.1.2453.6
Data file 2011-11-10 - TFD - EP 3-5.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●

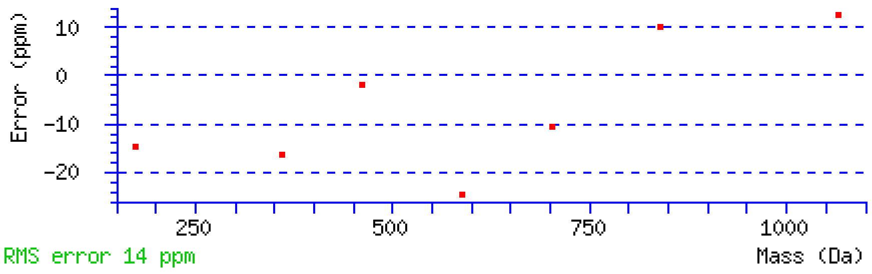


```
Monoisotopic mass of neutral peptide Mr(calc): 1342.699341
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 32  Expect: 0.0013
Matches : 7/106 fragment ions using 20 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.070605	82.538940					Y							11
2	279.097548	140.052412			261.086983	131.047130	D	1180.643298	590.825287	1163.616749	582.312013	1162.632733	581.820004	10
3	378.165962	189.586619			360.155397	180.581337	V	***1065.616355***	533.311815	1048.589806	524.798541	1047.605790	524.306533	9
4	506.224540	253.615908	489.197991	245.102634	488.213975	244.610626	Q	966.547941	483.777609	949.521392	475.264334	948.537376	474.772326	8
5	643.283452	322.145364	626.256903	313.632090	625.272887	313.140087	H	***838.489363***	419.748319	821.462814	411.235045	820.478798	410.743037	7
6	756.367516	378.687396	739.340967	370.174122	738.356951	369.682114	L	***701.430451***	351.218864	684.403902	342.705589	683.419886	342.213581	6
7	884.426094	442.716685	867.399545	434.203411	866.415529	433.711403	Q	***588.346387***	294.676831	571.319838	286.163557	570.335822	285.671549	5
8	985.473773	493.240525	968.447224	484.727250	967.463208	484.235242	T	***460.287809***	230.647542	443.261260	222.134268	442.277244	221.642260	4
9	1056.510887	528.759082	1039.484338	520.245807	1038.500322	519.753799	A	***359.240130***	180.123703	342.213581	171.610428			3
10	1169.594951	585.301114	1152.568402	576.787839	1151.584386	576.295831	L	288.203016	144.605146	271.176467	136.091871			2
11							R	***175.118952***	88.063114	158.092403	79.549839			1



RMS error 14 ppm



RMS error 14 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.2	1342.699341	-0.001089	YDVQHLQTALR
1.3	1342.709229	-0.010977	DLEVLEGGAATLR

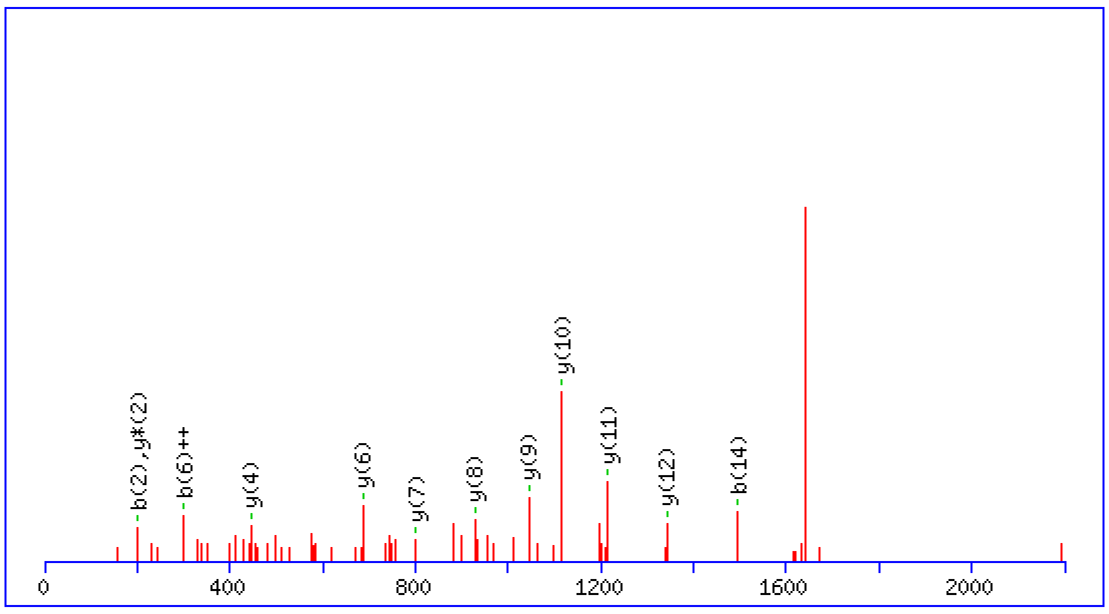
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AEVEVADELLENLAK**
Found in **GET4_HUMAN**, Golgi to ER traffic protein 4 homolog OS=Homo sapiens GN=GET4 PE=1 SV=1

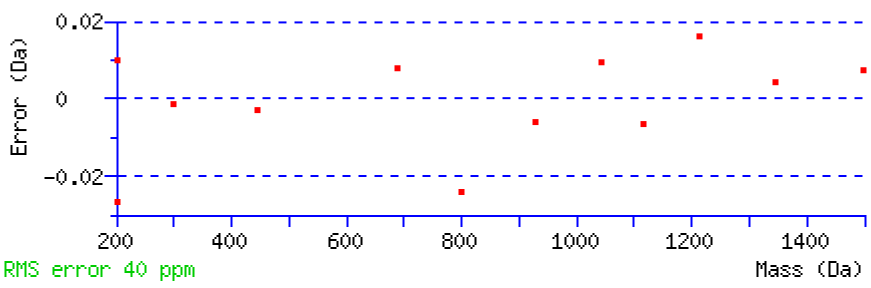
Match to Query 53138: 1641.854108 from(821.934330,2+) rtinseconds(3897) index(57768)
Title: Locus:1.1.1.2893.32
Data file 2011-11-12 - TFD - EP 5-4.mgf

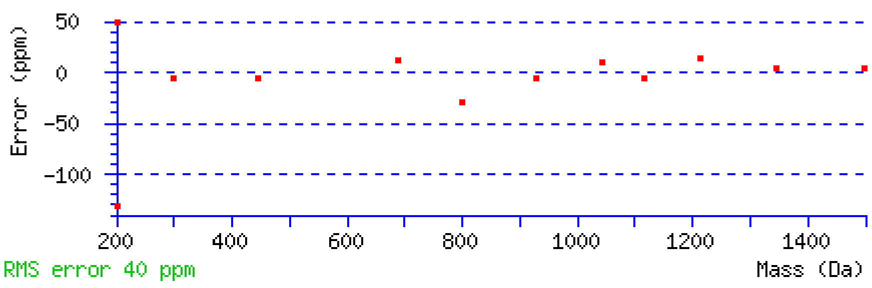
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1641.846085
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 67  Expect: 1.2e-006
Matches : 13/136 fragment ions using 14 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							15
2	**201.086983**	101.047130			183.076418	92.041847	E	1571.816294	786.411785	1554.789745	777.898510	1553.805729	777.406502	14
3	**300.155397**	150.581336			282.144832	141.576054	V	1442.773701	721.890488	1425.747152	713.377214	1424.763136	712.885206	13
4	429.197990	215.102633			411.187425	206.097351	E	***1343.705287***	672.356281	1326.678738	663.843007	1325.694722	663.350999	12
5	528.266404	264.636840			510.255839	255.631558	V	***1214.662694***	607.834985	1197.636145	599.321710	1196.652129	598.829702	11
6	599.303518	300.155397			581.292953	291.150115	A	***1115.594280***	558.300778	1098.567731	549.787503	1097.583715	549.295495	10
7	714.330461	357.668869			696.319896	348.663586	D	***1044.557166***	522.782221	1027.530617	514.268946	1026.546601	513.776938	9
8	843.373054	422.190165			825.362489	413.184883	E	***929.530223***	465.268749	912.503674	456.755475	911.519658	456.263467	8
9	956.457118	478.732197			938.446553	469.726915	L	***800.487630***	400.747453	783.461081	392.234178	782.477065	391.742170	7
10	1069.541182	535.274229			1051.530617	526.268946	L	***687.403566***	344.205421	670.377017	335.692146	669.393001	335.200138	6
11	1198.583775	599.795525			1180.573210	590.790243	E	574.319502	287.663389	557.292953	279.150114	556.308937	278.658106	5
12	1312.626702	656.816989	1295.600153	648.303714	1294.616137	647.811706	N	***445.276909***	223.142092	428.250360	214.628818			4
13	1425.710766	713.359021	1408.684217	704.845746	1407.700201	704.353738	L	331.233982	166.120629	314.207433	157.607354			3
14	**1496.747880**	748.877578	1479.721331	740.364303	1478.737315	739.872295	A	218.149918	109.578597	201.123369	101.065322			2
15							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
66.5	1641.846085	0.008023	AEVEVADELLENLAK
3.3	1641.857346	-0.003238	SPALQDLSQPEGLKK
0.4	1641.846100	0.008008	ALDIDLDKPLADSEK

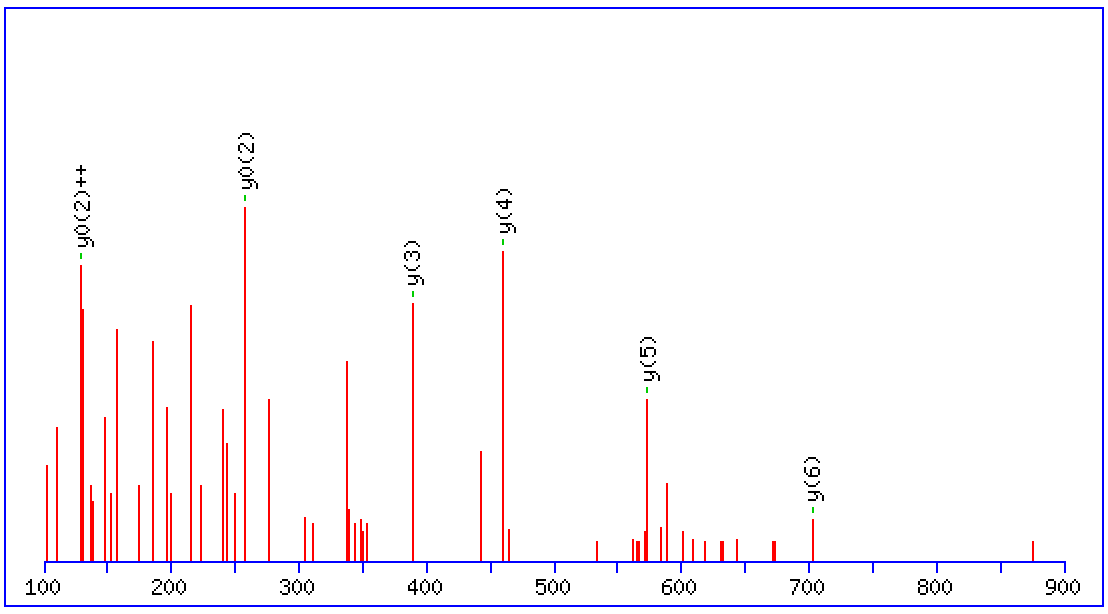
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LEIALEK**
Found in **GOGA1_HUMAN**, Golgin subfamily A member 1 OS=Homo sapiens GN=GOLGA1 PE=1 SV=3

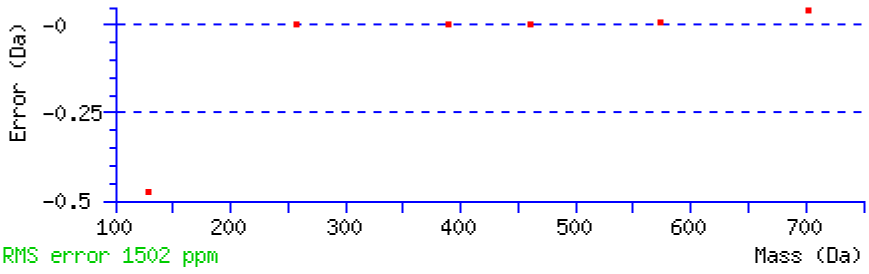
Match to Query 1212: 814.482148 from(408.248350,2+) rtinseconds(2090) index(24692)
Title: Locus:1.1.1.2114.3
Data file 2011-11-12 - TFD - EP 6-1.mgf

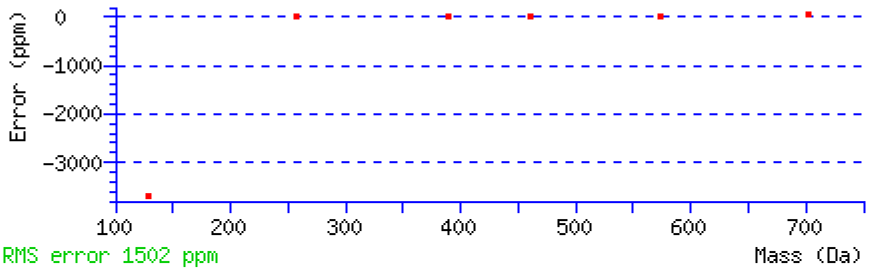
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 814.479980
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 33  Expect: 0.0026
Matches : 6/56 fragment ions using 7 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							7
2	243.133933	122.070605	225.123368	113.065322	E	***702.403232***	351.705254	685.376683	343.191980	684.392667	342.699972	6
3	356.217997	178.612637	338.207432	169.607354	I	***573.360639***	287.183958	556.334090	278.670683	555.350074	278.178675	5
4	427.255111	214.131193	409.244546	205.125911	A	***460.276575***	230.641925	443.250026	222.128651	442.266010	221.636643	4
5	540.339175	270.673226	522.328610	261.667943	L	***389.239461***	195.123369	372.212912	186.610094	371.228896	186.118086	3
6	669.381768	335.194522	651.371203	326.189240	E	276.155397	138.581336	259.128848	130.068062	258.144832	129.576054	2
7					K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.1	814.479980	0.002168	LEIALEK
28.2	814.479980	0.002168	LIEALEK
19.4	814.479980	0.002168	ELLALEK
17.6	814.479980	0.002168	LEALLEK
11.2	814.479980	0.002168	ELLLAEK
10.3	814.480011	0.002137	DVVLLEK
9.0	814.479996	0.002152	LEPIISK
8.6	814.480011	0.002137	VDLVLEK
7.4	814.479980	0.002168	IILEAEK
7.4	814.480011	0.002137	ILVDVEK

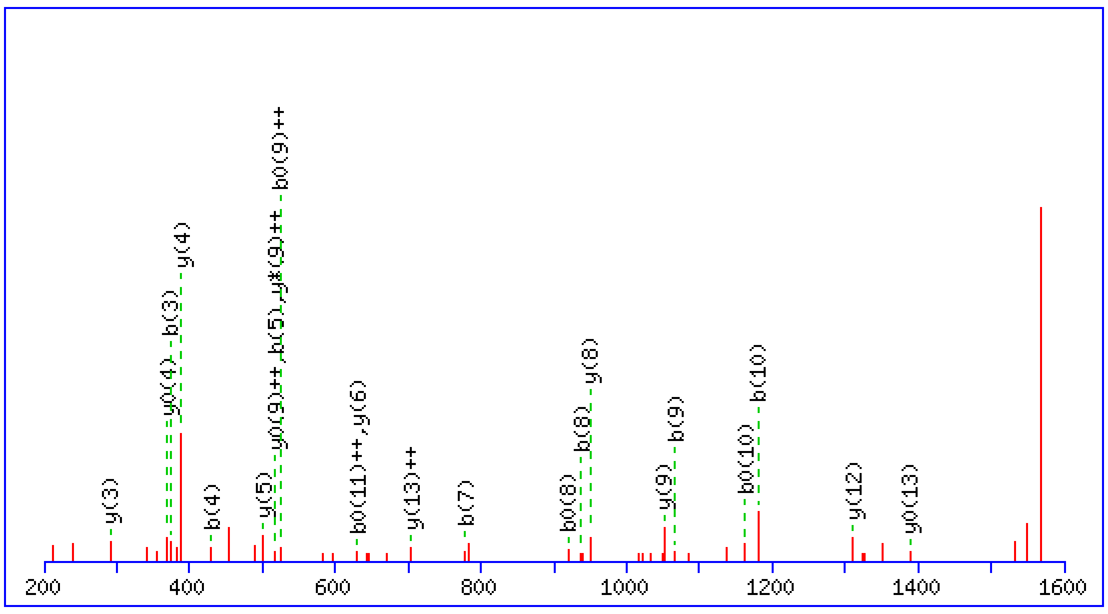
Mascot Search Results

Peptide View

MS/MS Fragmentation of **CPDGSTCCELPSGK**
Found in **GRN_HUMAN**, Granulins OS=Homo sapiens GN=GRN PE=1 SV=2

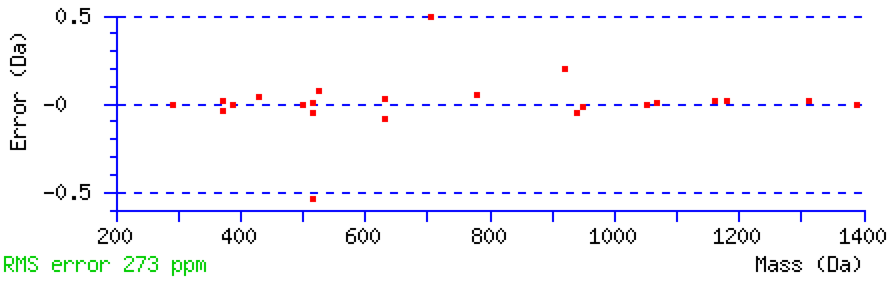
Match to Query 887303: 1566.611448 from(784.313000,2+) rtinseconds(1385) index(251100)
Title: Locus:1.1.1.971.44
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●

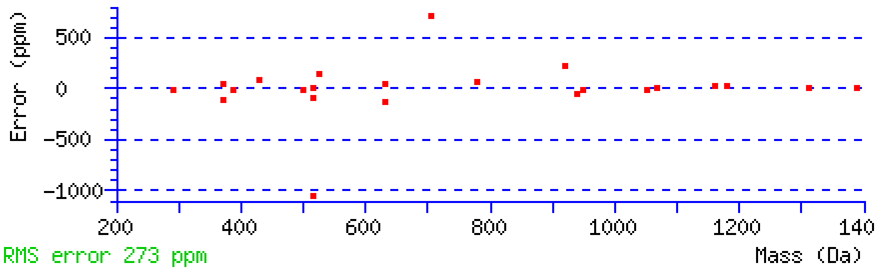


Monoisotopic mass of neutral peptide Mr(calc): 1566.611282
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 47 **Expect:** 2.9e-005
Matches : 23/122 fragment ions using 39 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	161.037925	81.022600			C							14
2	258.090689	129.548982			P	1407.587893	704.297585	1390.561344	695.784310	1389.577328	695.292302	13
3	***373.117632***	187.062454	355.107067	178.057172	D	***1310.535129***	655.771203	1293.508580	647.257928	1292.524564	646.765920	12
4	***430.139096***	215.573186	412.128531	206.567904	G	1195.508186	598.257731	1178.481637	589.744457	1177.497621	589.252449	11
5	***517.171124***	259.089200	499.160559	250.083918	S	1138.486722	569.746999	1121.460173	561.233725	1120.476157	560.741717	10
6	618.218803	309.613040	600.208238	300.607757	T	***1051.454694***	526.230985	1034.428145	517.717711	1033.444129	517.225703	9
7	***778.249452***	389.628364	760.238887	380.623082	C	***950.407015***	475.707146	933.380466	467.193871	932.396450	466.701863	8
8	***938.280101***	469.643689	920.269536	460.638406	C	790.376366	395.691821	773.349817	387.178547	772.365801	386.686539	7
9	***1067.322694***	534.164985	1049.312129	525.159703	E	***630.345717***	315.676497	613.319168	307.163222	612.335152	306.671214	6
10	***1180.406758***	590.707017	1162.396193	581.701735	L	***501.303124***	251.155200	484.276575	242.641925	483.292559	242.149917	5
11	1277.459522	639.233399	1259.448957	630.228117	P	***388.219060***	194.613168	371.192511	186.099894	370.208495	185.607886	4
12	1364.491550	682.749413	1346.480985	673.744131	S	***291.166296***	146.086786	274.139747	137.573512	273.155731	137.081504	3
13	1421.513014	711.260145	1403.502449	702.254863	G	204.134268	102.570772	187.107719	94.057497			2
14					K	147.112804	74.060040	130.086255	65.546765			1



RMS error 273 ppm



RMS error 273 ppm

NCBI **BLAST** search of CPDGSTCCELPSGK
(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	1566.611282	0.000166	CPDGSTCCELPSGK
0.2	1566.612610	-0.001162	CVQASNCPCYHR

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

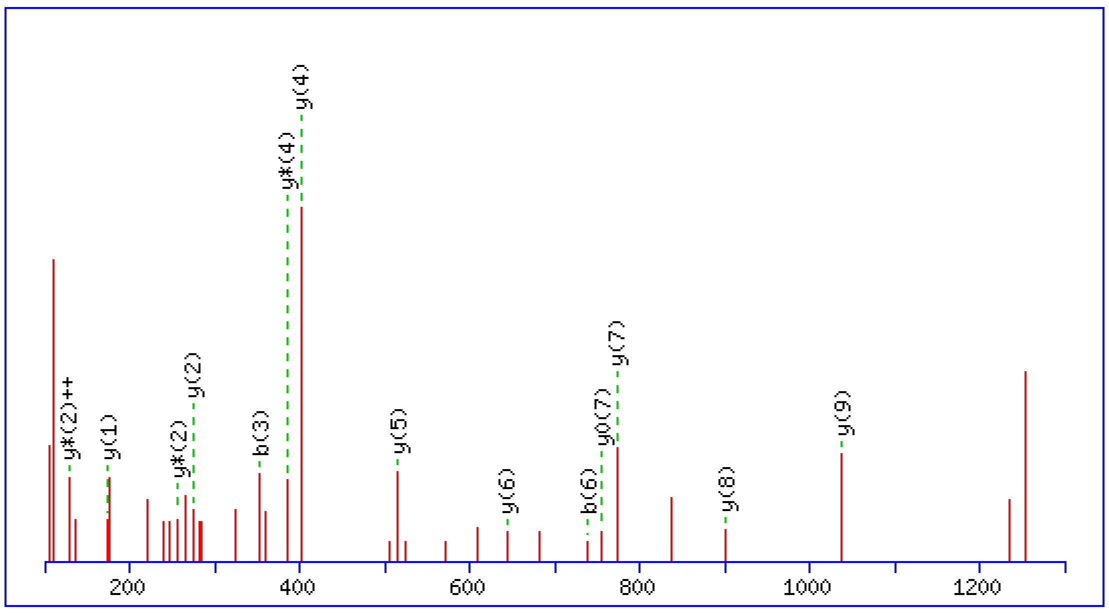
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SQHKEELGAVR**
Found in **GRAP1_HUMAN**, GRIP1-associated protein 1 OS=Homo sapiens GN=GRIPAP1 PE=1 SV=1

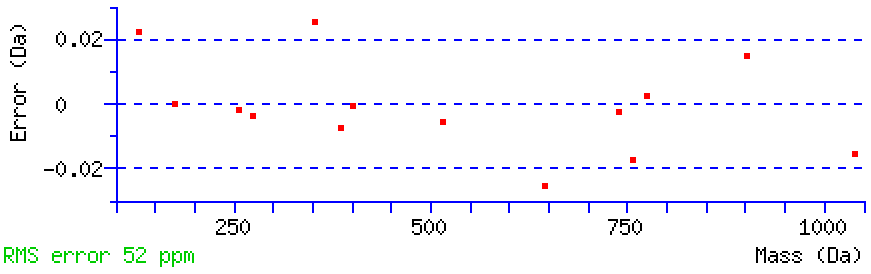
Match to Query 586243: 1252.652742 from(418.558190,3+) rtinseconds(831) index(817382)
Title: Locus:1.1.1.859.4
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

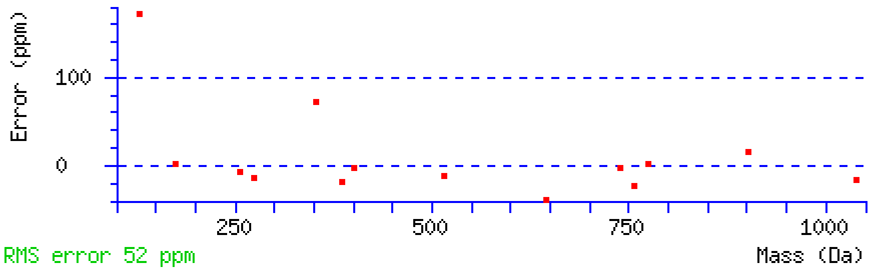
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1252.652374
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 48  Expect: 0.00018
Matches : 14/108 fragment ions using 32 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							11
2	216.097882	108.552579	199.071333	100.039305	198.087317	99.547296	Q	1166.627647	583.817462	1149.601098	575.304187	1148.617082	574.812179	10
3	**353.156794**	177.082035	336.130245	168.568761	335.146229	168.076753	H	***1038.569069***	519.788173	1021.542520	511.274898	1020.558504	510.782890	9
4	481.251757	241.129516	464.225208	232.616242	463.241192	232.124234	K	***901.510157***	451.258717	884.483608	442.745442	883.499592	442.253434	8
5	610.294350	305.650813	593.267801	297.137539	592.283785	296.645531	E	***773.415194***	387.211235	756.388645	378.697961	755.404629	378.205953	7
6	**739.336943**	370.172110	722.310394	361.658835	721.326378	361.166827	E	***644.372601***	322.689939	627.346052	314.176664	626.362036	313.684656	6
7	852.421007	426.714142	835.394458	418.200867	834.410442	417.708859	L	***515.330008***	258.168642	498.303459	249.655368			5
8	909.442471	455.224874	892.415922	446.711599	891.431906	446.219591	G	***402.245944***	201.626610	385.219395	193.113335			4
9	980.479585	490.743431	963.453036	482.230156	962.469020	481.738148	A	345.224480	173.115878	328.197931	164.602603			3
10	1079.547999	540.277638	1062.521450	531.764363	1061.537434	531.272355	V	***274.187366***	137.597321	257.160817	129.084046			2
11							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.4	1252.652374	0.000368	SQHKEELGAVR
8.2	1252.652374	0.000368	LSPESAPGPARR
6.7	1252.641205	0.011537	VGVTGPPDPQVR
6.7	1252.641205	0.011537	VGVTGPPDPQVR
5.6	1252.652390	0.000352	RPEIGGELGGPR
2.4	1252.648560	0.004182	MAVDGTLVYIR
0.7	1252.652390	0.000352	AAPPQIPDTRR

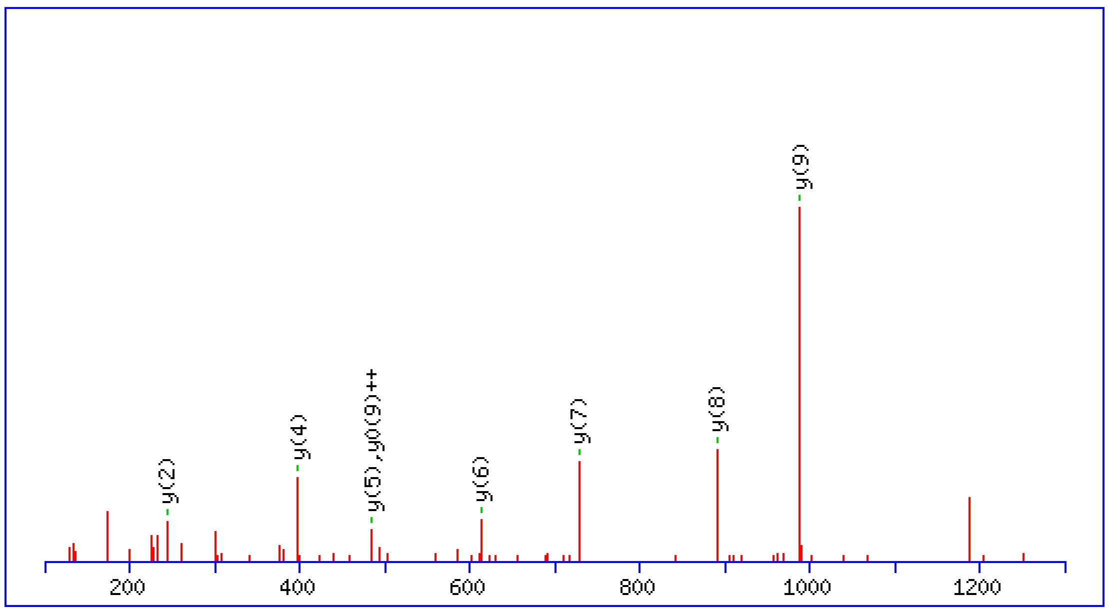
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SIPYDQSPGPK**
Found in **GHITM_HUMAN**, Growth hormone-inducible transmembrane protein OS=Homo sapiens GN=GHITM PE=1 SV=2

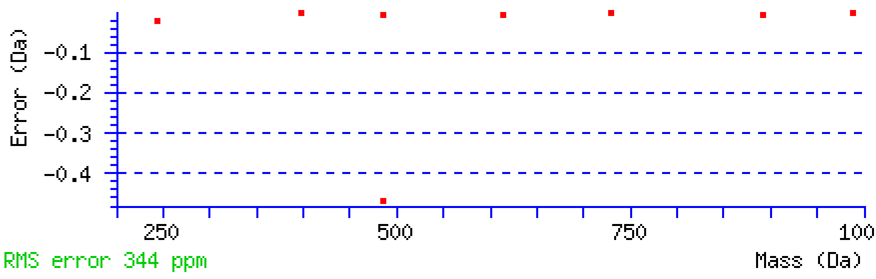
Match to Query 504363: 1187.584168 from(594.799360,2+) rtinseconds(1546) index(338723)
Title: Locus:1.1.1.926.32
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

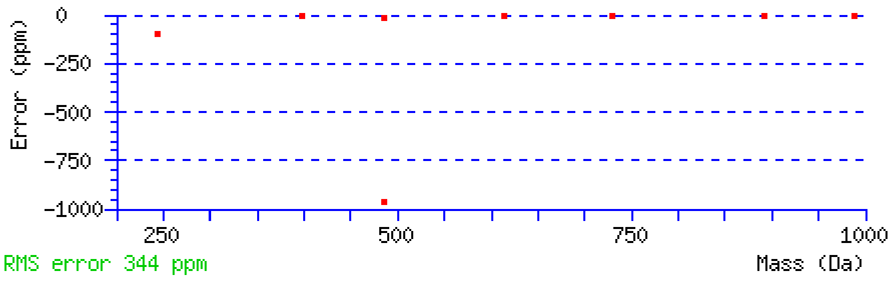
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1187.582245
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 65 **Expect:** 2.7e-006
Matches : 8/102 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							11
2	201.123368	101.065322			183.112803	92.060039	I	1101.557502	551.282389	1084.530953	542.769115	1083.546937	542.277107	10
3	298.176132	149.591704			280.165567	140.586422	P	***988.473438***	494.740357	971.446889	486.227083	970.462873	485.735075	9
4	461.239461	231.123369			443.228896	222.118086	Y	***891.420674***	446.213975	874.394125	437.700701	873.410109	437.208693	8
5	576.266404	288.636840			558.255839	279.631558	D	***728.357345***	364.682311	711.330796	356.169036	710.346780	355.677028	7
6	704.324982	352.666129	687.298433	344.152855	686.314417	343.660847	Q	***613.330402***	307.168839	596.303853	298.655565	595.319837	298.163557	6
7	791.357010	396.182143	774.330461	387.668869	773.346445	387.176861	S	***485.271824***	243.139550	468.245275	234.626276	467.261259	234.134268	5
8	888.409774	444.708525	871.383225	436.195251	870.399209	435.703243	P	***398.239796***	199.623536	381.213247	191.110262			4
9	945.431238	473.219257	928.404689	464.705983	927.420673	464.213975	G	301.187032	151.097154	284.160483	142.583880			3
10	1042.484002	521.745639	1025.457453	513.232365	1024.473437	512.740357	P	***244.165568***	122.586422	227.139019	114.073148			2
11							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
65.0	1187.582245	0.001923	SIPYDQSPGPK
5.3	1187.578217	0.005951	GGPGLSKNGEEK
2.4	1187.574371	0.009797	EALMPPLEQL
1.8	1187.593475	-0.009307	SPQRFPESPK
1.6	1187.589462	-0.005294	DGARSDPVSLR
0.9	1187.586975	-0.002807	VTMGWPRPGR
0.6	1187.578201	0.005967	PSDANLNSINK

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

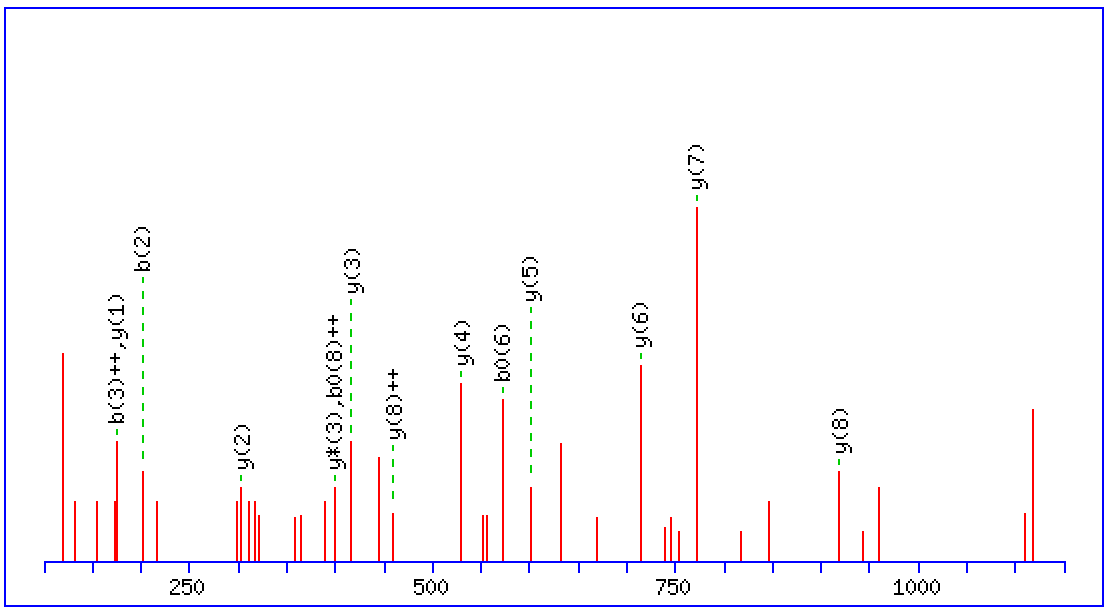
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EAFGNALLQR**
Found in **GSKIP_HUMAN**, GSK3-beta interaction protein OS=Homo sapiens GN=GSKIP PE=1 SV=2

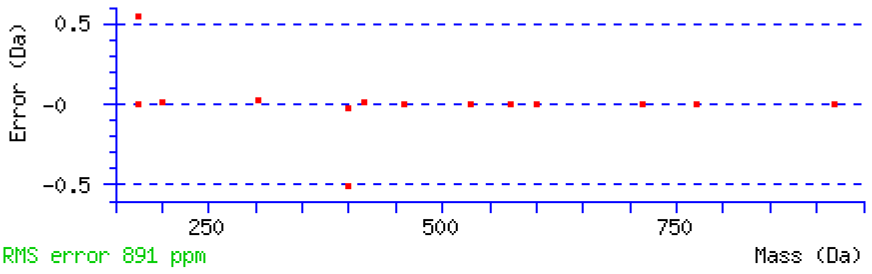
Match to Query 29375: 1117.581768 from(559.798160,2+) rtinseconds(2461) index(29624)
Title: Locus:1.1.1.2194.28
Data file 2011-11-10 - TFD - EP 4-6.mgf

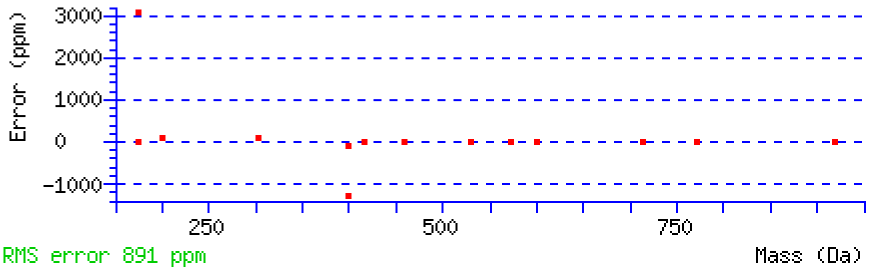
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1117.587982
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 44  Expect: 0.00047
Matches : 14/82 fragment ions using 25 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	130.049869	65.528572			112.039304	56.523290	E					10
2	201.086983	101.047130			183.076418	92.041847	A	989.552691	495.279984	972.526142	486.766709	9
3	348.155397	174.581336			330.144832	165.576054	F	***918.515577***	459.761427	901.489028	451.248152	8
4	405.176861	203.092068			387.166296	194.086786	G	***771.447163***	386.227220	754.420614	377.713945	7
5	519.219788	260.113532	502.193239	251.600258	501.209223	251.108250	N	***714.425699***	357.716488	697.399150	349.203213	6
6	590.256902	295.632089	573.230353	287.118814	572.246337	286.626806	A	***600.382772***	300.695024	583.356223	292.181750	5
7	703.340966	352.174121	686.314417	343.660846	685.330401	343.168838	L	***529.345658***	265.176467	512.319109	256.663193	4
8	816.425030	408.716153	799.398481	400.202879	798.414465	399.710871	L	***416.261594***	208.634435	399.235045	200.121160	3
9	944.483608	472.745442	927.457059	464.232168	926.473043	463.740160	Q	***303.177530***	152.092403	286.150981	143.579128	2
10							R	***175.118952***	88.063114	158.092403	79.549839	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.5	1117.587982	-0.006214	EAFGNALLQR
18.0	1117.588013	-0.006245	GTWSTGLPKR
14.2	1117.576767	0.005001	SADTLWGIQK
10.6	1117.572708	0.009060	SAEAELQSKR
7.4	1117.591354	-0.009586	DACQTLLKR
6.9	1117.583954	-0.002186	SSAQNGSALKR
4.4	1117.591354	-0.009586	KCIQAVETR
3.2	1117.572739	0.009029	NDGVETIKSR
0.1	1117.591354	-0.009586	VAKDMAAAVR

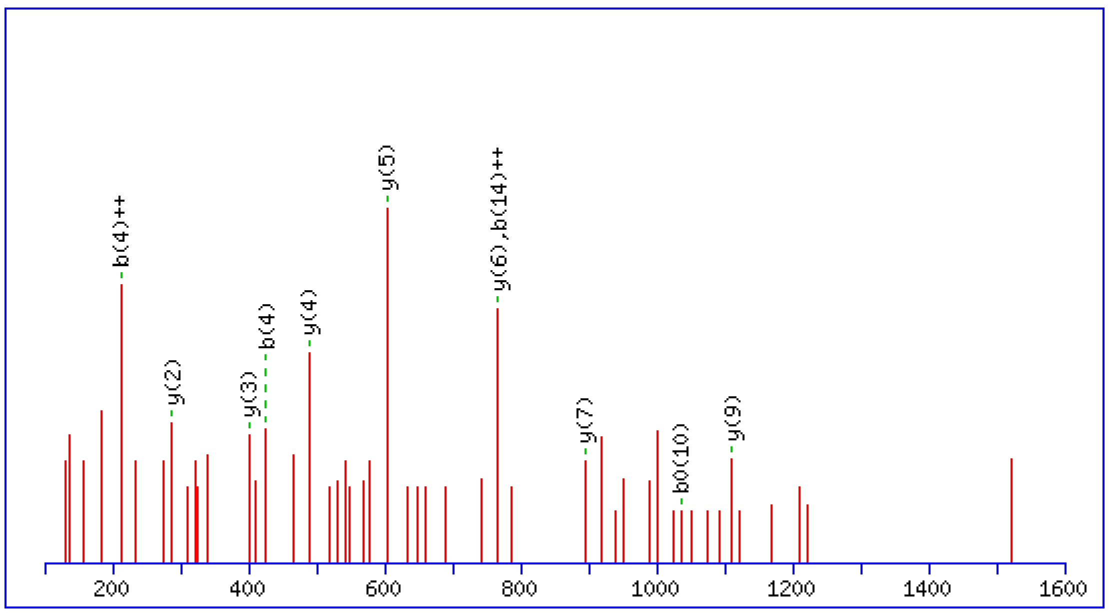
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LVLVSPTSEQYDSLLR**
Found in **GTPB1_HUMAN**, GTP-binding protein 1 OS=Homo sapiens GN=GTPBP1 PE=1 SV=3

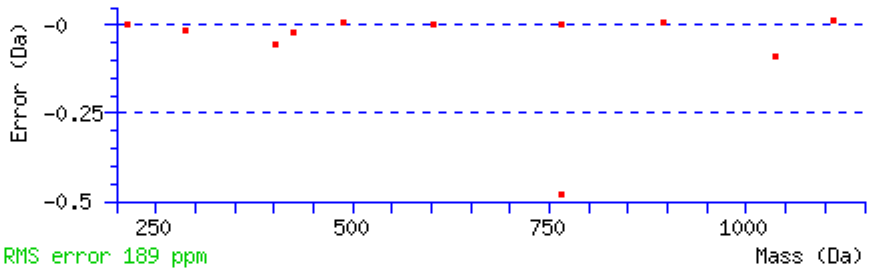
Match to Query 58416: 1818.975012 from(607.332280,3+) rtinseconds(3287) index(45824)
Title: Locus:1.1.1.2736.15
Data file 2011-11-10 - TFD - EP 4-2.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●

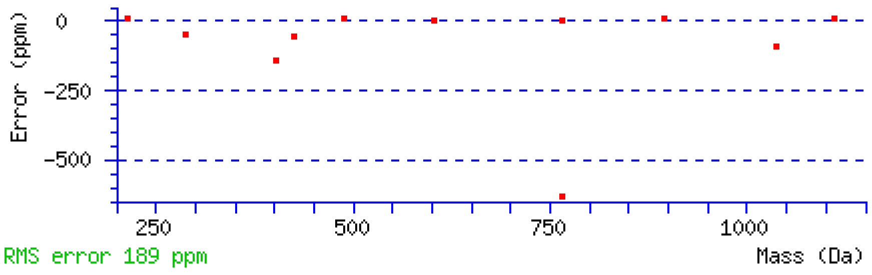


```
Monoisotopic mass of neutral peptide Mr(calc): 1818.972717
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 31  Expect: 0.0017
Matches : 12/148 fragment ions using 23 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					L							16
2	**213.159754**	107.083515					V	1706.895942	853.951609	1689.869393	845.438335	1688.885377	844.946327	15
3	326.243818	163.625547					L	1607.827528	804.417402	1590.800979	795.904128	1589.816963	795.412120	14
4	**425.312232**	**213.159754**					V	1494.743464	747.875370	1477.716915	739.362096	1476.732899	738.870088	13
5	512.344260	256.675768			494.333695	247.670486	S	1395.675050	698.341163	1378.648501	689.827889	1377.664485	689.335881	12
6	609.397024	305.202150			591.386459	296.196868	P	1308.643022	654.825149	1291.616473	646.311875	1290.632457	645.819867	11
7	710.444703	355.725990			692.434138	346.720707	T	1211.590258	606.298767	1194.563709	597.785493	1193.579693	597.293485	10
8	797.476731	399.242004			779.466166	390.236721	S	***1110.542579***	555.774928	1093.516030	547.261653	1092.532014	546.769645	9
9	926.519324	463.763300			908.508759	454.758018	E	1023.510551	512.258914	1006.484002	503.745639	1005.499986	503.253631	8
10	1054.577902	527.792589	1037.551353	519.279315	1036.567337	518.787307	Q	***894.467958***	447.737617	877.441409	439.224343	876.457393	438.732335	7
11	1217.641231	609.324254	1200.614682	600.810979	1199.630666	600.318971	Y	***766.409380***	383.708328	749.382831	375.195054	748.398815	374.703046	6
12	1332.668174	666.837725	1315.641625	658.324451	1314.657609	657.832443	D	***603.346051***	302.176664	586.319502	293.663389	585.335486	293.171381	5
13	1419.700202	710.353739	1402.673653	701.840465	1401.689637	701.348457	S	***488.319108***	244.663192	471.292559	236.149917	470.308543	235.657909	4
14	1532.784266	**766.895771**	1515.757717	758.382497	1514.773701	757.890489	L	***401.287080***	201.147178	384.260531	192.633903			3
15	1645.868330	823.437803	1628.841781	814.924529	1627.857765	814.432521	L	***288.203016***	144.605146	271.176467	136.091871			2
16							R	175.118952	88.063114	158.092403	79.549839			1



RMS error 189 ppm



RMS error 189 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.4	1818.972717	0.002295	LVLVSPTSEQYDSLLR
1.8	1818.976074	-0.001062	TEGLSVLSQAMAVIKEK
0.6	1818.963684	0.011328	LQKMGPFQPMNIFLR
0.5	1818.983948	-0.008936	NALGPGLSPELGPLPALR

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

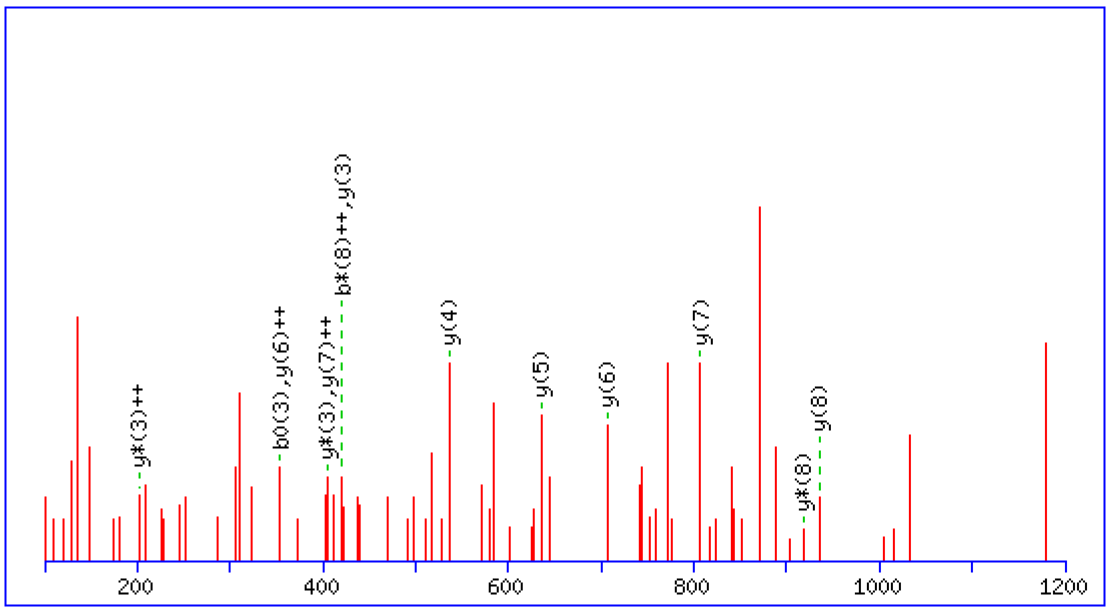
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ENQTAVDVFR**
Found in **RHEB_HUMAN**, GTP-binding protein Rheb OS=Homo sapiens GN=RHEB PE=1 SV=1

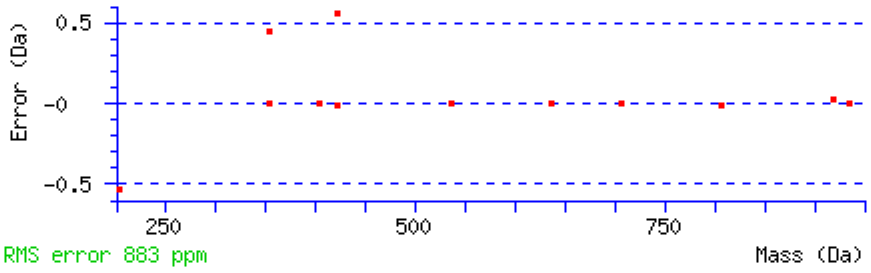
Match to Query 33590: 1177.580268 from(589.797410,2+) rtinseconds(2113) index(22979)
Title: Locus:1.1.1.2061.32
Data file 2011-11-10 - TFD - EP 4-6.mgf

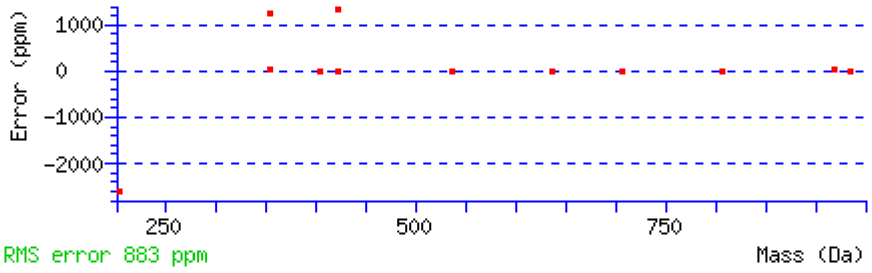
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1177.572754
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.0031
Matches : 13/100 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	E							10
2	244.092796	122.550036	227.066247	114.036762	226.082231	113.544754	N	1049.537435	525.272356	1032.510886	516.759081	1031.526870	516.267073	9
3	372.151374	186.579325	355.124825	178.066051	354.140809	177.574043	Q	***935.494508***	468.250892	918.467959	459.737618	917.483943	459.245610	8
4	473.199053	237.103165	456.172504	228.589890	455.188488	228.097882	T	***807.435930***	404.221603	790.409381	395.708329	789.425365	395.216321	7
5	544.236167	272.621722	527.209618	264.108447	526.225602	263.616439	A	***706.388251***	353.697764	689.361702	345.184489	688.377686	344.692481	6
6	643.304581	322.155929	626.278032	313.642654	625.294016	313.150646	V	***635.351137***	318.179207	618.324588	309.665932	617.340572	309.173924	5
7	758.331524	379.669400	741.304975	371.156126	740.320959	370.664118	D	***536.282723***	268.645000	519.256174	260.131725	518.272158	259.639717	4
8	857.399938	429.203607	840.373389	420.690333	839.389373	420.198325	V	***421.255780***	211.131528	404.229231	202.618253			3
9	1004.468352	502.737814	987.441803	494.224539	986.457787	493.732531	F	322.187366	161.597321	305.160817	153.084047			2
10							R	175.118952	88.063114	158.092403	79.549840			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.2	1177.572754	0.007514	ENQTAVDVFR
4.3	1177.583481	-0.003213	EMEVKCKPK
0.5	1177.583969	-0.003701	YGLSPAGRGER

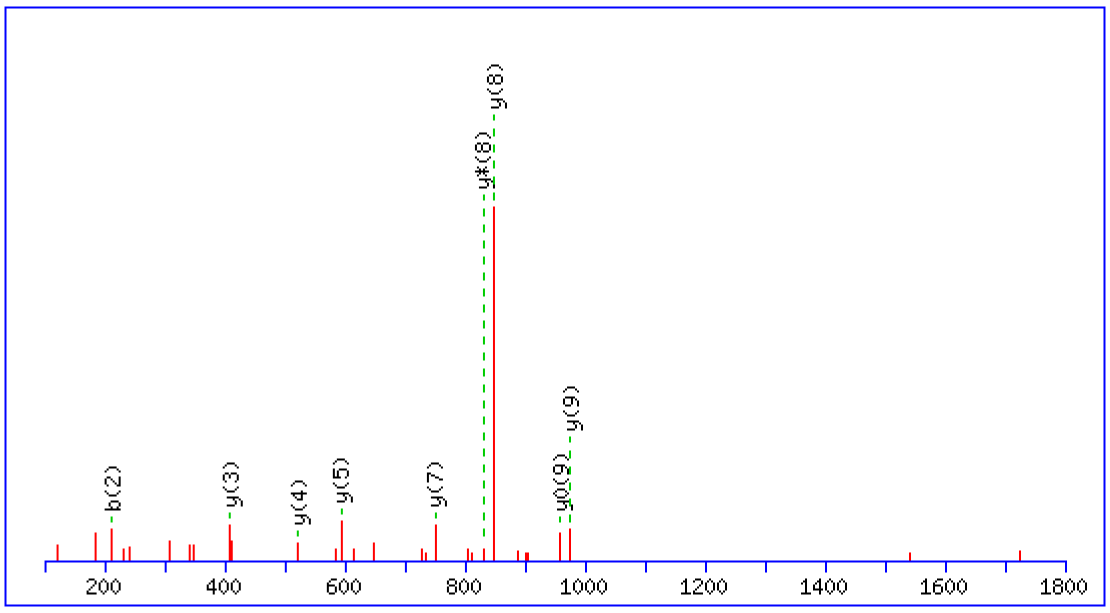
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLQPGTALFSR**
Found in **MSS4_HUMAN**, Guanine nucleotide exchange factor MSS4 OS=Homo sapiens GN=RABIF PE=1 SV=2

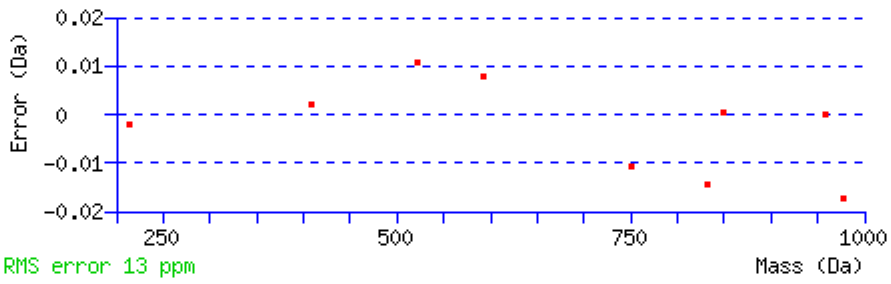
Match to Query 25909: 1187.662148 from(594.838350,2+) rtinseconds(2604) index(27560)
Title: Locus:1.1.1.2401.19
Data file 2011-11-10 - TFD - EP 3-7.mgf

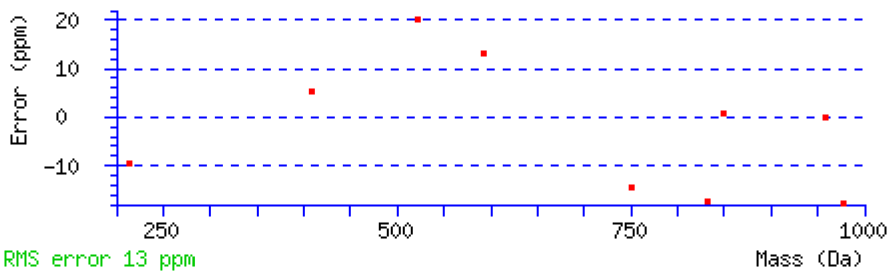
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1187.666260
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 40 **Expect:** 0.0011
Matches : 9/104 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							11
2	213.159754	107.083515					L	1089.605121	545.306198	1072.578572	536.792924	1071.594556	536.300916	10
3	341.218332	171.112804	324.191783	162.599529			Q	*976.521057*	488.764166	959.494508	480.250892	958.510492	479.758884	9
4	438.271096	219.639186	421.244547	211.125912			P	*848.462479*	424.734877	831.435930	416.221603	830.451914	415.729595	8
5	495.292560	248.149918	478.266011	239.636643			G	*751.409715*	376.208495	734.383166	367.695221	733.399150	367.203213	7
6	596.340239	298.673758	579.313690	290.160483	578.329674	289.668475	T	694.388251	347.697763	677.361702	339.184489	676.377686	338.692481	6
7	667.377353	334.192315	650.350804	325.679040	649.366788	325.187032	A	*593.340572*	297.173924	576.314023	288.660649	575.330007	288.168641	5
8	780.461417	390.734347	763.434868	382.221072	762.450852	381.729064	L	*522.303458*	261.655367	505.276909	253.142092	504.292893	252.650084	4
9	927.529831	464.268554	910.503282	455.755279	909.519266	455.263271	F	*409.219394*	205.113335	392.192845	196.600060	391.208829	196.108052	3
10	1014.561859	507.784567	997.535310	499.271293	996.551294	498.779285	S	262.150980	131.579128	245.124431	123.065853	244.140415	122.573845	2
11							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.0	1187.666260	-0.004112	VLQPGTALFSR

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

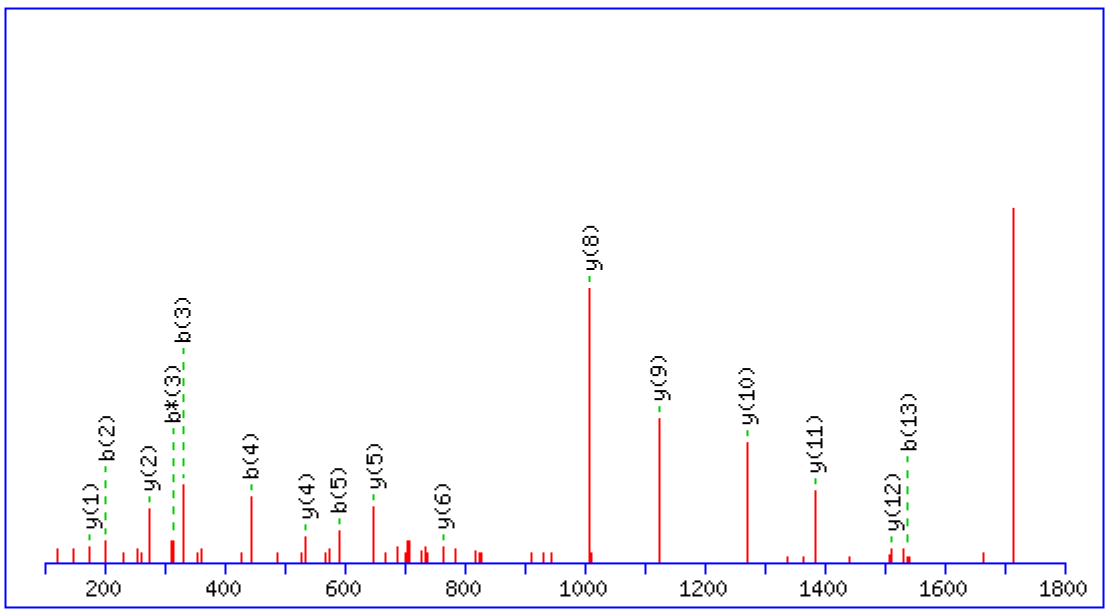
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NSELFDPFDLFDVR**
Found in **VAV2_HUMAN**, Guanine nucleotide exchange factor VAV2 OS=Homo sapiens GN=VAV2 PE=1 SV=2

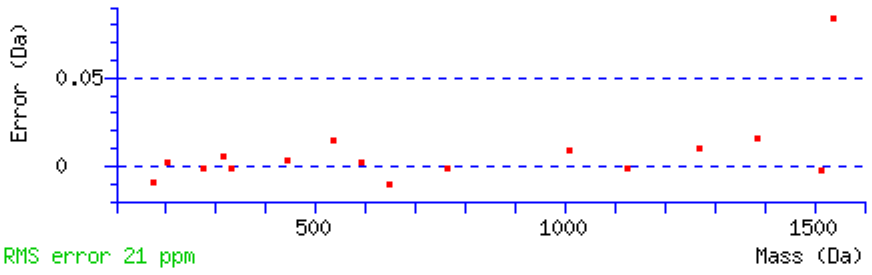
Match to Query 55744: 1712.808128 from(857.411340,2+) rtinseconds(4728) index(69953)
Title: Locus:1.1.1.3171.12
Data file 2011-11-12 - TFD - EP 6-2.mgf

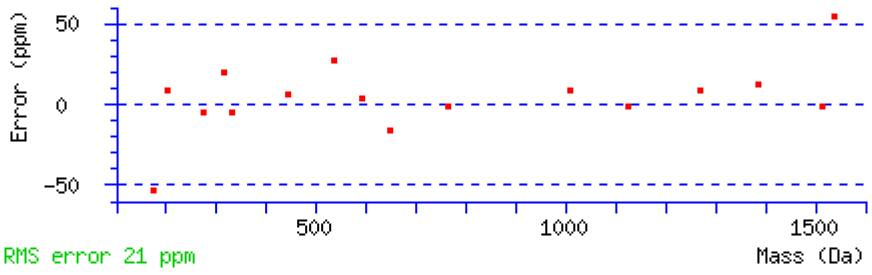
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1712.804611
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 71 **Expect:** 6e-007
Matches : 16/150 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			N							14
2	**202.082231**	101.544753	185.055682	93.031479	184.071666	92.539471	S	1599.768950	800.388113	1582.742401	791.874839	1581.758385	791.382831	13
3	**331.124824**	166.066050	314.098275	157.552776	313.114259	157.060768	E	***1512.736922***	756.872099	1495.710373	748.358825	1494.726357	747.866817	12
4	**444.208888**	222.608082	427.182339	214.094808	426.198323	213.602800	L	***1383.694329***	692.350803	1366.667780	683.837528	1365.683764	683.345520	11
5	**591.277302**	296.142289	574.250753	287.629015	573.266737	287.137007	F	***1270.610265***	635.808771	1253.583716	627.295496	1252.599700	626.803488	10
6	706.304245	353.655761	689.277696	345.142486	688.293680	344.650478	D	***1123.541851***	562.274564	1106.515302	553.761289	1105.531286	553.269281	9
7	803.357009	402.182143	786.330460	393.668868	785.346444	393.176860	P	***1008.514908***	504.761092	991.488359	496.247818	990.504343	495.755810	8
8	950.425423	475.716350	933.398874	467.203075	932.414858	466.711067	F	911.462144	456.234710	894.435595	447.721436	893.451579	447.229428	7
9	1065.452366	533.229821	1048.425817	524.716547	1047.441801	524.224538	D	***764.393730***	382.700503	747.367181	374.187229	746.383165	373.695221	6
10	1178.536430	589.771853	1161.509881	581.258579	1160.525865	580.766570	L	***649.366787***	325.187032	632.340238	316.673757	631.356222	316.181749	5
11	1325.604844	663.306060	1308.578295	654.792786	1307.594279	654.300777	F	***536.282723***	268.645000	519.256174	260.131725	518.272158	259.639717	4
12	1440.631787	720.819532	1423.605238	712.306257	1422.621222	711.814249	D	389.214309	195.110793	372.187760	186.597518	371.203744	186.105510	3
13	**1539.700201**	770.353739	1522.673652	761.840464	1521.689636	761.348456	V	***274.187366***	137.597321	257.160817	129.084047			2
14							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
71.4	1712.804611	0.003517	NSELFDPFDLFDVR
4.9	1712.810486	-0.002358	IGTEPSTAPAPSPPAPK
3.0	1712.815186	-0.007058	LQGGTPQEPPNPRMK
3.0	1712.815186	-0.007058	LQGGTPQEPPNPRMK
3.0	1712.821716	-0.013588	VSTEIPASEPDGPSVGR
2.3	1712.821716	-0.013588	VSTEIPASEPDGPSVGR

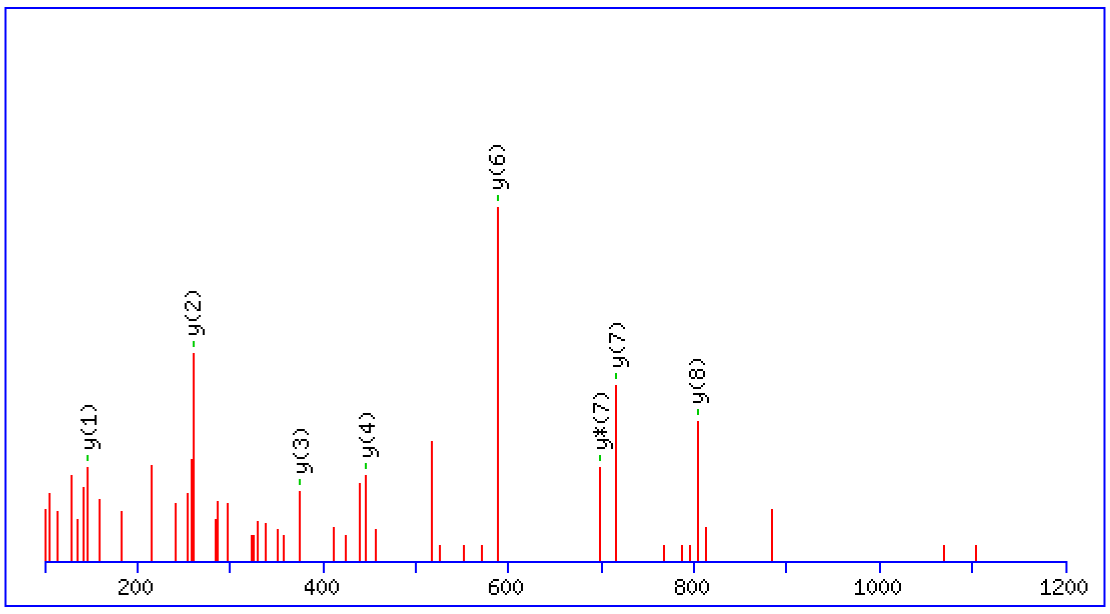
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VSQAAADLK**
Found in **GBG5_HUMAN**, Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-5 OS=Homo sapiens GN=GNG5 PE=1 SV=3

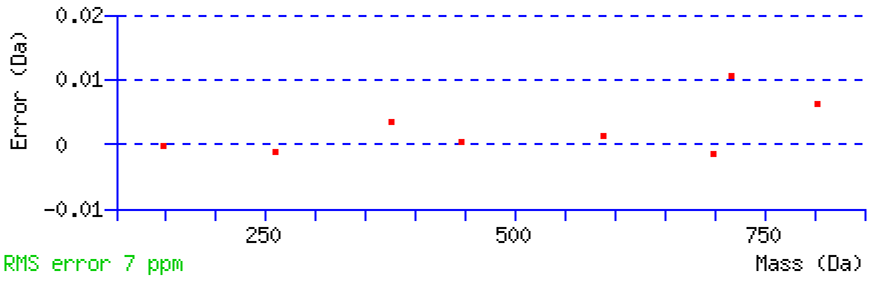
Match to Query 6160: 901.485628 from(451.750090,2+) rtinseconds(990) index(371)
Title: Locus:1.1.1.2010.3
Data file 2011-11-12 - TFD - EP 5-8.mgf

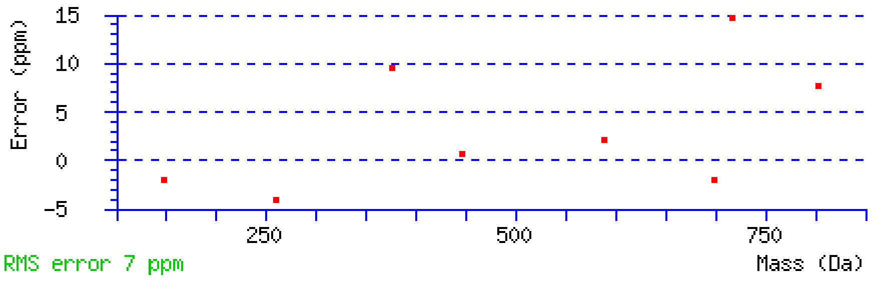
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 901.486877
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 79  Expect: 2.3e-007
Matches : 8/86 fragment ions using 8 most intense peaks   (help)
```

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	100.075690	50.541483					V							9
2	187.107718	94.057497			169.097153	85.052214	S	***803.425759***	402.216518	786.399210	393.703243	785.415194	393.211235	8
3	315.166296	158.086786	298.139747	149.573512	297.155731	149.081504	Q	***716.393731***	358.700504	699.367182	350.187229	698.383166	349.695221	7
4	386.203410	193.605343	369.176861	185.092069	368.192845	184.600061	A	***588.335153***	294.671215	571.308604	286.157940	570.324588	285.665932	6
5	457.240524	229.123900	440.213975	220.610626	439.229959	220.118618	A	517.298039	259.152658	500.271490	250.639383	499.287474	250.147375	5
6	528.277638	264.642457	511.251089	256.129183	510.267073	255.637175	A	***446.260925***	223.634100	429.234376	215.120826	428.250360	214.628818	4
7	643.304581	322.155929	626.278032	313.642654	625.294016	313.150646	D	***375.223811***	188.115543	358.197262	179.602269	357.213246	179.110261	3
8	756.388645	378.697961	739.362096	370.184686	738.378080	369.692678	L	***260.196868***	130.602072	243.170319	122.088798			2
9							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
79.0	901.486877	-0.001249	VSQAAADLK
15.0	901.486877	-0.001249	QEKAPVSK
12.7	901.486893	-0.001265	GSPGASLGIK
11.2	901.476974	0.008654	KWAAGQNK
11.0	901.486877	-0.001249	VSEQLQAK
9.9	901.486877	-0.001249	AASQVLGEK
8.6	901.486877	-0.001249	QEQSAVIK
8.2	901.486877	-0.001249	VNASAPSLK
7.6	901.490906	-0.005278	DLVEWLK
7.4	901.490921	-0.005293	AFVPPDLK

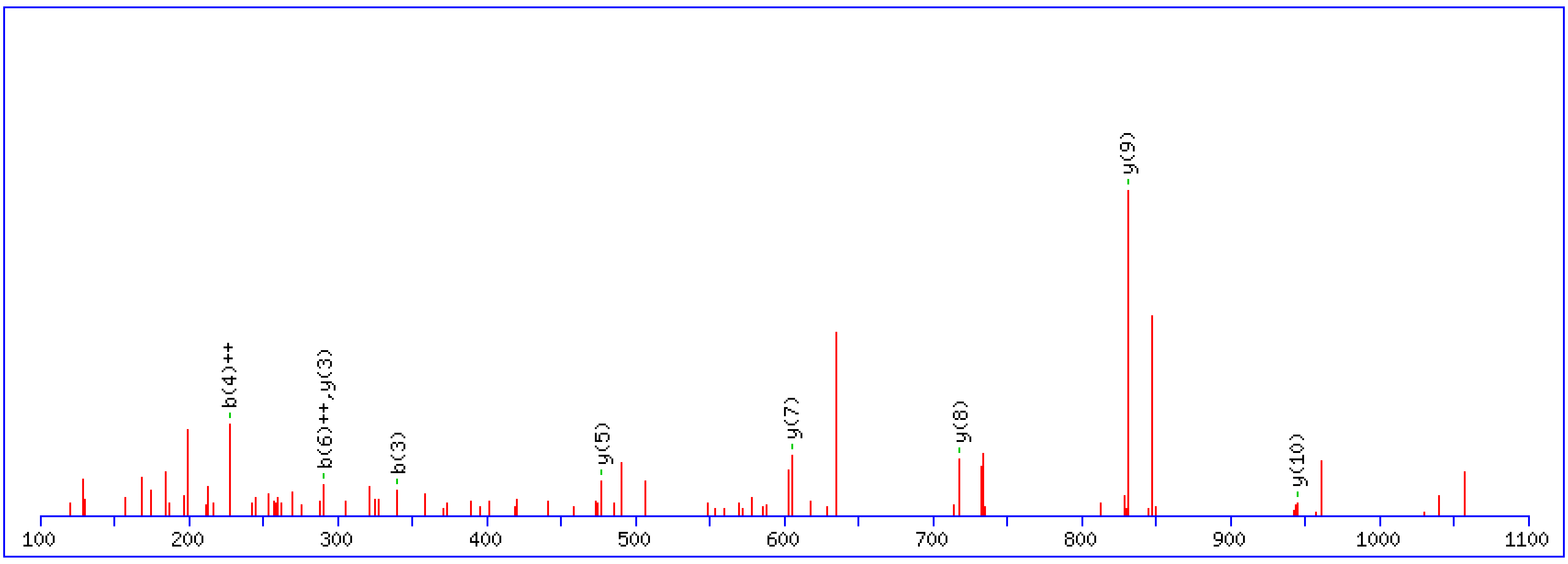
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILLLGAGESGK**
Found in **GNA12_HUMAN**, Guanine nucleotide-binding protein subunit alpha-12 OS=Homo sapiens GN=GNA12 PE=1 SV=4

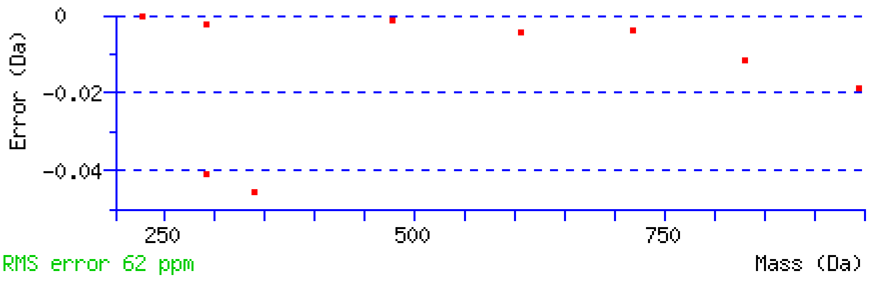
Match to Query 18675: 1056.607628 from(529.311090,2+) rtinseconds(2410) index(31002)
Title: Locus:1.1.1.1307.15
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 1.mgf

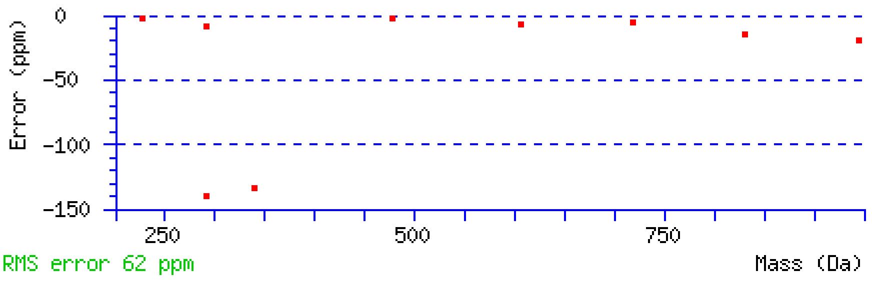
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1056.617889
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31  Expect: 0.0082
Matches : 10/82 fragment ions using 20 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							11
2	**227.175404**	114.091340			L	***944.541123***	472.774200	927.514574	464.260925	926.530558	463.768917	10
3	**340.259468**	170.633372			L	***831.457059***	416.232168	814.430510	407.718893	813.446494	407.226885	9
4	453.343532	**227.175404**			L	***718.372995***	359.690136	701.346446	351.176861	700.362430	350.684853	8
5	510.364996	255.686136			G	***605.288931***	303.148104	588.262382	294.634829	587.278366	294.142821	7
6	581.402110	**291.204693**			A	548.267467	274.637372	531.240918	266.124097	530.256902	265.632089	6
7	638.423574	319.715425			G	***477.230353***	239.118815	460.203804	230.605540	459.219788	230.113532	5
8	767.466167	384.236722	749.455602	375.231439	E	420.208889	210.608082	403.182340	202.094808	402.198324	201.602800	4
9	854.498195	427.752736	836.487630	418.747453	S	***291.166296***	146.086786	274.139747	137.573512	273.155731	137.081504	3
10	911.519659	456.263468	893.509094	447.258185	G	204.134268	102.570772	187.107719	94.057498			2
11					K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.6	1056.617889	-0.010261	ILLLGAGESGK
30.6	1056.617889	-0.010261	LLLLGAGESGK
29.6	1056.608002	-0.000374	ILPVGAANFR
11.8	1056.606659	0.000969	LLPDTILEK
6.2	1056.606659	0.000969	LPLTDLEIK
3.8	1056.617874	-0.010246	LLDQEAKLK
3.1	1056.600143	0.007485	IPVSRPILM
2.0	1056.617905	-0.010277	ILVQLGETGK

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

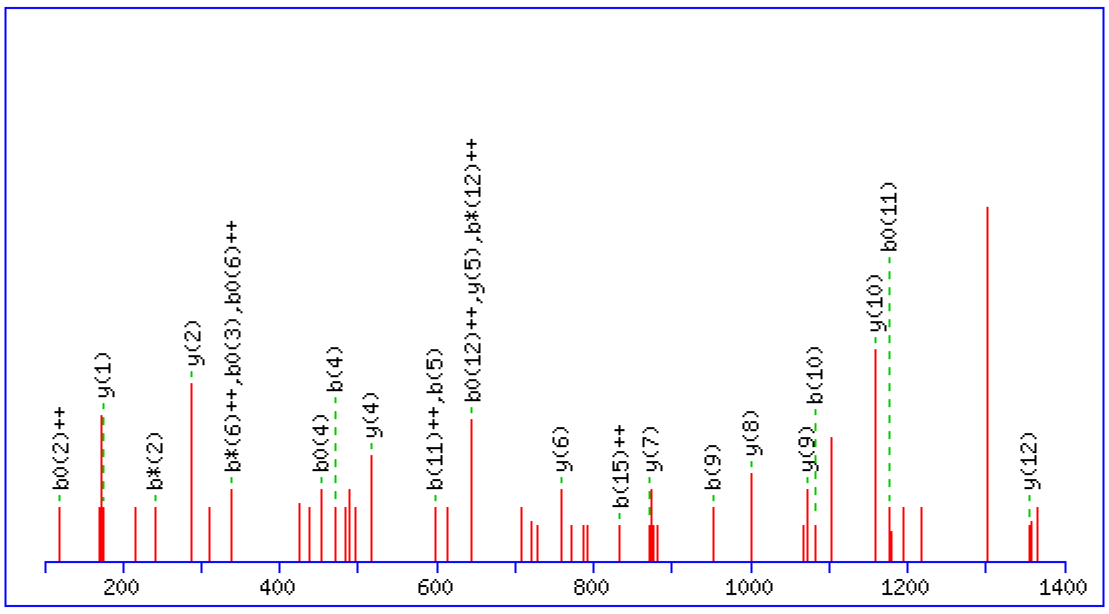
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EQVLQPVSAELLELDIR**
Found in **GNL1_HUMAN**, Guanine nucleotide-binding protein-like 1 OS=Homo sapiens GN=GNL1 PE=1 SV=2

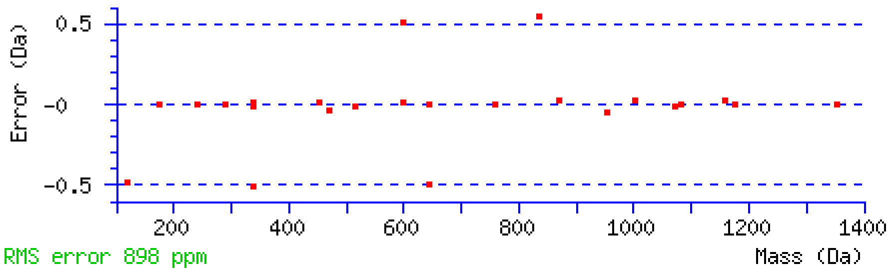
Match to Query 60313: 1951.056762 from(651.359530,3+) rtinseconds(3937) index(55270)
Title: Locus:1.1.1.3128.24
Data file 2011-11-12 - TFD - EP 5-2.mgf

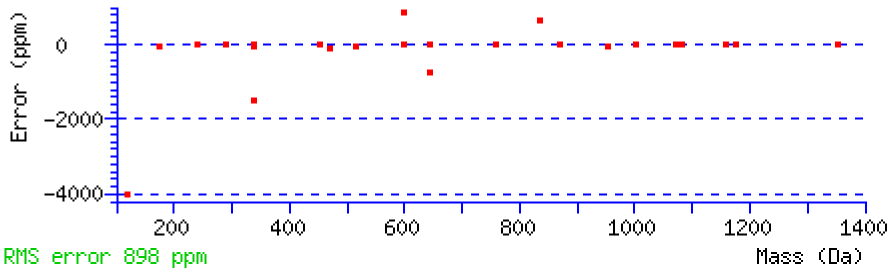
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1951.062576
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 48 **Expect:** 4.9e-005
Matches : 25/186 fragment ions using 44 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	E							17
2	258.108447	129.557862	241.081898	121.044587	240.097882	120.552579	Q	1823.027291	912.017284	1806.000742	903.504009	1805.016726	903.012001	16
3	357.176861	179.092069	340.150312	170.578794	339.166296	170.086786	V	1694.968713	847.987995	1677.942164	839.474720	1676.958148	838.982712	15
4	**470.260925**	235.634101	453.234376	227.120826	452.250360	226.628818	L	1595.900299	798.453787	1578.873750	789.940513	1577.889734	789.448505	14
5	**598.319503**	299.663390	581.292954	291.150115	580.308938	290.658107	Q	1482.816235	741.911756	1465.789686	733.398481	1464.805670	732.906473	13
6	695.372267	348.189772	678.345718	339.676497	677.361702	339.184489	P	***1354.757657***	677.882466	1337.731108	669.369192	1336.747092	668.877184	12
7	794.440681	397.723979	777.414132	389.210704	776.430116	388.718696	V	1257.704893	629.356084	1240.678344	620.842810	1239.694328	620.350802	11
8	881.472709	441.239993	864.446160	432.726718	863.462144	432.234710	S	***1158.636479***	579.821878	1141.609930	571.308603	1140.625914	570.816595	10
9	**952.509823**	476.758550	935.483274	468.245275	934.499258	467.753267	A	***1071.604451***	536.305863	1054.577902	527.792589	1053.593886	527.300581	9
10	**1081.552416**	541.279846	1064.525867	532.766572	1063.541851	532.274564	E	***1000.567337***	500.787307	983.540788	492.274032	982.556772	491.782024	8
11	1194.636480	597.821878	1177.609931	589.308604	1176.625915	588.816596	L	***871.524744***	436.266010	854.498195	427.752735	853.514179	427.260727	7
12	1307.720544	654.363910	1290.693995	645.850636	1289.709979	645.358628	L	***758.440680***	379.723978	741.414131	371.210703	740.430115	370.718695	6
13	1436.763137	718.885207	1419.736588	710.371932	1418.752572	709.879924	E	***645.356616***	323.181946	628.330067	314.668672	627.346051	314.176664	5
14	1549.847201	775.427239	1532.820652	766.913964	1531.836636	766.421956	L	***516.314023***	258.660649	499.287474	250.147375	498.303458	249.655367	4
15	1664.874144	832.940710	1647.847595	824.427436	1646.863579	823.935428	D	403.229959	202.118617	386.203410	193.605343	385.219394	193.113335	3
16	1777.958208	889.482742	1760.931659	880.969468	1759.947643	880.477460	I	***288.203016***	144.605146	271.176467	136.091871			2
17							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.8	1951.062576	-0.005814	EQVLQPVSAELLELDIR
1.8	1951.067307	-0.010545	CHLGQLAKGTEVSVGLLR

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

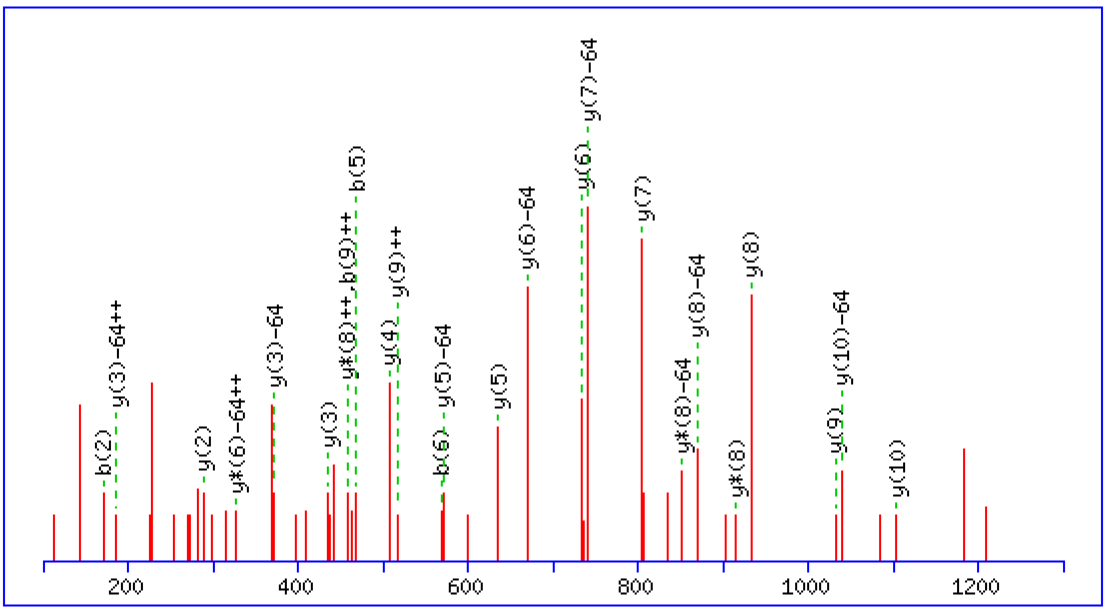
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VAVQAVQAMNR**
Found in **KGUA_HUMAN**, Guanylate kinase OS=Homo sapiens GN=GUK1 PE=1 SV=2

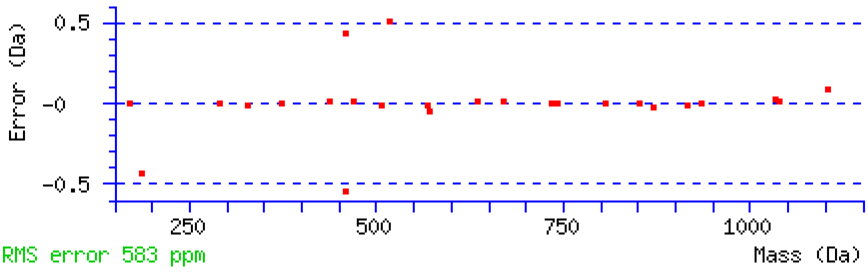
Match to Query 30318: 1201.624548 from(601.819550,2+) rtinseconds(1205) index(4496)
Title: Locus:1.1.1.1729.34
Data file 2011-11-14 - TFD - EP 8-6.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●

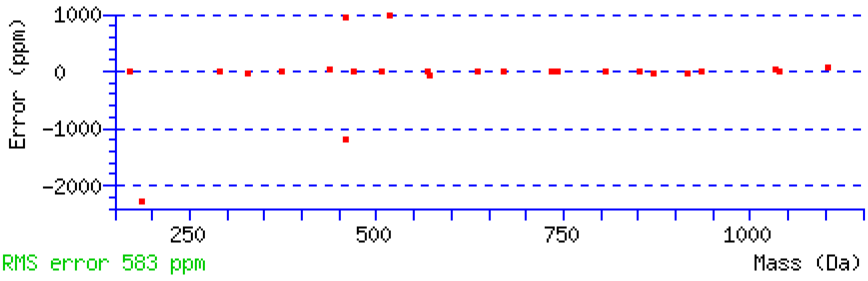


```
Monoisotopic mass of neutral peptide Mr(calc): 1201.623734
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M9      : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 60  Expect: 1.4e-005
Matches : 25/114 fragment ions using 42 most intense peaks    (help)
```

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	100.075690	50.541483			V					11
2	**171.112804**	86.060040			A	***1103.562605***	552.284940	1086.536056	543.771666	10
3	270.181218	135.594247			V	***1032.525491***	516.766383	1015.498942	508.253109	9
4	398.239796	199.623536	381.213247	191.110262	Q	***933.457077***	467.232176	916.430528	458.718902	8
5	**469.276910**	235.142093	452.250361	226.628818	A	***805.398499***	403.202887	788.371950	394.689613	7
6	**568.345324**	284.676300	551.318775	276.163026	V	***734.361385***	367.684330	717.334836	359.171056	6
7	696.403902	348.705589	679.377353	340.192315	Q	***635.292971***	318.150124	618.266422	309.636849	5
8	767.441016	384.224146	750.414467	375.710872	A	***507.234393***	254.120834	490.207844	245.607560	4
9	914.476416	457.741846	897.449867	449.228571	M	***436.197279***	218.602277	419.170730	210.089003	3
10	1028.519343	514.763309	1011.492794	506.250035	N	***289.161879***	145.084577	272.135330	136.571303	2
11					R	175.118952	88.063114	158.092403	79.549839	1



RMS error 583 ppm



RMS error 583 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
60.4	1201.623734	0.000814	VAVQAVQAMNR

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

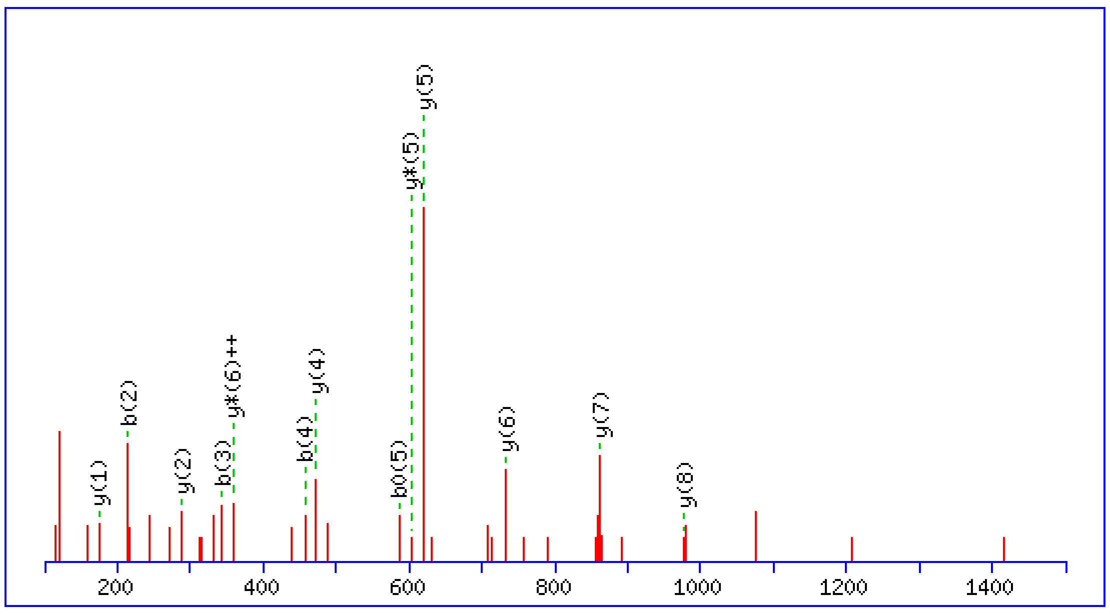
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VDEIFGQLR**
Found in **GAR1_HUMAN**, H/ACA ribonucleoprotein complex subunit 1 OS=Homo sapiens GN=GAR1 PE=1 SV=1

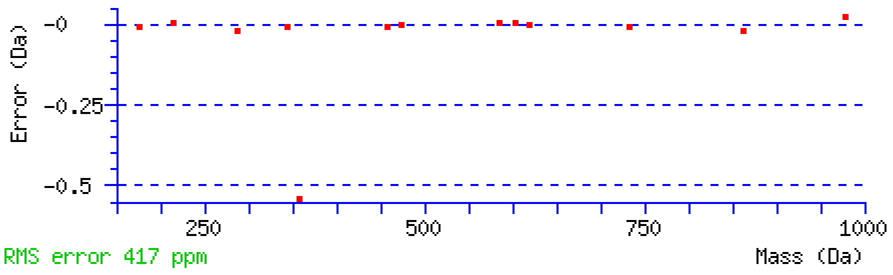
Match to Query 21858: 1075.565308 from(538.789930,2+) rtinseconds(2700) index(34301)
Title: Locus:1.1.1.2343.20
Data file 2011-11-10 - TFD - EP 4-5.mgf

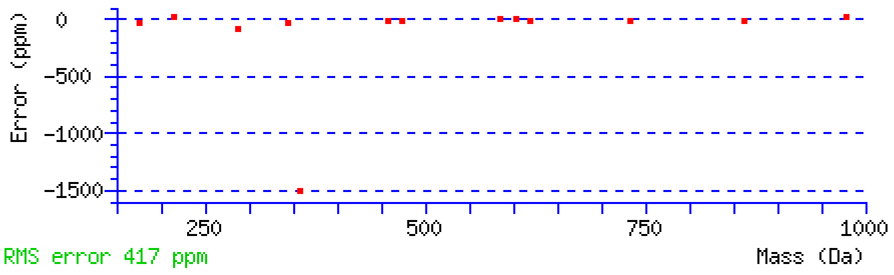
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1075.566208
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 59  Expect: 1.6e-005
Matches : 13/70 fragment ions using 18 most intense peaks    (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	100.075690	50.541483					V							9
2	**215.102633**	108.054954			197.092068	99.049672	D	***977.505072***	489.256174	960.478523	480.742900	959.494507	480.250892	8
3	**344.145226**	172.576251			326.134661	163.570969	E	***862.478129***	431.742703	845.451580	423.229428	844.467564	422.737420	7
4	**457.229290**	229.118283			439.218725	220.113001	I	***733.435536***	367.221406	716.408987	358.708132			6
5	604.297704	302.652490			586.287139	293.647208	F	***620.351472***	310.679374	603.324923	302.166100			5
6	661.319168	331.163222			643.308603	322.157940	G	***473.283058***	237.145167	456.256509	228.631893			4
7	789.377746	395.192511	772.351197	386.679237	771.367181	386.187229	Q	416.261594	208.634435	399.235045	200.121161			3
8	902.461810	451.734543	885.435261	443.221269	884.451245	442.729261	L	***288.203016***	144.605146	271.176467	136.091872			2
9							R	***175.118952***	88.063114	158.092403	79.549840			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
59.3	1075.566208	-0.000900	VDEIFGQLR
9.2	1075.569565	-0.004257	MLVLDSDKR
7.4	1075.569550	-0.004242	LTEGKIMER
4.1	1075.570236	-0.004928	VEPFLGTWK
3.3	1075.566223	-0.000915	VLFSTQPPR
2.1	1075.573593	-0.008285	DMPLNIFVK
1.7	1075.573395	-0.008087	SGLSRSSNLR

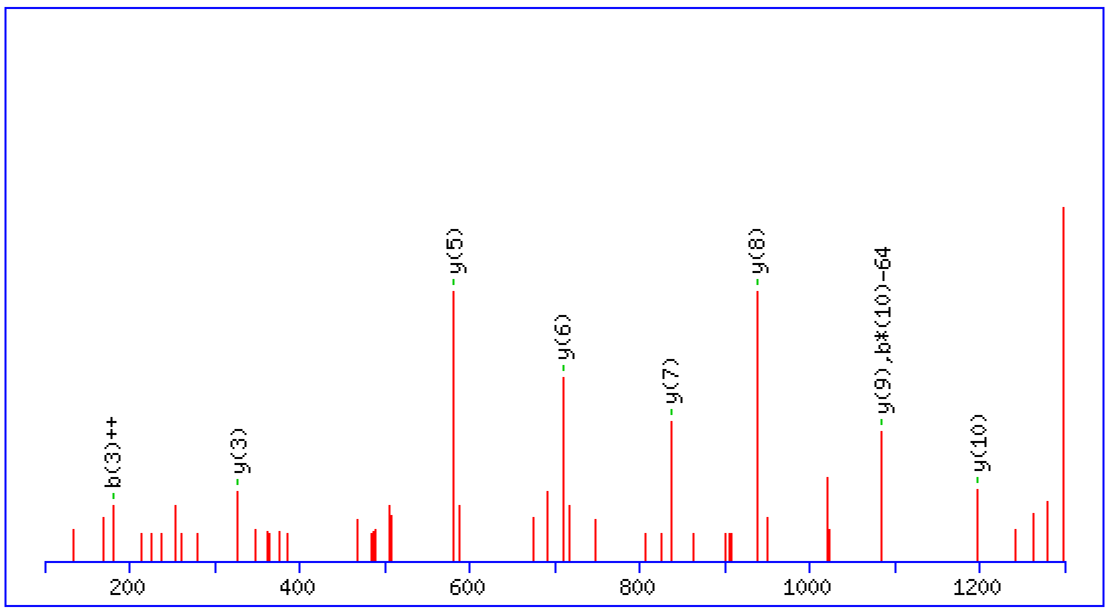
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLMTQQPRPVL**
Found in **NOP10_HUMAN**, H/ACA ribonucleoprotein complex subunit 3 OS=Homo sapiens GN=NOP10 PE=1 SV=1

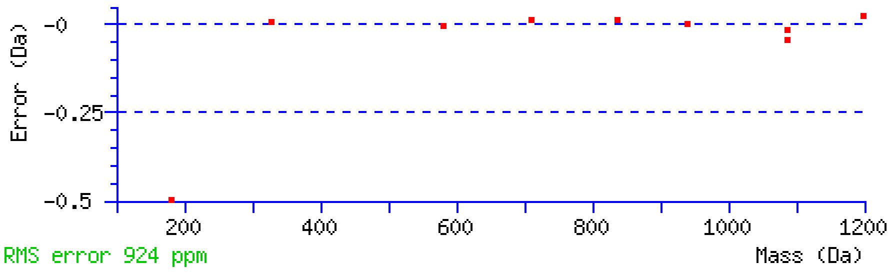
Match to Query 19692: 1296.725708 from(649.370130,2+) rtinseconds(2047) index(9602)
Title: Locus:1.1.1.2295.42
Data file 2011-11-12 - TFD - EP 6-8.mgf

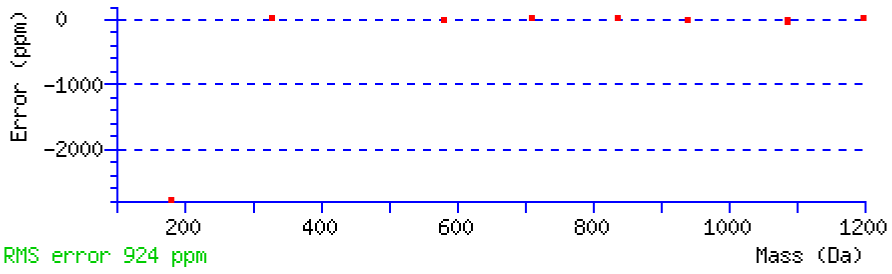
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1296.722397
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M3 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 55 **Expect:** 1.6e-005
Matches : 9/140 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							11
2	213.159754	107.083515					L	***1198.661257***	599.834267	1181.634708	591.320992	1180.650692	590.828984	10
3	360.195154	180.601215					M	***1085.577193***	543.292235	1068.550644	534.778960	1067.566628	534.286952	9
4	461.242833	231.125054			443.232268	222.119772	T	***938.541793***	469.774535	921.515244	461.261260	920.531228	460.769252	8
5	589.301411	295.154344	572.274862	286.641069	571.290846	286.149061	Q	***837.494114***	419.250695	820.467565	410.737421			7
6	717.359989	359.183633	700.333440	350.670358	699.349424	350.178350	Q	***709.435536***	355.221406	692.408987	346.708132			6
7	814.412753	407.710015	797.386204	399.196740	796.402188	398.704732	P	***581.376958***	291.192117	564.350409	282.678843			5
8	970.513864	485.760570	953.487315	477.247296	952.503299	476.755288	R	484.324194	242.665735	467.297645	234.152460			4
9	1067.566628	534.286952	1050.540079	525.773678	1049.556063	525.281670	P	***328.223083***	164.615179					3
10	1166.635042	583.821159	1149.608493	575.307885	1148.624477	574.815877	V	231.170319	116.088797					2
11							L	132.101905	66.554590					1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.3	1296.722397	0.003311	VLMTQQPRPVL
4.4	1296.722382	0.003326	VLSHNLCTVLK
4.0	1296.722397	0.003311	VLMTQQPRPVL
3.9	1296.719009	0.006699	VIPPKEWKPR

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

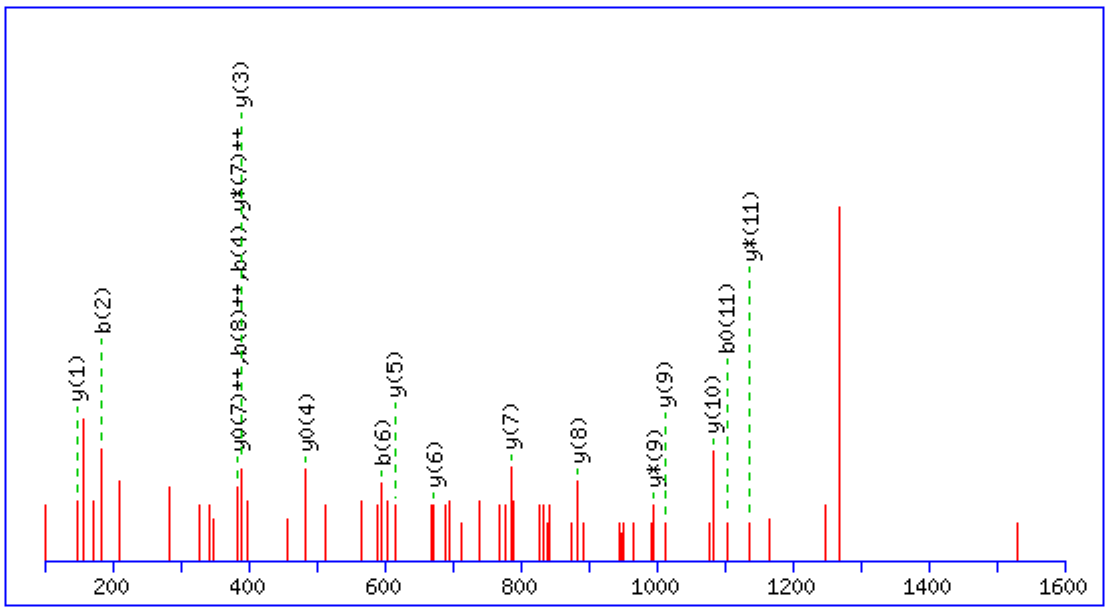
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LAAQVLGLLLEK**
Found in **HTR7A_HUMAN**, HEAT repeat-containing protein 7A OS=Homo sapiens GN=HEATR7A PE=1 SV=3

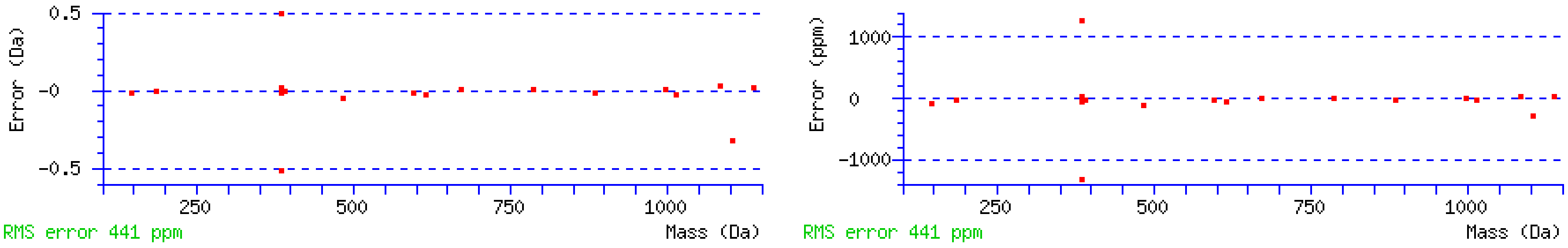
Match to Query 33042: 1266.794728 from(634.404640,2+) rtinseconds(3883) index(56876)
Title: Locus:1.1.1.2889.22
Data file 2011-11-10 - TFD - EP 3-1.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1266.791092
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 37 **Expect:** 0.00018
Matches : 18/104 fragment ions using 39 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							12
2	**185.128454**	93.067865					A	1154.714337	577.860807	1137.687788	569.347532	1136.703772	568.855524	11
3	256.165568	128.586422					A	***1083.677223***	542.342250	1066.650674	533.828975	1065.666658	533.336967	10
4	**384.224146**	192.615711	367.197597	184.102436			Q	***1012.640109***	506.823693	995.613560	498.310418	994.629544	497.818410	9
5	483.292560	242.149918	466.266011	233.636643			V	***884.581531***	442.794404	867.554982	434.281129	866.570966	433.789121	8
6	**596.376624**	298.691950	579.350075	290.178676			L	***785.513117***	393.260197	768.486568	384.746922	767.502552	384.254914	7
7	653.398088	327.202682	636.371539	318.689408			G	***672.429053***	336.718165	655.402504	328.204890	654.418488	327.712882	6
8	766.482152	383.744714	749.455603	375.231440			L	***615.407589***	308.207433	598.381040	299.694158	597.397024	299.202150	5
9	879.566216	440.286746	862.539667	431.773472			L	502.323525	251.665401	485.296976	243.152126	484.312960	242.660118	4
10	992.650280	496.828778	975.623731	488.315504			L	***389.239461***	195.123369	372.212912	186.610094	371.228896	186.118086	3
11	1121.692873	561.350075	1104.666324	552.836800	1103.682308	552.344792	E	276.155397	138.581337	259.128848	130.068062	258.144832	129.576054	2
12							K	***147.112804***	74.060040	130.086255	65.546765			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.4	1266.791092	0.003636	LAAQVLGLLLEK

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

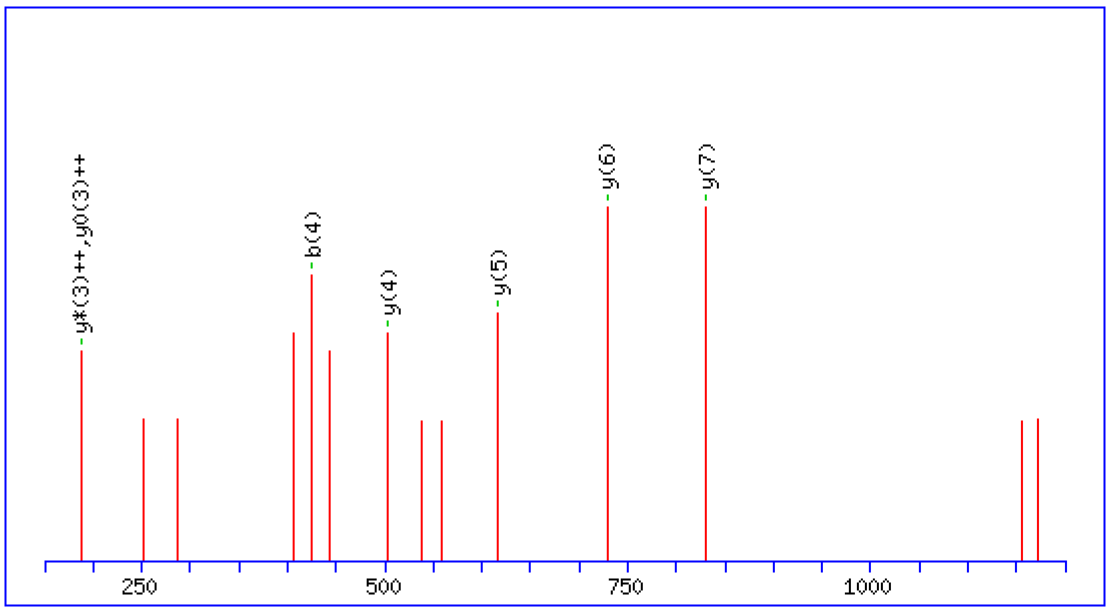
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLPTLPPDKK**
Found in **HEN1_HUMAN**, Helix-loop-helix protein 1 OS=Homo sapiens GN=NHLH1 PE=2 SV=1

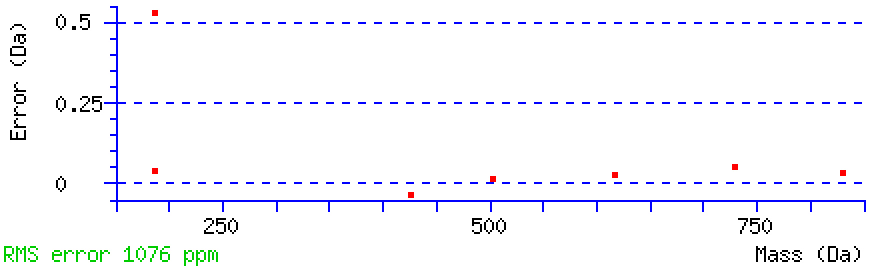
Match to Query 26864: 1152.682408 from(577.348480,2+) rtinseconds(4305) index(64107)
Title: Locus:1.1.1.2969.17
Data file 2011-11-10 - TFD - EP 3-4.mgf

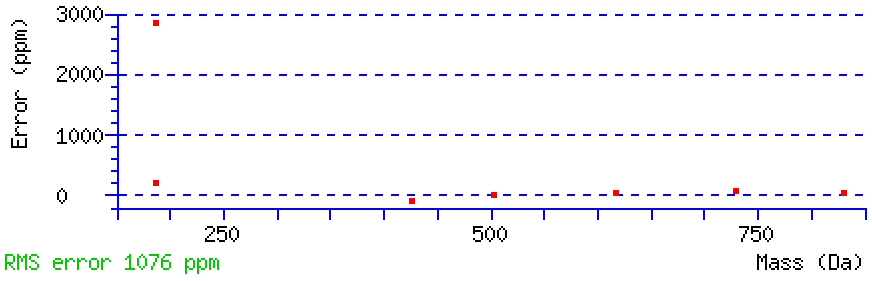
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [150] to [1200] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1152.675415
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P6 : Oxidation (P)
P7 : Oxidation (P)
Ions Score: 33 **Expect:** 0.0017
Matches : 7/82 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							10
2	227.175404	114.091340					L	1040.598639	520.802958	1023.572090	512.289683	1022.588074	511.797675	9
3	324.228168	162.617722					P	927.514575	464.260926	910.488026	455.747651	909.504010	455.255643	8
4	425.275847	213.141561			407.265282	204.136279	T	***830.461811***	415.734544	813.435262	407.221269	812.451246	406.729261	7
5	538.359911	269.683594			520.349346	260.678311	L	***729.414132***	365.210704	712.387583	356.697430	711.403567	356.205422	6
6	651.407590	326.207433			633.397025	317.202151	P	***616.330068***	308.668672	599.303519	300.155398	598.319503	299.663390	5
7	764.455269	382.731273			746.444704	373.725990	P	***503.282389***	252.144833	486.255840	243.631558	485.271824	243.139550	4
8	879.482212	440.244744			861.471647	431.239462	D	390.234710	195.620993	373.208161	187.107719	372.224145	186.615711	3
9	1007.577175	504.292226	990.550626	495.778951	989.566610	495.286943	K	275.207767	138.107522	258.181218	129.594247			2
10							K	147.112804	74.060040	130.086255	65.546766			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.0	1152.675415	0.006993	LLPTLPPDKK
2.3	1152.686615	-0.004207	LAKPKPNLEK

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

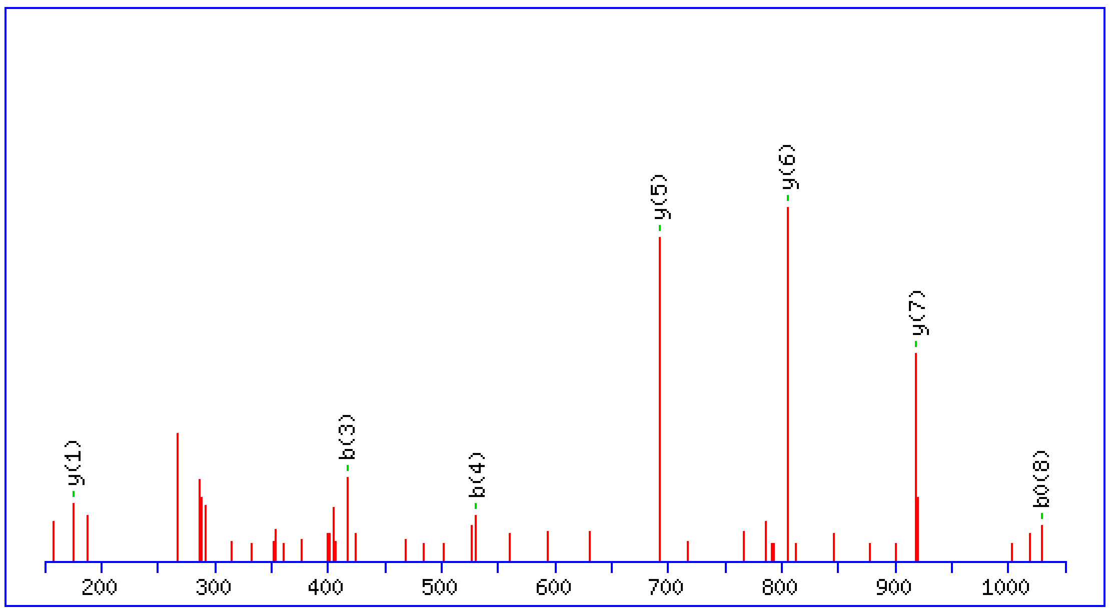
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **RFLIHHENR**
Found in **ENH1_HUMAN**, HERV-H_2q24.3 provirus ancestral Env polyprotein OS=Homo sapiens PE=2 SV=1

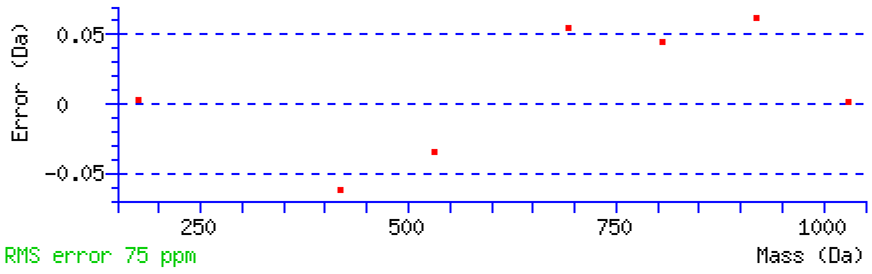
Match to Query 32185: 1220.650868 from(611.332710,2+) rtinseconds(3788) index(53798)
Title: Locus:1.1.1.2762.9
Data file 2011-11-14 - TFD - EP 8-5.mgf

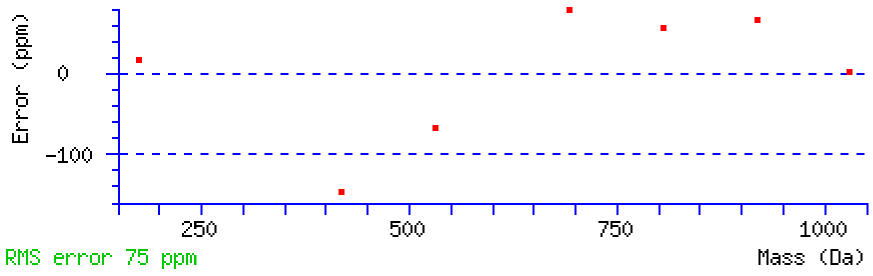
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1220.652649
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 32  Expect: 0.0067
Matches : 7/80 fragment ions using 9 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	157.108387	79.057831	140.081838	70.544557			R							9
2	304.176801	152.592039	287.150252	144.078764			F	1065.558838	533.283057	1048.532289	524.769783	1047.548273	524.277775	8
3	**417.260865**	209.134071	400.234316	200.620796			L	***918.490424***	459.748850	901.463875	451.235576	900.479859	450.743568	7
4	**530.344929**	265.676103	513.318380	257.162828			I	***805.406360***	403.206818	788.379811	394.693544	787.395795	394.201536	6
5	667.403841	334.205559	650.377292	325.692284			H	***692.322296***	346.664786	675.295747	338.151512	674.311731	337.659504	5
6	804.462753	402.735015	787.436204	394.221740			H	555.263384	278.135330	538.236835	269.622056	537.252819	269.130048	4
7	933.505346	467.256311	916.478797	458.743037	915.494781	458.251029	E	418.204472	209.605874	401.177923	201.092600	400.193907	200.600592	3
8	1047.548273	524.277775	1030.521724	515.764500	1029.537708	515.272492	N	289.161879	145.084577	272.135330	136.571303			2
9							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.5	1220.652649	-0.001781	RFLIHHENR
27.6	1220.640076	0.010792	ASSGLLYPLER
10.9	1220.640076	0.010792	LFASADISLER
9.0	1220.640091	0.010777	SDVDQLYLIR
7.5	1220.662537	-0.011669	RESPSPAPKPR
5.1	1220.640091	0.010777	SFDALLADLTR
1.3	1220.658707	-0.007839	CNKTLPIAFK

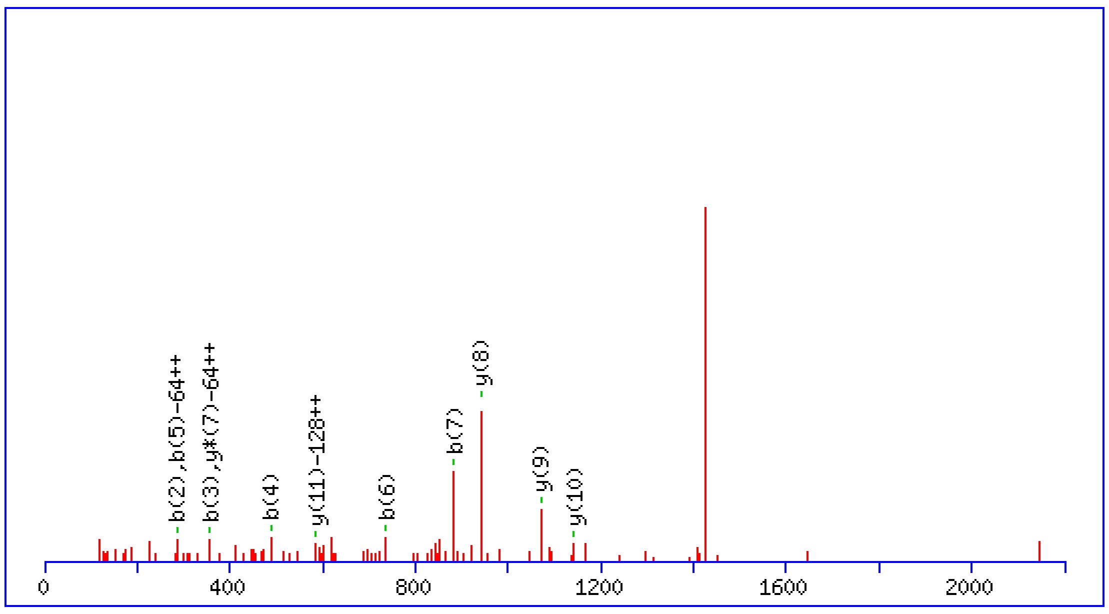
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ERAMMTMVVLSK**
Found in **ENK1_HUMAN**, HERV-K_12q14.1 provirus ancestral Env polyprotein OS=Homo sapiens PE=1 SV=1

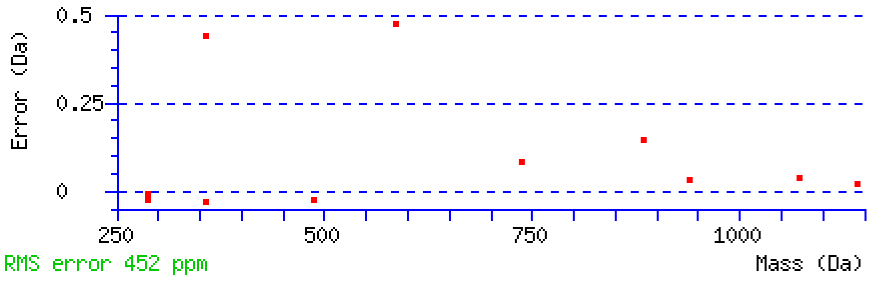
Match to Query 41244: 1426.709568 from(714.362060,2+) rtinseconds(2482) index(28139)
Title: Locus:1.1.1.2585.42
Data file 2011-11-12 - TFD - EP 5-2.mgf

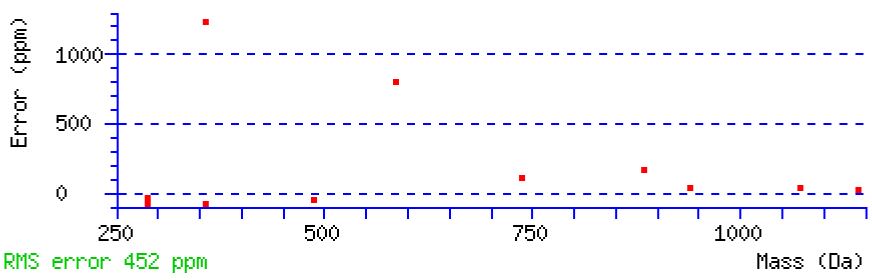
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1426.698212
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M5      : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
M7      : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 35  Expect: 0.005
Matches : 11/206 fragment ions using 13 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	130.049869	65.528572			112.039304	56.523290	E							12
2	***286.150980***	143.579128	269.124431	135.065854	268.140415	134.573846	R	1298.662913	649.835094	1281.636364	641.321820	1280.652348	640.829812	11
3	***357.188094***	179.097685	340.161545	170.584411	339.177529	170.092403	A	**1142.561802**	571.784539	1125.535253	563.271265	1124.551237	562.779256	10
4	***488.228579***	244.617928	471.202030	236.104653	470.218014	235.612645	M	**1071.524688**	536.265982	1054.498139	527.752708	1053.514123	527.260699	9
5	635.263979	318.135628	618.237430	309.622353	617.253414	309.130345	M	**940.484203**	470.745740	923.457654	462.232465	922.473638	461.740457	8
6	***736.311658***	368.659467	719.285109	360.146193	718.301093	359.654185	T	793.448803	397.228040	776.422254	388.714765	775.438238	388.222757	7
7	***883.347058***	442.177167	866.320509	433.663893	865.336493	433.171885	M	692.401124	346.704200	675.374575	338.190925	674.390559	337.698917	6
8	982.415472	491.711374	965.388923	483.198100	964.404907	482.706092	V	545.365724	273.186500	528.339175	264.673226	527.355159	264.181218	5
9	1081.483886	541.245581	1064.457337	532.732307	1063.473321	532.240298	V	446.297310	223.652293	429.270761	215.139018	428.286745	214.647010	4
10	1194.567950	597.787613	1177.541401	589.274339	1176.557385	588.782330	L	347.228896	174.118086	330.202347	165.604811	329.218331	165.112803	3
11	1281.599978	641.303627	1264.573429	632.790353	1263.589413	632.298344	S	234.144832	117.576054	217.118283	109.062780	216.134267	108.570772	2
12							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.8	1426.698212	0.011356	ERAMMTMVVLSK
32.0	1426.706070	0.003498	MGPAMGPALGAGIER
18.5	1426.698212	0.011356	ERAMMTMVVLSK
8.8	1426.698212	0.011356	ERAMMTMVVLSK
3.6	1426.698700	0.010868	SVEDGGMPGLGRPR
1.9	1426.709244	0.000324	GDAIYSAVYDVVR

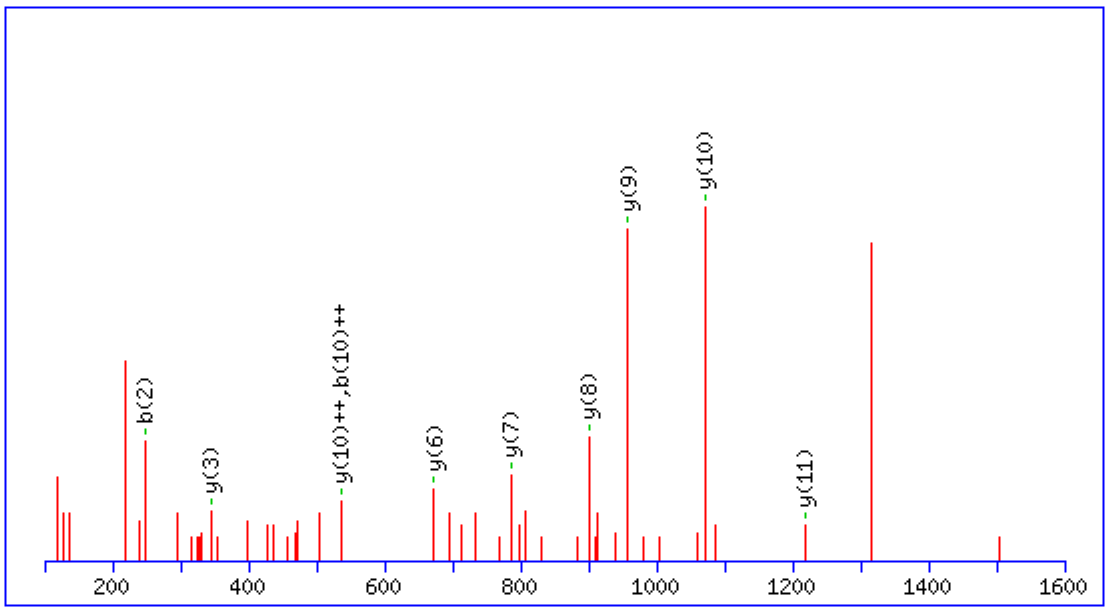
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VFIGNLNTLVVK**
Found in **HNRCL_HUMAN**, Heterogeneous nuclear ribonucleoprotein C-like 1 OS=Homo sapiens GN=HNRNPCL1 PE=1 SV=1

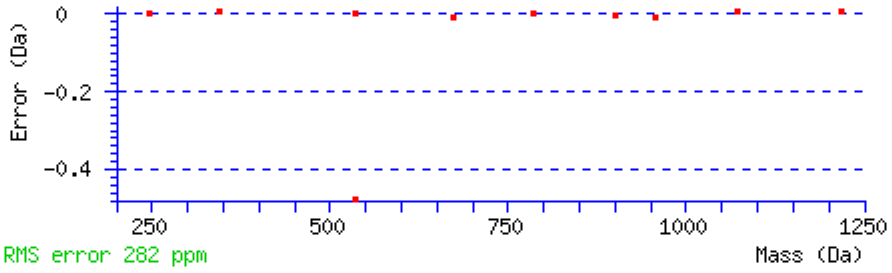
Match to Query 32880: 1315.786808 from(658.900680,2+) rtinseconds(3217) index(37858)
Title: Locus:1.1.1.2560.22
Data file 2011-11-12 - TFD - EP 6-7.mgf

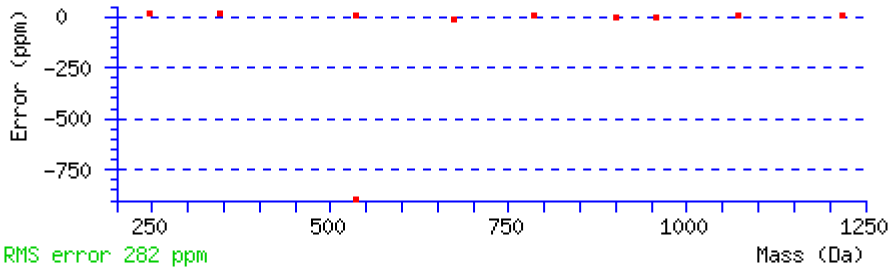
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1315.786377
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 55 **Expect:** 4.9e-006
Matches : 10/102 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	100.075690	50.541483					**V**							12
2	247.144104	124.075690					**F**	***1217.725235***	609.366256	1200.698686	600.852981	1199.714670	600.360973	11
3	360.228168	180.617722					**I**	***1070.656821***	535.832049	1053.630272	527.318774	1052.646256	526.826766	10
4	417.249632	209.128454					**G**	***957.572757***	479.290017	940.546208	470.776742	939.562192	470.284734	9
5	531.292559	266.149918	514.266010	257.636643			**N**	***900.551293***	450.779285	883.524744	442.266010	882.540728	441.774002	8
6	644.376623	322.691950	627.350074	314.178675			**L**	***786.508366***	393.757821	769.481817	385.244547	768.497801	384.752539	7
7	758.419550	379.713413	741.393001	371.200138			**N**	***673.424302***	337.215789	656.397753	328.702515	655.413737	328.210507	6
8	859.467229	430.237253	842.440680	421.723978	841.456664	421.231970	**T**	559.381375	280.194326	542.354826	271.681051	541.370810	271.189043	5
9	972.551293	486.779285	955.524744	478.266010	954.540728	477.774002	**L**	458.333696	229.670486	441.307147	221.157212			4
10	1071.619707	536.313492	1054.593158	527.800217	1053.609142	527.308209	**V**	***345.249632***	173.128454	328.223083	164.615180			3
11	1170.688121	585.847699	1153.661572	577.334424	1152.677556	576.842416	**V**	246.181218	123.594247	229.154669	115.080973			2
12							**K**	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.6	1315.786377	0.000431	VFIGNLNTLVVK

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

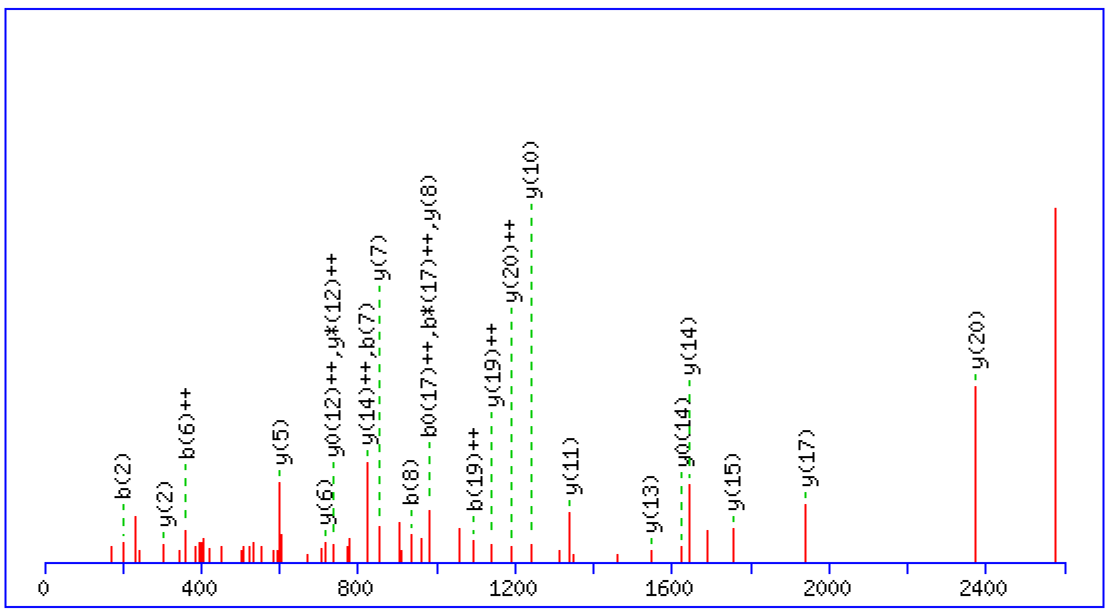
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AEPYCSVLPGFTFIQHLPLSER**
Found in **HNRL1_HUMAN**, Heterogeneous nuclear ribonucleoprotein U-like protein 1 OS=Homo sapiens GN=HNRNPUL1 PE=1 SV=2

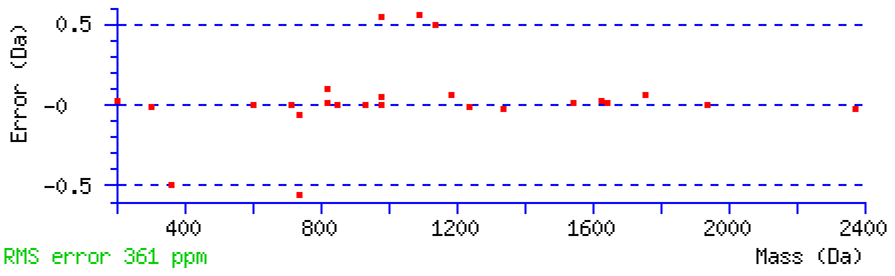
Match to Query 66639: 2574.300732 from(859.107520,3+) rtinseconds(4130) index(59944)
Title: Locus:1.1.1.3012.22
Data file 2011-11-14 - TFD - EP 7-2.mgf

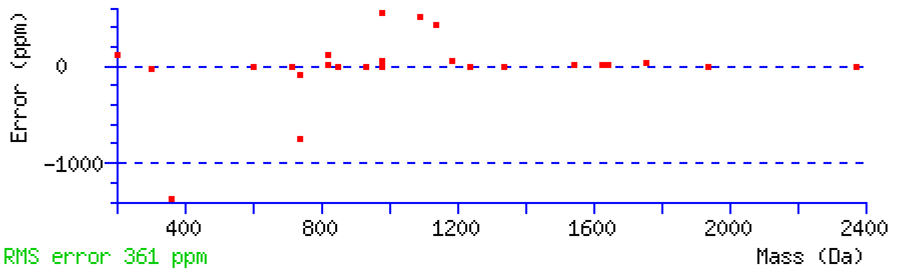
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2574.294067
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 82  Expect: 4.1e-008
Matches : 25/220 fragment ions using 32 most intense peaks   (help)
```

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	72.044390	36.525833					A							22
2	**201.086983**	101.047130			183.076418	92.041847	E	2504.264245	1252.635760	2487.237696	1244.122486	2486.253680	1243.630478	21
3	298.139747	149.573512			280.129182	140.568229	P	***2375.221652***	1188.114464	2358.195103	1179.601189	2357.211087	1179.109181	20
4	461.203076	231.105176			443.192511	222.099894	Y	2278.168888	1139.588082	2261.142339	1131.074807	2260.158323	1130.582799	19
5	635.249375	318.128326			617.238810	309.123043	C	2115.105559	1058.056417	2098.079010	1049.543143	2097.094994	1049.051135	18
6	722.281403	**361.644340**			704.270838	352.639057	S	***1941.059260***	971.033268	1924.032711	962.519993	1923.048695	962.027985	17
7	**821.349817**	411.178547			803.339252	402.173264	V	1854.027232	927.517254	1837.000683	919.003979	1836.016667	918.511971	16
8	**934.433881**	467.720579			916.423316	458.715296	L	***1754.958818***	877.983047	1737.932269	869.469772	1736.948253	868.977764	15
9	1031.486645	516.246961			1013.476080	507.241678	P	***1641.874754***	821.441015	1624.848205	812.927740	1623.864189	812.435732	14
10	1088.508109	544.757692			1070.497544	535.752410	G	***1544.821990***	772.914633	1527.795441	764.401359	1526.811425	763.909350	13
11	1235.576523	618.291900			1217.565958	609.286617	F	1487.800526	744.403901	1470.773977	735.890627	1469.789961	735.398619	12
12	1336.624202	668.815739			1318.613637	659.810456	T	***1340.732112***	670.869694	1323.705563	662.356420	1322.721547	661.864411	11
13	1483.692616	742.349946			1465.682051	733.344664	F	***1239.684433***	620.345854	1222.657884	611.832580	1221.673868	611.340572	10
14	1596.776680	798.891978			1578.766115	789.886695	I	1092.616019	546.811647	1075.589470	538.298373	1074.605454	537.806365	9
15	1724.835258	862.921267	1707.808709	854.407992	1706.824693	853.915984	Q	***979.531955***	490.269615	962.505406	481.756341	961.521390	481.264333	8
16	1861.894170	931.450723	1844.867621	922.937448	1843.883605	922.445440	H	***851.473377***	426.240327	834.446828	417.727052	833.462812	417.235044	7
17	1974.978234	987.992755	1957.951685	979.479480	1956.967669	978.987472	L	***714.414465***	357.710871	697.387916	349.197596	696.403900	348.705588	6
18	2072.030998	1036.519137	2055.004449	1028.005862	2054.020433	1027.513854	P	***601.330401***	301.168839	584.303852	292.655564	583.319836	292.163556	5
19	2185.115062	**1093.061169**	2168.088513	1084.547894	2167.104497	1084.055886	L	504.277637	252.642457	487.251088	244.129182	486.267072	243.637174	4
20	2272.147090	1136.577183	2255.120541	1128.063908	2254.136525	1127.571900	S	391.193573	196.100425	374.167024	187.587150	373.183008	187.095142	3
21	2401.189683	1201.098479	2384.163134	1192.585205	2383.179118	1192.093197	E	***304.161545***	152.584411	287.134996	144.071136	286.150980	143.579128	2
22							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
82.1	2574.294067	0.006665	AEPYCSVLPGFTFIQHLPLSER
3.2	2574.286194	0.014538	LSPQEISYFQFPGELLMRMLK
2.5	2574.286194	0.014538	LSPQEISYFQFPGELLMRMLK
1.5	2574.319748	-0.019016	GGACQTPTVGNRQTPTLGIHARPR
0.1	2574.311157	-0.010425	LPMDLLVLEDEKHHGAQSAALQK

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

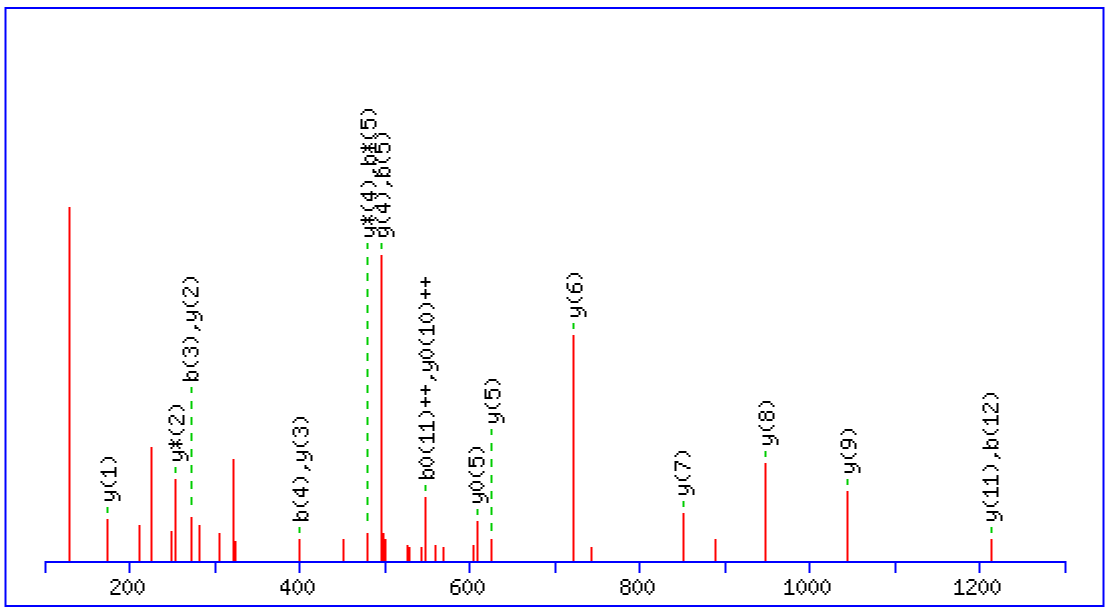
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSAKPAPPKPEPKPR**
Found in **HMGN3_HUMAN**, High mobility group nucleosome-binding domain-containing protein 3 OS=Homo sapiens GN=HMGN3 PE=1 SV=2

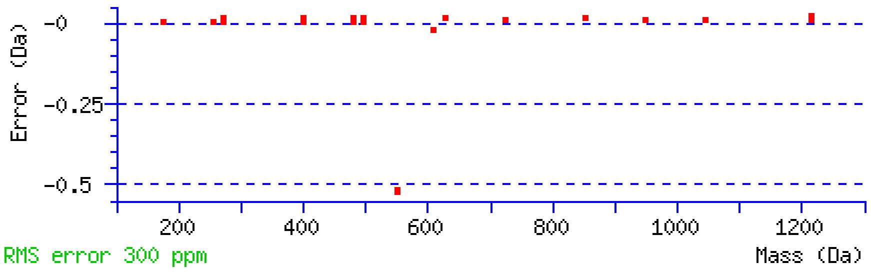
Match to Query 47639: 1611.944736 from(403.993460,4+) rtinseconds(862) index(871)
Title: Locus:1.1.1.1599.2
Data file 2011-11-14 - TFD - EP 8-6.mgf

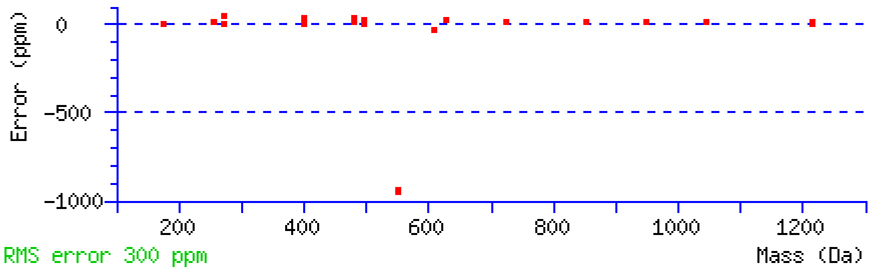
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1611.946014
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 83 **Expect:** 9.2e-009
Matches : 20/152 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					L							15
2	201.123368	101.065322			183.112803	92.060039	S	1499.869274	750.438275	1482.842725	741.925001	1481.858709	741.432993	14
3	**272.160482**	136.583879			254.149917	127.578596	A	1412.837246	706.922261	1395.810697	698.408987	1394.826681	697.916979	13
4	**400.255445**	200.631360	383.228896	192.118086	382.244880	191.626078	K	1341.800132	671.403704	1324.773583	662.890430	1323.789567	662.398422	12
5	**497.308209**	249.157742	480.281660	240.644468	479.297644	240.152460	P	***1213.705169***	607.356223	1196.678620	598.842948	1195.694604	598.350940	11
6	568.345323	284.676300	551.318774	276.163025	550.334758	275.671017	A	1116.652405	558.829841	1099.625856	550.316566	1098.641840	549.824558	10
7	665.398087	333.202682	648.371538	324.689407	647.387522	324.197399	P	***1045.615291***	523.311284	1028.588742	514.798009	1027.604726	514.306001	9
8	762.450851	381.729064	745.424302	373.215789	744.440286	372.723781	P	***948.562527***	474.784902	931.535978	466.271627	930.551962	465.779619	8
9	890.545814	445.776545	873.519265	437.263271	872.535249	436.771263	K	***851.509763***	426.258520	834.483214	417.745245	833.499198	417.253237	7
10	987.598578	494.302927	970.572029	485.789653	969.588013	485.297645	P	***723.414800***	362.211038	706.388251	353.697764	705.404235	353.205756	6
11	1116.641171	558.824224	1099.614622	550.310949	1098.630606	549.818941	E	***626.362036***	313.684656	609.335487	305.171382	608.351471	304.679374	5
12	**1213.693935**	607.350606	1196.667386	598.837331	1195.683370	598.345323	P	***497.319443***	249.163359	480.292894	240.650085			4
13	1341.788898	671.398087	1324.762349	662.884813	1323.778333	662.392805	K	***400.266679***	200.636977	383.240130	192.123703			3
14	1438.841662	719.924469	1421.815113	711.411195	1420.831097	710.919187	P	***272.171716***	136.589496	255.145167	128.076221			2
15							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
83.4	1611.946014	-0.001278	LSAKPAPPKPEPKPR
54.0	1611.946014	-0.001278	LSAKPAPPKPEPRPK

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

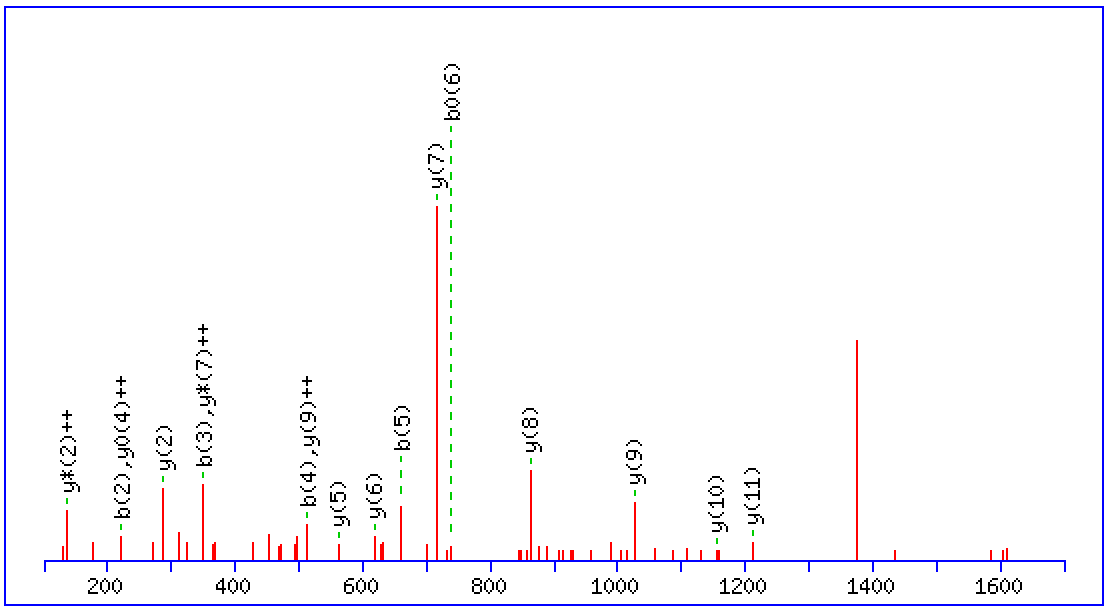
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YGEYFPGTGDLR**
Found in **HDAC1_HUMAN**, Histone deacetylase 1 OS=Homo sapiens GN=HDAC1 PE=1 SV=1

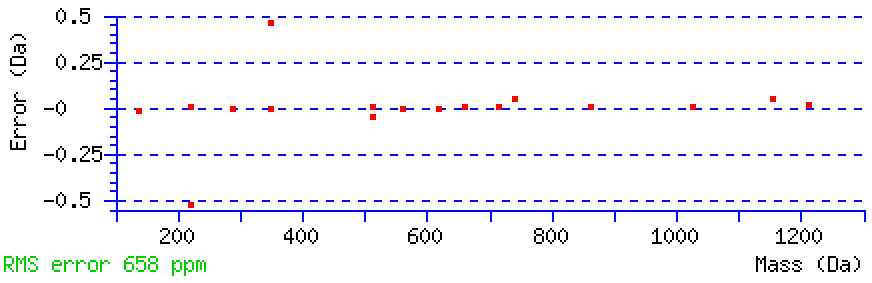
Match to Query 38024: 1373.630788 from(687.822670,2+) rtinseconds(2598) index(34681)
Title: Locus:1.1.1.2408.36
Data file 2011-11-10 - TFD - EP 3-3.mgf

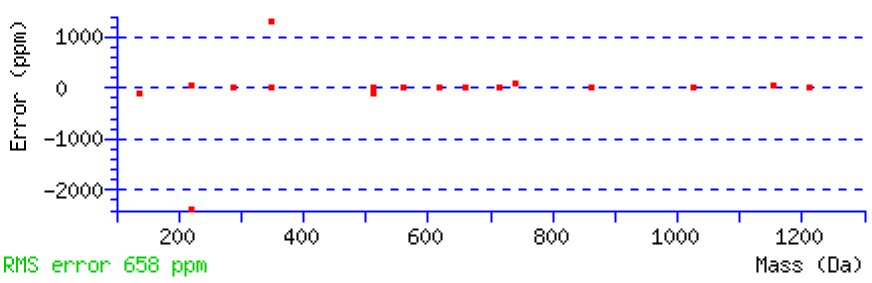
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1373.625183
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 59  Expect: 3.2e-006
Matches : 17/102 fragment ions using 22 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.070605	82.538940			Y							12
2	**221.092069**	111.049673			G	***1211.569130***	606.288203	1194.542581	597.774928	1193.558565	597.282920	11
3	**350.134662**	175.570969	332.124097	166.565687	E	***1154.547666***	577.777471	1137.521117	569.264197	1136.537101	568.772188	10
4	**513.197991**	257.102634	495.187426	248.097351	Y	***1025.505073***	513.256175	1008.478524	504.742900	1007.494508	504.250892	9
5	**660.266405**	330.636841	642.255840	321.631558	F	***862.441744***	431.724510	845.415195	423.211235	844.431179	422.719227	8
6	757.319169	379.163223	739.308604	370.157940	P	***715.373330***	358.190303	698.346781	349.677029	697.362765	349.185021	7
7	814.340633	407.673955	796.330068	398.668672	G	***618.320566***	309.663921	601.294017	301.150646	600.310001	300.658639	6
8	915.388312	458.197794	897.377747	449.192512	T	***561.299102***	281.153189	544.272553	272.639914	543.288537	272.147906	5
9	972.409776	486.708526	954.399211	477.703244	G	460.251423	230.629349	443.224874	222.116075	442.240858	221.624067	4
10	1087.436719	544.221998	1069.426154	535.216715	D	403.229959	202.118617	386.203410	193.605343	385.219394	193.113335	3
11	1200.520783	600.764029	1182.510218	591.758747	L	***288.203016***	144.605146	271.176467	136.091871			2
12					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of YGEYFPGTGDLR
(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	1373.625183	0.005605	YGEYFPGTGDLR
0.6	1373.624527	0.006261	MPDHDSTALLSR

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

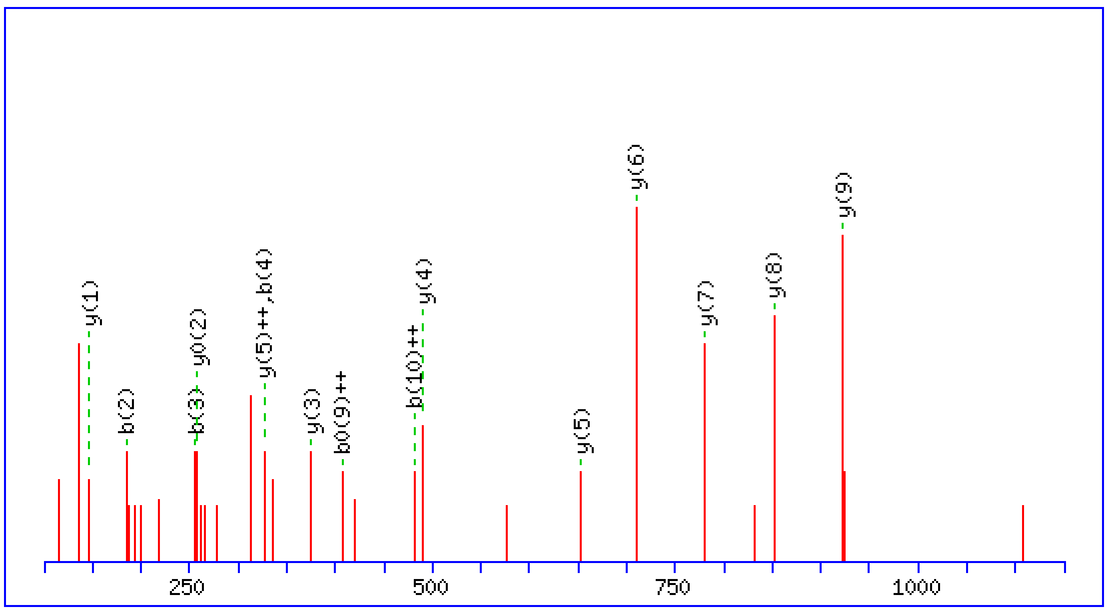
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALAAAGYDVEK**
Found in **H11_HUMAN**, Histone H1.1 OS=Homo sapiens GN=HIST1H1A PE=1 SV=3

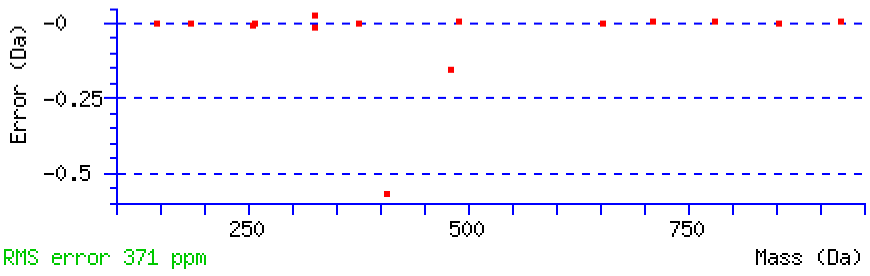
Match to Query 15263: 1106.565888 from(554.290220,2+) rtinseconds(1743) index(5423)
Title: Locus:1.1.1.2320.26
Data file 2011-11-13 - TFD - EP 7-8.mgf

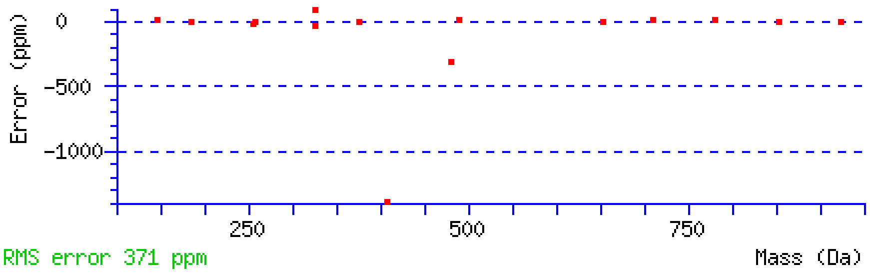
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1106.560760
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 59  Expect: 1.2e-005
Matches : 15/84 fragment ions using 23 most intense peaks   (help)
```

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	72.044390	36.525833			A							11
2	**185.128454**	93.067865			L	1036.530953	518.769115	1019.504404	510.255840	1018.520388	509.763832	10
3	**256.165568**	128.586422			A	***923.446889***	462.227082	906.420340	453.713808	905.436324	453.221800	9
4	**327.202682**	164.104979			A	***852.409775***	426.708526	835.383226	418.195251	834.399210	417.703243	8
5	398.239796	199.623536			A	***781.372661***	391.189968	764.346112	382.676694	763.362096	382.184686	7
6	455.261260	228.134268			G	***710.335547***	355.671411	693.308998	347.158137	692.324982	346.666129	6
7	618.324589	309.665933			Y	***653.314083***	327.160680	636.287534	318.647405	635.303518	318.155397	5
8	733.351532	367.179404	715.340967	358.174122	D	***490.250754***	245.629015	473.224205	237.115740	472.240189	236.623732	4
9	832.419946	416.713611	814.409381	407.708328	V	***375.223811***	188.115543	358.197262	179.602269	357.213246	179.110261	3
10	961.462539	481.234908	943.451974	472.229625	E	276.155397	138.581336	259.128848	130.068062	258.144832	129.576054	2
11					K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.9	1106.560760	0.005128	ALAAAGYDVEK
6.1	1106.560776	0.005112	NVLQFTEEK
5.6	1106.572006	-0.006118	NRDEVSFIK
3.6	1106.564148	0.001740	TMIQKDLDK
3.3	1106.572006	-0.006118	RVINDPSYK
2.9	1106.560806	0.005082	IGVVGGSDFEK
2.4	1106.560776	0.005112	LTNAEGVEFK

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

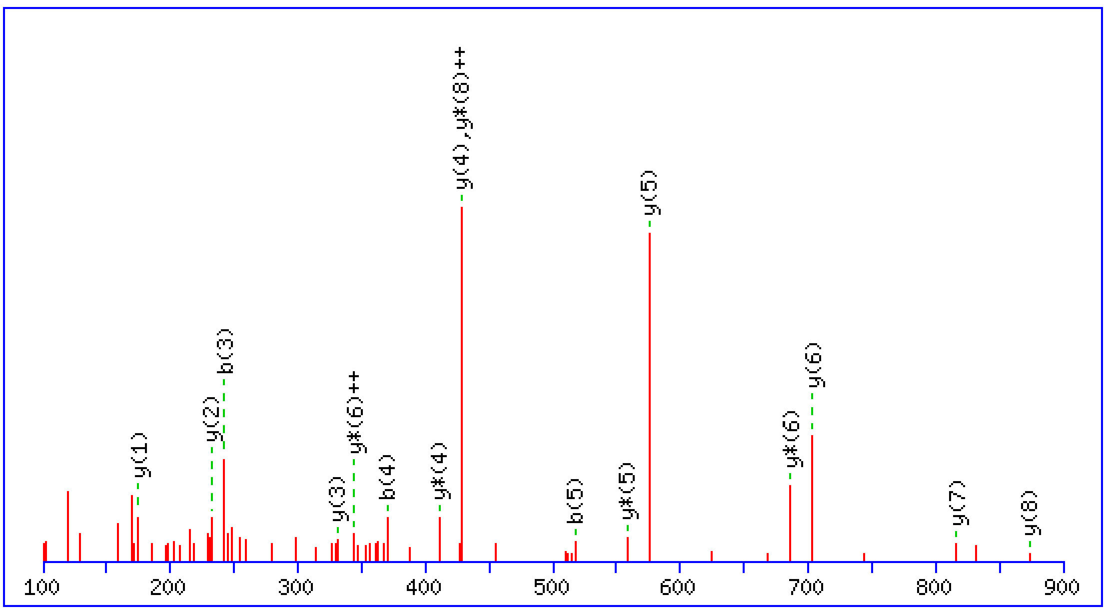
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AGLQFPVGR**
Found in **H2A1A_HUMAN**, Histone H2A type 1-A OS=Homo sapiens GN=HIST1H2AA PE=1 SV=3

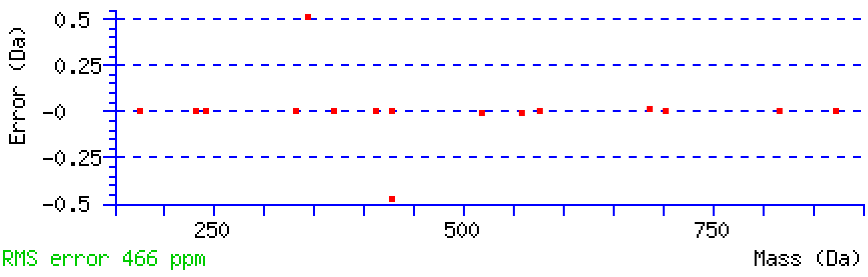
Match to Query 8651: 943.524448 from(472.769500,2+) rtinseconds(2398) index(9203)
Title: Locus:1.1.1.2527.5
Data file 2011-11-10 - TFD - EP 4-8.mgf

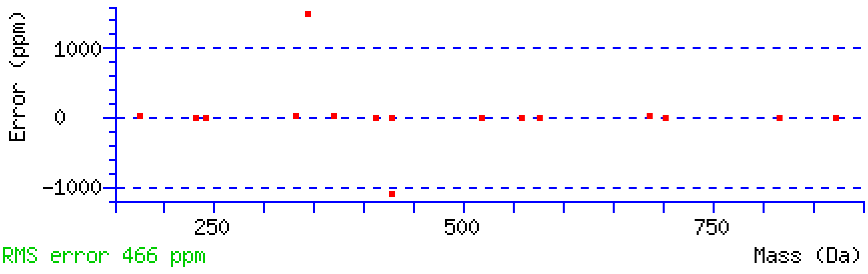
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 943.523956
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 72  Expect: 1e-006
Matches : 16/58 fragment ions using 23 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	72.044390	36.525833			A					9
2	129.065854	65.036565			G	***873.494114***	437.250695	856.467565	428.737421	8
3	**242.149918**	121.578597			L	***816.472650***	408.739963	799.446101	400.226689	7
4	**370.208496**	185.607886	353.181947	177.094612	Q	***703.388586***	352.197931	686.362037	343.684657	6
5	**517.276910**	259.142093	500.250361	250.628819	F	***575.330008***	288.168642	558.303459	279.655368	5
6	614.329674	307.668475	597.303125	299.155201	P	***428.261594***	214.634435	411.235045	206.121160	4
7	713.398088	357.202682	696.371539	348.689408	V	***331.208830***	166.108053	314.182281	157.594778	3
8	770.419552	385.713414	753.393003	377.200140	G	***232.140416***	116.573846	215.113867	108.060571	2
9					R	***175.118952***	88.063114	158.092403	79.549839	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
72.2	943.523956	0.000492	AGLQFPVGR
18.7	943.523926	0.000522	KIQNQWK
18.7	943.533813	-0.009365	QLKGLEEK
16.0	943.533829	-0.009381	KTTPQELK
12.9	943.533829	-0.009381	LQKSPVEK
12.0	943.527298	-0.002850	AGLLGLCAR
11.4	943.533813	-0.009365	KLGELQEK
10.3	943.519913	0.004535	QLSRDIGR
10.0	943.533829	-0.009381	KIPVENTK
8.6	943.519913	0.004535	QIRQGNTK

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

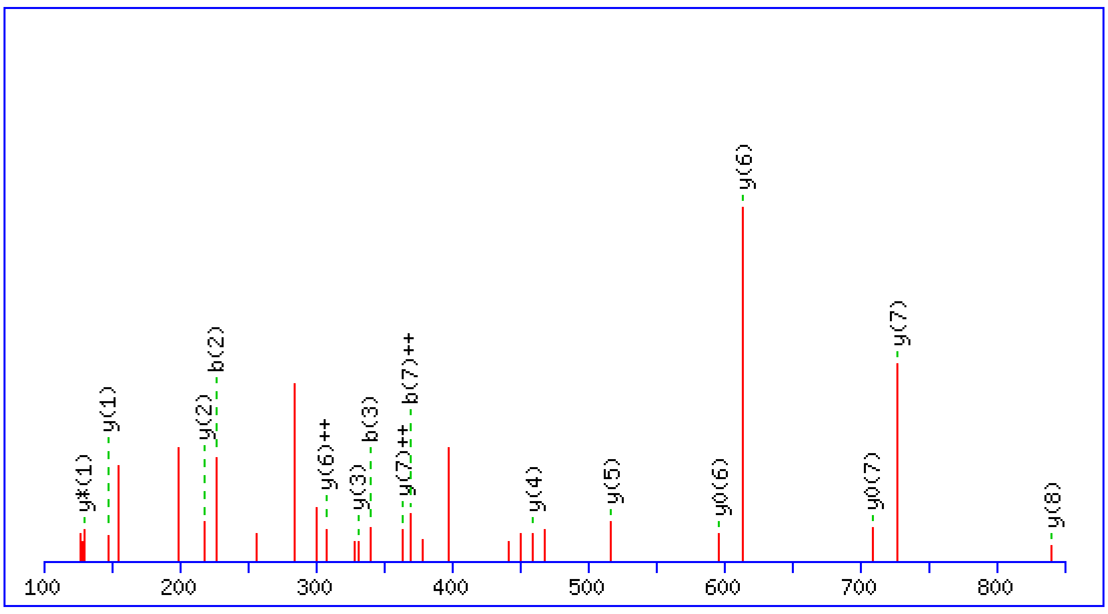
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLLPGELAK**
Found in **H2B1A_HUMAN**, Histone H2B type 1-A OS=Homo sapiens GN=HIST1H2BA PE=1 SV=3

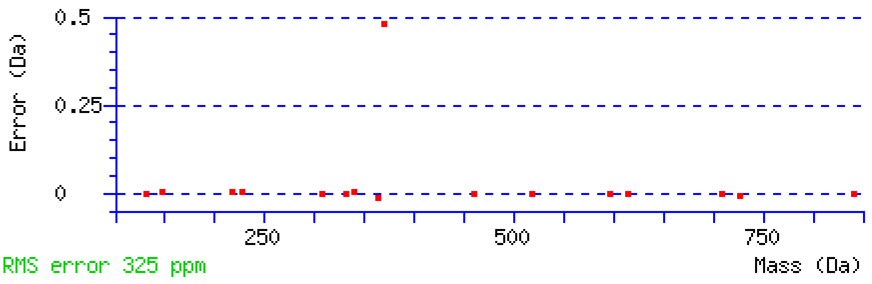
Match to Query 9083: 952.597768 from(477.306160,2+) rtinseconds(2621) index(9806)
Title: Locus:1.1.1.2611.5
Data file 2011-11-10 - TFD - EP 4-8.mgf

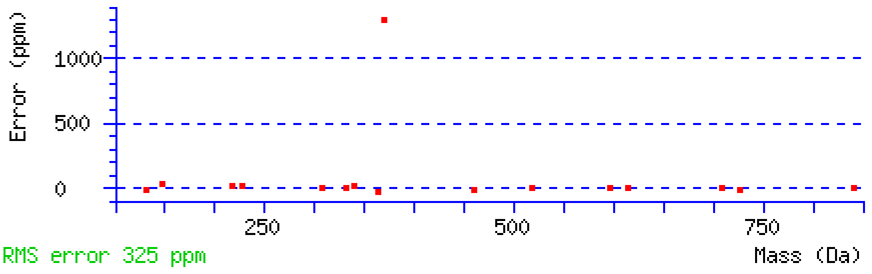
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 952.595688
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 61 **Expect:** 1.9e-006
Matches : 16/64 fragment ions using 29 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							9
2	**227.175404**	114.091340			L	***840.518931***	420.763104	823.492382	412.249829	822.508366	411.757821	8
3	**340.259468**	170.633372			L	***727.434867***	364.221072	710.408318	355.707797	709.424302	355.215789	7
4	437.312232	219.159754			P	***614.350803***	307.679040	597.324254	299.165765	596.340238	298.673757	6
5	494.333696	247.670486			G	***517.298039***	259.152658	500.271490	250.639383	499.287474	250.147375	5
6	623.376289	312.191783	605.365724	303.186500	E	***460.276575***	230.641926	443.250026	222.128651	442.266010	221.636643	4
7	736.460353	368.733815	718.449788	359.728532	L	***331.233982***	166.120629	314.207433	157.607354			3
8	807.497467	404.252372	789.486902	395.247089	A	***218.149918***	109.578597	201.123369	101.065322			2
9					K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
61.1	952.595688	0.002080	LLLPGELAK
30.8	952.595688	0.002080	IIIPEIQK
25.2	952.606918	-0.009150	LILPNKQK
22.8	952.597031	0.000737	LLIPRWR
22.0	952.606934	-0.009166	LLLGATLPR
20.5	952.595703	0.002065	ILGILPPSK
19.2	952.606934	-0.009166	EPLKVVLR
19.1	952.595688	0.002080	ILLLEAGPK
18.3	952.595688	0.002080	LLIKEPPK
17.4	952.595688	0.002080	LLIKEPPK

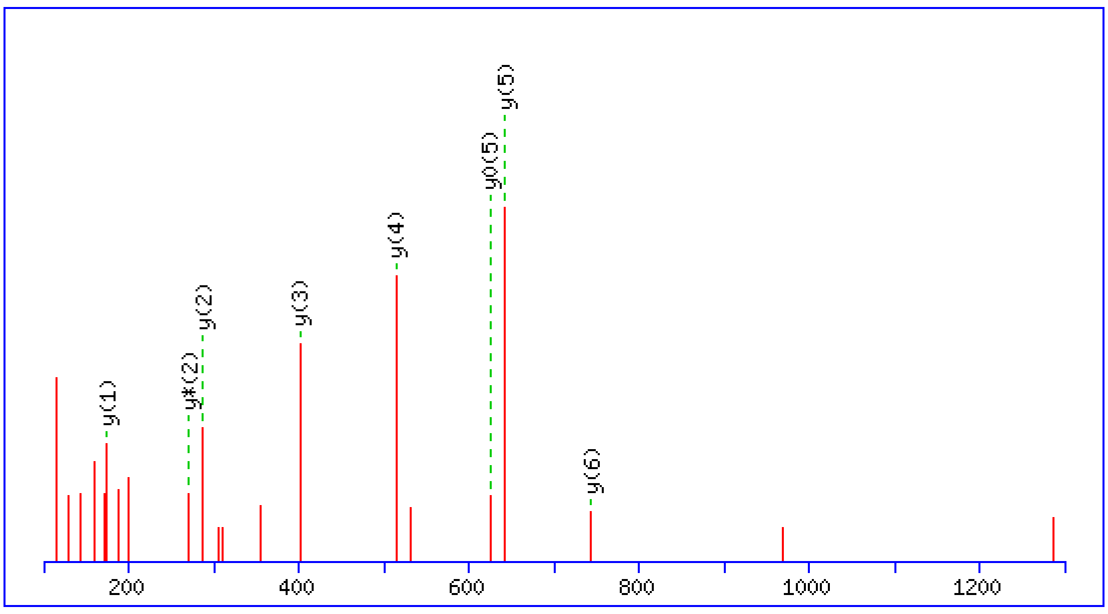
Mascot Search Results

Peptide View

MS/MS Fragmentation of **STELLIR**
Found in **H31T_HUMAN**, Histone H3.1t OS=Homo sapiens GN=HIST3H3 PE=1 SV=3

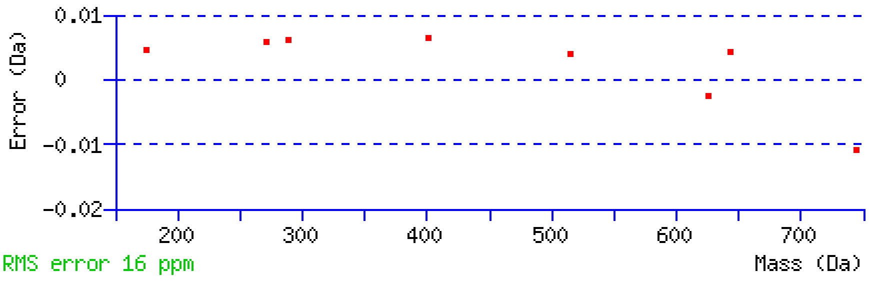
Match to Query 2823: 830.491748 from(416.253150,2+) rtinseconds(1888) index(19168)
Title: Locus:1.1.1.2041.5
Data file 2011-11-14 - TFD - EP 8-5.mgf

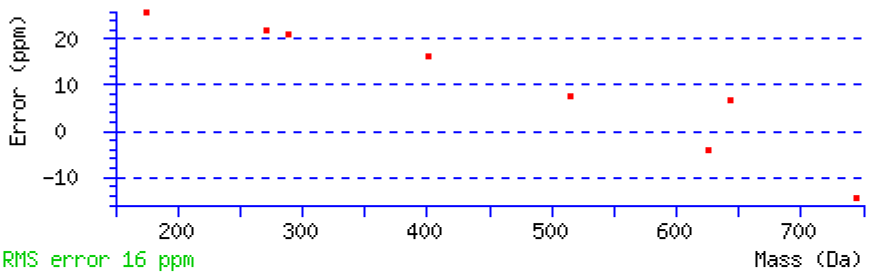
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 830.486145
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 55 **Expect:** 3e-005
Matches : 8/52 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	**S**							7
2	189.086983	95.047129	171.076418	86.041847	**T**	***744.461416***	372.734346	727.434867	364.221072	726.450851	363.729064	6
3	318.129576	159.568426	300.119011	150.563144	**E**	***643.413737***	322.210507	626.387188	313.697232	625.403172	313.205224	5
4	431.213640	216.110458	413.203075	207.105176	**L**	***514.371144***	257.689210	497.344595	249.175936			4
5	544.297704	272.652490	526.287139	263.647208	**L**	***401.287080***	201.147178	384.260531	192.633904			3
6	657.381768	329.194522	639.371203	320.189240	**I**	***288.203016***	144.605146	271.176467	136.091872			2
7					**R**	***175.118952***	88.063114	158.092403	79.549840			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.0	830.486145	0.005603	STELLIR
10.8	830.486145	0.005603	TELSLLR
9.5	830.486145	0.005603	ESLTLLR
9.5	830.487503	0.004245	HVGHLLR
9.5	830.497375	-0.005627	KSNTLLR
9.5	830.498718	-0.006970	RHHLIR
8.3	830.497391	-0.005643	AGTSVKLR
7.9	830.497375	-0.005627	SKLSQLR
7.6	830.497391	-0.005643	SVAKTLGR
5.6	830.486160	0.005588	STAPVKTK

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

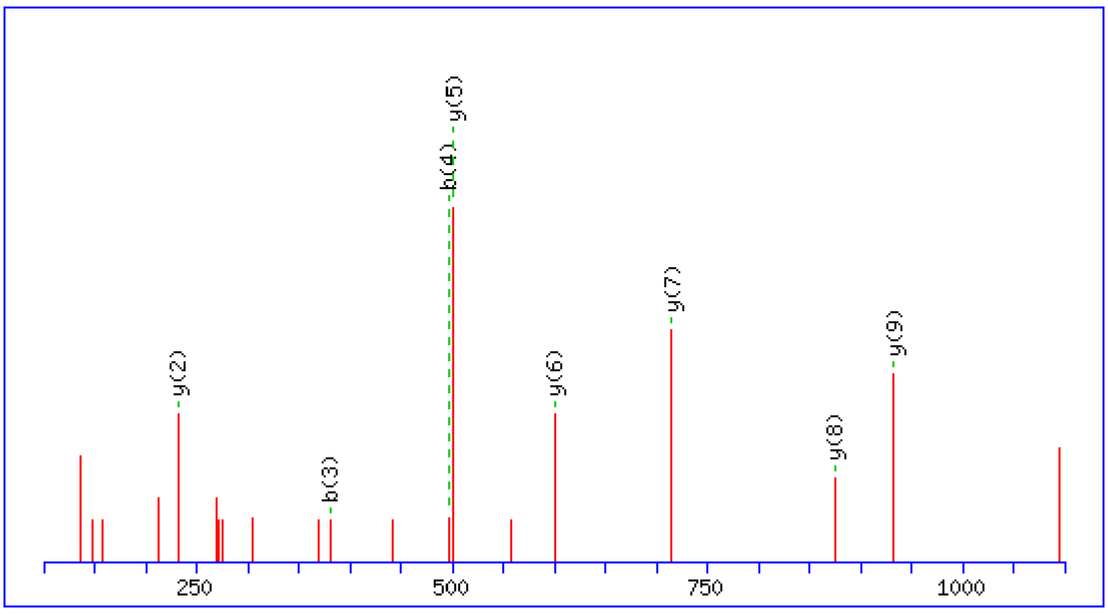
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YGCDVGPDGR**
Found in **1A01_HUMAN**, HLA class I histocompatibility antigen, A-1 alpha chain OS=Homo sapiens GN=HLA-A PE=1 SV=1

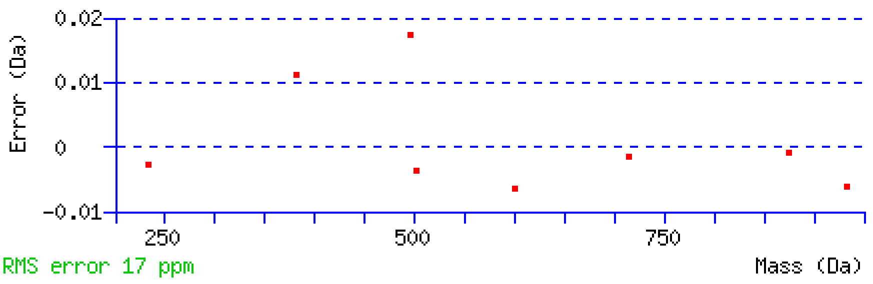
Match to Query 387291: 1094.443468 from(548.229010,2+) rtinseconds(1141) index(414283)
Title: Locus:1.1.1.770.31
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

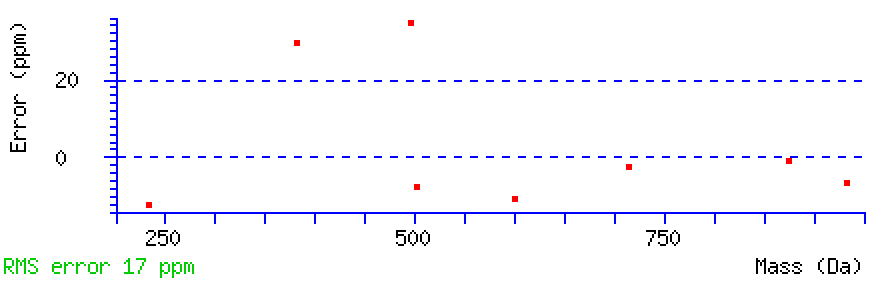
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1094.445129
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 46 **Expect:** 0.00014
Matches : 8/80 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.070605	82.538940			Y							10
2	221.092069	111.049673			G	***932.389057***	466.698167	915.362508	458.184892	914.378492	457.692884	9
3	**381.122718**	191.064997			C	***875.367593***	438.187435	858.341044	429.674160	857.357028	429.182152	8
4	**496.149661**	248.578469	478.139096	239.573186	D	***715.336944***	358.172110	698.310395	349.658836	697.326379	349.166828	7
5	595.218075	298.112676	577.207510	289.107393	V	***600.310001***	300.658639	583.283452	292.145364	582.299436	291.653356	6
6	652.239539	326.623408	634.228974	317.618125	G	***501.241587***	251.124431	484.215038	242.611157	483.231022	242.119149	5
7	749.292303	375.149790	731.281738	366.144507	P	444.220123	222.613699	427.193574	214.100425	426.209558	213.608417	4
8	864.319246	432.663261	846.308681	423.657979	D	347.167359	174.087317	330.140810	165.574043	329.156794	165.082035	3
9	921.340710	461.173993	903.330145	452.168711	G	***232.140416***	116.573846	215.113867	108.060571			2
10					R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.8	1094.445129	-0.001661	YGCDVGPDGR

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

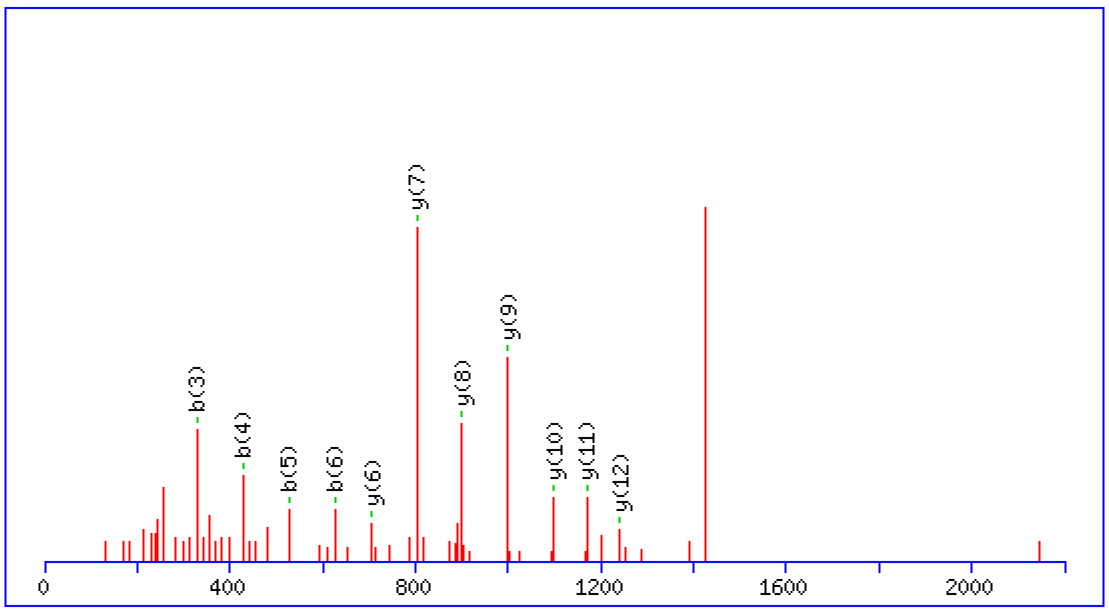
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **WAAVVVPSGEEQR**
Found in **1A01_HUMAN**, HLA class I histocompatibility antigen, A-1 alpha chain OS=Homo sapiens GN=HLA-A PE=1 SV=1

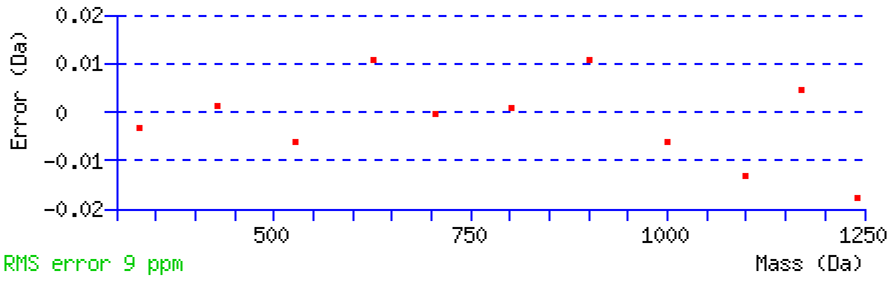
Match to Query 42630: 1426.722108 from(714.368330,2+) rtinseconds(2286) index(28422)
Title: Locus:1.1.1.2197.43
Data file 2011-11-10 - TFD - EP 4-4.mgf

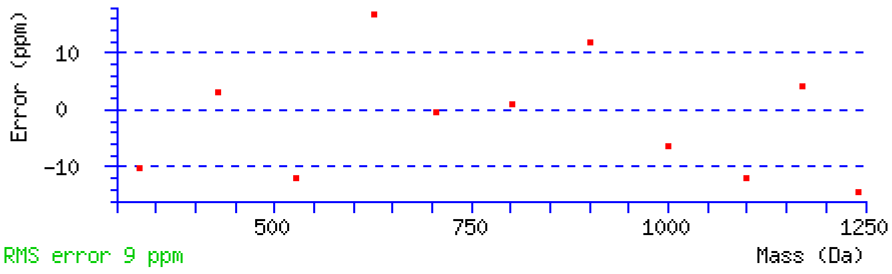
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1426.720474
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 63 **Expect:** 2.5e-006
Matches : 11/104 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	187.086589	94.046932					W							13
2	258.123703	129.565490					A	***1241.648442***	621.327859	1224.621893	612.814585	1223.637877	612.322577	12
3	**329.160817**	165.084047					A	***1170.611328***	585.809302	1153.584779	577.296028	1152.600763	576.804020	11
4	**428.229231**	214.618254					V	***1099.574214***	550.290745	1082.547665	541.777471	1081.563649	541.285462	10
5	**527.297645**	264.152461					V	***1000.505800***	500.756538	983.479251	492.243264	982.495235	491.751256	9
6	**626.366059**	313.686668					V	***901.437386***	451.222331	884.410837	442.709057	883.426821	442.217049	8
7	723.418823	362.213050					P	***802.368972***	401.688124	785.342423	393.174850	784.358407	392.682842	7
8	810.450851	405.729064			792.440286	396.723781	S	***705.316208***	353.161742	688.289659	344.648468	687.305643	344.156460	6
9	867.472315	434.239796			849.461750	425.234513	G	618.284180	309.645728	601.257631	301.132454	600.273615	300.640446	5
10	996.514908	498.761092			978.504343	489.755810	E	561.262716	281.134996	544.236167	272.621722	543.252151	272.129714	4
11	1125.557501	563.282389			1107.546936	554.277106	E	432.220123	216.613699	415.193574	208.100425	414.209558	207.608417	3
12	1253.616079	627.311678	1236.589530	618.798403	1235.605514	618.306395	Q	303.177530	152.092403	286.150981	143.579129			2
13							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
62.5	1426.720474	0.001634	WAAVVVPSGEEQR
2.7	1426.709915	0.012193	VQRPEPSCRPR

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

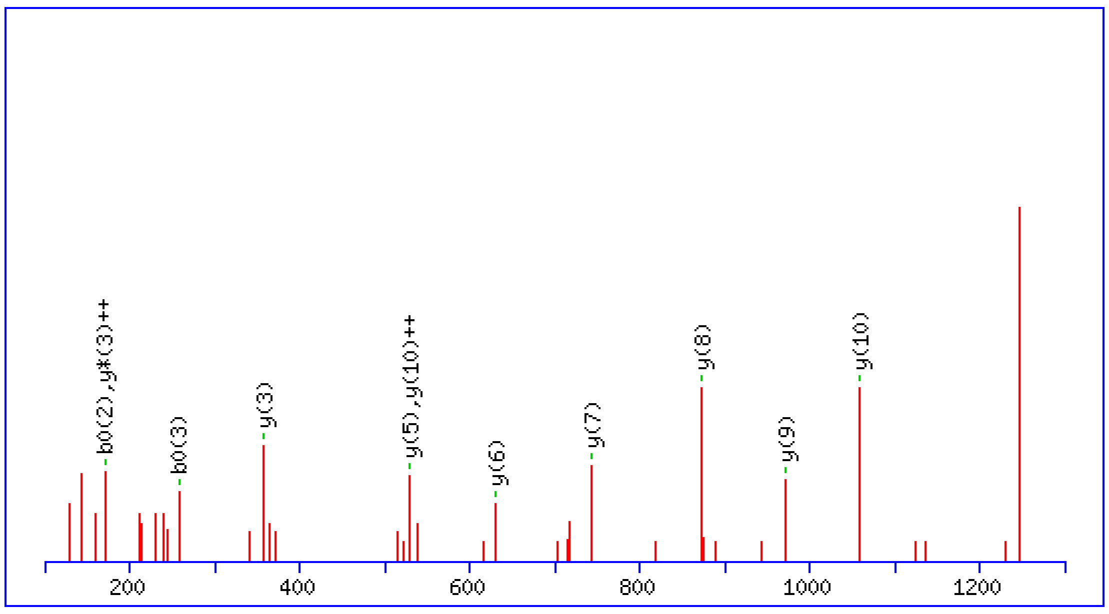
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **STSVELTGDPNK**
Found in **HCAR2_HUMAN**, Hydroxycarboxylic acid receptor 2 OS=Homo sapiens GN=HCAR2 PE=1 SV=1

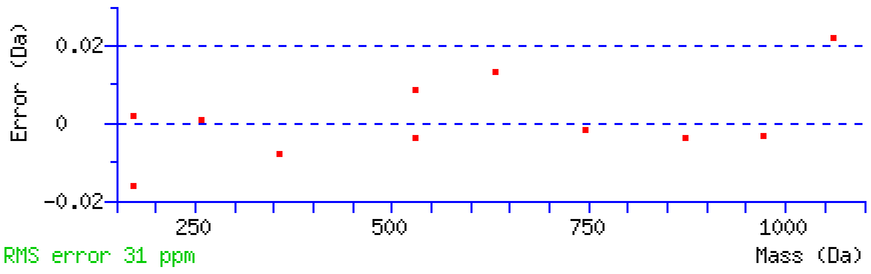
Match to Query 31877: 1246.605228 from(624.309890,2+) rtinseconds(1356) index(10769)
Title: Locus:1.1.1.1844.40
Data file 2011-11-10 - TFD - EP 4-4.mgf

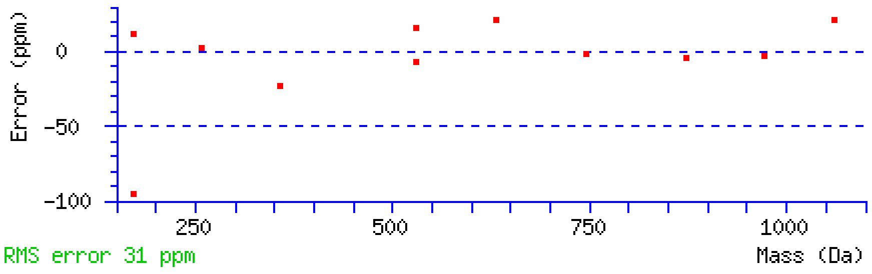
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1246.604111
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 59 **Expect:** 1.2e-005
Matches : 11/106 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							12
2	189.086983	95.047129			171.076418	86.041847	T	1160.579359	580.793318	1143.552810	572.280043	1142.568794	571.788035	11
3	276.119011	138.563143			258.108446	129.557861	S	***1059.531680***	530.269478	1042.505131	521.756204	1041.521115	521.264196	10
4	375.187425	188.097350			357.176860	179.092068	V	***972.499652***	486.753464	955.473103	478.240190	954.489087	477.748182	9
5	504.230018	252.618647			486.219453	243.613364	E	***873.431238***	437.219257	856.404689	428.705983	855.420673	428.213975	8
6	617.314082	309.160679			599.303517	300.155396	L	***744.388645***	372.697961	727.362096	364.184686	726.378080	363.692678	7
7	718.361761	359.684519			700.351196	350.679236	T	***631.304581***	316.155929	614.278032	307.642654	613.294016	307.150646	6
8	775.383225	388.195251			757.372660	379.189968	G	***530.256902***	265.632089	513.230353	257.118815	512.246337	256.626807	5
9	890.410168	445.708722			872.399603	436.703440	D	473.235438	237.121357	456.208889	228.608083	455.224873	228.116075	4
10	987.462932	494.235104			969.452367	485.229822	P	***358.208495***	179.607886	341.181946	171.094611			3
11	1101.505859	551.256568	1084.479310	542.743293	1083.495294	542.251285	N	261.155731	131.081504	244.129182	122.568229			2
12							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
59.3	1246.604111	0.001117	STSVELTGDPNK
6.6	1246.604065	0.001163	KELDEEESIR
6.0	1246.615356	-0.010128	TTAVEDTVQAGR
4.0	1246.597565	0.007663	KDNETIPCTR
3.6	1246.615326	-0.010098	QTDAQSASSPKK
3.6	1246.615326	-0.010098	KQTDAQSASSPK

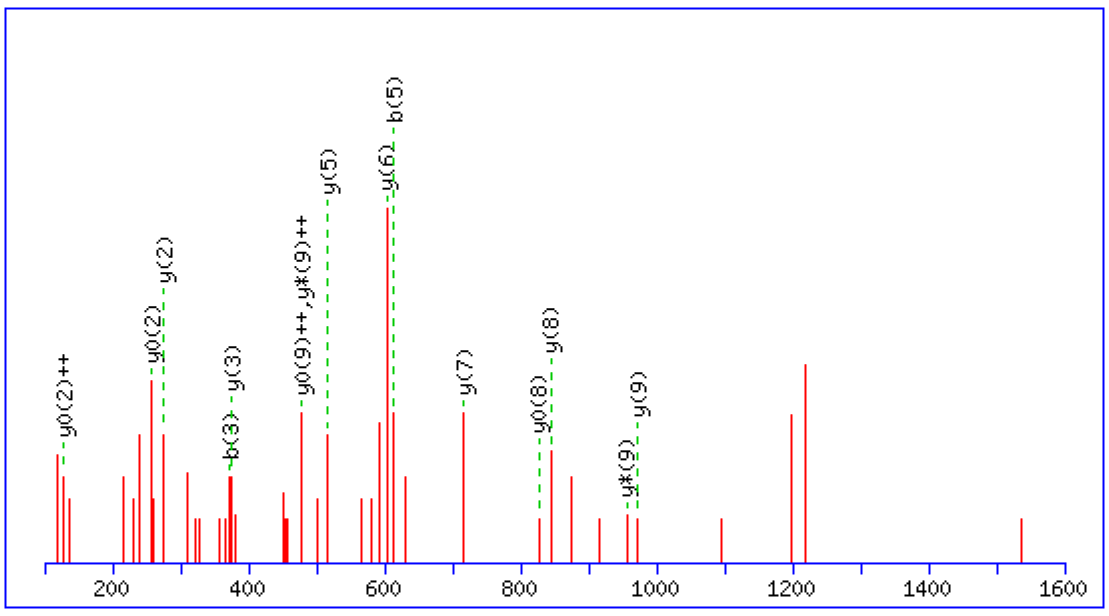
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DEQQISAAVEK**
Found in **HSDL2_HUMAN**, Hydroxysteroid dehydrogenase-like protein 2 OS=Homo sapiens GN=HSDL2 PE=1 SV=1

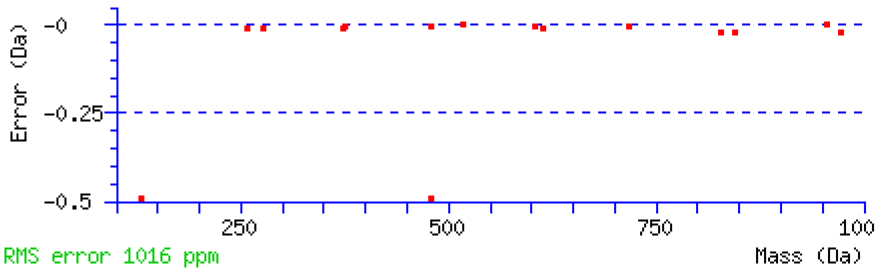
Match to Query 541580: 1216.603888 from(609.309220,2+) rtinseconds(1545) index(253999)
Title: Locus:1.1.1.1034.22
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

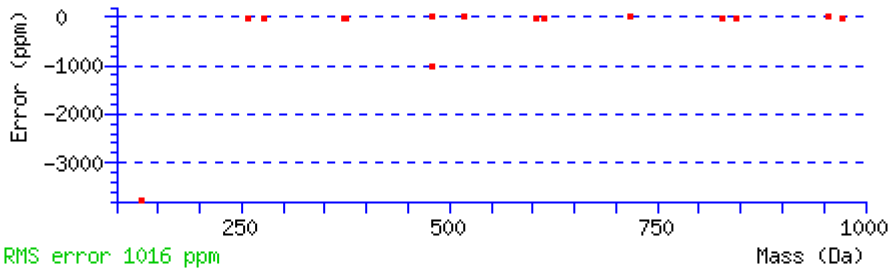
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1216.593521
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 52 **Expect:** 4.4e-005
Matches : 15/114 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	116.034219	58.520748			98.023654	49.515465	D							11
2	245.076812	123.042044			227.066247	114.036762	E	1102.573880	551.790578	1085.547331	543.277304	1084.563315	542.785295	10
3	**373.135390**	187.071333	356.108841	178.558059	355.124825	178.066051	Q	***973.531287***	487.269282	956.504738	478.756007	955.520722	478.263999	9
4	501.193968	251.100622	484.167419	242.587348	483.183403	242.095340	Q	***845.472709***	423.239992	828.446160	414.726718	827.462144	414.234710	8
5	**614.278032**	307.642654	597.251483	299.129380	596.267467	298.637372	I	***717.414131***	359.210704	700.387582	350.697429	699.403566	350.205421	7
6	701.310060	351.158668	684.283511	342.645394	683.299495	342.153386	S	***604.330067***	302.668672	587.303518	294.155397	586.319502	293.663389	6
7	772.347174	386.677225	755.320625	378.163951	754.336609	377.671943	A	***517.298039***	259.152658	500.271490	250.639383	499.287474	250.147375	5
8	843.384288	422.195782	826.357739	413.682507	825.373723	413.190499	A	446.260925	223.634100	429.234376	215.120826	428.250360	214.628818	4
9	942.452702	471.729989	925.426153	463.216714	924.442137	462.724706	V	***375.223811***	188.115543	358.197262	179.602269	357.213246	179.110261	3
10	1071.495295	536.251285	1054.468746	527.738011	1053.484730	527.246003	E	***276.155397***	138.581336	259.128848	130.068062	258.144832	129.576054	2
11							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.6	1216.593521	0.010367	DEQQISAAVEK
5.0	1216.604767	-0.000879	AGEAKGQAPTGSK
3.9	1216.604752	-0.000864	EENQTKLSPR
3.2	1216.604767	-0.000879	AAPTSAPPSKSR
2.6	1216.616013	-0.012125	ESRPVQQTTR
1.4	1216.612137	-0.008249	QELQKQAELM
1.4	1216.600937	0.002951	QEVGVIESPLM
1.1	1216.598907	0.004981	QEFTRSFFR
0.9	1216.604767	-0.000879	RSEGPSLSPSGK

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

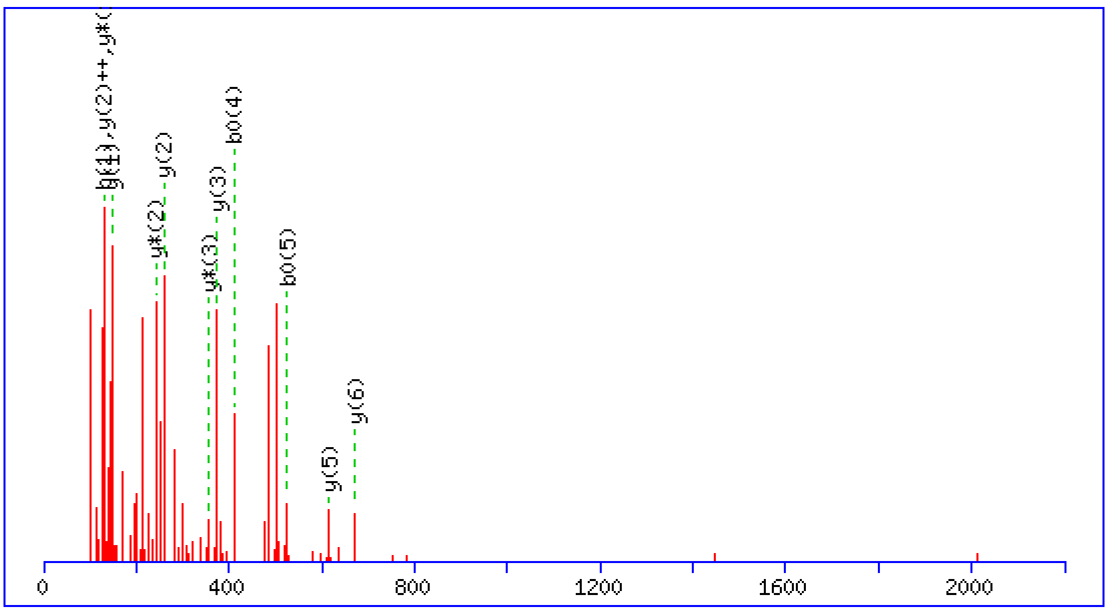
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EGKNLLK**
Found in **IDS_HUMAN**, Iduronate 2-sulfatase OS=Homo sapiens GN=IDS PE=1 SV=1

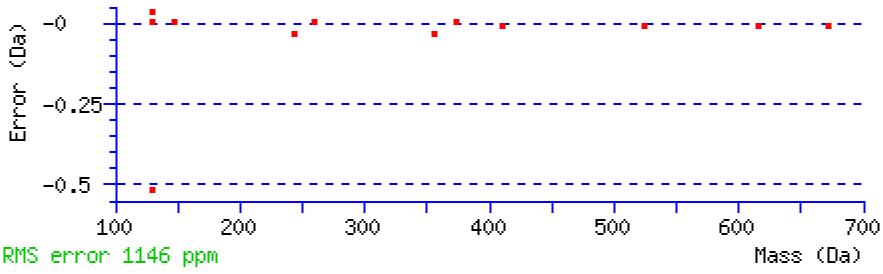
Match to Query 274: 800.468008 from(401.241280,2+) rtinseconds(2291) index(28798)
Title: Locus:1.1.1.2291.3
Data file 2011-11-10 - TFD - EP 3-3.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●

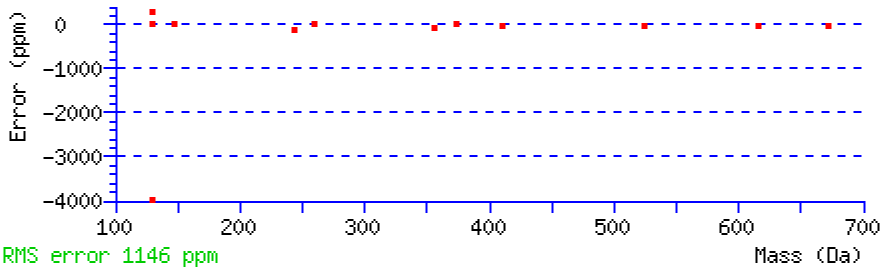


Monoisotopic mass of neutral peptide Mr(calc): 800.475571
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.0042
Matches : 12/56 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	130.049869	65.528572			112.039304	56.523290	E					7
2	187.071333	94.039305			169.060768	85.034022	G	***672.440286***	336.723781	655.413737	328.210507	6
3	315.166296	158.086786	298.139747	149.573512	297.155731	149.081504	K	***615.418822***	308.213049	598.392273	299.699775	5
4	429.209223	215.108250	412.182674	206.594975	411.198658	206.102967	N	487.323859	244.165567	470.297310	235.652293	4
5	542.293287	271.650282	525.266738	263.137007	524.282722	262.644999	L	***373.280932***	187.144104	356.254383	178.630829	3
6	655.377351	328.192314	638.350802	319.679039	637.366786	319.187031	L	***260.196868***	130.602072	243.170319	122.088798	2
7							K	***147.112804***	74.060040	130.086255	65.546765	1



RMS error 1146 ppm



RMS error 1146 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.9	800.464340	0.003668	EGLELLK
35.8	800.475571	-0.007563	EGKNLLK
23.0	800.464340	0.003668	EAEVLLK
23.0	800.464355	0.003653	EVLSPLK
21.7	800.464340	0.003668	EILGEIK
21.0	800.475586	-0.007578	VSLQNLK
20.9	800.464355	0.003653	EIPVSIK
20.4	800.475586	-0.007578	EGKQVLK
17.5	800.475586	-0.007578	SNGAVLIK
15.1	800.475586	-0.007578	QKVGELK

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

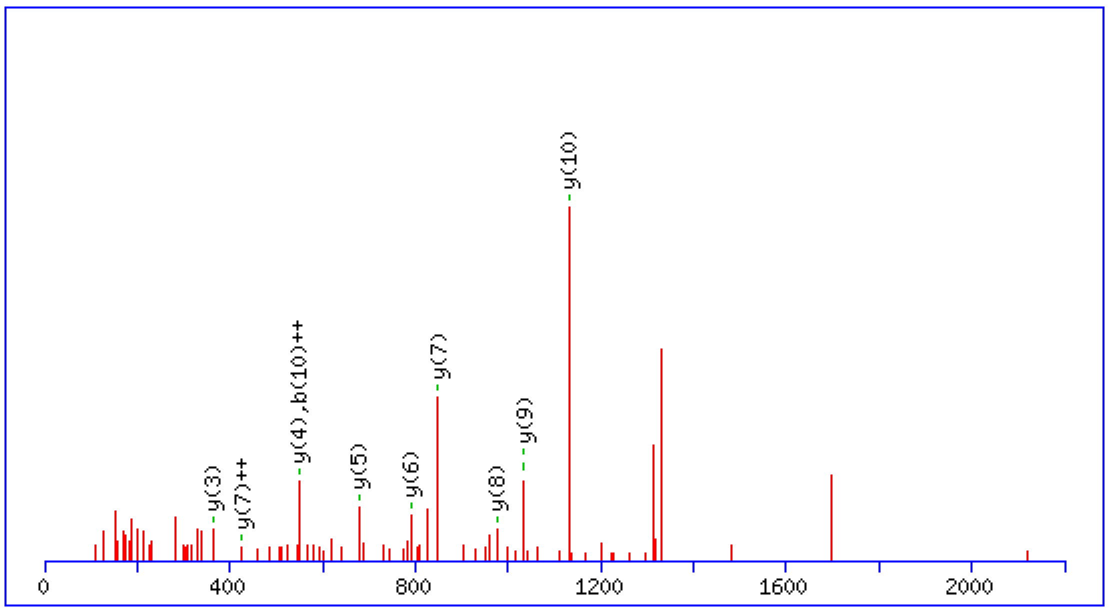
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QAPGQGLEWMGR**
Found in **HV103_HUMAN**, Ig heavy chain V-I region V35 OS=Homo sapiens PE=1 SV=1

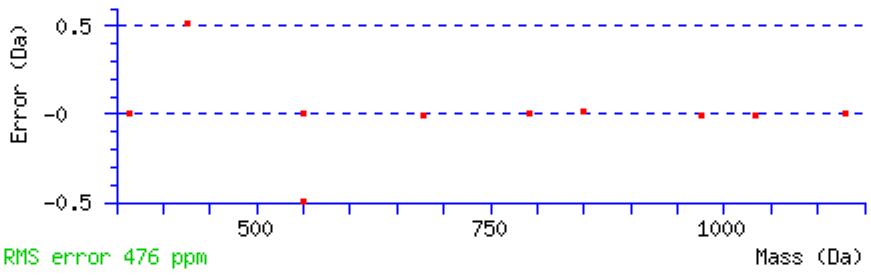
Match to Query 29786: 1328.632348 from(665.323450,2+) rtinseconds(2468) index(31123)
Title: Locus:1.1.1.2455.36
Data file 2011-11-12 - TFD - EP 5-3.mgf

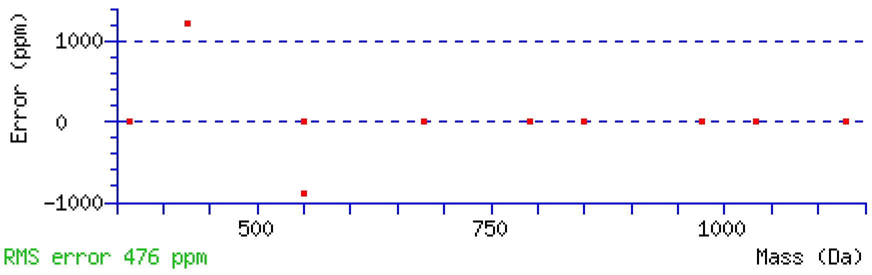
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1328.629547
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 68 **Expect:** 1.6e-006
Matches : 10/110 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	129.065854	65.036565	112.039305	56.523291			Q							12
2	200.102968	100.555122	183.076419	92.041848			A	1201.578255	601.292766	1184.551706	592.779491	1183.567690	592.287483	11
3	297.155732	149.081504	280.129183	140.568230			P	***1130.541141***	565.774208	1113.514592	557.260934	1112.530576	556.768926	10
4	354.177196	177.592236	337.150647	169.078961			G	***1033.488377***	517.247827	1016.461828	508.734552	1015.477812	508.242544	9
5	482.235774	241.621525	465.209225	233.108251			Q	***976.466913***	488.737095	959.440364	480.223820	958.456348	479.731812	8
6	539.257238	270.132257	522.230689	261.618983			G	***848.408335***	424.707806	831.381786	416.194531	830.397770	415.702523	7
7	652.341302	326.674289	635.314753	318.161015			L	***791.386871***	396.197074	774.360322	387.683799	773.376306	387.191791	6
8	781.383895	391.195586	764.357346	382.682311	763.373330	382.190303	E	***678.302807***	339.655042	661.276258	331.141767	660.292242	330.649759	5
9	967.463208	484.235242	950.436659	475.721968	949.452643	475.229960	W	***549.260214***	275.133745	532.233665	266.620471			4
10	1098.503693	549.755485	1081.477144	541.242210	1080.493128	540.750202	M	***363.180901***	182.094088	346.154352	173.580814			3
11	1155.525157	578.266217	1138.498608	569.752942	1137.514592	569.260934	G	232.140416	116.573846	215.113867	108.060571			2
12							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
67.8	1328.629547	0.002801	QAPGQGLEWMGR

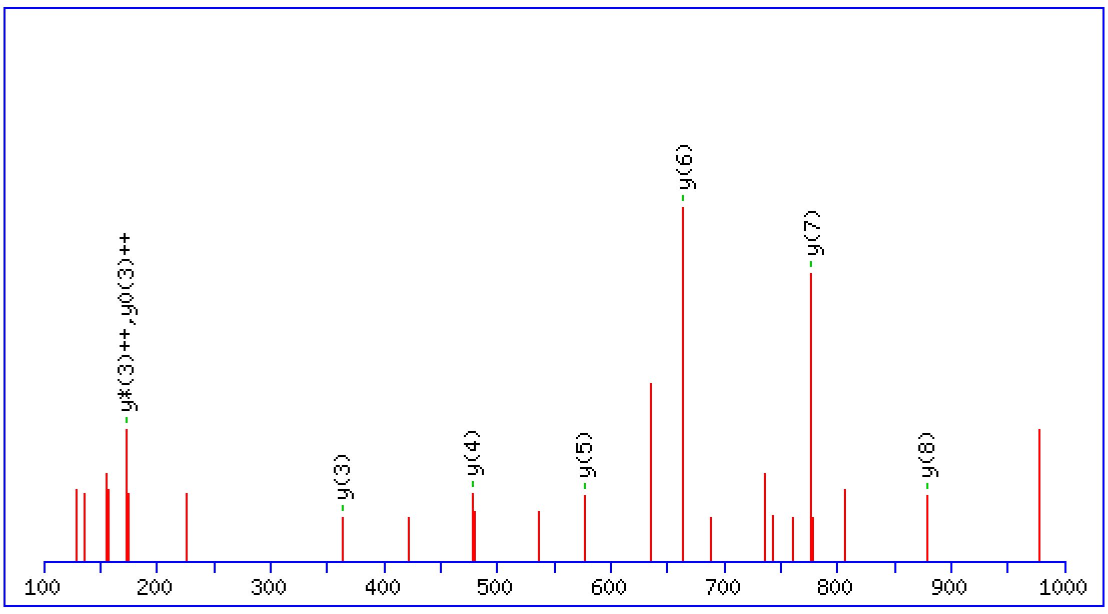
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VTISVDTSR**
Found in **HV206_HUMAN**, Ig heavy chain V-II region WAH OS=Homo sapiens PE=1 SV=1

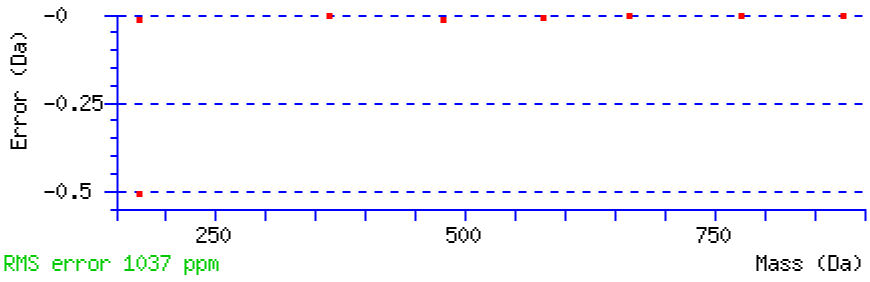
Match to Query 230428: 976.517788 from(489.266170,2+) rtinseconds(1602) index(339801)
Title: Locus:1.1.1.948.11
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

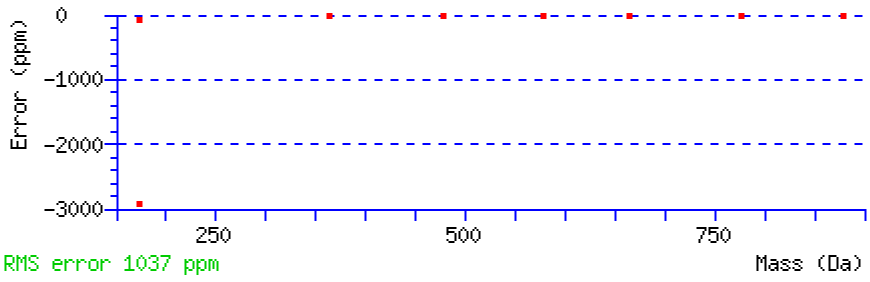
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 976.518936
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 65  Expect: 1.1e-005
Matches : 8/76 fragment ions using 7 most intense peaks   (help)
```

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	100.075690	50.541483			V							9
2	201.123369	101.065322	183.112804	92.060040	T	***878.457787***	439.732532	861.431238	431.219257	860.447222	430.727249	8
3	314.207433	157.607354	296.196868	148.602072	I	***777.410108***	389.208692	760.383559	380.695418	759.399543	380.203410	7
4	401.239461	201.123368	383.228896	192.118086	S	***664.326044***	332.666660	647.299495	324.153386	646.315479	323.661378	6
5	500.307875	250.657575	482.297310	241.652293	V	***577.294016***	289.150646	560.267467	280.637372	559.283451	280.145364	5
6	615.334818	308.171047	597.324253	299.165765	D	***478.225602***	239.616439	461.199053	231.103165	460.215037	230.611157	4
7	716.382497	358.694887	698.371932	349.689604	T	***363.198659***	182.102968	346.172110	173.589693	345.188094	173.097685	3
8	803.414525	402.210901	785.403960	393.205618	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
9					R	175.118952	88.063114	158.092403	79.549840			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
65.0	976.518936	-0.001148	VTISVDTSR
13.3	976.526306	-0.008518	VTLQEMLK
11.0	976.526306	-0.008518	ISSIVISQM
9.9	976.509033	0.008755	TVSPPPAHR
1.7	976.526291	-0.008503	SIIMLQEK
1.7	976.526321	-0.008533	SLLVGITSGM

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

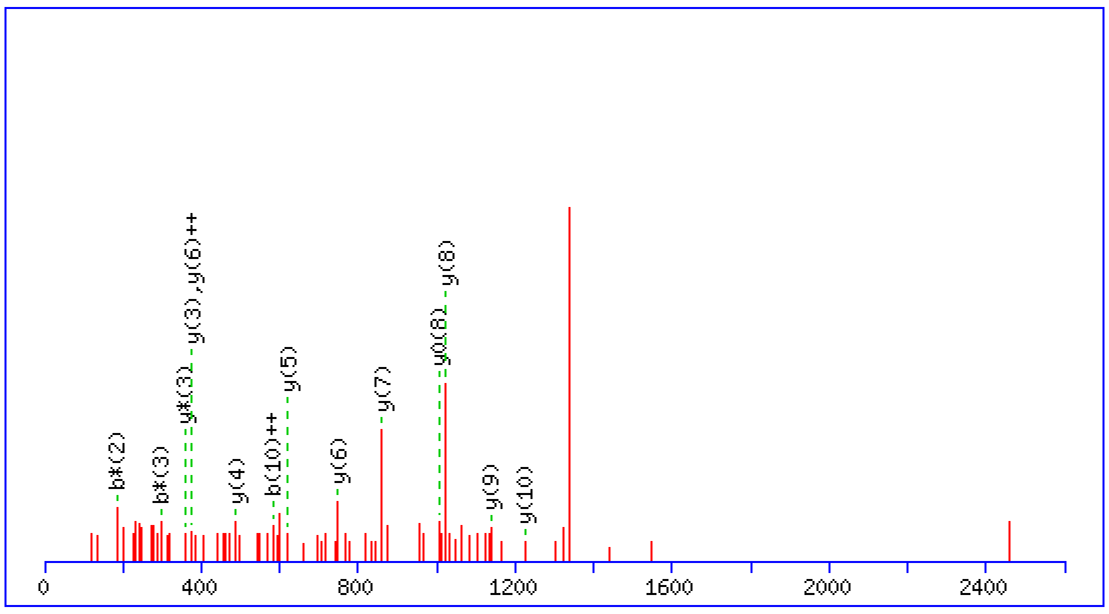
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NSLYLQMNSLR**
Found in **HV320_HUMAN**, Ig heavy chain V-III region GAL OS=Homo sapiens PE=1 SV=1

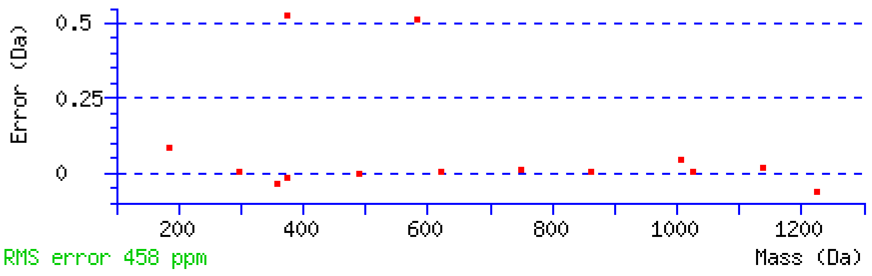
Match to Query 35829: 1337.683448 from(669.849000,2+) rtinseconds(2758) index(37679)
Title: Locus:1.1.1.2468.34
Data file 2011-11-10 - TFD - EP 3-3.mgf

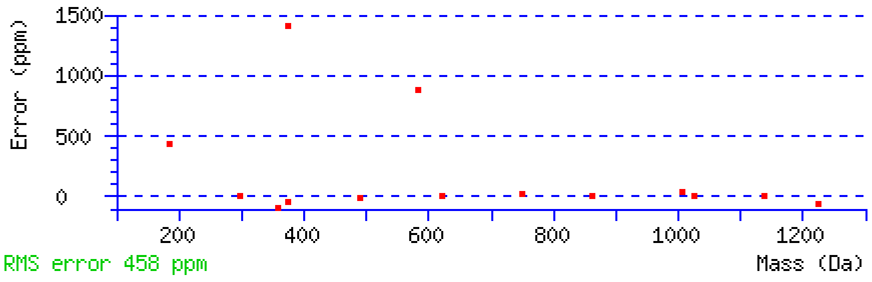
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1337.676132
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 44 **Expect:** 0.00047
Matches : 14/114 fragment ions using 25 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	115.050203	58.028740	98.023654	49.515465			N							11
2	202.082231	101.544753	185.055682	93.031479	184.071666	92.539471	S	***1224.640519***	612.823898	1207.613970	604.310623	1206.629954	603.818615	10
3	315.166295	158.086785	298.139746	149.573511	297.155730	149.081503	L	***1137.608491***	569.307884	1120.581942	560.794609	1119.597926	560.302601	9
4	478.229624	239.618450	461.203075	231.105176	460.219059	230.613168	Y	***1024.524427***	512.765851	1007.497878	504.252577	1006.513862	503.760569	8
5	591.313688	296.160482	574.287139	287.647208	573.303123	287.155200	L	***861.461098***	431.234187	844.434549	422.720913	843.450533	422.228905	7
6	719.372266	360.189771	702.345717	351.676497	701.361701	351.184489	Q	***748.377034***	374.692155	731.350485	366.178880	730.366469	365.686872	6
7	850.412751	425.710014	833.386202	417.196739	832.402186	416.704731	M	***620.318456***	310.662866	603.291907	302.149591	602.307891	301.657583	5
8	964.455678	482.731477	947.429129	474.218203	946.445113	473.726195	N	***489.277971***	245.142623	472.251422	236.629349	471.267406	236.137341	4
9	1051.487706	526.247491	1034.461157	517.734217	1033.477141	517.242209	S	***375.235044***	188.121160	358.208495	179.607885	357.224479	179.115877	3
10	1164.571770	582.789523	1147.545221	574.276249	1146.561205	573.784241	L	288.203016	144.605146	271.176467	136.091871			2
11							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
43.6	1337.676132	0.007316	NSLYLQMNSLR
32.1	1337.676147	0.007301	BTVYLQMBSLR
1.8	1337.676132	0.007316	NTLYLNMNSLR
1.3	1337.693436	-0.009988	KMSDLLELMVK

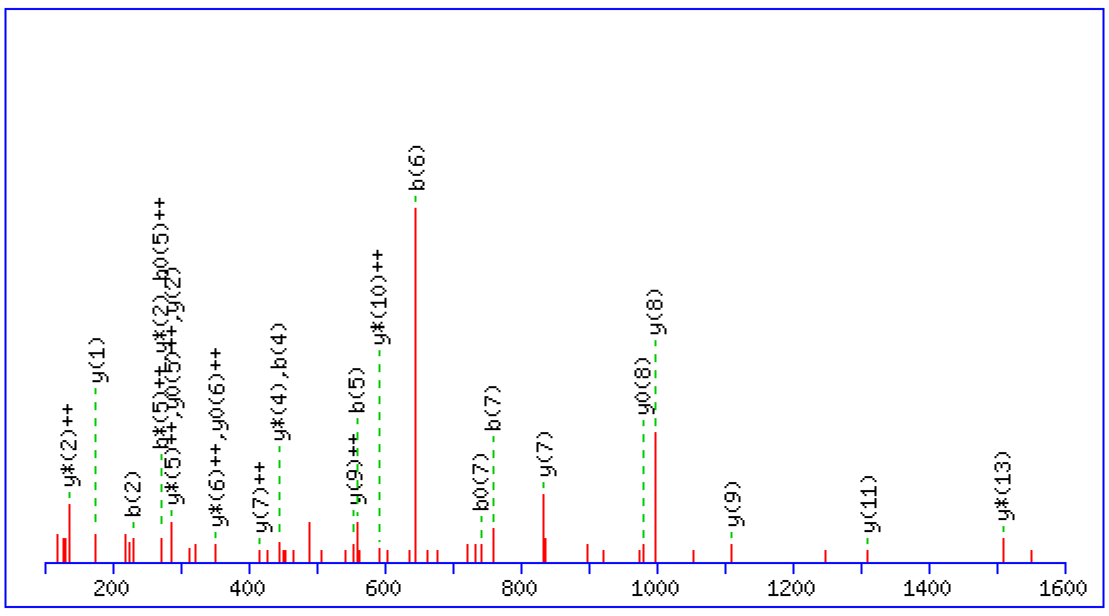
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NDSKNSLYLQMSSLR**
Found in **HV302_HUMAN**, Ig heavy chain V-III region WEA OS=Homo sapiens PE=1 SV=1

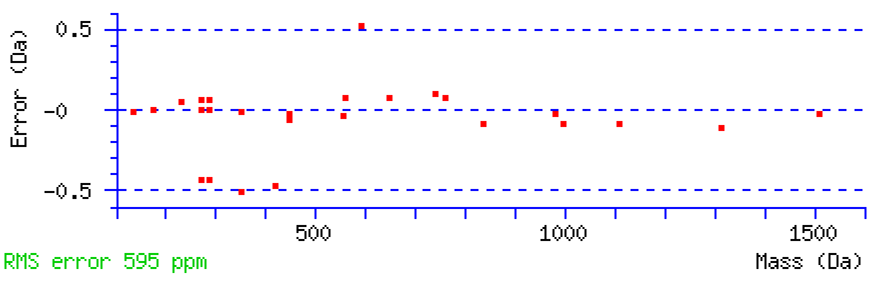
Match to Query 41146: 1754.850912 from(585.957580,3+) rtinseconds(2542) index(26501)
Title: Locus:1.1.1.2377.31
Data file 2011-11-10 - TFD - EP 3-7.mgf

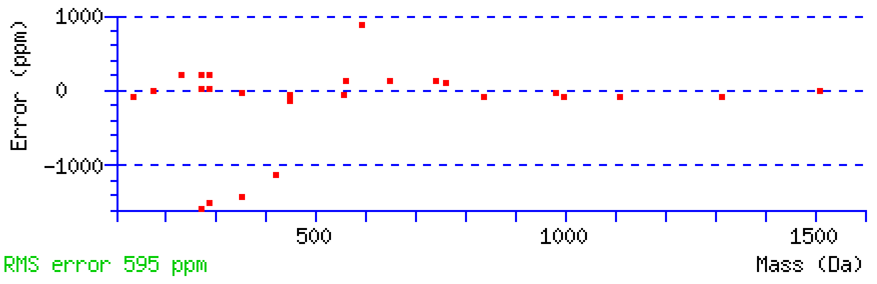
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1754.862091
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 35 **Expect:** 0.0032
Matches : 26/162 fragment ions using 33 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			N							15
2	***230.077146***	115.542211	213.050597	107.028937	212.066581	106.536928	D	1641.826481	821.416879	1624.799932	812.903604	1623.815916	812.411596	14
3	317.109174	159.058225	300.082625	150.544951	299.098609	150.052943	S	1526.799538	763.903407	1509.772989	755.390133	1508.788973	754.898124	13
4	***445.204137***	223.105707	428.177588	214.592432	427.193572	214.100424	K	1439.767510	720.387393	1422.740961	711.874119	1421.756945	711.382110	12
5	***559.247064***	280.127170	542.220515	271.613896	541.236499	271.121888	N	***1311.672547***	656.339911	1294.645998	647.826637	1293.661982	647.334629	11
6	***646.279092***	323.643184	629.252543	315.129910	628.268527	314.637902	S	1197.629620	599.318448	1180.603071	590.805174	1179.619055	590.313165	10
7	***759.363156***	380.185216	742.336607	371.671942	741.352591	371.179934	L	***1110.597592***	555.802434	1093.571043	547.289160	1092.587027	546.797152	9
8	922.426485	461.716881	905.399936	453.203606	904.415920	452.711598	Y	***997.513528***	499.260402	980.486979	490.747128	979.502963	490.255120	8
9	1035.510549	518.258912	1018.484000	509.745638	1017.499984	509.253630	L	***834.450199***	417.728738	817.423650	409.215463	816.439634	408.723455	7
10	1163.569127	582.288202	1146.542578	573.774927	1145.558562	573.282919	Q	721.366135	361.186706	704.339586	352.673431	703.355570	352.181423	6
11	1294.609612	647.808444	1277.583063	639.295170	1276.599047	638.803161	M	593.307557	297.157417	576.281008	288.644142	575.296992	288.152134	5
12	1381.641640	691.324458	1364.615091	682.811184	1363.631075	682.319176	S	462.267072	231.637174	445.240523	223.123899	444.256507	222.631891	4
13	1468.673668	734.840472	1451.647119	726.327198	1450.663103	725.835190	S	375.235044	188.121160	358.208495	179.607885	357.224479	179.115877	3
14	1581.757732	791.382504	1564.731183	782.869230	1563.747167	782.377222	L	***288.203016***	144.605146	271.176467	136.091871			2
15							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.5	1754.862091	-0.011179	NBSKNSLYLQMSSLR
22.5	1754.843491	0.007421	EGTEAAAAKPAGGSPQGPK
12.7	1754.843491	0.007421	EGTEAAAAKPAGGSPQGPK
10.6	1754.850906	0.000006	ALSGGGSVASPPPSPAMPK
8.2	1754.862122	-0.011210	GASPDMAPILEPVDRR
8.2	1754.862122	-0.011210	GASPDMAPILEPVDRR
7.2	1754.850906	0.000006	ALSGGGSVASPPPSPAMPK
7.2	1754.850906	0.000006	ALSGGGSVASPPPSPAMPK
7.2	1754.850906	0.000006	ALSGGGSVASPPPSPAMPK
7.2	1754.850906	0.000006	ALSGGGSVASPPPSPAMPK

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

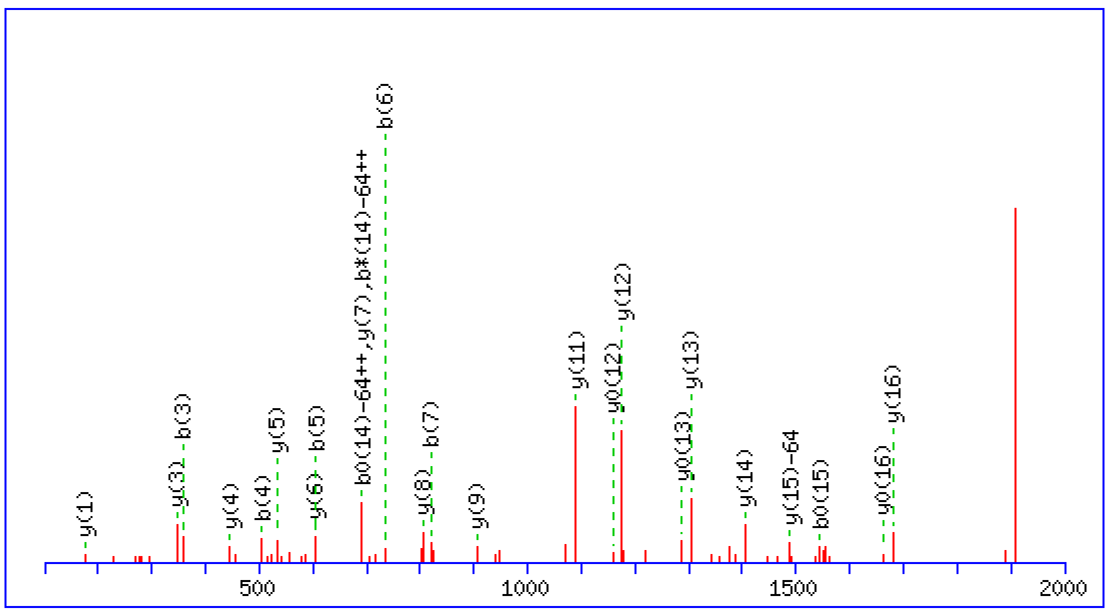
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **DIQMTQSPSTLSASVGDR**
Found in **KV104_HUMAN**, Ig kappa chain V-I region CAR OS=Homo sapiens PE=1 SV=1

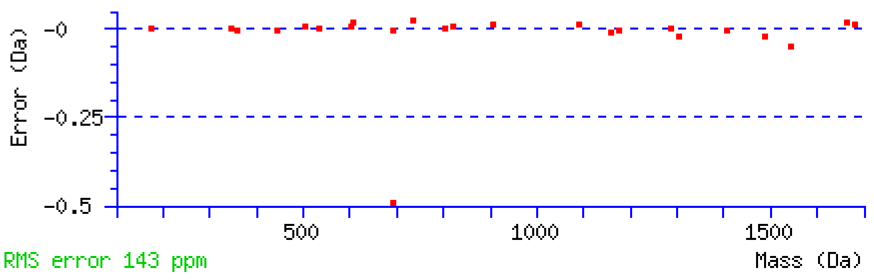
Match to Query 54418: 1907.885988 from(954.950270,2+) rtinseconds(2011) index(20688)
Title: Locus:1.1.1.2184.51
Data file 2011-11-13 - TFD - EP 7-5.mgf

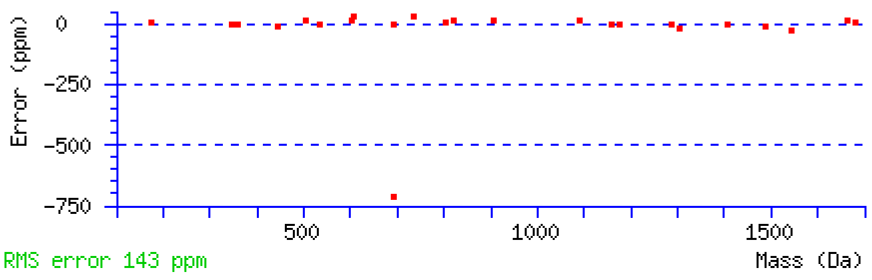
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1907.889481
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M4 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 123 **Expect:** 5.1e-012
Matches : 25/300 fragment ions using 30 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.034219	58.520748			98.023654	49.515465	**D**							**18**
2	229.118283	115.062779			211.107718	106.057497	**I**	1793.869805	897.438541	1776.843256	888.925266	1775.859240	888.433258	**17**
3	**357.176861**	179.092068	340.150312	170.578794	339.166296	170.086786	**Q**	***1680.785741***	840.896509	1663.759192	832.383234	1662.775176	831.891226	**16**
4	**504.212261**	252.609768	487.185712	244.096494	486.201696	243.604486	**M**	1552.727163	776.867220	1535.700614	768.353945	1534.716598	767.861937	**15**
5	**605.259940**	303.133608	588.233391	294.620334	587.249375	294.128326	**T**	***1405.691763***	703.349520	1388.665214	694.836245	1387.681198	694.344237	**14**
6	**733.318518**	367.162897	716.291969	358.649623	715.307953	358.157615	**Q**	***1304.644084***	652.825680	1287.617535	644.312406	1286.633519	643.820398	**13**
7	**820.350546**	410.678911	803.323997	402.165637	802.339981	401.673629	**S**	***1176.585506***	588.796391	1159.558957	580.283117	1158.574941	579.791109	**12**
8	917.403310	459.205293	900.376761	450.692019	899.392745	450.200011	**P**	***1089.553478***	545.280377	1072.526929	536.767103	1071.542913	536.275095	**11**
9	1004.435338	502.721307	987.408789	494.208033	986.424773	493.716025	**S**	992.500714	496.753995	975.474165	488.240721	974.490149	487.748713	**10**
10	1105.483017	553.245147	1088.456468	544.731872	1087.472452	544.239864	**T**	***905.468686***	453.237981	888.442137	444.724707	887.458121	444.232699	**9**
11	1218.567081	609.787178	1201.540532	601.273904	1200.556516	600.781896	**L**	***804.421007***	402.714142	787.394458	394.200867	786.410442	393.708859	**8**
12	1305.599109	653.303193	1288.572560	644.789918	1287.588544	644.297910	**S**	***691.336943***	346.172110	674.310394	337.658835	673.326378	337.166827	**7**
13	1376.636223	688.821750	1359.609674	680.308475	1358.625658	679.816467	**A**	***604.304915***	302.656096	587.278366	294.142821	586.294350	293.650813	**6**
14	1463.668251	732.337764	1446.641702	723.824489	1445.657686	723.332481	**S**	***533.267801***	267.137539	516.241252	258.624264	515.257236	258.132256	**5**
15	1562.736665	781.871971	1545.710116	773.358696	1544.726100	772.866688	**V**	***446.235773***	223.621524	429.209224	215.108250	428.225208	214.616242	**4**
16	1619.758129	810.382703	1602.731580	801.869428	1601.747564	801.377420	**G**	***347.167359***	174.087317	330.140810	165.574043	329.156794	165.082035	**3**
17	1734.785072	867.896174	1717.758523	859.382900	1716.774507	858.890892	**D**	290.145895	145.576585	273.119346	137.063311	272.135330	136.571303	**2**
18							**R**	***175.118952***	88.063114	158.092403	79.549839			**1**





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
123.4	1907.889481	-0.003493	DIQMTQSPSTLSASVGDR
76.2	1907.889481	-0.003493	DIQMTQSPSSLSATVGDR
44.8	1907.889481	-0.003493	DIQMTQSPSTLSASVGDR
16.0	1907.889481	-0.003493	DIQMTQSPSSLSATVGDR
11.7	1907.870834	0.015154	SEGKSLPSSPSSPSSPASR
9.2	1907.882080	0.003908	LDSSDSDSASGQGQVKATR
2.6	1907.896851	-0.010863	VMLEGDSEEMGVIPSKR
1.6	1907.901382	-0.015394	GGGGDPGPGPAPAPAPPPAPDK
1.3	1907.886932	-0.000944	LPEYTREALCPPACR
0.5	1907.901382	-0.015394	GGGGDPGPGPAPAPAPPPAPDK

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

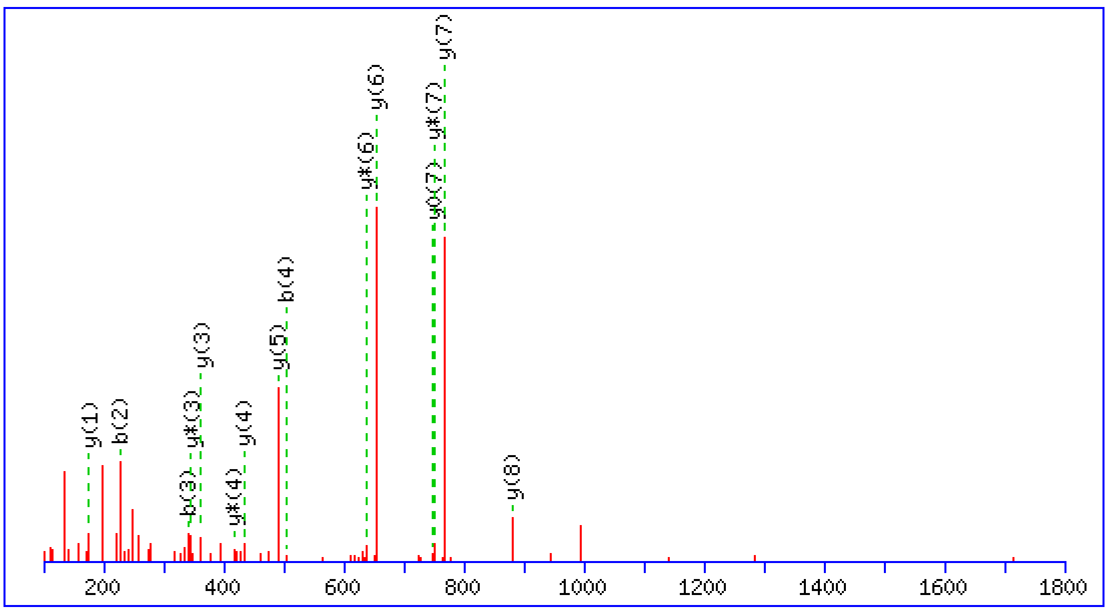
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLIYGASTR**
Found in **KV113_HUMAN**, Ig kappa chain V-I region Lay OS=Homo sapiens PE=1 SV=1

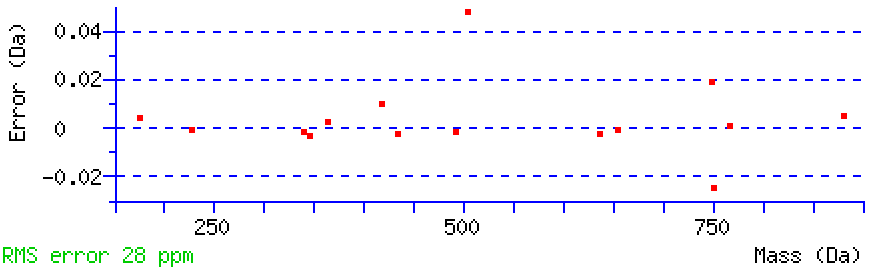
Match to Query 14707: 992.567568 from(497.291060,2+) rtinseconds(2077) index(21905)
Title: Locus:1.1.1.2209.18
Data file 2011-11-13 - TFD - EP 7-5.mgf

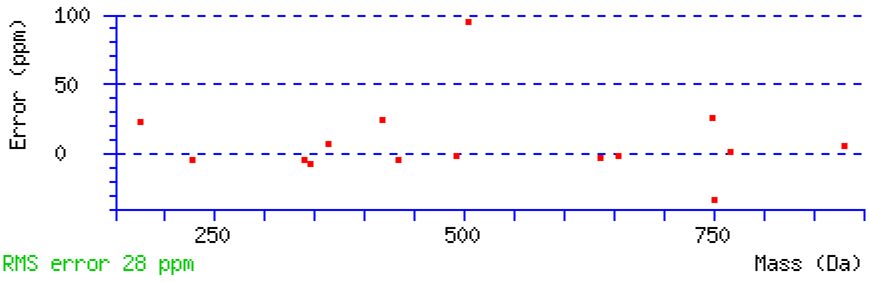
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 992.565460
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 58  Expect: 7e-006
Matches : 15/66 fragment ions using 22 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							9
2	**227.175404**	114.091340			L	***880.488694***	440.747985	863.462145	432.234711	862.478129	431.742703	8
3	**340.259468**	170.633372			I	***767.404630***	384.205953	750.378081	375.692679	749.394065	375.200671	7
4	**503.322797**	252.165036			Y	***654.320566***	327.663921	637.294017	319.150647	636.310001	318.658639	6
5	560.344261	280.675769			G	***491.257237***	246.132256	474.230688	237.618982	473.246672	237.126974	5
6	631.381375	316.194326			A	***434.235773***	217.621524	417.209224	209.108250	416.225208	208.616242	4
7	718.413403	359.710340	700.402838	350.705057	S	***363.198659***	182.102967	346.172110	173.589693	345.188094	173.097685	3
8	819.461082	410.234179	801.450517	401.228897	T	276.166631	138.586953	259.140082	130.073679	258.156066	129.581671	2
9					R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.4	992.565460	0.002108	LLIYGASTR
58.4	992.565460	0.002108	LLIYGATSR
5.9	992.576691	-0.009123	LRPLPPER
5.7	992.565475	0.002093	EPLHVVATK
4.8	992.576691	-0.009123	LRPLPPER
0.9	992.565460	0.002108	IPKPELHK
0.9	992.576706	-0.009138	LPPRPVNGK
0.8	992.576706	-0.009138	LIHVLDAGR
0.6	992.565460	0.002108	LLQTLSYR
0.0	992.576691	-0.009123	LRPLPPER

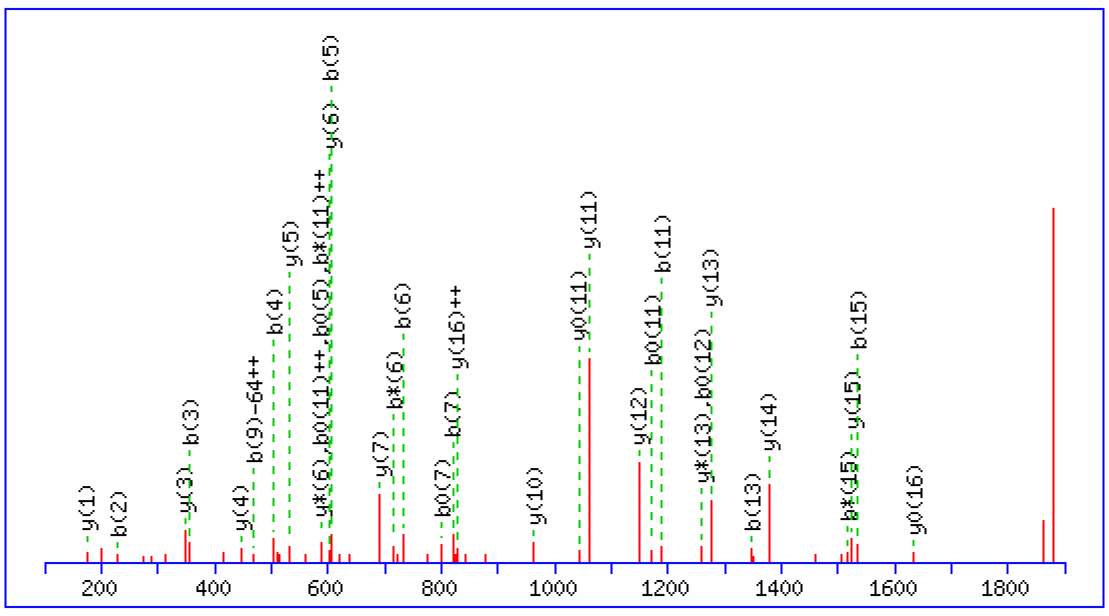
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DIQMTQSPSSVSASVGDR**
Found in **KV119_HUMAN**, Ig kappa chain V-I region Wes OS=Homo sapiens PE=1 SV=1

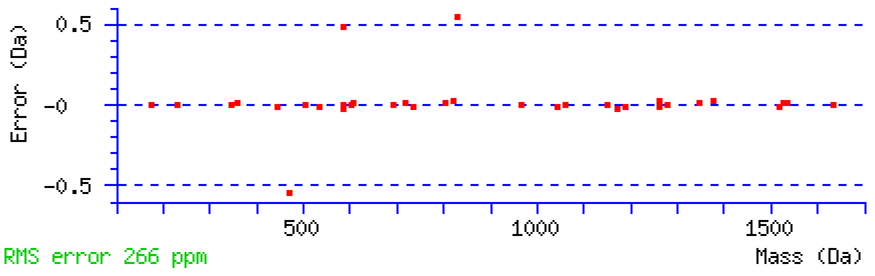
Match to Query 54748: 1879.854168 from(940.934360,2+) rtinseconds(1769) index(16967)
Title: Locus:1.1.1.1965.51
Data file 2011-11-12 - TFD - EP 6-5.mgf

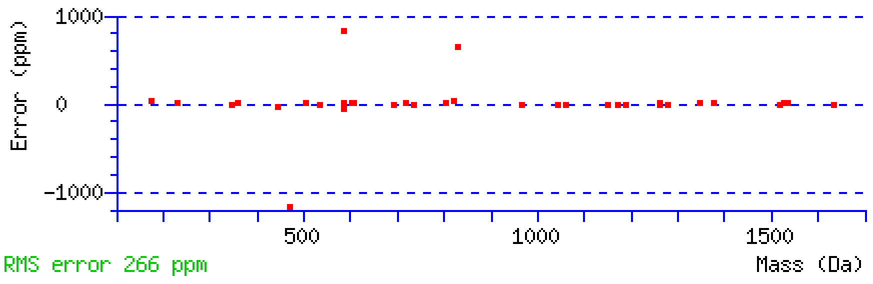
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1879.858185
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M4 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 101 **Expect:** 6.5e-010
Matches : 35/300 fragment ions using 40 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.034219	58.520748			98.023654	49.515465	D							18
2	**229.118283**	115.062779			211.107718	106.057497	I	1765.838504	883.422890	1748.811955	874.909616	1747.827939	874.417608	17
3	**357.176861**	179.092068	340.150312	170.578794	339.166296	170.086786	Q	1652.754440	826.880858	1635.727891	818.367584	1634.743875	817.875576	16
4	**504.212261**	252.609768	487.185712	244.096494	486.201696	243.604486	M	***1524.695862***	762.851569	1507.669313	754.338295	1506.685297	753.846287	15
5	**605.259940**	303.133608	588.233391	294.620334	587.249375	294.128326	T	***1377.660462***	689.333869	1360.633913	680.820595	1359.649897	680.328587	14
6	**733.318518**	367.162897	716.291969	358.649623	715.307953	358.157615	Q	***1276.612783***	638.810030	1259.586234	630.296755	1258.602218	629.804747	13
7	**820.350546**	410.678911	803.323997	402.165637	802.339981	401.673629	S	***1148.554205***	574.780741	1131.527656	566.267466	1130.543640	565.775458	12
8	917.403310	459.205293	900.376761	450.692019	899.392745	450.200011	P	***1061.522177***	531.264727	1044.495628	522.751452	1043.511612	522.259444	11
9	1004.435338	502.721307	987.408789	494.208033	986.424773	493.716025	S	***964.469413***	482.738345	947.442864	474.225070	946.458848	473.733062	10
10	1091.467366	546.237321	1074.440817	537.724047	1073.456801	537.232039	S	877.437385	439.222331	860.410836	430.709056	859.426820	430.217048	9
11	**1190.535780**	595.771528	1173.509231	587.258254	1172.525215	586.766246	V	790.405357	395.706317	773.378808	387.193042	772.394792	386.701034	8
12	1277.567808	639.287542	1260.541259	630.774268	1259.557243	630.282260	S	***691.336943***	346.172110	674.310394	337.658835	673.326378	337.166827	7
13	**1348.604922**	674.806099	1331.578373	666.292825	1330.594357	665.800817	A	***604.304915***	302.656096	587.278366	294.142821	586.294350	293.650813	6
14	1435.636950	718.322113	1418.610401	709.808839	1417.626385	709.316831	S	***533.267801***	267.137539	516.241252	258.624264	515.257236	258.132256	5
15	**1534.705364**	767.856320	1517.678815	759.343046	1516.694799	758.851038	V	***446.235773***	223.621524	429.209224	215.108250	428.225208	214.616242	4
16	1591.726828	796.367052	1574.700279	787.853778	1573.716263	787.361770	G	***347.167359***	174.087317	330.140810	165.574043	329.156794	165.082035	3
17	1706.753771	853.880524	1689.727222	845.367249	1688.743206	844.875241	D	290.145895	145.576585	273.119346	137.063311	272.135330	136.571303	2
18							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
100.8	1879.858185	-0.004017	DIQMTQSPSSVSASVGDR
38.3	1879.858185	-0.004017	DIQMTQSPSSVSASVGDR
16.2	1879.858185	-0.004017	DVQMTQSPSSLSASVGDR
16.0	1879.858185	-0.004017	DVQMTQSPSSLSASVGDR
15.4	1879.846893	0.007275	ETDSGDKEMAEAISELR
4.8	1879.852295	0.001873	VFHEDCHIPPVEAER
3.2	1879.837006	0.017162	TPSECSYYSSRISSAR

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

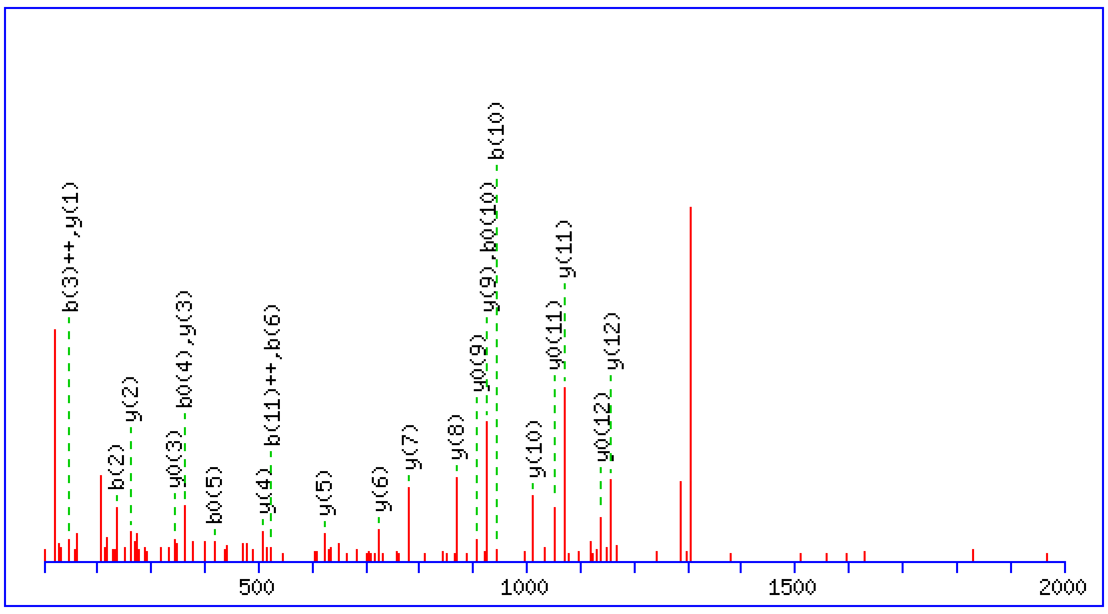
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FSGSGSGTDFTLK**
Found in **KV201_HUMAN**, Ig kappa chain V-II region Cum OS=Homo sapiens PE=1 SV=1

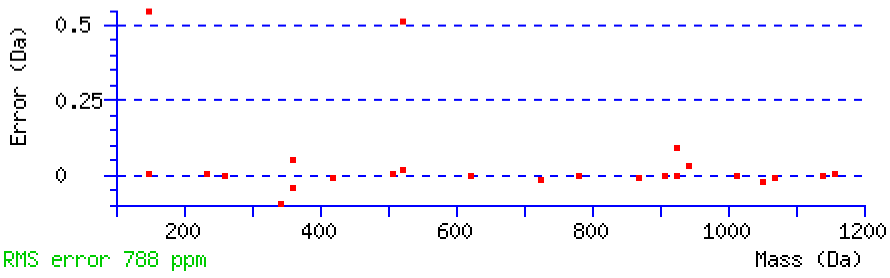
Match to Query 36233: 1302.603688 from(652.309120,2+) rtinseconds(2150) index(23881)
Title: Locus:1.1.1.2134.37
Data file 2011-11-10 - TFD - EP 4-5.mgf

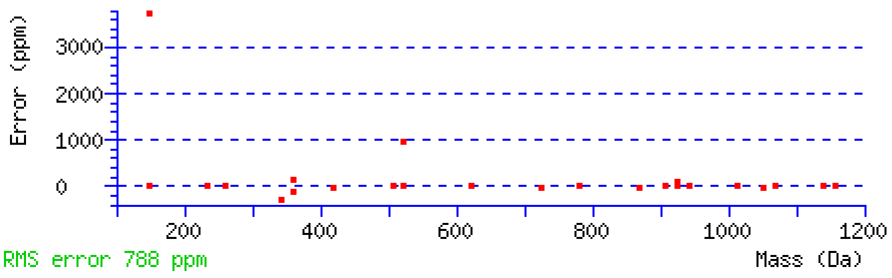
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1302.609222
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 101  Expect: 9.7e-010
Matches : 24/114 fragment ions using 36 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.075690	74.541483			F							13
2	**235.107718**	118.057497	217.097153	109.052214	S	***1156.548059***	578.777667	1139.521510	570.264393	1138.537494	569.772385	12
3	292.129182	146.568229	274.118617	137.562946	G	***1069.516031***	535.261653	1052.489482	526.748379	1051.505466	526.256371	11
4	379.161210	190.084243	361.150645	181.078960	S	***1012.494567***	506.750921	995.468018	498.237647	994.484002	497.745639	10
5	436.182674	218.594975	418.172109	209.589692	G	***925.462539***	463.234907	908.435990	454.721633	907.451974	454.229625	9
6	**523.214702**	262.110989	505.204137	253.105707	S	***868.441075***	434.724176	851.414526	426.210901	850.430510	425.718893	8
7	580.236166	290.621721	562.225601	281.616439	G	***781.409047***	391.208161	764.382498	382.694887	763.398482	382.202879	7
8	681.283845	341.145561	663.273280	332.140278	T	***724.387583***	362.697429	707.361034	354.184155	706.377018	353.692147	6
9	796.310788	398.659032	778.300223	389.653750	D	***623.339904***	312.173590	606.313355	303.660315	605.329339	303.168307	5
10	**943.379202**	472.193239	925.368637	463.187956	F	***508.312961***	254.660118	491.286412	246.146844	490.302396	245.654836	4
11	1044.426881	522.717078	1026.416316	513.711796	T	***361.244547***	181.125911	344.217998	172.612637	343.233982	172.120629	3
12	1157.510945	579.259110	1139.500380	570.253828	L	***260.196868***	130.602072	243.170319	122.088797			2
13					K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
100.5	1302.609222	-0.005534	FSGSGSGTDFTLK
100.5	1302.609222	-0.005534	FSGSGSGTBFTLK
5.9	1302.602676	0.001012	HPFTGDNCTIK
3.1	1302.593948	0.009740	TDENIDTPGTPK

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

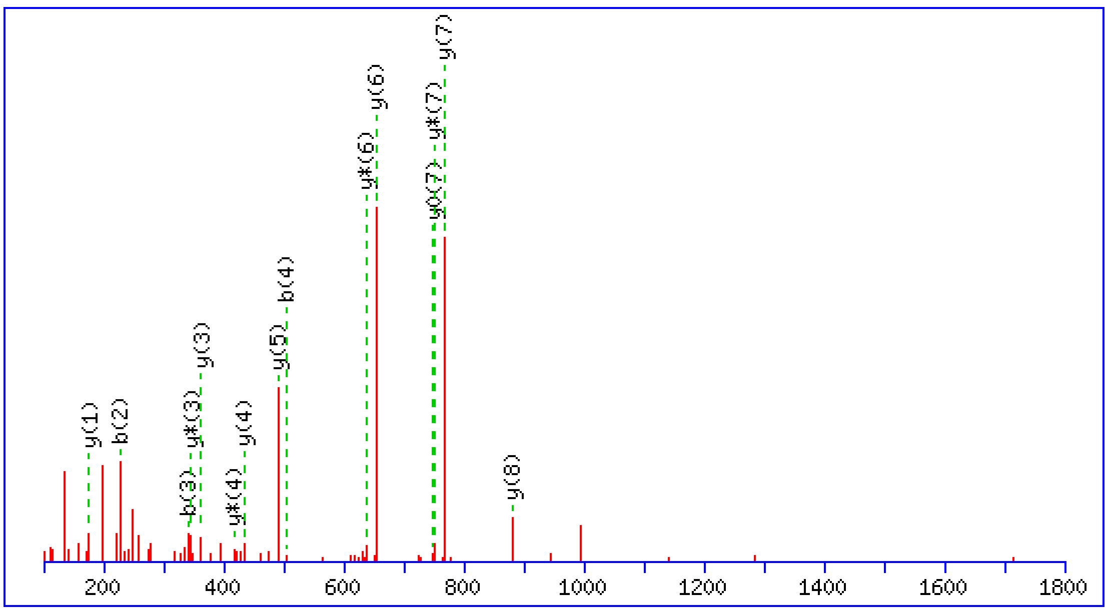
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLIYGASTR**
Found in **KV113_HUMAN**, Ig kappa chain V-I region Lay OS=Homo sapiens PE=1 SV=1

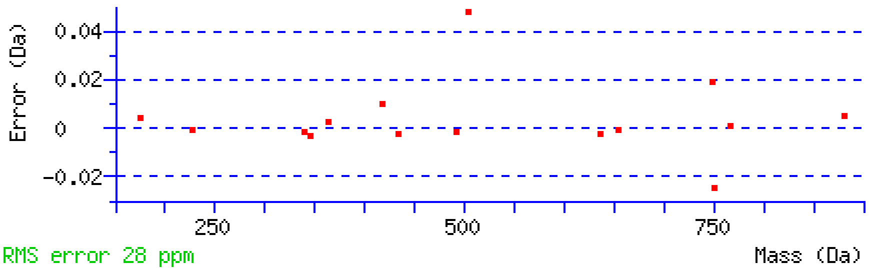
Match to Query 14707: 992.567568 from(497.291060,2+) rtinseconds(2077) index(21905)
Title: Locus:1.1.1.2209.18
Data file 2011-11-13 - TFD - EP 7-5.mgf

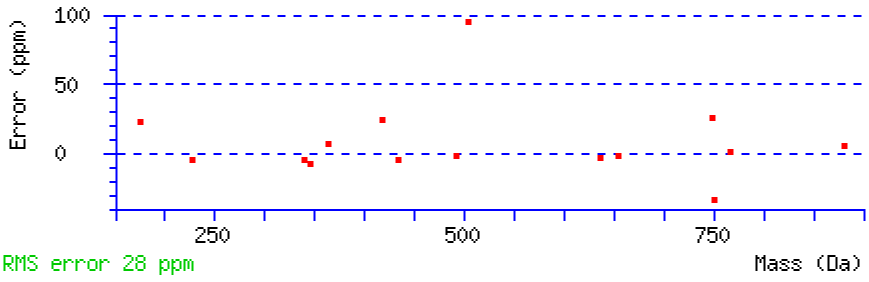
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 992.565460
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 58  Expect: 7e-006
Matches : 15/66 fragment ions using 22 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							9
2	227.175404	114.091340			L	880.488694	440.747985	863.462145	432.234711	862.478129	431.742703	8
3	340.259468	170.633372			I	767.404630	384.205953	750.378081	375.692679	749.394065	375.200671	7
4	503.322797	252.165036			Y	654.320566	327.663921	637.294017	319.150647	636.310001	318.658639	6
5	560.344261	280.675769			G	491.257237	246.132256	474.230688	237.618982	473.246672	237.126974	5
6	631.381375	316.194326			A	434.235773	217.621524	417.209224	209.108250	416.225208	208.616242	4
7	718.413403	359.710340	700.402838	350.705057	S	363.198659	182.102967	346.172110	173.589693	345.188094	173.097685	3
8	819.461082	410.234179	801.450517	401.228897	T	276.166631	138.586953	259.140082	130.073679	258.156066	129.581671	2
9					R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.4	992.565460	0.002108	LLIYGASTR
58.4	992.565460	0.002108	LLIYGATSR
5.9	992.576691	-0.009123	LRPLPPER
5.7	992.565475	0.002093	EPLHVVATK
4.8	992.576691	-0.009123	LRPLPPER
0.9	992.565460	0.002108	IPKPELHK
0.9	992.576706	-0.009138	LPPRPVNGK
0.8	992.576706	-0.009138	LIHVLDAGR
0.6	992.565460	0.002108	LLQTLSYR
0.0	992.576691	-0.009123	LRPLPPER

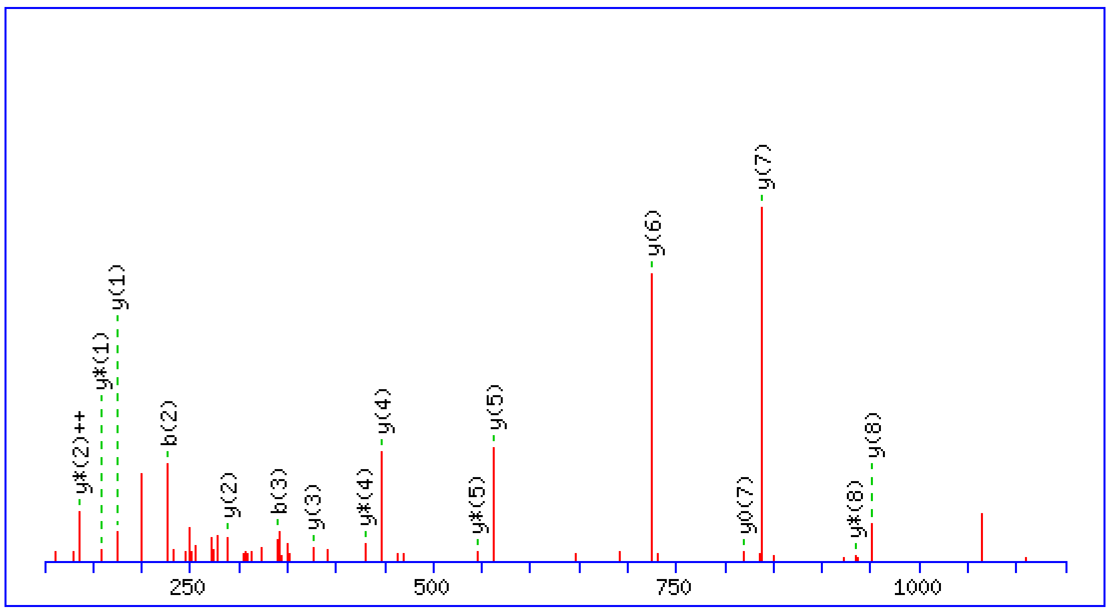
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLIYDASNR**
Found in **KV309_HUMAN**, Ig kappa chain V-III region VG (Fragment) OS=Homo sapiens PE=1 SV=1

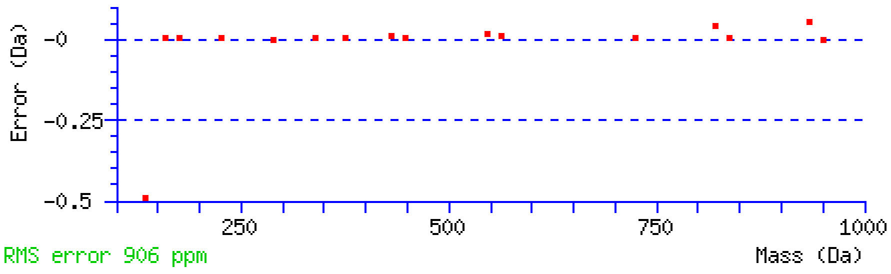
Match to Query 18062: 1063.569028 from(532.791790,2+) rtinseconds(2115) index(19960)
Title: Locus:1.1.1.2427.24
Data file 2011-11-10 - TFD - EP 3-5.mgf

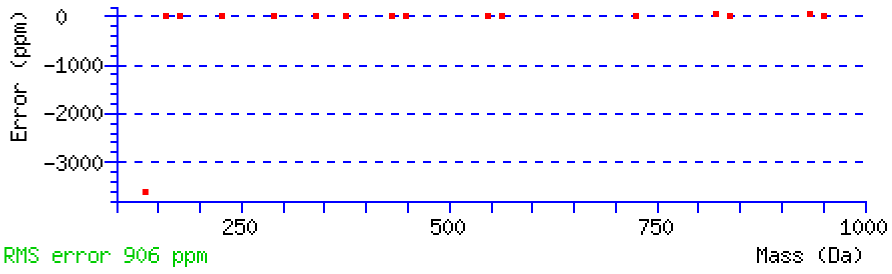
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1063.566177
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 57  Expect: 1.9e-005
Matches : 16/70 fragment ions using 30 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							9
2	**227.175404**	114.091340					L	***951.489421***	476.248348	934.462872	467.735074	933.478856	467.243066	8
3	**340.259468**	170.633372					I	***838.405357***	419.706316	821.378808	411.193042	820.394792	410.701034	7
4	503.322797	252.165036					Y	***725.321293***	363.164285	708.294744	354.651010	707.310728	354.159002	6
5	618.349740	309.678508			600.339175	300.673226	D	***562.257964***	281.632620	545.231415	273.119345	544.247399	272.627337	5
6	689.386854	345.197065			671.376289	336.191782	A	***447.231021***	224.119148	430.204472	215.605874	429.220456	215.113866	4
7	776.418882	388.713079			758.408317	379.707796	S	***376.193907***	188.600591	359.167358	180.087317	358.183342	179.595309	3
8	890.461809	445.734542	873.435260	437.221268	872.451244	436.729260	N	***289.161879***	145.084577	272.135330	136.571303			2
9							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
57.4	1063.566177	0.002851	LLIYDASNR
13.5	1063.577408	-0.008380	LLPAAEAHAR
9.9	1063.577423	-0.008395	IIALPHDNR
9.8	1063.576950	-0.007922	IIMGLDKMK
3.4	1063.566208	0.002820	ATPLPPPSPR
2.0	1063.570221	-0.001193	LLNAFFDPK
1.8	1063.566208	0.002820	ATPLPPPSPR
1.7	1063.559662	0.009366	LLNRMFDR
1.6	1063.566177	0.002851	LNSAIIYDR
0.9	1063.566162	0.002866	IIYKENER

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

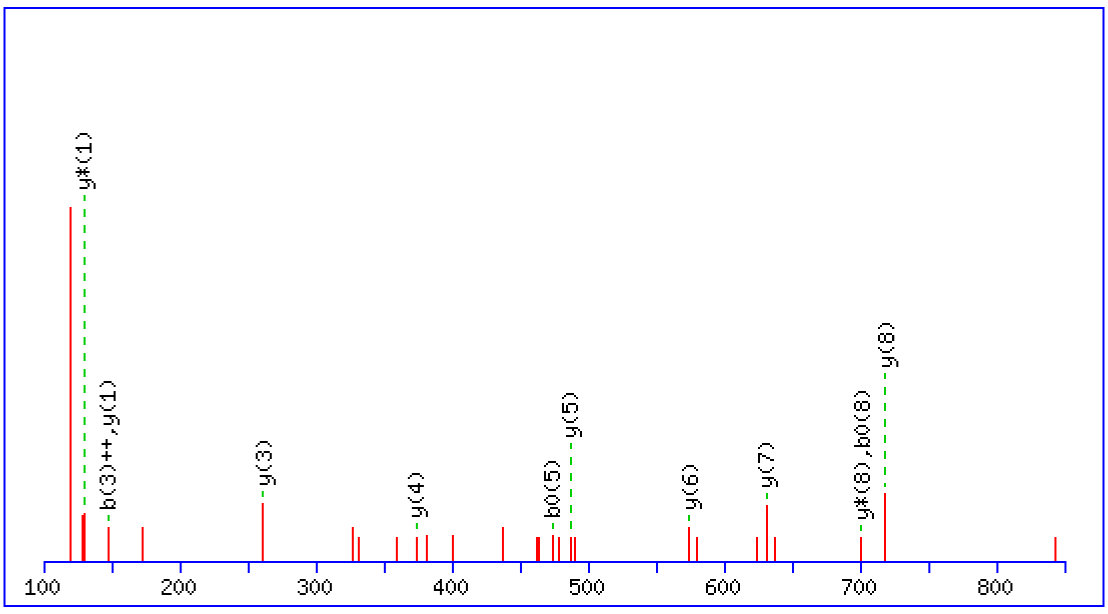
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FSGSLLGGK**
Found in **LV001_HUMAN**, Ig lambda chain V region 4A OS=Homo sapiens PE=4 SV=1

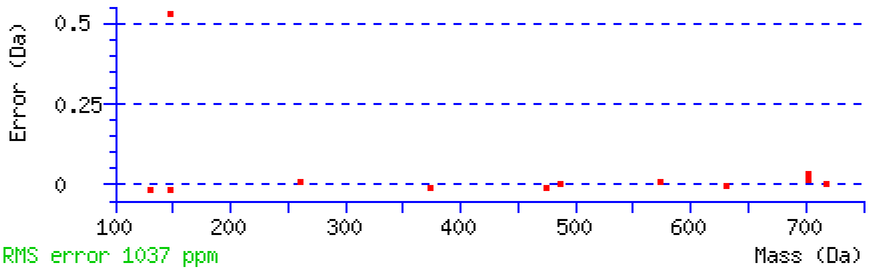
Match to Query 4763: 864.477528 from(433.246040,2+) rtinseconds(1984) index(17494)
Title: Locus:1.1.1.2378.8
Data file 2011-11-10 - TFD - EP 3-5.mgf

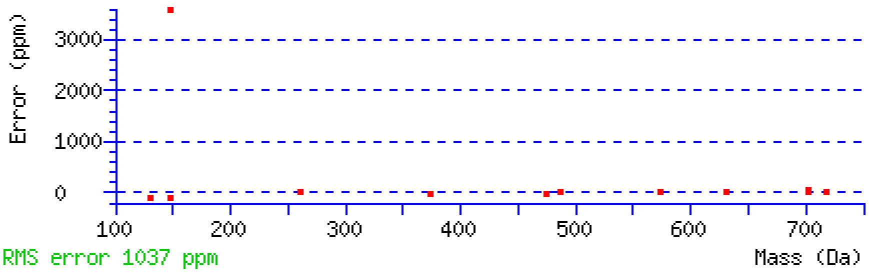
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 864.470520
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 45  Expect: 0.00028
Matches : 12/68 fragment ions using 20 most intense peaks   (help)
```

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	148.075690	74.541483			F							9
2	235.107718	118.057497	217.097153	109.052214	S	***718.409380***	359.708328	701.382831	351.195054	700.398815	350.703046	8
3	292.129182	146.568229	274.118617	137.562946	G	***631.377352***	316.192314	614.350803	307.679040	613.366787	307.187032	7
4	379.161210	190.084243	361.150645	181.078960	S	***574.355888***	287.681582	557.329339	279.168308	556.345323	278.676300	6
5	492.245274	246.626275	474.234709	237.620992	L	***487.323860***	244.165568	470.297311	235.652294			5
6	605.329338	303.168307	587.318773	294.163025	L	***374.239796***	187.623536	357.213247	179.110262			4
7	662.350802	331.679039	644.340237	322.673757	G	***261.155732***	131.081504	244.129183	122.568230			3
8	719.372266	360.189771	701.361701	351.184489	G	204.134268	102.570772	187.107719	94.057498			2
9					K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.7	864.470520	0.007008	FSGSLLGGK
7.8	864.474548	0.002980	FFPDVIK
3.7	864.481735	-0.004207	FSIRNTK
3.1	864.473877	0.003651	MVVASSKK
3.1	864.481735	-0.004207	HPEKVAGK
0.7	864.481735	-0.004207	KIHPDQK

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

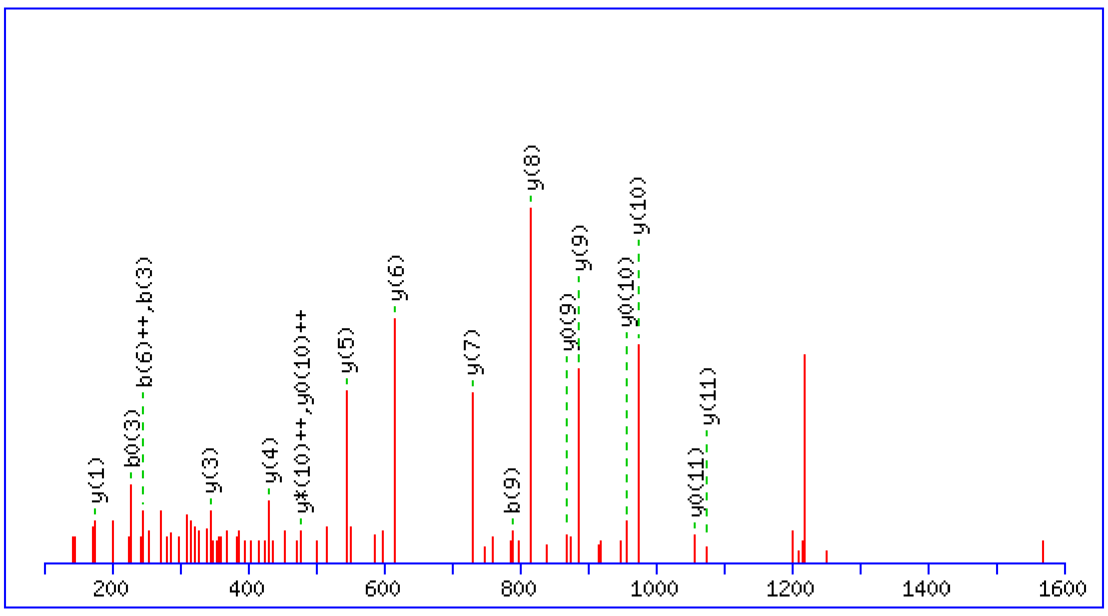
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SGTSASLAISGLR**
Found in **LV102_HUMAN**, Ig lambda chain V-I region HA OS=Homo sapiens PE=1 SV=1

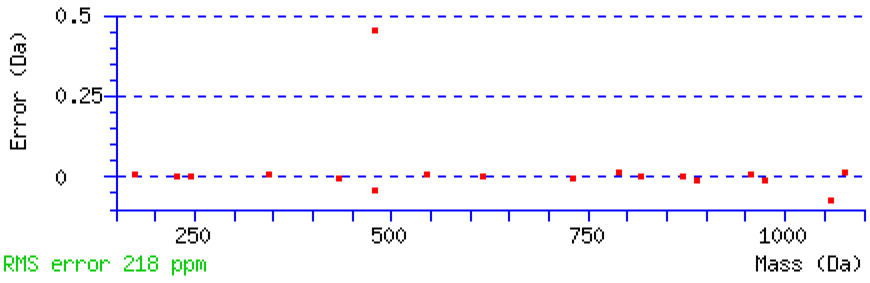
Match to Query 32105: 1218.656188 from(610.335370,2+) rtinseconds(2269) index(26399)
Title: Locus:1.1.1.2185.36
Data file 2011-11-14 - TFD - EP 8-5.mgf

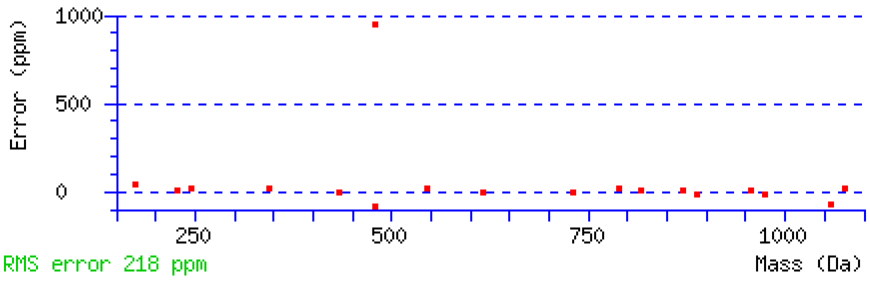
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1218.656799
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 100  Expect: 1.1e-009
Matches : 19/114 fragment ions using 21 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	S							13
2	145.060768	73.034022	127.050203	64.028740	G	1132.632063	566.819669	1115.605514	558.306395	1114.621498	557.814387	12
3	**246.108447**	123.557862	228.097882	114.552579	T	***1075.610599***	538.308937	1058.584050	529.795663	1057.600034	529.303655	11
4	333.140475	167.073875	315.129910	158.068593	S	***974.562920***	487.785098	957.536371	479.271823	956.552355	478.779815	10
5	404.177589	202.592432	386.167024	193.587150	A	***887.530892***	444.269084	870.504343	435.755809	869.520327	435.263801	9
6	491.209617	246.108446	473.199052	237.103164	S	***816.493778***	408.750527	799.467229	400.237252	798.483213	399.745244	8
7	604.293681	302.650479	586.283116	293.645196	L	***729.461750***	365.234513	712.435201	356.721238	711.451185	356.229230	7
8	675.330795	338.169036	657.320230	329.163753	A	***616.377686***	308.692481	599.351137	300.179206	598.367121	299.687198	6
9	**788.414859**	394.711068	770.404294	385.705785	I	***545.340572***	273.173924	528.314023	264.660649	527.330007	264.168641	5
10	875.446887	438.227082	857.436322	429.221799	S	***432.256508***	216.631892	415.229959	208.118617	414.245943	207.626609	4
11	932.468351	466.737814	914.457786	457.732531	G	***345.224480***	173.115878	328.197931	164.602603			3
12	1045.552415	523.279845	1027.541850	514.274563	L	288.203016	144.605146	271.176467	136.091871			2
13					R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
99.8	1218.656799	-0.000611	SGTSASLAISGLR
5.1	1218.660812	-0.004624	AEFQAKIDAVK
2.4	1218.649597	0.006591	IAEGPYIDVVK
2.2	1218.650940	0.005248	FYRPPTPGLR
1.9	1218.654297	0.001891	GGCIPFLKAAR
1.5	1218.662170	-0.005982	KPRGWSFGIR
0.1	1218.650940	0.005248	FYRPPTPGLR

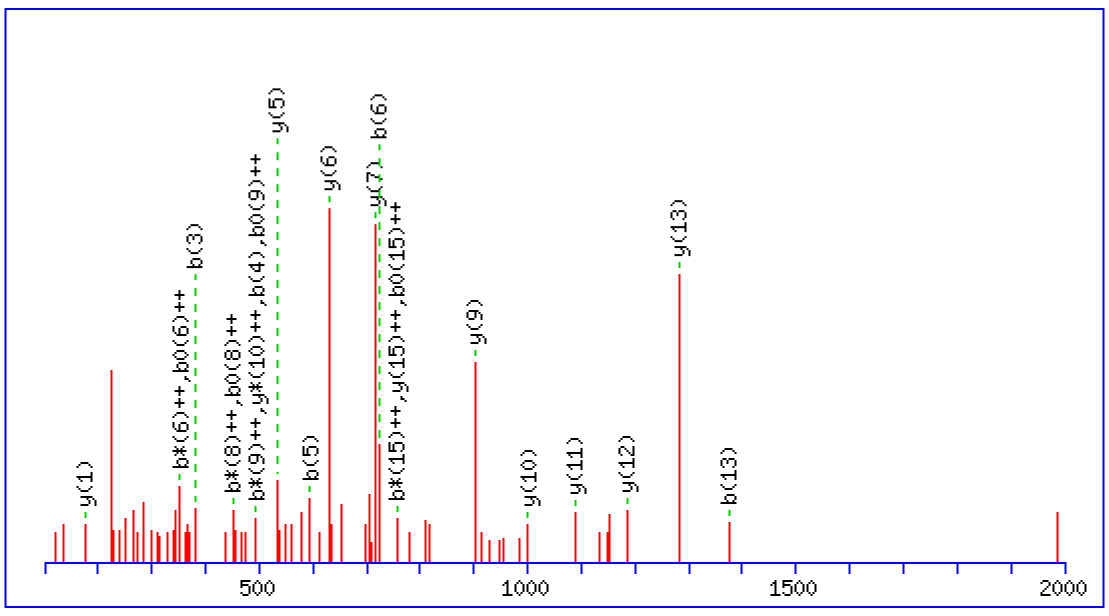
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SYELTQPPSVSVSPGQTAR**
Found in **LV403_HUMAN**, Ig lambda chain V-IV region Hil OS=Homo sapiens PE=1 SV=1

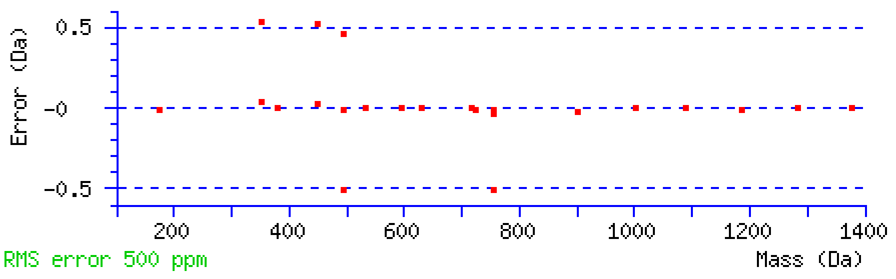
Match to Query 57824: 2002.985682 from(668.669170,3+) rtinseconds(2381) index(28593)
Title: Locus:1.1.1.2198.44
Data file 2011-11-12 - TFD - EP 6-5.mgf

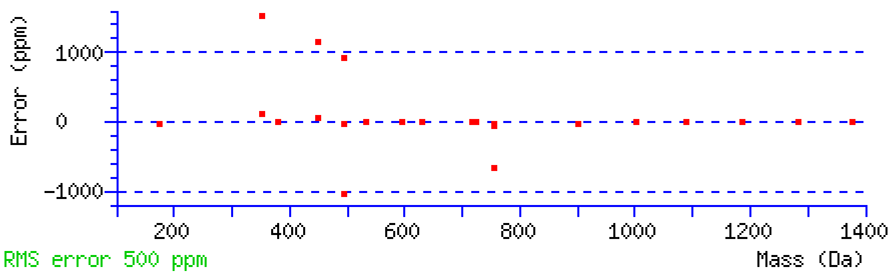
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2002.995987
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 66  Expect: 1.1e-006
Matches : 24/202 fragment ions using 25 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							19
2	251.102633	126.054954			233.092068	117.049672	Y	1916.971234	958.989255	1899.944685	950.475981	1898.960669	949.983973	18
3	***380.145226***	190.576251			362.134661	181.570969	E	1753.907905	877.457591	1736.881356	868.944316	1735.897340	868.452308	17
4	***493.229290***	247.118283			475.218725	238.113001	L	1624.865312	812.936294	1607.838763	804.423020	1606.854747	803.931012	16
5	***594.276969***	297.642123			576.266404	288.636840	T	1511.781248	756.394262	1494.754699	747.880988	1493.770683	747.388980	15
6	***722.335547***	361.671412	705.308998	353.158137	704.324982	352.666129	Q	1410.733569	705.870423	1393.707020	697.357148	1392.723004	696.865140	14
7	819.388311	410.197794	802.361762	401.684519	801.377746	401.192511	P	***1282.674991***	641.841134	1265.648442	633.327859	1264.664426	632.835851	13
8	916.441075	458.724176	899.414526	450.210901	898.430510	449.718893	P	***1185.622227***	593.314752	1168.595678	584.801477	1167.611662	584.309469	12
9	1003.473103	502.240190	986.446554	493.726915	985.462538	493.234907	S	***1088.569463***	544.788370	1071.542914	536.275095	1070.558898	535.783087	11
10	1102.541517	551.774397	1085.514968	543.261122	1084.530952	542.769114	V	***1001.537435***	501.272356	984.510886	492.759081	983.526870	492.267073	10
11	1189.573545	595.290411	1172.546996	586.777136	1171.562980	586.285128	S	***902.469021***	451.738149	885.442472	443.224874	884.458456	442.732866	9
12	1288.641959	644.824618	1271.615410	636.311343	1270.631394	635.819335	V	815.436993	408.222135	798.410444	399.708860	797.426428	399.216852	8
13	***1375.673987***	688.340632	1358.647438	679.827357	1357.663422	679.335349	S	***716.368579***	358.687928	699.342030	350.174653	698.358014	349.682645	7
14	1472.726751	736.867014	1455.700202	728.353739	1454.716186	727.861731	P	***629.336551***	315.171914	612.310002	306.658639	611.325986	306.166631	6
15	1529.748215	765.377746	1512.721666	756.864471	1511.737650	756.372463	G	***532.283787***	266.645532	515.257238	258.132257	514.273222	257.640249	5
16	1657.806793	829.407035	1640.780244	820.893760	1639.796228	820.401752	Q	475.262323	238.134800	458.235774	229.621525	457.251758	229.129517	4
17	1758.854472	879.930874	1741.827923	871.417600	1740.843907	870.925592	T	347.203745	174.105510	330.177196	165.592236	329.193180	165.100228	3
18	1829.891586	915.449431	1812.865037	906.936157	1811.881021	906.444149	A	246.156066	123.581671	229.129517	115.068396			2
19							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
66.2	2002.995987	-0.010305	SYELTQPPSVSVSPGQTAR
2.3	2002.991959	-0.006277	ASSKPATSGPSSAVVPNTSSR
1.9	2002.970856	0.014826	LEDSGVHVIIGGHDSPSPR
1.2	2002.971680	0.014002	HAPGAHGGPGEMAAMIEVKK
0.8	2002.971695	0.013987	GAVAMAPEMLPKHPHTPR
0.5	2002.989426	-0.003744	SAAKIALMNSVFNEHPSR
0.4	2002.991959	-0.006277	ASSKPATSGPSSAVVPNTSSR
0.3	2002.967010	0.018672	TAVFVEGGSEVGPPPAQAMK
0.2	2002.967010	0.018672	TAVFVEGGSEVGPPPAQAMK
0.2	2002.967010	0.018672	TAVFVEGGSEVGPPPAQAMK

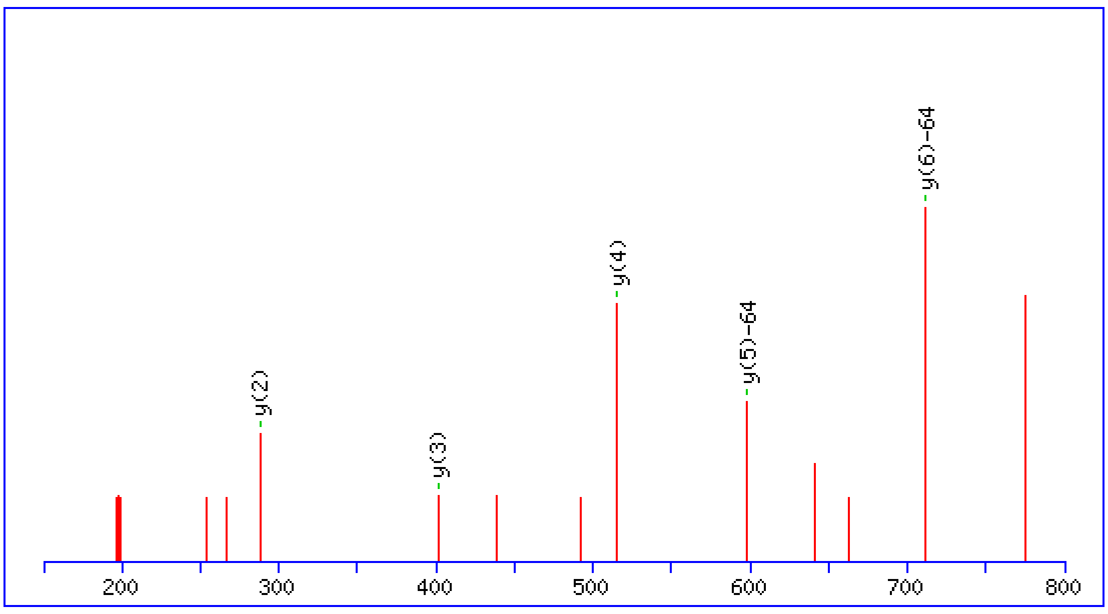
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SQLMNLIR**
Found in **IR3IP_HUMAN**, Immediate early response 3-interacting protein 1 OS=Homo sapiens GN=IER3IP1 PE=1 SV=1

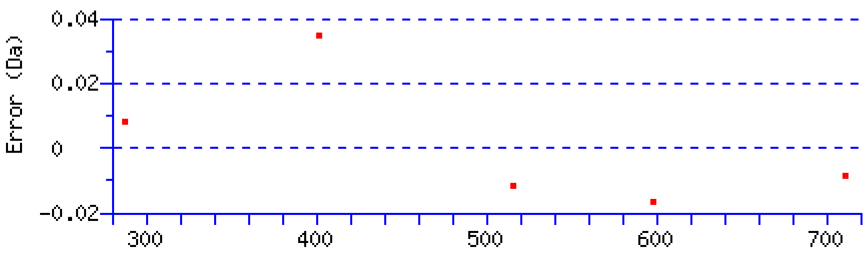
Match to Query 10685: 989.536848 from(495.775700,2+) rtinseconds(2175) index(11259)
Title: Locus:1.1.1.2344.13
Data file 2011-11-12 - TFD - EP 6-8.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●

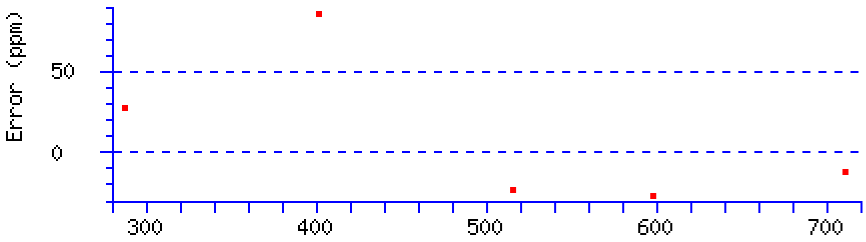


```
Monoisotopic mass of neutral peptide Mr(calc): 989.532776
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M4       : Oxidation (M), with neutral losses 63.998285(shown in table), 0.000000
Ions Score: 52  Expect: 8.3e-005
Matches : 5/104 fragment ions using 5 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	88.039304	44.523290			70.028739	35.518008	S					8
2	216.097882	108.552579	199.071333	100.039305	198.087317	99.547296	Q	839.509764	420.258520	822.483215	411.745246	7
3	329.181946	165.094611	312.155397	156.581336	311.171381	156.089328	L	***711.451186***	356.229231	694.424637	347.715957	6
4	412.219061	206.613168	395.192512	198.099894	394.208496	197.607886	M	***598.367122***	299.687199	581.340573	291.173925	5
5	526.261988	263.634632	509.235439	255.121357	508.251423	254.629349	N	***515.330007***	258.168642	498.303458	249.655367	4
6	639.346052	320.176664	622.319503	311.663389	621.335487	311.171382	L	***401.287080***	201.147178	384.260531	192.633904	3
7	752.430116	376.718696	735.403567	368.205422	734.419551	367.713414	I	***288.203016***	144.605146	271.176467	136.091872	2
8							R	175.118952	88.063114	158.092403	79.549840	1



RMS error 43 ppm



RMS error 43 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.7	989.532776	0.004072	SQLMNLIR
16.1	989.532776	0.004072	SISINLMGR
8.3	989.532791	0.004057	CSVQTLLR
4.3	989.532776	0.004072	NTIMRDLK
2.7	989.532791	0.004057	SQIQMLVR
1.5	989.529434	0.007414	AFGSLGPGLR

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

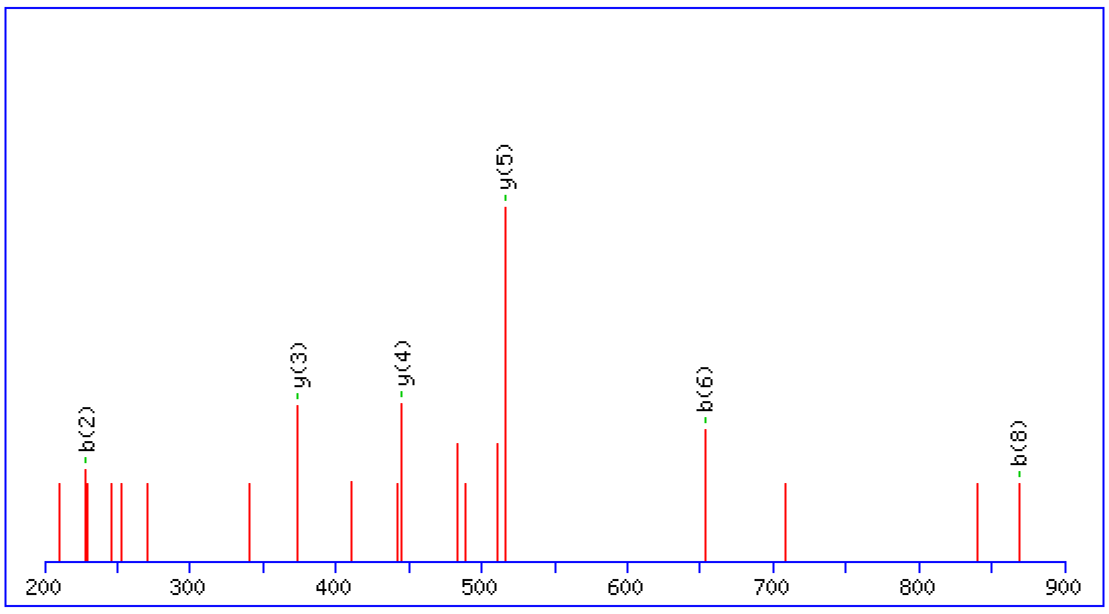
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NLRPGDSQTAAQAR**
Found in **IRGQ_HUMAN**, Immunity-related GTPase family Q protein OS=Homo sapiens GN=IRGQ PE=1 SV=1

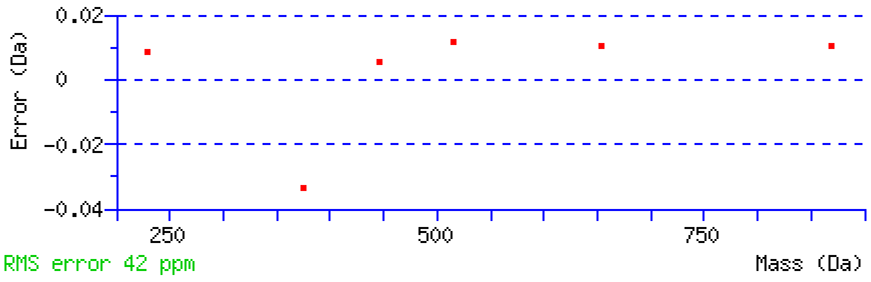
Match to Query 39325: 1483.742412 from(495.588080,3+) rtinseconds(911) index(1329)
Title: Locus:1.1.1.1857.26
Data file 2011-11-12 - TFD - EP 5-3.mgf

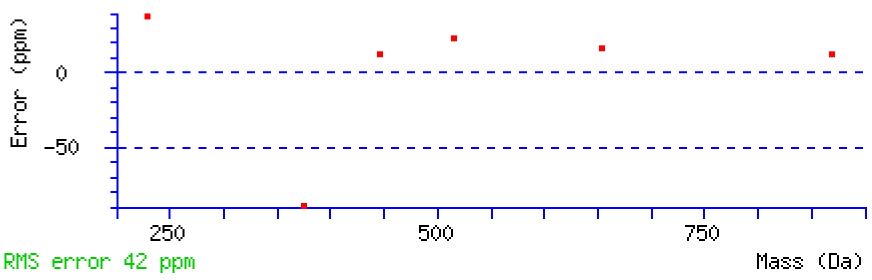
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1483.749130
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 37  Expect: 0.00053
Matches : 6/136 fragment ions using 6 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			N							14
2	***228.134267***	114.570771	211.107718	106.057497			L	1370.713503	685.860390	1353.686954	677.347115	1352.702938	676.855107	13
3	384.235378	192.621327	367.208829	184.108053			R	1257.629439	629.318357	1240.602890	620.805083	1239.618874	620.313075	12
4	481.288142	241.147709	464.261593	232.634435			P	1101.528328	551.267802	1084.501779	542.754527	1083.517763	542.262519	11
5	538.309606	269.658441	521.283057	261.145167			G	1004.475564	502.741420	987.449015	494.228145	986.464999	493.736137	10
6	***653.336549***	327.171913	636.310000	318.658638	635.325984	318.166630	D	947.454100	474.230688	930.427551	465.717413	929.443535	465.225405	9
7	740.368577	370.687927	723.342028	362.174652	722.358012	361.682644	S	832.427157	416.717216	815.400608	408.203942	814.416592	407.711934	8
8	***868.427155***	434.717216	851.400606	426.203941	850.416590	425.711933	Q	745.395129	373.201202	728.368580	364.687928	727.384564	364.195920	7
9	969.474834	485.241055	952.448285	476.727781	951.464269	476.235773	T	617.336551	309.171913	600.310002	300.658639	599.325986	300.166631	6
10	1040.511948	520.759612	1023.485399	512.246337	1022.501383	511.754330	A	***516.288872***	258.648074	499.262323	250.134799			5
11	1111.549062	556.278169	1094.522513	547.764895	1093.538497	547.272887	A	***445.251758***	223.129517	428.225209	214.616242			4
12	1239.607640	620.307458	1222.581091	611.794184	1221.597075	611.302175	Q	***374.214644***	187.610960	357.188095	179.097685			3
13	1310.644754	655.826015	1293.618205	647.312741	1292.634189	646.820732	A	246.156066	123.581671	229.129517	115.068396			2
14							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.4	1483.749130	-0.006718	NLRPGDSQTAAQAR
2.4	1483.738098	0.004314	YLPGPLQDMFKK
1.4	1483.746628	-0.004216	ACAQAGRPLQGWR
1.4	1483.752701	-0.010289	FTMLALRDLGMGK
1.0	1483.737930	0.004482	VQHSDTPSGARSVK

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

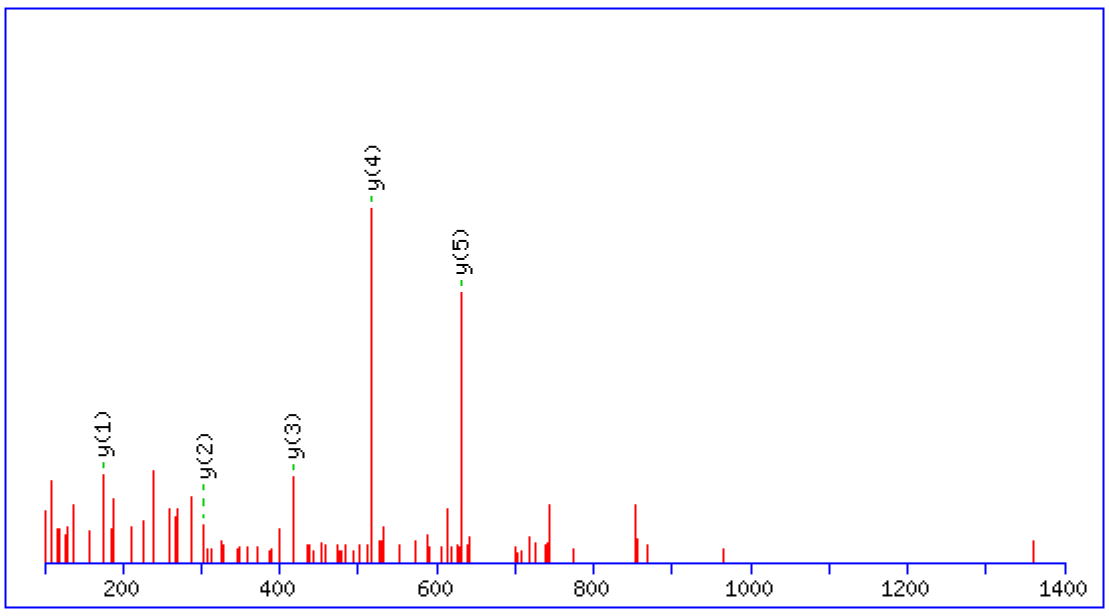
Mascot Search Results

Peptide View

MS/MS Fragmentation of **HNYRELTLQR**
Found in **IGS10_HUMAN**, Immunoglobulin superfamily member 10 OS=Homo sapiens GN=IGSF10 PE=1 SV=1

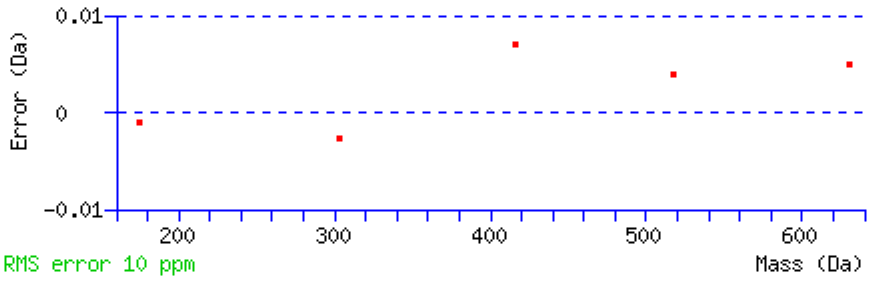
Match to Query 37614: 1328.707602 from(443.909810,3+) rtinseconds(2120) index(25247)
Title: Locus:1.1.1.2125.8
Data file 2011-11-12 - TFD - EP 6-1.mgf

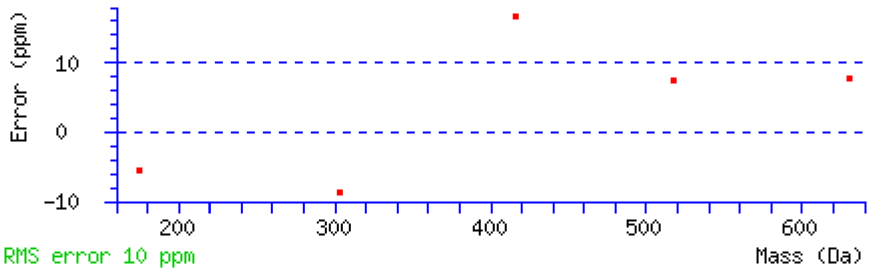
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1328.694901
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 30  Expect: 0.011
Matches : 5/92 fragment ions using 9 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	138.066188	69.536732					H							10
2	252.109115	126.558195	235.082566	118.044921			N	1192.643297	596.825286	1175.616748	588.312012	1174.632732	587.820004	9
3	415.172444	208.089860	398.145895	199.576585			Y	1078.600370	539.803823	1061.573821	531.290549	1060.589805	530.798540	8
4	571.273555	286.140416	554.247006	277.627141			R	915.537041	458.272158	898.510492	449.758884	897.526476	449.266876	7
5	700.316148	350.661712	683.289599	342.148438	682.305583	341.656430	E	759.435930	380.221603	742.409381	371.708328	741.425365	371.216320	6
6	813.400212	407.203744	796.373663	398.690470	795.389647	398.198462	L	***630.393337***	315.700306	613.366788	307.187032	612.382772	306.695024	5
7	914.447891	457.727584	897.421342	449.214309	896.437326	448.722301	T	***517.309273***	259.158274	500.282724	250.645000	499.298708	250.152992	4
8	1027.531955	514.269615	1010.505406	505.756341	1009.521390	505.264333	L	***416.261594***	208.634435	399.235045	200.121160			3
9	1155.590533	578.298904	1138.563984	569.785630	1137.579968	569.293622	Q	***303.177530***	152.092403	286.150981	143.579128			2
10							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.1	1328.694901	0.012701	HNYRELTLQR
16.6	1328.708862	-0.001260	FGIGPPVETIQR
16.6	1328.708862	-0.001260	FGIGPPVETIQR
9.0	1328.712219	-0.004617	MVIQDIPAVTSR
8.6	1328.718750	-0.011148	VSSPLSPLSPGIK
7.4	1328.716049	-0.008447	VSRASSVAGDKPR
6.8	1328.704788	0.002814	AEDLASGILRER
6.4	1328.704803	0.002799	QSVEADINGLRK
6.4	1328.708832	-0.001230	VSATAAELAPFPR
3.1	1328.704803	0.002799	QKADTIQELQR

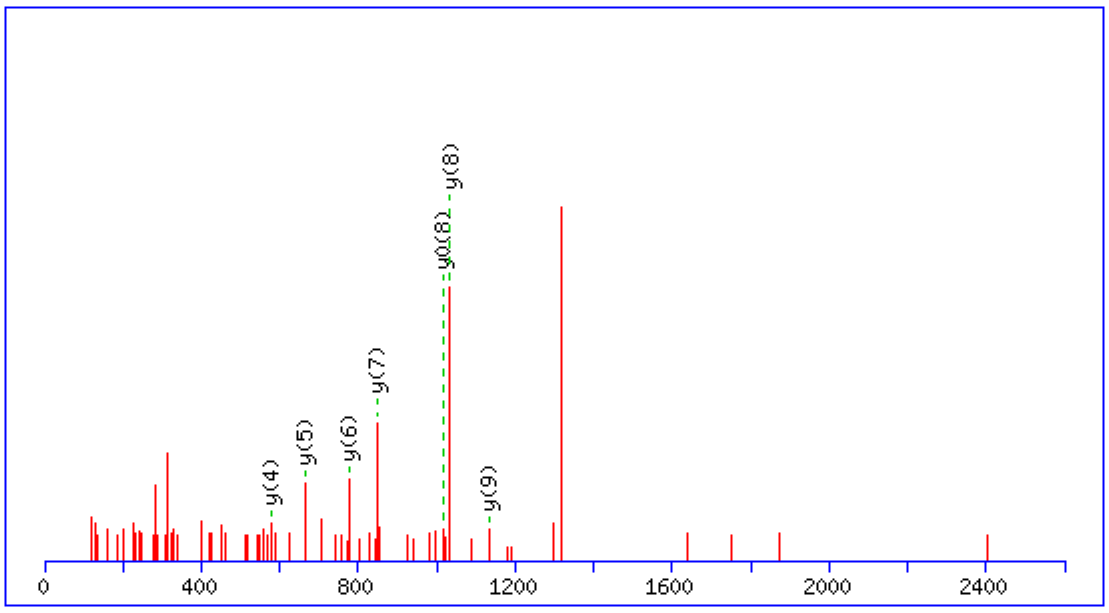
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NAVWALSNLCR**
Found in **IMA1_HUMAN**, Importin subunit alpha-1 OS=Homo sapiens GN=KPNA1 PE=1 SV=3

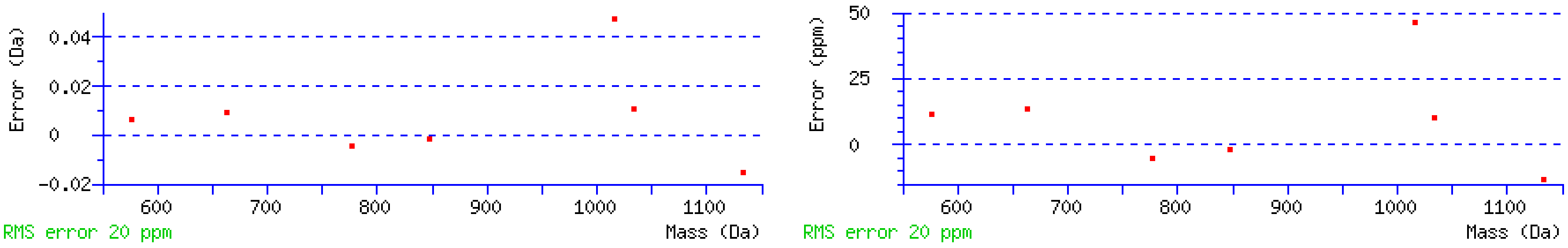
Match to Query 33874: 1316.669328 from(659.341940,2+) rtinseconds(3043) index(42731)
Title: Locus:1.1.1.2528.31
Data file 2011-11-12 - TFD - EP 6-3.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1316.665909
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 42 **Expect:** 0.00057
Matches : 7/100 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			N							11
2	186.087317	93.547296	169.060768	85.034022			A	1203.630289	602.318783	1186.603740	593.805508	1185.619724	593.313500	10
3	285.155731	143.081504	268.129182	134.568229			V	*1132.593175*	566.800226	1115.566626	558.286951	1114.582610	557.794943	9
4	471.235044	236.121160	454.208495	227.607886			W	*1033.524761*	517.266019	1016.498212	508.752744	1015.514196	508.260736	8
5	542.272158	271.639717	525.245609	263.126443			A	*847.445448*	424.226362	830.418899	415.713088	829.434883	415.221080	7
6	655.356222	328.181749	638.329673	319.668475			L	*776.408334*	388.707805	759.381785	380.194531	758.397769	379.702523	6
7	742.388250	371.697763	725.361701	363.184489	724.377685	362.692481	S	*663.324270*	332.165773	646.297721	323.652499	645.313705	323.160491	5
8	856.431177	428.719227	839.404628	420.205952	838.420612	419.713944	N	*576.292242*	288.649759	559.265693	280.136485			4
9	969.515241	485.261259	952.488692	476.747984	951.504676	476.255976	L	462.249315	231.628296	445.222766	223.115021			3
10	1143.561540	572.284408	1126.534991	563.771134	1125.550975	563.279126	C	349.165251	175.086264	332.138702	166.572989			2
11							R	175.118952	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.3	1316.665909	0.003419	NAVWALSNLCR
7.7	1316.657181	0.012147	ANENSLPSTQLK

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

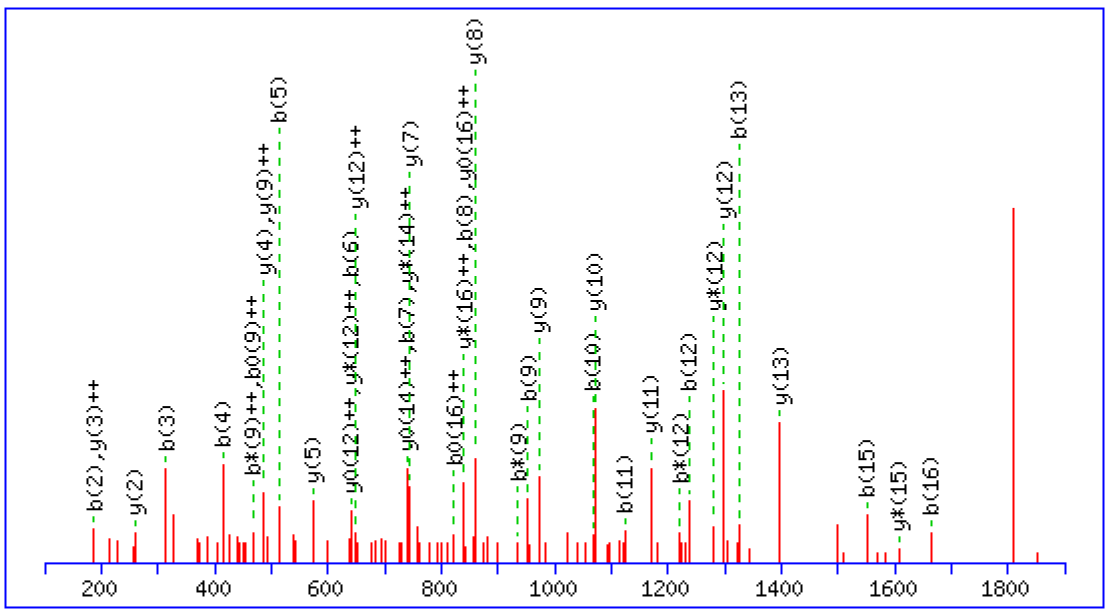
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DAQVVQVVLDGLSNILK**
Found in **IMA4_HUMAN**, Importin subunit alpha-4 OS=Homo sapiens GN=KPNA4 PE=1 SV=1

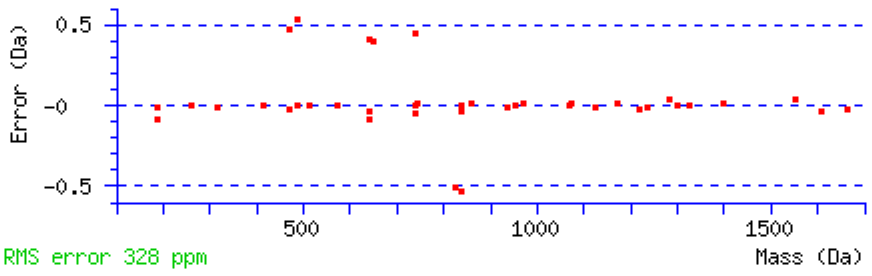
Match to Query 54429: 1810.031748 from(906.023150,2+) rtinseconds(5183) index(82783)
Title: Locus:1.1.1.3457.27
Data file 2011-11-10 - TFD - EP 4-3.mgf

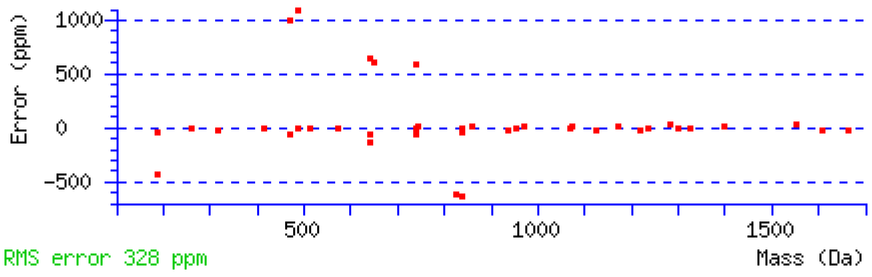
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1810.020020
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 121 **Expect:** 1.6e-012
Matches : 40/180 fragment ions using 43 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	116.034219	58.520748			98.023654	49.515465	D							17
2	*187.071333*	94.039304			169.060768	85.034022	A	1696.000348	848.503812	1678.973799	839.990537	1677.989783	839.498529	16
3	*315.129911*	158.068593	298.103362	149.555319	297.119346	149.063311	Q	1624.963234	812.985255	1607.936685	804.471980	1606.952669	803.979972	15
4	*414.198325*	207.602801	397.171776	199.089526	396.187760	198.597518	V	1496.904656	748.955966	1479.878107	740.442691	1478.894091	739.950683	14
5	*513.266739*	257.137008	496.240190	248.623733	495.256174	248.131725	V	**1397.836242**	699.421759	1380.809693	690.908484	1379.825677	690.416476	13
6	*641.325317*	321.166297	624.298768	312.653022	623.314752	312.161014	Q	**1298.767828**	649.887552	1281.741279	641.374277	1280.757263	640.882269	12
7	*740.393731*	370.700504	723.367182	362.187229	722.383166	361.695221	V	**1170.709250**	585.858263	1153.682701	577.344988	1152.698685	576.852980	11
8	*839.462145*	420.234711	822.435596	411.721436	821.451580	411.229428	V	**1071.640836**	536.324056	1054.614287	527.810781	1053.630271	527.318773	10
9	*952.546209*	476.776743	935.519660	468.263468	934.535644	467.771460	L	**972.572422**	486.789849	955.545873	478.276574	954.561857	477.784566	9
10	*1067.573152*	534.290214	1050.546603	525.776940	1049.562587	525.284931	D	**859.488358**	430.247817	842.461809	421.734542	841.477793	421.242534	8
11	*1124.594616*	562.800946	1107.568067	554.287671	1106.584051	553.795663	G	**744.461415**	372.734345	727.434866	364.221071	726.450850	363.729063	7
12	*1237.678680*	619.342978	1220.652131	610.829703	1219.668115	610.337695	L	687.439951	344.223613	670.413402	335.710339	669.429386	335.218331	6
13	*1324.710708*	662.858992	1307.684159	654.345717	1306.700143	653.853709	S	**574.355887**	287.681581	557.329338	279.168307	556.345322	278.676299	5
14	1438.753635	719.880455	1421.727086	711.367181	1420.743070	710.875173	N	**487.323859**	244.165567	470.297310	235.652293			4
15	*1551.837699*	776.422487	1534.811150	767.909213	1533.827134	767.417205	I	373.280932	187.144104	356.254383	178.630829			3
16	*1664.921763*	832.964519	1647.895214	824.451245	1646.911198	823.959237	L	**260.196868**	130.602072	243.170319	122.088797			2
17							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
121.3	1810.020020	0.011728	DAQVVQVVLDGLSNILK
1.9	1810.038620	-0.006872	NVLMTLPIPILSAQLR
1.8	1810.024704	0.007044	CISLIPVNGRPRTGLK

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

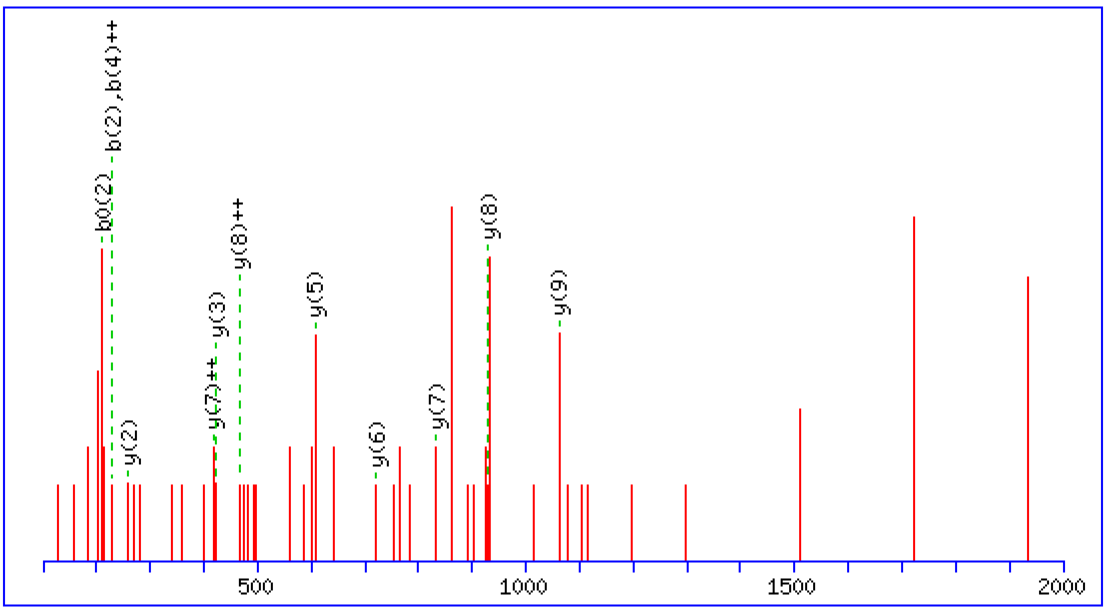
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EVMPLLLAYLK**
Found in **IPO4_HUMAN**, Importin-4 OS=Homo sapiens GN=IPO4 PE=1 SV=2

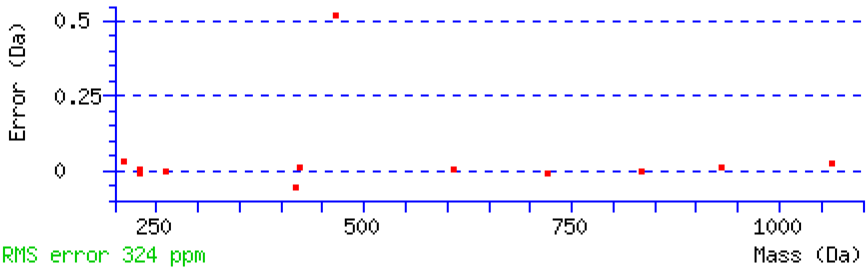
Match to Query 35071: 1288.744688 from(645.379620,2+) rtinseconds(4266) index(65010)
Title: Locus:1.1.1.2920.23
Data file 2011-11-12 - TFD - EP 6-1.mgf

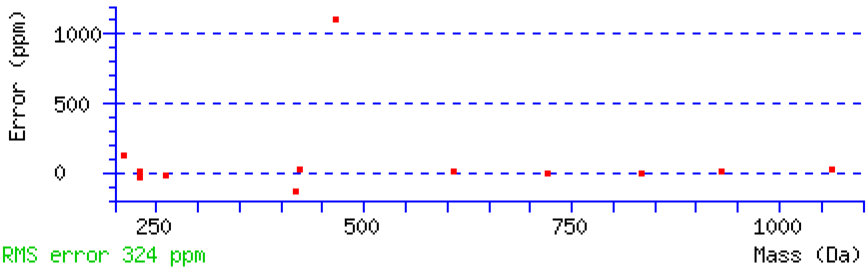
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1288.746445
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.0011
Matches : 12/80 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	130.049869	65.528572	112.039304	56.523290	**E**					**11**
2	229.118283	115.062780	211.107718	106.057497	**V**	1160.711166	580.859221	1143.684617	572.345946	**10**
3	360.158768	180.583022	342.148203	171.577740	**M**	***1061.642752***	531.325014	1044.616203	522.811740	**9**
4	457.211532	229.109404	439.200967	220.104121	**P**	***930.602267***	465.804772	913.575718	457.291497	**8**
5	570.295596	285.651436	552.285031	276.646154	**L**	***833.549503***	417.278390	816.522954	408.765115	**7**
6	683.379660	342.193468	665.369095	333.188186	**L**	***720.465439***	360.736358	703.438890	352.223083	**6**
7	796.463724	398.735500	778.453159	389.730218	**L**	***607.381375***	304.194325	590.354826	295.681051	**5**
8	867.500838	434.254057	849.490273	425.248775	**A**	494.297311	247.652293	477.270762	239.139019	**4**
9	1030.564167	515.785722	1012.553602	506.780439	**Y**	***423.260197***	212.133736	406.233648	203.620462	**3**
10	1143.648231	572.327753	1125.637666	563.322471	**L**	***260.196868***	130.602072	243.170319	122.088797	**2**
11					**K**	147.112804	74.060040	130.086255	65.546765	**1**





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.9	1288.746445	-0.001757	EVMPLLLAYLK
3.0	1288.736374	0.008314	QHLLDARPAIR

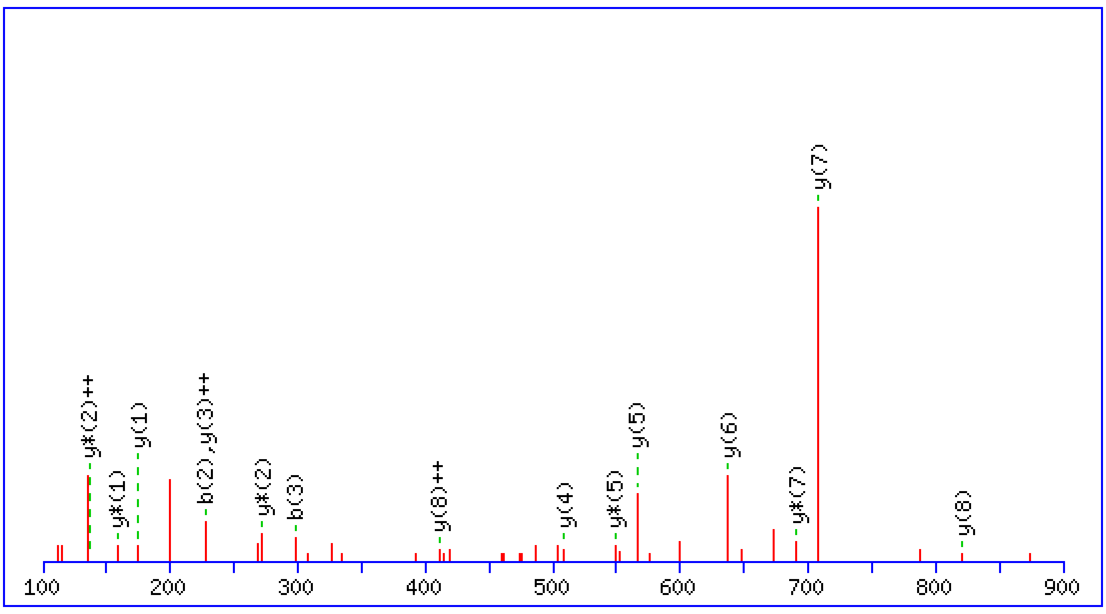
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LIAAGGYNR**
Found in **NS1BP_HUMAN**, Influenza virus NS1A-binding protein OS=Homo sapiens GN=IVNS1ABP PE=1 SV=3

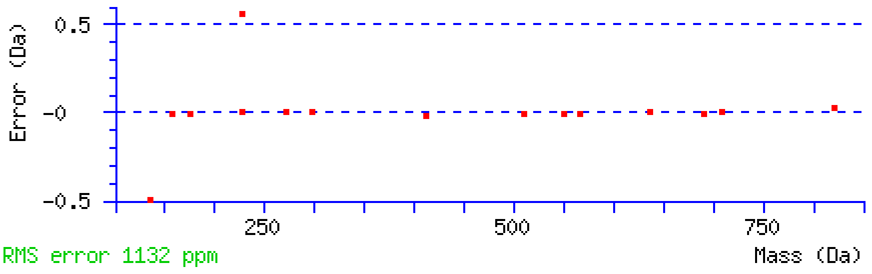
Match to Query 172456: 933.501908 from(467.758230,2+) rtinseconds(1355) index(500041)
Title: Locus:1.1.1.843.13
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

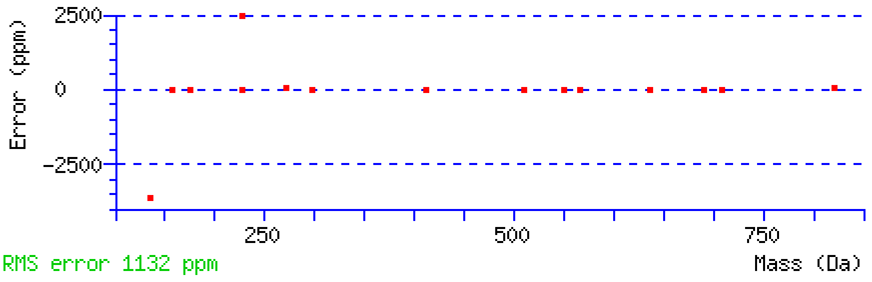
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 933.503189
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33  Expect: 0.0057
Matches : 15/50 fragment ions using 32 most intense peaks   (help)
```

#	b	b^{++}	b*	b*$^{++}$	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	114.091340	57.549308			L					9
2	227.175404	114.091340			I	821.426428	411.216852	804.399879	402.703577	8
3	298.212518	149.609897			A	708.342364	354.674820	691.315815	346.161545	7
4	369.249632	185.128454			A	637.305250	319.156263	620.278701	310.642988	6
5	426.271096	213.639186			G	566.268136	283.637706	549.241587	275.124431	5
6	483.292560	242.149918			G	509.246672	255.126974	492.220123	246.613699	4
7	646.355889	323.681582			Y	452.225208	226.616242	435.198659	218.102967	3
8	760.398816	380.703046	743.372267	372.189771	N	289.161879	145.084577	272.135330	136.571303	2
9					R	175.118952	88.063114	158.092403	79.549839	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.7	933.503189	-0.001281	LIAAGGYNR
10.1	933.499374	0.002534	LLVASWVM
7.2	933.493317	0.008591	LAHGHFPR
6.4	933.499374	0.002534	LLLPQFGM
4.4	933.495346	0.006562	LLTDGIMR
3.4	933.503220	-0.001312	GPPKPGPPR
3.4	933.503220	-0.001312	GPPKPGPPR
1.9	933.499374	0.002534	IPPSFVKM
1.9	933.507217	-0.005309	IIHYFNK
1.9	933.502731	-0.000823	IIQMGLLM

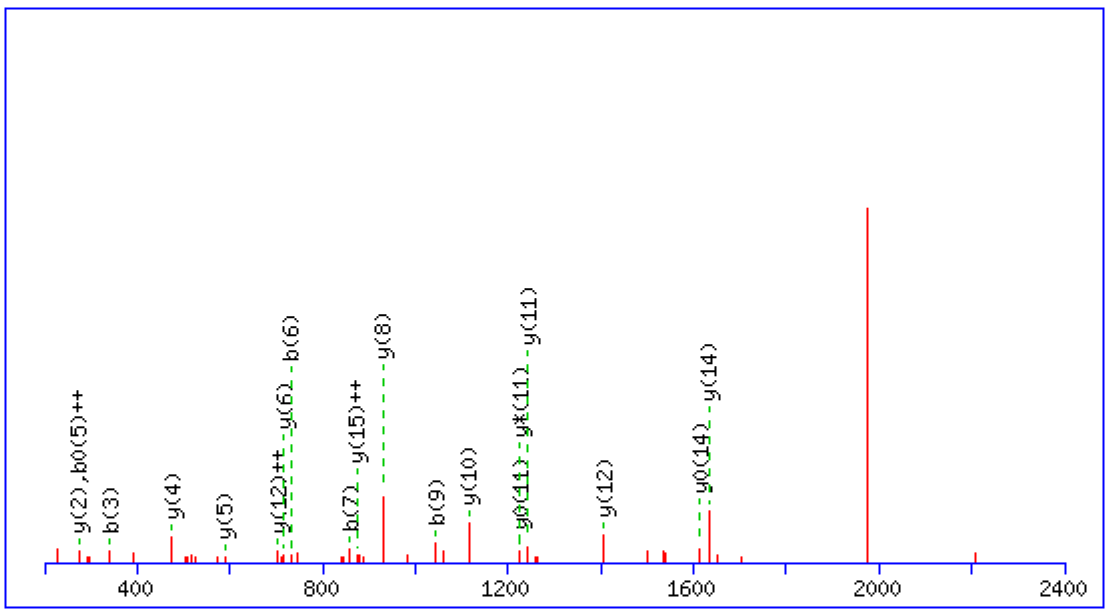
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IDLPEYQGEPDEISIQK**
Found in **ITPA_HUMAN**, Inosine triphosphate pyrophosphatase OS=Homo sapiens GN=ITPA PE=1 SV=2

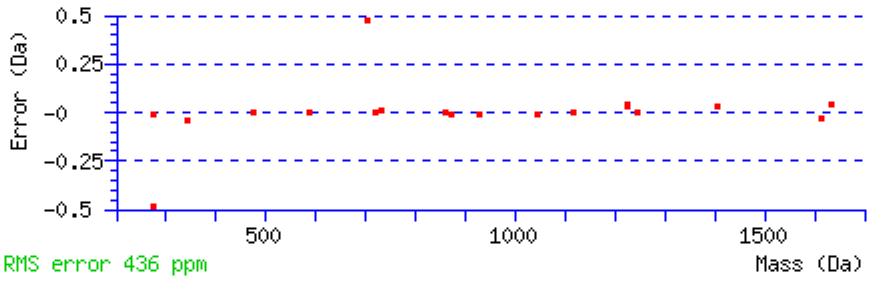
Match to Query 56349: 1972.967108 from(987.490830,2+) rtinseconds(2898) index(37851)
Title: Locus:1.1.1.2255.51
Data file 2011-11-12 - TFD - EP 6-6.mgf

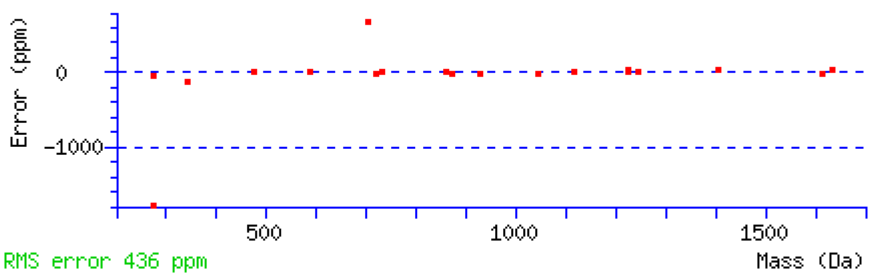
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1972.962921
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 60  Expect: 3.7e-006
Matches : 19/172 fragment ions using 28 most intense peaks   (help)
```

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					I							17
2	229.118283	115.062779			211.107718	106.057497	D	1860.886166	930.946721	1843.859617	922.433447	1842.875601	921.941439	16
3	**342.202347**	171.604811			324.191782	162.599529	L	1745.859223	873.433250	1728.832674	864.919975	1727.848658	864.427967	15
4	439.255111	220.131193			421.244546	211.125911	P	***1632.775159***	816.891218	1615.748610	808.377943	1614.764594	807.885935	14
5	568.297704	284.652490			550.287139	275.647208	E	1535.722395	768.364836	1518.695846	759.851561	1517.711830	759.359553	13
6	**731.361033**	366.184155			713.350468	357.178872	Y	***1406.679802***	703.843539	1389.653253	695.330265	1388.669237	694.838257	12
7	**859.419611**	430.213444	842.393062	421.700169	841.409046	421.208161	Q	***1243.616473***	622.311875	1226.589924	613.798600	1225.605908	613.306592	11
8	916.441075	458.724176	899.414526	450.210901	898.430510	449.718893	G	***1115.557895***	558.282586	1098.531346	549.769311	1097.547330	549.277303	10
9	**1045.483668**	523.245472	1028.457119	514.732198	1027.473103	514.240190	E	1058.536431	529.771854	1041.509882	521.258579	1040.525866	520.766571	9
10	1142.536432	571.771854	1125.509883	563.258580	1124.525867	562.766572	P	***929.493838***	465.250557	912.467289	456.737283	911.483273	456.245275	8
11	1257.563375	629.285326	1240.536826	620.772051	1239.552810	620.280043	D	832.441074	416.724175	815.414525	408.210901	814.430509	407.718893	7
12	1386.605968	693.806622	1369.579419	685.293348	1368.595403	684.801340	E	***717.414131***	359.210704	700.387582	350.697429	699.403566	350.205421	6
13	1499.690032	750.348654	1482.663483	741.835380	1481.679467	741.343371	I	***588.371538***	294.689407	571.344989	286.176133	570.360973	285.684125	5
14	1586.722060	793.864668	1569.695511	785.351394	1568.711495	784.859386	S	***475.287474***	238.147375	458.260925	229.634101	457.276909	229.142093	4
15	1699.806124	850.406700	1682.779575	841.893426	1681.795559	841.401417	I	388.255446	194.631361	371.228897	186.118087			3
16	1827.864702	914.435989	1810.838153	905.922715	1809.854137	905.430707	Q	***275.171382***	138.089329	258.144833	129.576055			2
17							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
60.0	1972.962921	0.004187	IDLPEYQGEPDEISIQK
2.1	1972.981583	-0.014475	DLMPPPDLATSPTKSPFK
2.1	1972.981583	-0.014475	DLMPPPDLATSPTKSPFK

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

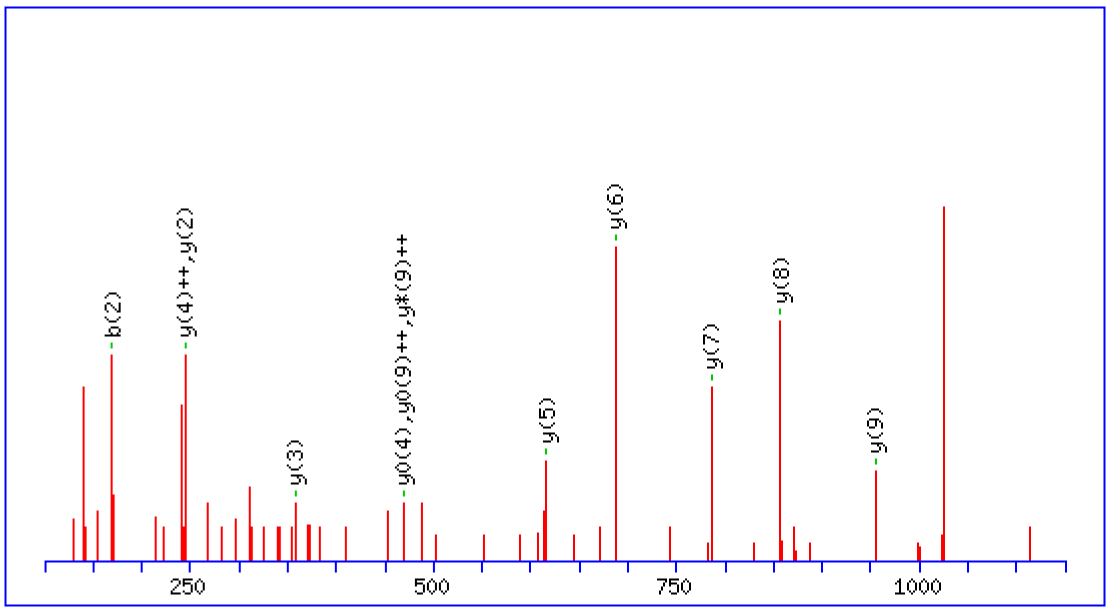
Mascot Search Results

Peptide View

MS/MS Fragmentation of **APAVAEENPK**
Found in **IBP6_HUMAN**, Insulin-like growth factor-binding protein 6 OS=Homo sapiens GN=IGFBP6 PE=1 SV=1

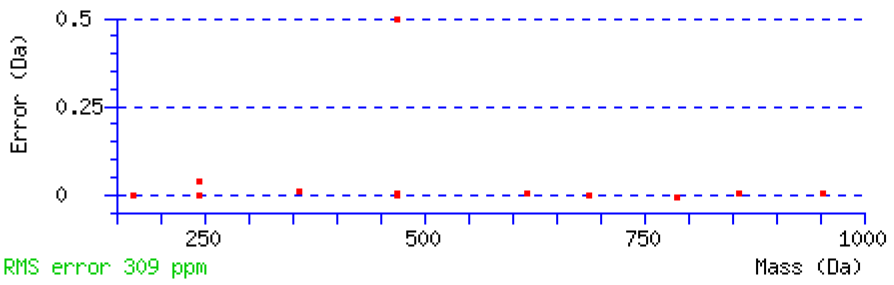
Match to Query 293741: 1024.516468 from(513.265510,2+) rtinseconds(928) index(242456)
Title: Locus:1.1.1.793.21
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

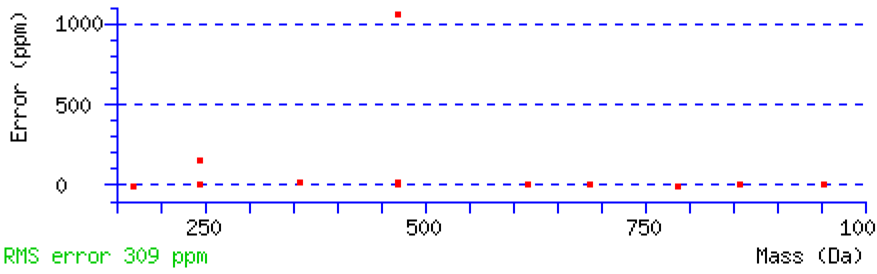
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1024.518890
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 71  Expect: 8.3e-007
Matches : 12/78 fragment ions using 9 most intense peaks   (help)
```

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	72.044390	36.525833					**A**							**10**
2	169.097154	85.052215					**P**	***954.489087***	477.748182	937.462538	469.234907	936.478522	468.742899	**9**
3	240.134268	120.570772					**A**	***857.436323***	429.221800	840.409774	420.708525	839.425758	420.216517	**8**
4	339.202682	170.104979					**V**	***786.399209***	393.703243	769.372660	385.189968	768.388644	384.697960	**7**
5	410.239796	205.623536					**A**	***687.330795***	344.169036	670.304246	335.655761	669.320230	335.163753	**6**
6	539.282389	270.144833			521.271824	261.139550	**E**	***616.293681***	308.650479	599.267132	300.137204	598.283116	299.645196	**5**
7	668.324982	334.666129			650.314417	325.660847	**E**	487.251088	244.129182	470.224539	235.615907	469.240523	235.123899	**4**
8	782.367909	391.687593	765.341360	383.174318	764.357344	382.682310	**N**	***358.208495***	179.607885	341.181946	171.094611			**3**
9	879.420673	440.213975	862.394124	431.700700	861.410108	431.208692	**P**	***244.165568***	122.586422	227.139019	114.073148			**2**
10							**K**	147.112804	74.060040	130.086255	65.546765			**1**





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
70.8	1024.518890	-0.002422	APAVAEENPK
10.6	1024.516418	0.000050	APAFAFVRM
0.1	1024.512375	0.004093	APPASRAPQM

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

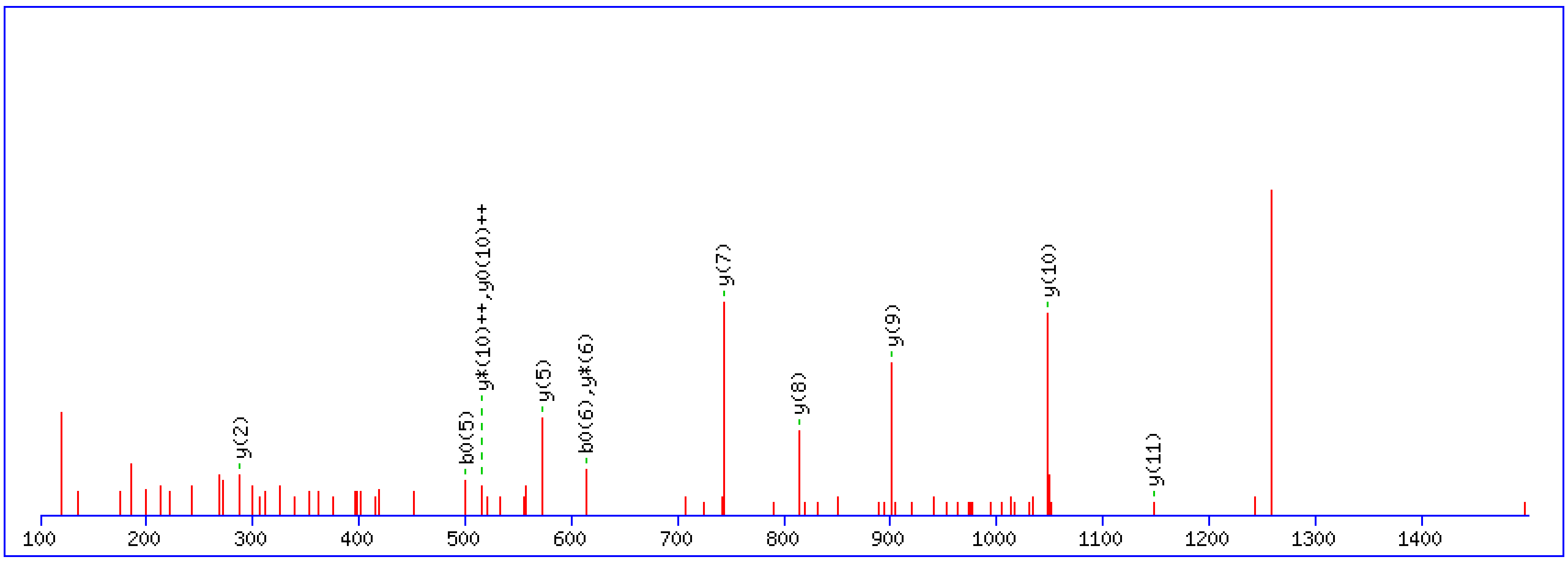
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LVFSALGPTSLR**
Found in **ITB4_HUMAN**, Integrin beta-4 OS=Homo sapiens GN=ITGB4 PE=1 SV=5

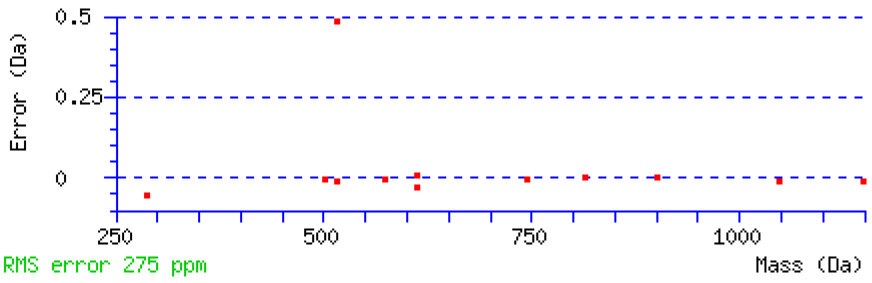
Match to Query 36132: 1259.717888 from(630.866220,2+) rtinseconds(3076) index(43612)
Title: Locus:1.1.1.1559.25
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 1.mgf

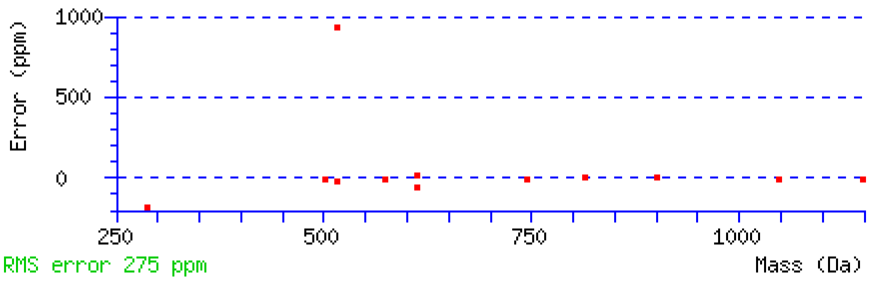
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1259.723770
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 39  Expect: 0.00026
Matches : 12/100 fragment ions using 22 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							12
2	213.159754	107.083515			V	***1147.646985***	574.327131	1130.620436	565.813856	1129.636420	565.321848	11
3	360.228168	180.617722			F	***1048.578571***	524.792924	1031.552022	516.279649	1030.568006	515.787641	10
4	447.260196	224.133736	429.249631	215.128454	S	***901.510157***	451.258716	884.483608	442.745442	883.499592	442.253434	9
5	518.297310	259.652293	500.286745	250.647011	A	***814.478129***	407.742703	797.451580	399.229428	796.467564	398.737420	8
6	631.381374	316.194325	613.370809	307.189043	L	***743.441015***	372.224146	726.414466	363.710871	725.430450	363.218863	7
7	688.402838	344.705057	670.392273	335.699775	G	630.356951	315.682114	613.330402	307.168839	612.346386	306.676831	6
8	785.455602	393.231439	767.445037	384.226157	P	***573.335487***	287.171382	556.308938	278.658107	555.324922	278.166099	5
9	886.503281	443.755279	868.492716	434.749996	T	476.282723	238.644999	459.256174	230.131725	458.272158	229.639717	4
10	973.535309	487.271293	955.524744	478.266010	S	375.235044	188.121160	358.208495	179.607885	357.224479	179.115877	3
11	1086.619373	543.813325	1068.608808	534.808042	L	***288.203016***	144.605146	271.176467	136.091871			2
12					R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.7	1259.723770	-0.005882	LVFSALGPTSLR
0.5	1259.712524	0.005364	LVLYPEGIQTK

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

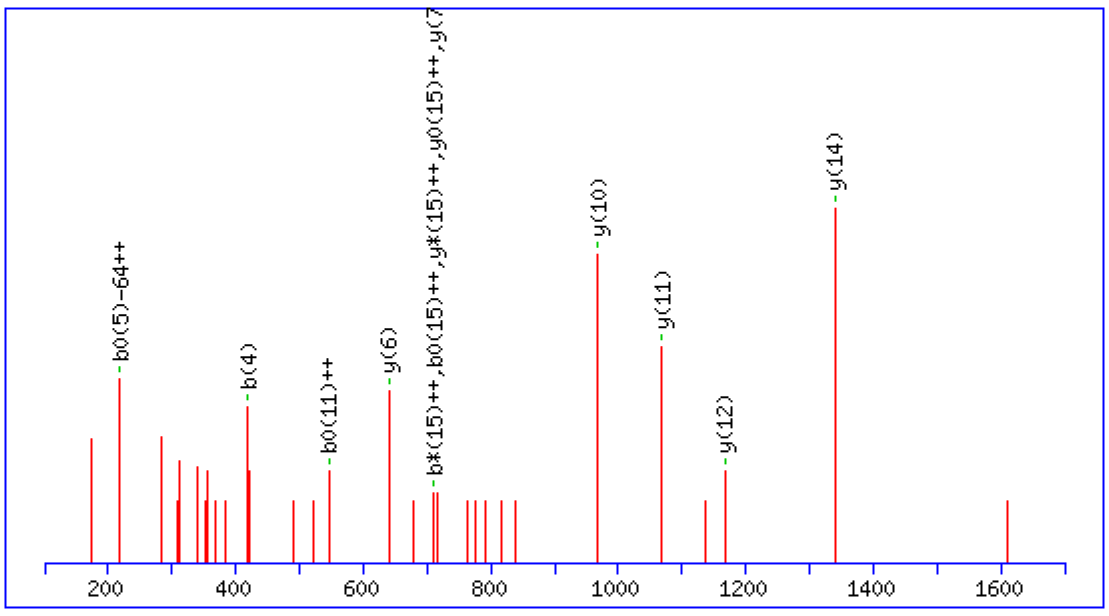
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVGDVTGAQAYASTAK**
Found in **IFM1_HUMAN**, Interferon-induced transmembrane protein 1 OS=Homo sapiens GN=IFITM1 PE=1 SV=3

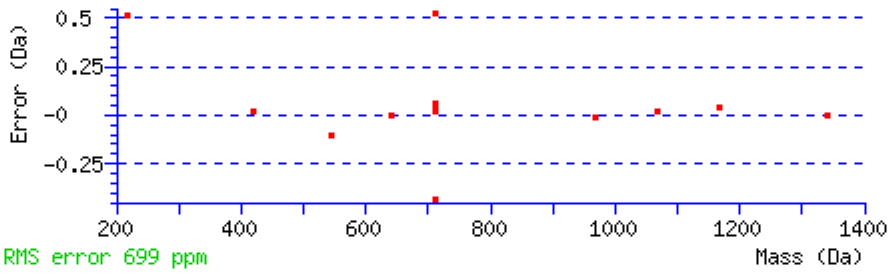
Match to Query 40501: 1584.750248 from(793.382400,2+) rtinseconds(1802) index(11514)
Title: Locus:1.1.1.2142.42
Data file 2011-11-10 - TFD - EP 4-7.mgf

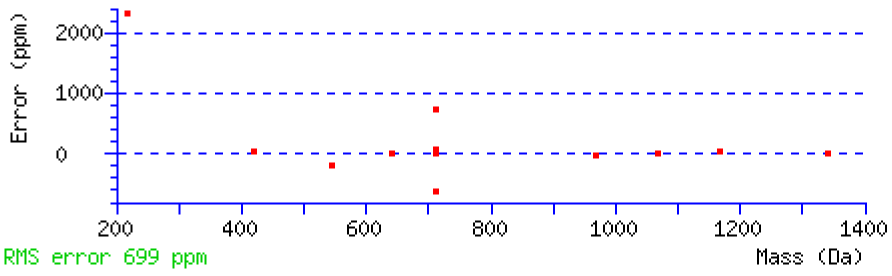
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1584.745377
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 36 **Expect:** 0.0025
Matches : 13/222 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.042676	74.524976					M							16
2	247.111090	124.059183					V	1438.717252	719.862264	1421.690703	711.348990	1420.706687	710.856982	15
3	304.132554	152.569915					G	***1339.648838***	670.328057	1322.622289	661.814783	1321.638273	661.322775	14
4	419.159497	210.083386			401.148932	201.078104	D	1282.627374	641.817325	1265.600825	633.304051	1264.616809	632.812043	13
5	518.227911	259.617594			500.217346	250.612311	V	***1167.600431***	584.303854	1150.573882	575.790579	1149.589866	575.298571	12
6	619.275590	310.141433			601.265025	301.136151	T	***1068.532017***	534.769647	1051.505468	526.256372	1050.521452	525.764364	11
7	676.297054	338.652165			658.286489	329.646883	G	***967.484338***	484.245807	950.457789	475.732533	949.473773	475.240525	10
8	747.334168	374.170722			729.323603	365.165440	A	910.462874	455.735075	893.436325	447.221801	892.452309	446.729793	9
9	875.392746	438.200011	858.366197	429.686737	857.382181	429.194729	Q	839.425760	420.216518	822.399211	411.703244	821.415195	411.211236	8
10	946.429860	473.718568	929.403311	465.205294	928.419295	464.713286	A	***711.367182***	356.187229	694.340633	347.673955	693.356617	347.181947	7
11	1109.493189	555.250233	1092.466640	546.736958	1091.482624	546.244950	Y	***640.330068***	320.668672	623.303519	312.155398	622.319503	311.663390	6
12	1180.530303	590.768790	1163.503754	582.255515	1162.519738	581.763507	A	477.266739	239.137008	460.240190	230.623733	459.256174	230.131725	5
13	1267.562331	634.284804	1250.535782	625.771529	1249.551766	625.279521	S	406.229625	203.618451	389.203076	195.105176	388.219060	194.613168	4
14	1368.610010	684.808643	1351.583461	676.295369	1350.599445	675.803361	T	319.197597	160.102436	302.171048	151.589162	301.187032	151.097154	3
15	1439.647124	720.327200	1422.620575	711.813926	1421.636559	711.321918	A	218.149918	109.578597	201.123369	101.065322			2
16							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.7	1584.745377	0.004871	MVGDVTGAQAYASTAK
13.4	1584.764465	-0.014217	TFPATTYSGNSRQR
4.0	1584.738861	0.011387	SMSTVIRMPDGGFR
1.0	1584.757446	-0.007198	LCMSLMQNKQFR
0.7	1584.738846	0.011402	FVRVLCGMSSDER

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

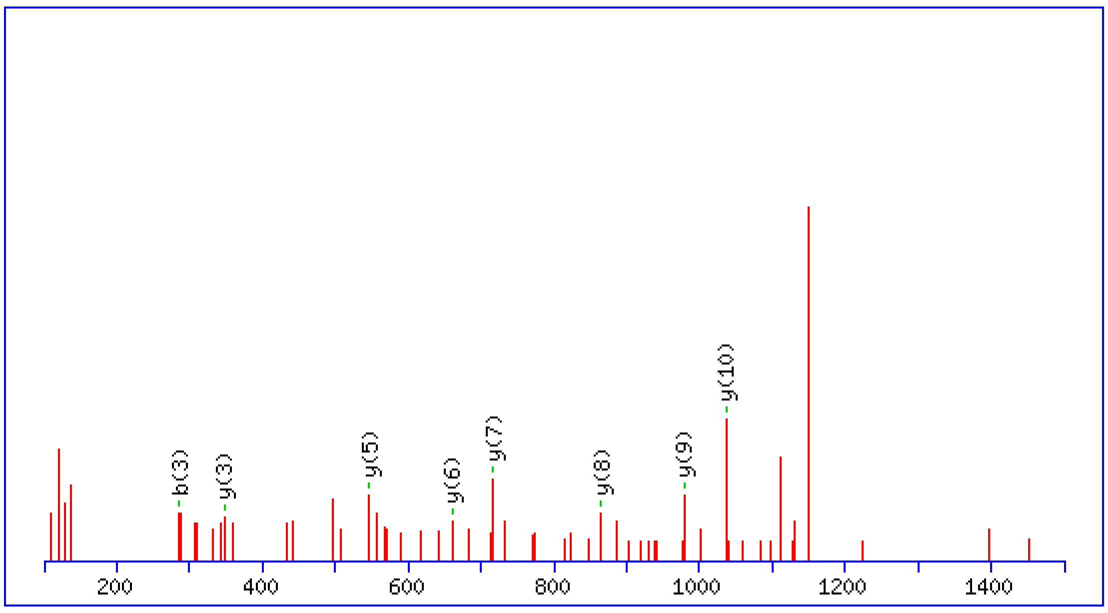
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IGDFGLVTSLK**
Found in **E2AK2_HUMAN**, Interferon-induced, double-stranded RNA-activated protein kinase OS=Homo sapiens GN=EIF2AK2 PE=1 SV=2

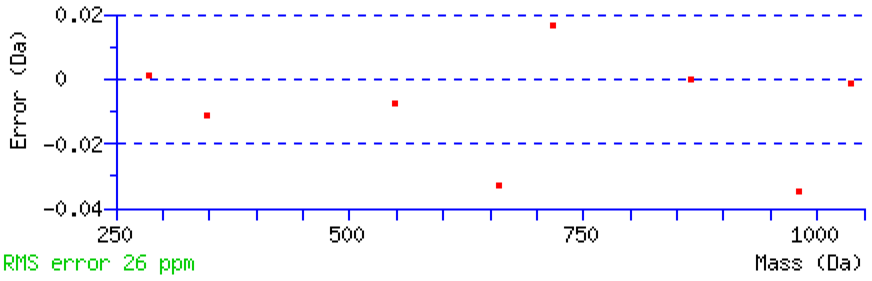
Match to Query 26804: 1148.647048 from(575.330800,2+) rtinseconds(3072) index(42486)
Title: Locus:1.1.1.2605.19
Data file 2011-11-10 - TFD - EP 3-2.mgf

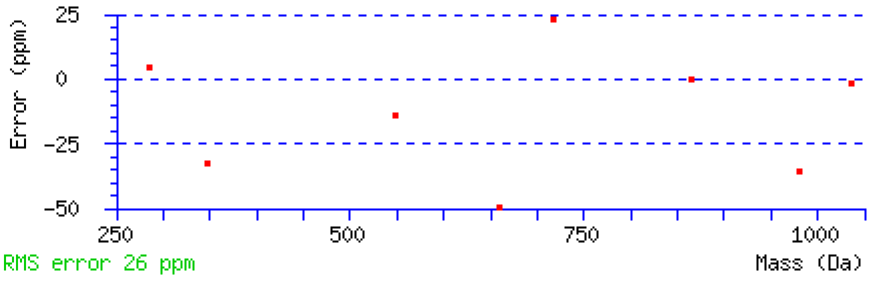
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1148.644135
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 54 **Expect:** 3e-005
Matches : 8/92 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							11
2	171.112804	86.060040			G	***1036.567338***	518.787307	1019.540789	510.274033	1018.556773	509.782025	10
3	286.139747	143.573512	268.129182	134.568229	D	***979.545874***	490.276575	962.519325	481.763300	961.535309	481.271292	9
4	433.208161	217.107718	415.197596	208.102436	F	***864.518931***	432.763104	847.492382	424.249829	846.508366	423.757821	8
5	490.229625	245.618450	472.219060	236.613168	G	***717.450517***	359.228897	700.423968	350.715622	699.439952	350.223614	7
6	603.313689	302.160483	585.303124	293.155200	L	***660.429053***	330.718165	643.402504	322.204890	642.418488	321.712882	6
7	702.382103	351.694689	684.371538	342.689407	V	***547.344989***	274.176133	530.318440	265.662858	529.334424	265.170850	5
8	803.429782	402.218529	785.419217	393.213246	T	448.276575	224.641925	431.250026	216.128651	430.266010	215.636643	4
9	890.461810	445.734543	872.451245	436.729260	S	***347.228896***	174.118086	330.202347	165.604811	329.218331	165.112803	3
10	1003.545874	502.276575	985.535309	493.271292	L	260.196868	130.602072	243.170319	122.088798			2
11					K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
53.5	1148.644135	0.002913	IGDFGLVTSLK

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

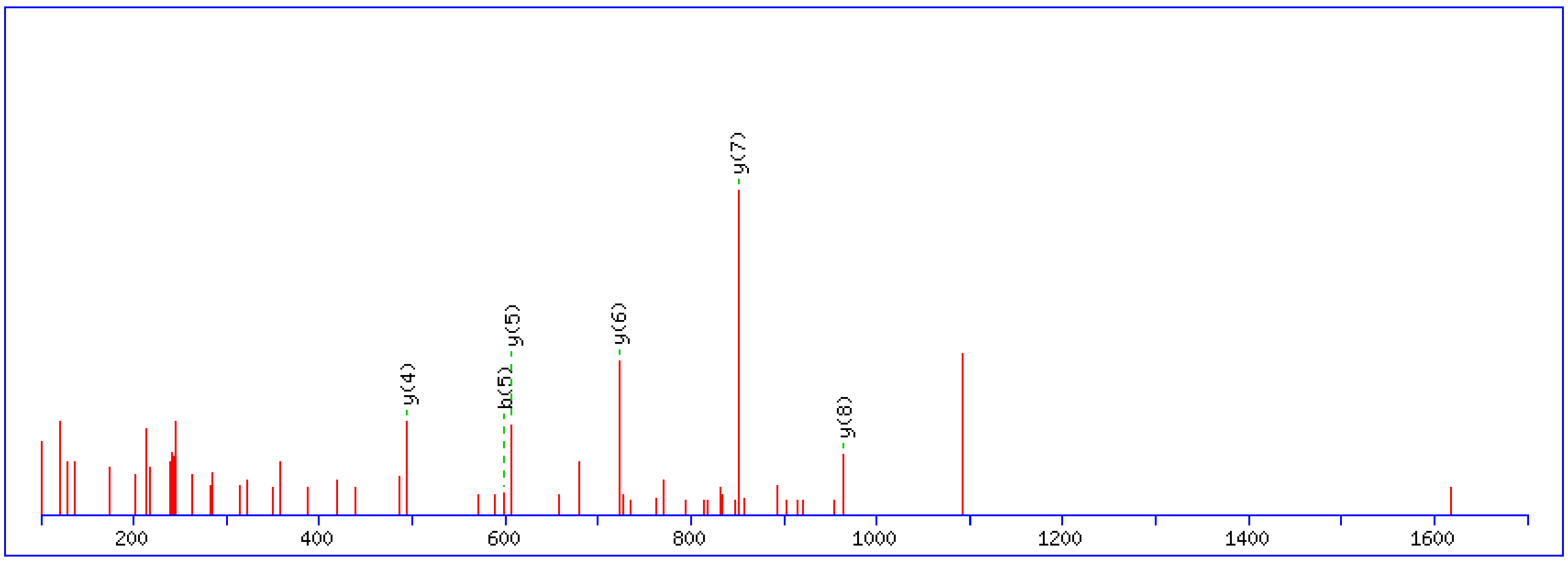
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KIEDLIQSM**
Found in **IL15_HUMAN**, Interleukin-15 OS=Homo sapiens GN=IL15 PE=1 SV=1

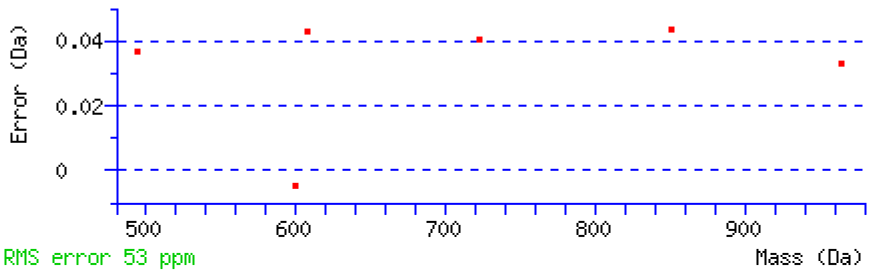
Match to Query 14458: 1091.560128 from(546.787340,2+) rtinseconds(2561) index(33279)
Title: Locus:1.1.1.1355.20
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 2.mgf

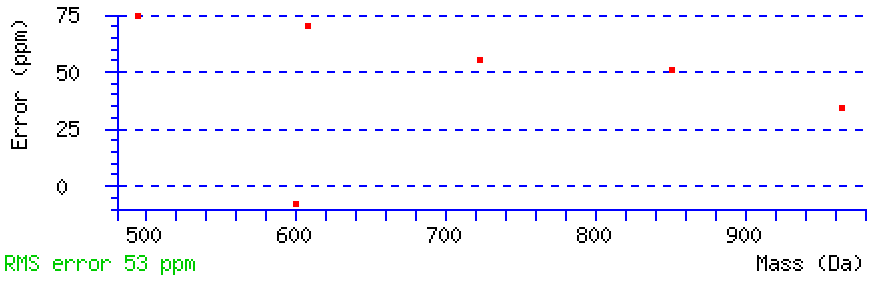
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1091.553238
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M9 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 32 **Expect:** 0.0064
Matches : 6/128 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	129.102239	65.054757	112.075690	56.541483			**K**							9
2	242.186303	121.596790	225.159754	113.083515			**I**	***964.465575***	482.736426	947.439026	474.223151	946.455010	473.731143	8
3	371.228896	186.118086	354.202347	177.604812	353.218331	177.112804	**E**	***851.381511***	426.194394	834.354962	417.681119	833.370946	417.189111	7
4	486.255839	243.631558	469.229290	235.118283	468.245274	234.626275	**D**	***722.338918***	361.673097	705.312369	353.159823	704.328353	352.667815	6
5	599.339903	300.173590	582.313354	291.660315	581.329338	291.168307	**L**	***607.311975***	304.159626	590.285426	295.646351	589.301410	295.154343	5
6	712.423967	356.715622	695.397418	348.202347	694.413402	347.710339	**I**	***494.227911***	247.617594	477.201362	239.104319	476.217346	238.612311	4
7	840.482545	420.744911	823.455996	412.231636	822.471980	411.739628	**Q**	381.143847	191.075562	364.117298	182.562287	363.133282	182.070279	3
8	927.514573	464.260925	910.488024	455.747650	909.504008	455.255642	**S**	253.085269	127.046273			235.074704	118.040990	2
9							**M**	166.053241	83.530259					1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.3	1091.553238	0.006890	KIEDLIQSM
8.6	1091.553238	0.006890	KLELQVESM
8.2	1091.564484	-0.004356	KIQTQISSGM
5.6	1091.561096	-0.000968	QLYELSPSR
3.4	1091.568497	-0.008369	FLPQLSMEK
2.8	1091.553253	0.006875	SILATLPTNM

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

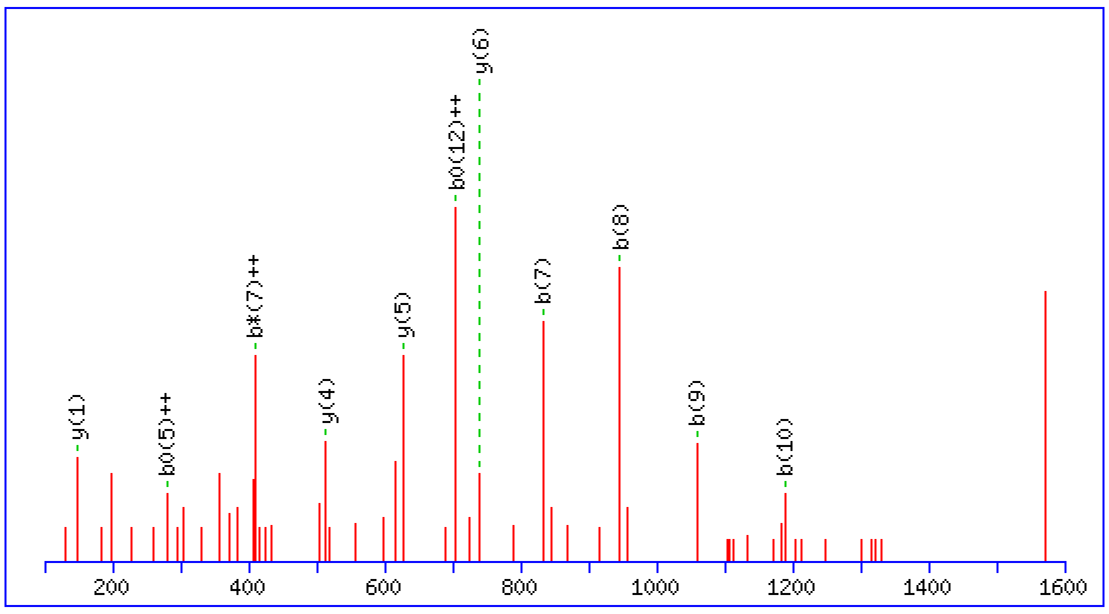
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EFLVSEKLPEHTK**
Found in **IL31R_HUMAN**, Interleukin-31 receptor subunit alpha OS=Homo sapiens GN=IL31RA PE=1 SV=1

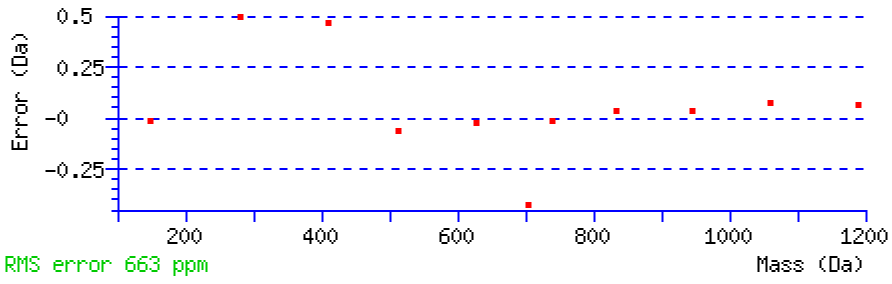
Match to Query 50176: 1571.830388 from(786.922470,2+) rtinseconds(4319) index(66296)
Title: Locus:1.1.1.2931.37
Data file 2011-11-12 - TFD - EP 6-4.mgf

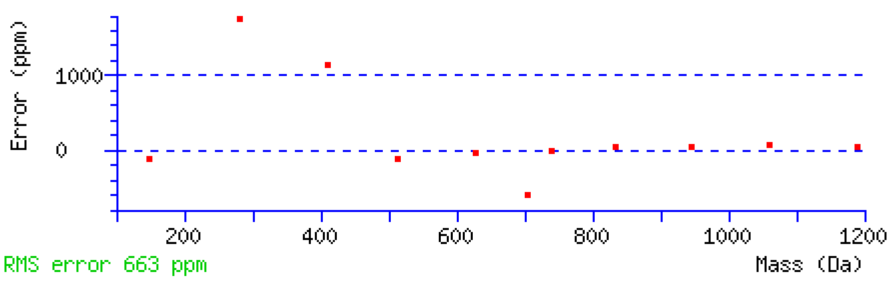
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1571.819504
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P9 : Oxidation (P)
Ions Score: 34 **Expect:** 0.0059
Matches : 11/130 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	E							13
2	277.118283	139.062779			259.107718	130.057497	F	1443.784207	722.395742	1426.757658	713.882467	1425.773642	713.390459	12
3	390.202347	195.604811			372.191782	186.599529	L	1296.715793	648.861535	1279.689244	640.348260	1278.705228	639.856252	11
4	489.270761	245.139018			471.260196	236.133736	V	1183.631729	592.319503	1166.605180	583.806228	1165.621164	583.314220	10
5	576.302789	288.655033			558.292224	279.649750	S	1084.563315	542.785296	1067.536766	534.272021	1066.552750	533.780013	9
6	705.345382	353.176329			687.334817	344.171047	E	997.531287	499.269282	980.504738	490.756007	979.520722	490.263999	8
7	***833.440345***	417.223811	816.413796	408.710536	815.429780	408.218528	K	868.488694	434.747985	851.462145	426.234711	850.478129	425.742703	7
8	***946.524409***	473.765843	929.497860	465.252568	928.513844	464.760560	L	***740.393731***	370.700504	723.367182	362.187229	722.383166	361.695221	6
9	***1059.572088***	530.289682	1042.545539	521.776408	1041.561523	521.284400	P	***627.309667***	314.158472	610.283118	305.645197	609.299102	305.153189	5
10	***1188.614681***	594.810979	1171.588132	586.297704	1170.604116	585.805696	E	***514.261988***	257.634632	497.235439	249.121358	496.251423	248.629350	4
11	1325.673593	663.340435	1308.647044	654.827160	1307.663028	654.335152	H	385.219395	193.113335	368.192846	184.600061	367.208830	184.108053	3
12	1426.721272	713.864274	1409.694723	705.351000	1408.710707	704.858992	T	248.160483	124.583879	231.133934	116.070605	230.149918	115.578597	2
13							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.7	1571.819504	0.010884	EFLVSEKLPEHTK

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

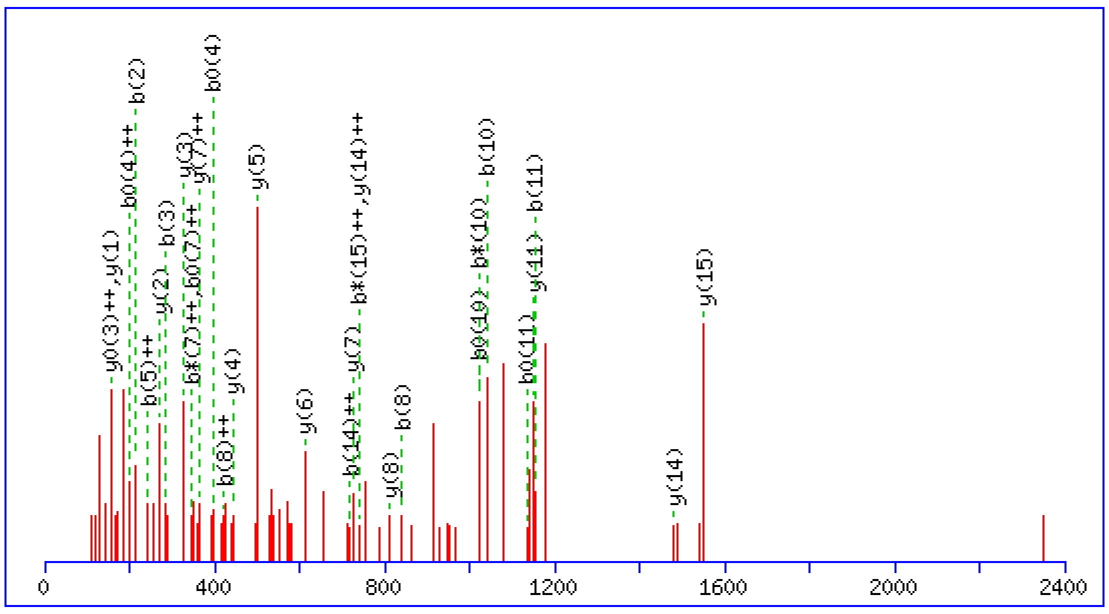
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DVAEAKPELSLLGDGDH**
Found in **IAH1_HUMAN**, Isoamyl acetate-hydrolyzing esterase 1 homolog OS=Homo sapiens GN=IAH1 PE=1 SV=1

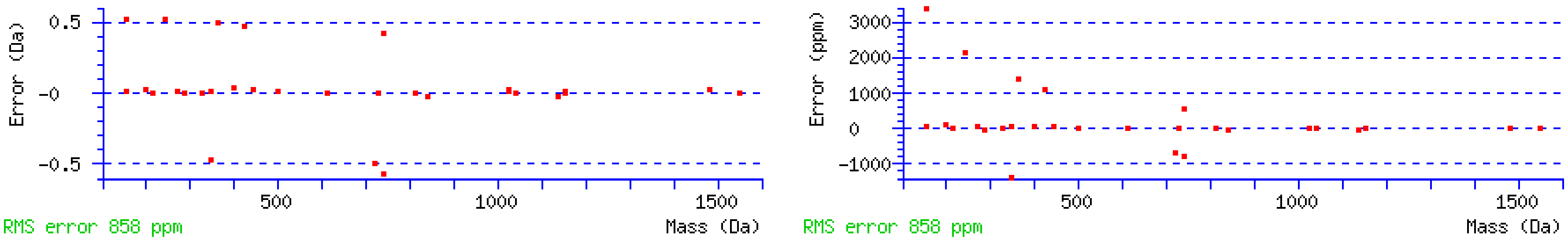
Match to Query 51151: 1764.845382 from(589.289070,3+) rtinseconds(2633) index(30458)
Title: Locus:1.1.1.2588.20
Data file 2011-11-12 - TFD - EP 5-5.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1764.852997
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 61  Expect: 9.4e-006
Matches : 30/158 fragment ions using 54 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	116.034219	58.520748			98.023654	49.515465	D							17
2	**215.102633**	108.054954			197.092068	99.049672	V	1650.833342	825.920309	1633.806793	817.407035	1632.822777	816.915026	16
3	**286.139747**	143.573512			268.129182	134.568229	A	***1551.764928***	776.386102	1534.738379	767.872828	1533.754363	767.380820	15
4	415.182340	208.094808			397.171775	199.089526	E	***1480.727814***	740.867545	1463.701265	732.354271	1462.717249	731.862263	14
5	486.219454	**243.613365**			468.208889	234.608082	A	1351.685221	676.346249	1334.658672	667.832974	1333.674656	667.340966	13
6	614.314417	307.660847	597.287868	299.147572	596.303852	298.655564	K	1280.648107	640.827692	1263.621558	632.314417	1262.637542	631.822409	12
7	711.367181	356.187229	694.340632	347.673954	693.356616	347.181946	P	***1152.553144***	576.780210			1134.542579	567.774927	11
8	**840.409774**	**420.708525**	823.383225	412.195251	822.399209	411.703243	E	1055.500380	528.253828			1037.489815	519.248545	10
9	953.493838	477.250557	936.467289	468.737283	935.483273	468.245275	L	926.457787	463.732531			908.447222	454.727249	9
10	**1040.525866**	520.766571	1023.499317	512.253297	1022.515301	511.761289	S	***813.373723***	407.190499			795.363158	398.185217	8
11	**1153.609930**	577.308603	1136.583381	568.795329	1135.599365	568.303321	L	***726.341695***	363.674485			708.331130	354.669203	7
12	1266.693994	633.850635	1249.667445	625.337361	1248.683429	624.845352	L	***613.257631***	307.132454			595.247066	298.127171	6
13	1323.715458	662.361367	1306.688909	653.848093	1305.704893	653.356084	G	***500.173567***	250.590421			482.163002	241.585139	5
14	1438.742401	**719.874839**	1421.715852	711.361564	1420.731836	710.869556	D	***443.152103***	222.079690			425.141538	213.074407	4
15	1495.763865	748.385570	1478.737316	739.872296	1477.753300	739.380288	G	***328.125160***	164.566218			310.114595	155.560935	3
16	1610.790808	805.899042	1593.764259	797.385768	1592.780243	796.893759	D	***271.103696***	136.055486			253.093131	127.050204	2
17							H	***156.076753***	78.542014					1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
60.9	1764.852997	-0.007615	DVAEAKPELSLLGDGDH

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

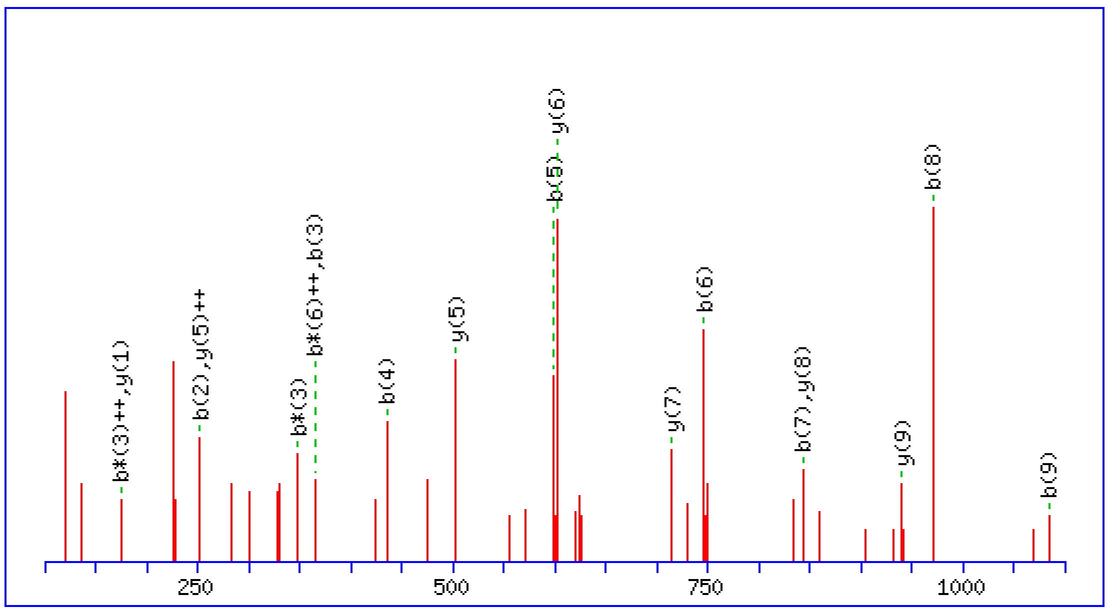
Mascot Search Results

Peptide View

MS/MS Fragmentation of **HNIAYFPQIVSVAAR**
Found in **ISOC2_HUMAN**, Isochorismatase domain-containing protein 2, mitochondrial OS=Homo sapiens GN=ISOC2 PE=1 SV=1

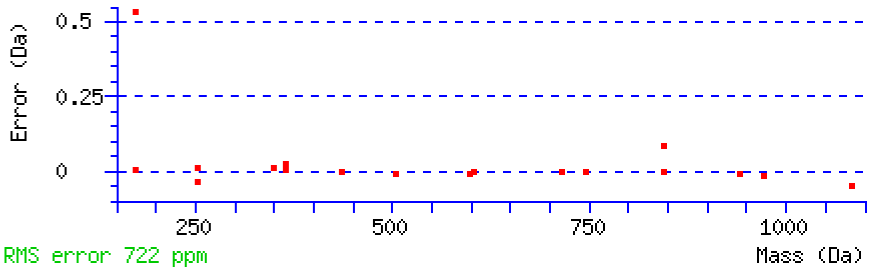
Match to Query 50632: 1684.905822 from(562.642550,3+) rtinseconds(2994) index(40164)
Title: Locus:1.1.1.2430.15
Data file 2011-11-12 - TFD - EP 6-5.mgf

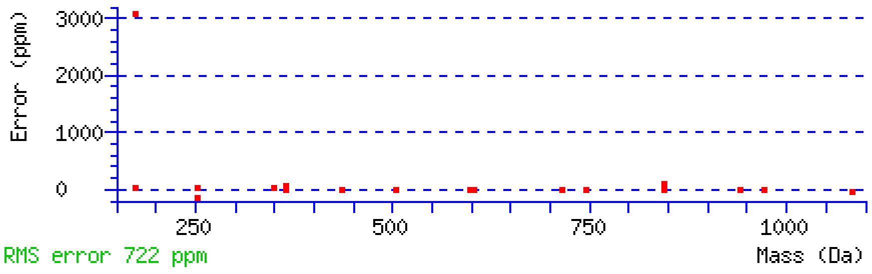
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1684.904907
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 46 **Expect:** 0.00016
Matches : 18/138 fragment ions using 29 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	138.066188	69.536732					H							15
2	***252.109115***	126.558195	235.082566	118.044921			N	1548.853290	774.930283	1531.826741	766.417009	1530.842725	765.925001	14
3	***365.193179***	183.100227	348.166630	174.586953			I	1434.810363	717.908820	1417.783814	709.395545	1416.799798	708.903537	13
4	***436.230293***	218.618785	419.203744	210.105510			A	1321.726299	661.366788	1304.699750	652.853513	1303.715734	652.361505	12
5	***599.293622***	300.150449	582.267073	291.637175			Y	1250.689185	625.848231	1233.662636	617.334956	1232.678620	616.842948	11
6	***746.362036***	373.684656	729.335487	365.171382			F	1087.625856	544.316566	1070.599307	535.803292	1069.615291	535.311284	10
7	***843.414800***	422.211038	826.388251	413.697764			P	***940.557442***	470.782359	923.530893	462.269085	922.546877	461.777077	9
8	***971.473378***	486.240327	954.446829	477.727053			Q	***843.504678***	422.255977	826.478129	413.742703	825.494113	413.250695	8
9	***1084.557442***	542.782359	1067.530893	534.269085			I	***715.446100***	358.226688	698.419551	349.713414	697.435535	349.221406	7
10	1183.625856	592.316566	1166.599307	583.803292			V	***602.362036***	301.684656	585.335487	293.171382	584.351471	292.679374	6
11	1270.657884	635.832580	1253.631335	627.319306	1252.647319	626.827298	S	***503.293622***	252.150449	486.267073	243.637175	485.283057	243.145167	5
12	1369.726298	685.366787	1352.699749	676.853513	1351.715733	676.361505	V	416.261594	208.634435	399.235045	200.121160			4
13	1440.763412	720.885344	1423.736863	712.372070	1422.752847	711.880062	A	317.193180	159.100228	300.166631	150.586953			3
14	1511.800526	756.403901	1494.773977	747.890627	1493.789961	747.398619	A	246.156066	123.581671	229.129517	115.068396			2
15							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.6	1684.904907	0.000915	HNIAYFPQIVSVAAR
4.8	1684.918182	-0.012360	CVDLVIQELINTVR
2.3	1684.903564	0.002258	WDGKDLEDLQILIK

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

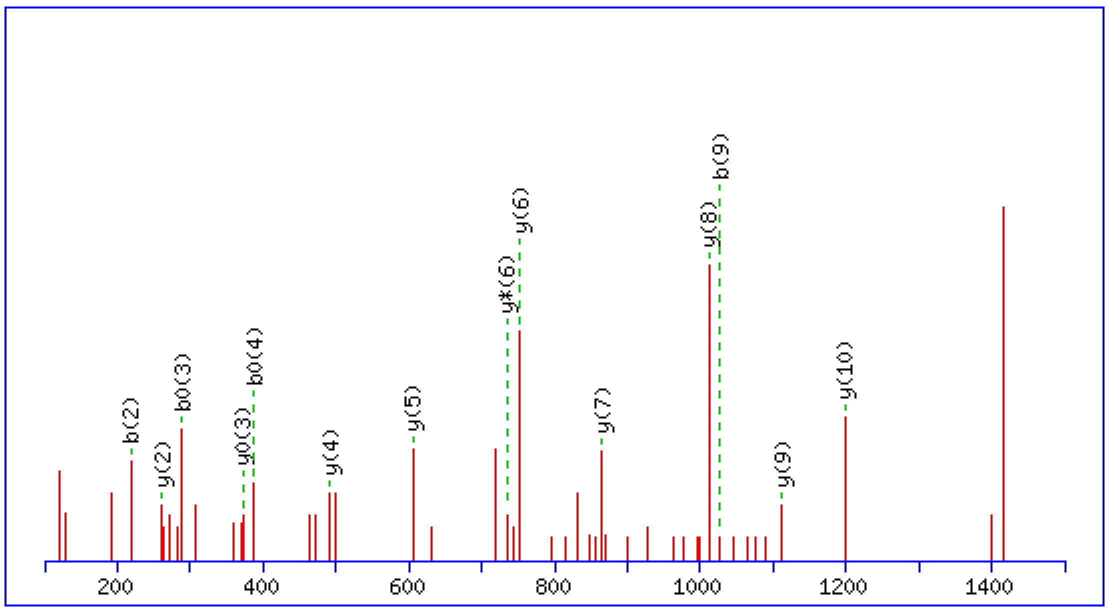
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AFSVFLFNTENK**
Found in **IDI1_HUMAN**, Isopentenyl-diphosphate Delta-isomerase 1 OS=Homo sapiens GN=IDI1 PE=1 SV=2

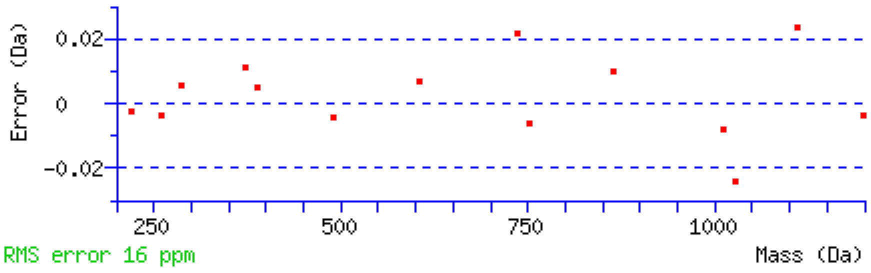
Match to Query 41860: 1415.705348 from(708.859950,2+) rtinseconds(3558) index(48135)
Title: Locus:1.1.1.2667.12
Data file 2011-11-10 - TFD - EP 4-5.mgf

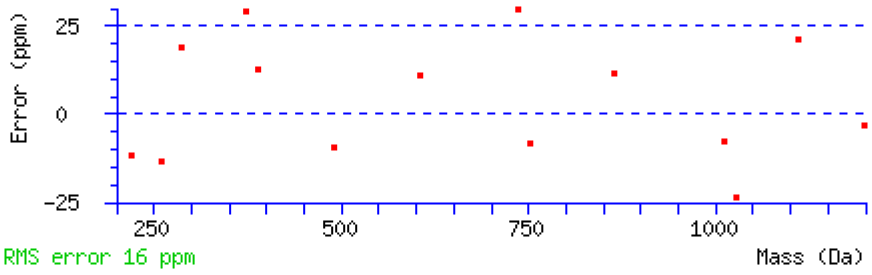
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1415.708511
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 59 **Expect:** 9e-006
Matches : 14/110 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							12
2	**219.112804**	110.060040					F	1345.678678	673.342977	1328.652129	664.829703	1327.668113	664.337695	11
3	306.144832	153.576054			288.134267	144.570772	S	***1198.610264***	599.808770	1181.583715	591.295496	1180.599699	590.803488	10
4	405.213246	203.110261			387.202681	194.104979	V	***1111.578236***	556.292756	1094.551687	547.779482	1093.567671	547.287474	9
5	552.281660	276.644468			534.271095	267.639186	F	***1012.509822***	506.758549	995.483273	498.245275	994.499257	497.753267	8
6	665.365724	333.186500			647.355159	324.181218	L	***865.441408***	433.224342	848.414859	424.711068	847.430843	424.219060	7
7	812.434138	406.720707			794.423573	397.715425	F	***752.357344***	376.682310	735.330795	368.169036	734.346779	367.677028	6
8	926.477065	463.742171	909.450516	455.228896	908.466500	454.736888	N	***605.288930***	303.148103	588.262381	294.634829	587.278365	294.142821	5
9	**1027.524744**	514.266010	1010.498195	505.752736	1009.514179	505.260728	T	***491.246003***	246.126640	474.219454	237.613365	473.235438	237.121357	4
10	1156.567337	578.787307	1139.540788	570.274032	1138.556772	569.782024	E	390.198324	195.602800	373.171775	187.089526	372.187759	186.597518	3
11	1270.610264	635.808770	1253.583715	627.295496	1252.599699	626.803488	N	***261.155731***	131.081503	244.129182	122.568229			2
12							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.9	1415.708511	-0.003163	AFSVFLFNTENK
5.1	1415.704498	0.000850	AFQVIETQDPPR

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

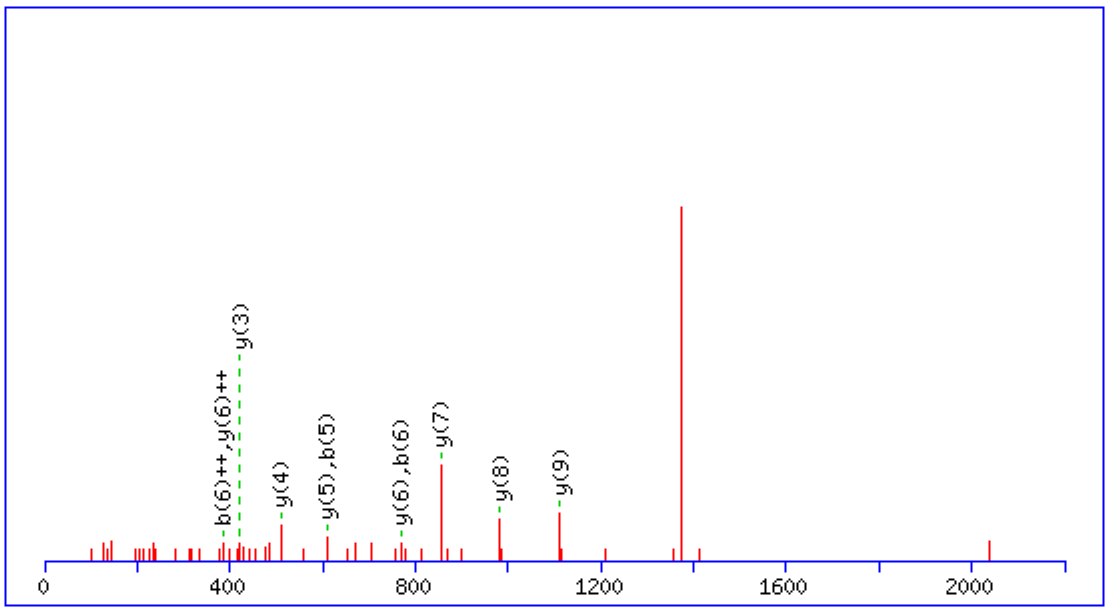
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TYQQSCVSSCR**
Found in **KR111_HUMAN**, Keratin-associated protein 11-1 OS=Homo sapiens GN=KRTAP11-1 PE=1 SV=1

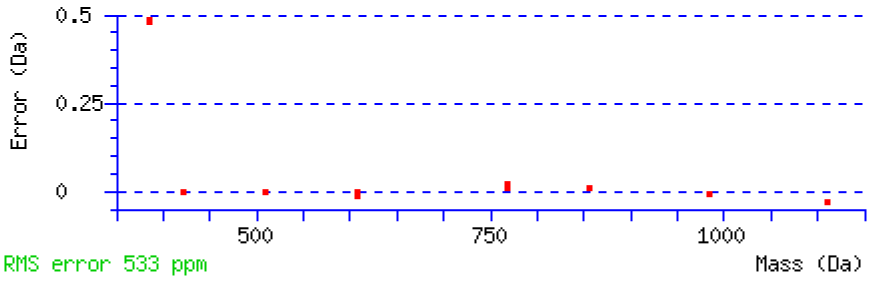
Match to Query 722686: 1374.577868 from(688.296210,2+) rtinseconds(1043) index(244586)
Title: Locus:1.1.1.838.39
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

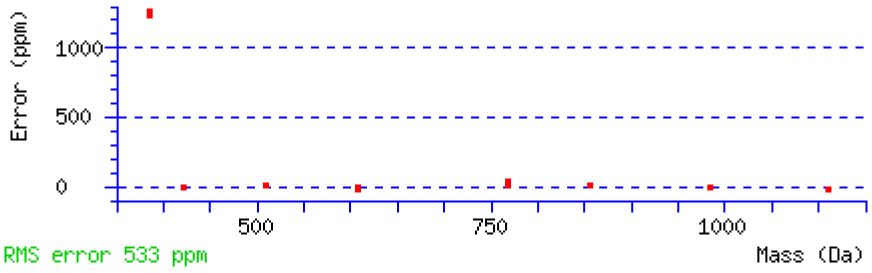
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1374.565643
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 53  Expect: 2.3e-005
Matches : 11/112 fragment ions using 12 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							11
2	265.118284	133.062780			247.107719	124.057498	Y	1274.525233	637.766255	1257.498684	629.252980	1256.514668	628.760972	10
3	393.176862	197.092069	376.150313	188.578795	375.166297	188.086787	Q	***1111.461904***	556.234590	1094.435355	547.721316	1093.451339	547.229308	9
4	521.235440	261.121358	504.208891	252.608084	503.224875	252.116076	Q	***983.403326***	492.205301	966.376777	483.692027	965.392761	483.200019	8
5	**608.267468**	304.637372	591.240919	296.124098	590.256903	295.632090	S	***855.344748***	428.176012	838.318199	419.662737	837.334183	419.170729	7
6	**768.298117**	384.652697	751.271568	376.139422	750.287552	375.647414	C	***768.312720***	384.659998	751.286171	376.146724	750.302155	375.654716	6
7	867.366531	434.186904	850.339982	425.673629	849.355966	425.181621	V	***608.282071***	304.644674	591.255522	296.131399	590.271506	295.639391	5
8	954.398559	477.702918	937.372010	469.189643	936.387994	468.697635	S	***509.213657***	255.110466	492.187108	246.597192	491.203092	246.105184	4
9	1041.430587	521.218932	1024.404038	512.705657	1023.420022	512.213649	S	***422.181629***	211.594452	405.155080	203.081178	404.171064	202.589170	3
10	1201.461236	601.234256	1184.434687	592.720982	1183.450671	592.228974	C	335.149601	168.078438	318.123052	159.565164			2
11							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.8	1374.565643	0.012225	TYQQSCVSSCR

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

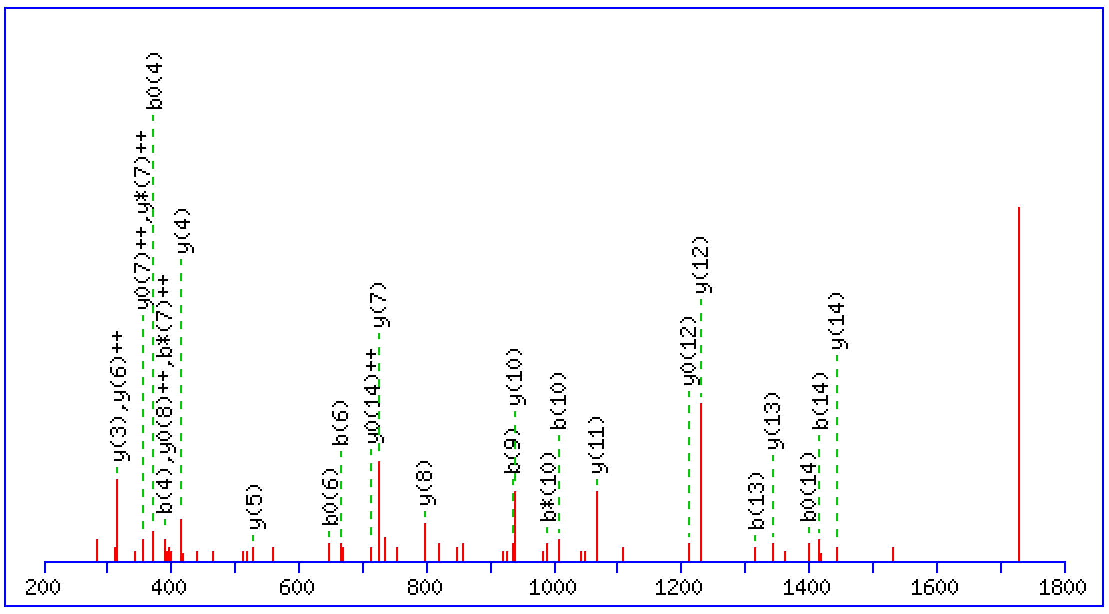
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ISSTLYQAAAPVLTPAK**
Found in **KTAP2_HUMAN**, Keratinocyte-associated protein 2 OS=Homo sapiens GN=KRTCAP2 PE=1 SV=1

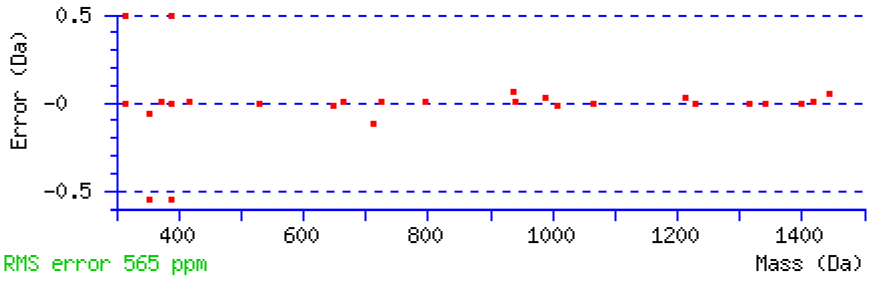
Match to Query 42658: 1729.964488 from(865.989520,2+) rtinseconds(2820) index(30370)
Title: Locus:1.1.1.2528.21
Data file 2011-11-13 - TFD - EP 7-7.mgf

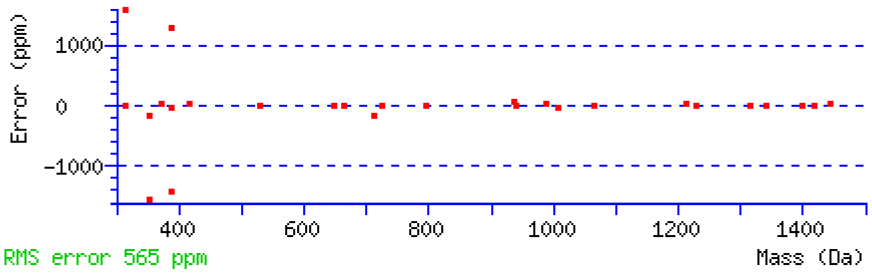
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1729.961411
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 75 **Expect:** 1.9e-007
Matches : 27/172 fragment ions using 34 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					I							17
2	201.123368	101.065322			183.112803	92.060039	S	1617.884651	809.445964	1600.858102	800.932689	1599.874086	800.440681	16
3	288.155396	144.581336			270.144831	135.576053	S	1530.852623	765.929950	1513.826074	757.416675	1512.842058	756.924667	15
4	**389.203075**	195.105175			371.192510	186.099893	T	***1443.820595***	722.413935	1426.794046	713.900661	1425.810030	713.408653	14
5	502.287139	251.647207			484.276574	242.641925	L	***1342.772916***	671.890096	1325.746367	663.376822	1324.762351	662.884814	13
6	**665.350468**	333.178872			647.339903	324.173590	Y	***1229.688852***	615.348064	1212.662303	606.834790	1211.678287	606.342782	12
7	793.409046	397.208161	776.382497	388.694887	775.398481	388.202879	Q	***1066.625523***	533.816399	1049.598974	525.303125	1048.614958	524.811117	11
8	864.446160	432.726718	847.419611	424.213444	846.435595	423.721436	A	***938.566945***	469.787110	921.540396	461.273836	920.556380	460.781828	10
9	**935.483274**	468.245275	918.456725	459.732001	917.472709	459.239993	A	867.529831	434.268554	850.503282	425.755279	849.519266	425.263271	9
10	**1006.520388**	503.763832	989.493839	495.250558	988.509823	494.758550	A	***796.492717***	398.749997	779.466168	390.236722	778.482152	389.744714	8
11	1103.573152	552.290214	1086.546603	543.776940	1085.562587	543.284931	P	***725.455603***	363.231440	708.429054	354.718165	707.445038	354.226157	7
12	1202.641566	601.824421	1185.615017	593.311147	1184.631001	592.819139	V	628.402839	314.705058	611.376290	306.191783	610.392274	305.699775	6
13	**1315.725630**	658.366453	1298.699081	649.853179	1297.715065	649.361170	L	***529.334425***	265.170851	512.307876	256.657576	511.323860	256.165568	5
14	**1416.773309**	708.890292	1399.746760	700.377018	1398.762744	699.885010	T	***416.250361***	208.628818	399.223812	200.115544	398.239796	199.623536	4
15	1513.826073	757.416675	1496.799524	748.903400	1495.815508	748.411392	P	***315.202682***	158.104979	298.176133	149.591704			3
16	1584.863187	792.935231	1567.836638	784.421957	1566.852622	783.929949	A	218.149918	109.578597	201.123369	101.065322			2
17							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
74.6	1729.961411	0.003077	ISSTLYQAAAPVLTPAK

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

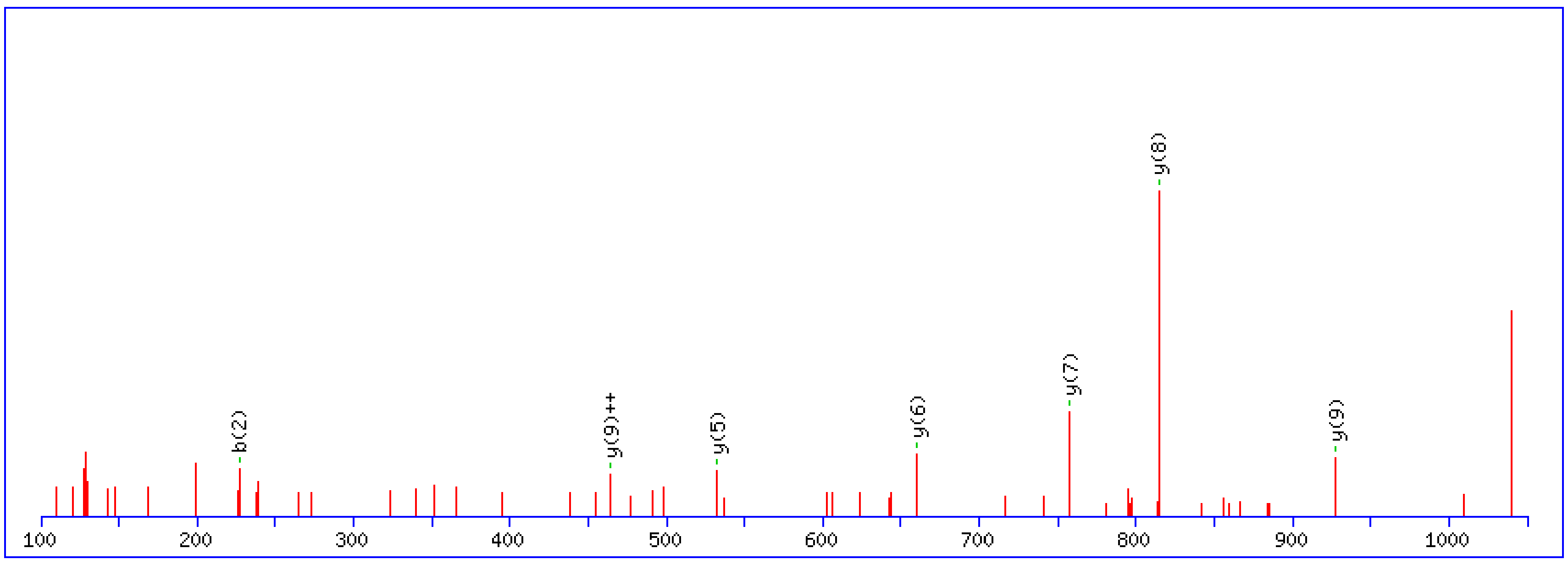
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILGPQGNTIK**
Found in **KHDR1_HUMAN**, KH domain-containing, RNA-binding, signal transduction-associated protein 1 OS=Homo sapiens GN=KHDRBS1 PE=1 SV=1

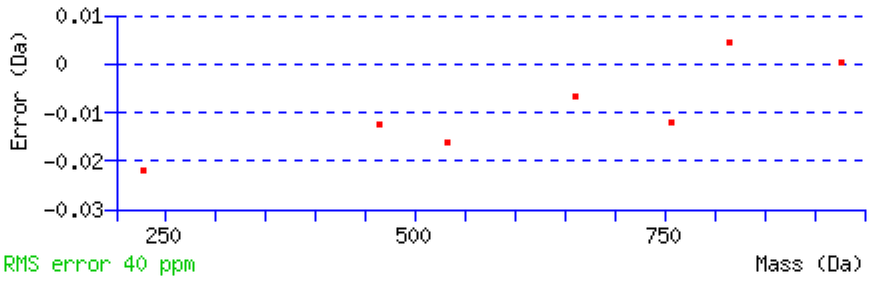
Match to Query 12357: 1039.599728 from(520.807140,2+) rtinseconds(1307) index(9443)
Title: Locus:1.1.1.944.23
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 3.mgf

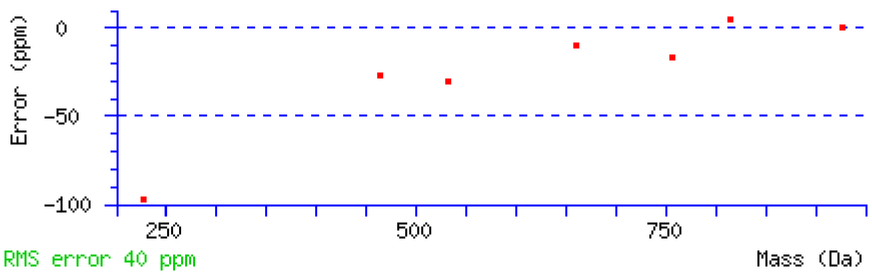
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1039.602585
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.0029
Matches : 7/82 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					I							10
2	227.175404	114.091340					L	***927.525808***	464.266542	910.499259	455.753268	909.515243	455.261260	9
3	284.196868	142.602072					G	***814.441744***	407.724510	797.415195	399.211236	796.431179	398.719228	8
4	381.249632	191.128454					P	***757.420280***	379.213778	740.393731	370.700504	739.409715	370.208496	7
5	509.308210	255.157743	492.281661	246.644468			Q	***660.367516***	330.687396	643.340967	322.174122	642.356951	321.682114	6
6	566.329674	283.668475	549.303125	275.155201			G	***532.308938***	266.658107	515.282389	258.144833	514.298373	257.652825	5
7	680.372601	340.689939	663.346052	332.176664			N	475.287474	238.147375	458.260925	229.634100	457.276909	229.142092	4
8	781.420280	391.213778	764.393731	382.700504	763.409715	382.208496	T	361.244547	181.125912	344.217998	172.612637	343.233982	172.120629	3
9	894.504344	447.755810	877.477795	439.242536	876.493779	438.750528	I	260.196868	130.602072	243.170319	122.088798			2
10							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.1	1039.602585	-0.002857	ILGPQGNTIK
9.5	1039.602585	-0.002857	IINTPEVVR
7.4	1039.591354	0.008374	IIPDPNVIK
7.4	1039.602585	-0.002857	IIPTPPRSK
7.4	1039.602585	-0.002857	IIPTPPRSK
7.4	1039.592682	0.007046	PILPSWRR
7.4	1039.602585	-0.002857	PINGTLKPGK
0.9	1039.602585	-0.002857	IIPTPPRSK
0.9	1039.591339	0.008389	IPPALISEGK
0.9	1039.591339	0.008389	LPPSVAEALK

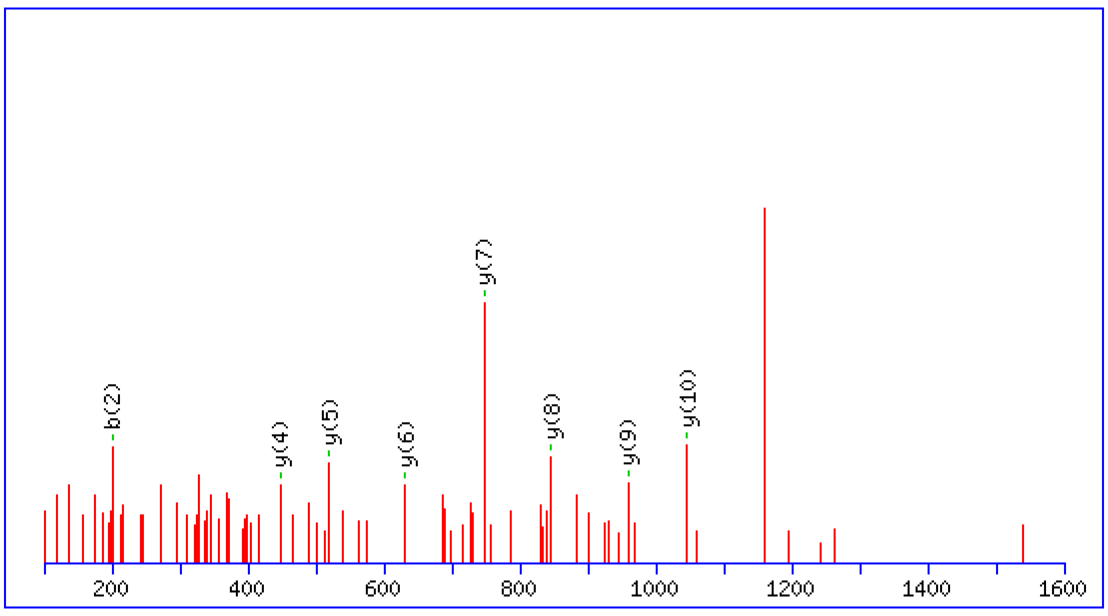
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ISLVDLAGSER**
Found in **KIF1A_HUMAN**, Kinesin-like protein KIF1A OS=Homo sapiens GN=KIF1A PE=2 SV=2

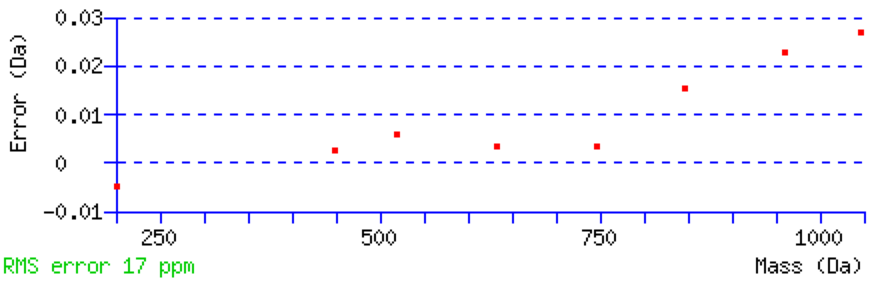
Match to Query 23721: 1158.627588 from(580.321070,2+) rtinseconds(2828) index(34886)
Title: Locus:1.1.1.2627.13
Data file 2011-11-12 - TFD - EP 5-1.mgf

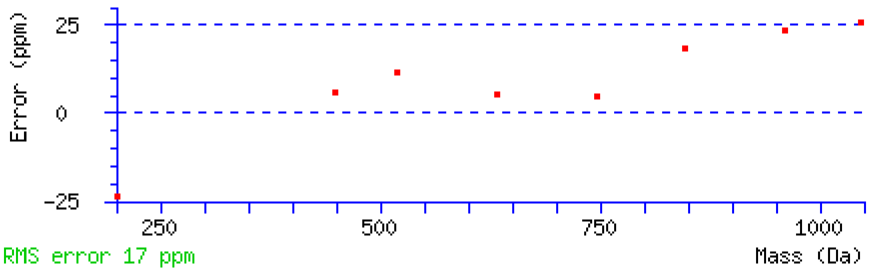
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1158.624435
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 57 **Expect:** 5e-005
Matches : 8/96 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							11
2	201.123368	101.065322	183.112803	92.060039	S	***1046.547664***	523.777470	1029.521115	515.264196	1028.537099	514.772188	10
3	314.207432	157.607354	296.196867	148.602071	L	***959.515636***	480.261456	942.489087	471.748182	941.505071	471.256174	9
4	413.275846	207.141561	395.265281	198.136279	V	***846.431572***	423.719424	829.405023	415.206150	828.421007	414.714142	8
5	528.302789	264.655033	510.292224	255.649750	D	***747.363158***	374.185217	730.336609	365.671943	729.352593	365.179935	7
6	641.386853	321.197065	623.376288	312.191782	L	***632.336215***	316.671746	615.309666	308.158471	614.325650	307.666463	6
7	712.423967	356.715622	694.413402	347.710339	A	***519.252151***	260.129714	502.225602	251.616439	501.241586	251.124431	5
8	769.445431	385.226354	751.434866	376.221071	G	***448.215037***	224.611156	431.188488	216.097882	430.204472	215.605874	4
9	856.477459	428.742368	838.466894	419.737085	S	391.193573	196.100424	374.167024	187.587150	373.183008	187.095142	3
10	985.520052	493.263664	967.509487	484.258382	E	304.161545	152.584410	287.134996	144.071136	286.150980	143.579128	2
11					R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
57.1	1158.624435	0.003153	ISLVDLAGSER
57.1	1158.624435	0.003153	LSLVDLAGSER
11.8	1158.624420	0.003168	LSAQKDLEQK
5.8	1158.617905	0.009683	LAELTGRPMR
5.8	1158.617905	0.009683	LAELTGRPMR
3.7	1158.624435	0.003153	TVPLTAKEER
3.4	1158.635666	-0.008078	LSEKTQQAVR
2.6	1158.624435	0.003153	LTVDGLEKER
2.6	1158.635681	-0.008093	VTGSVSININR
2.4	1158.635681	-0.008093	AVTEVREVTR

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

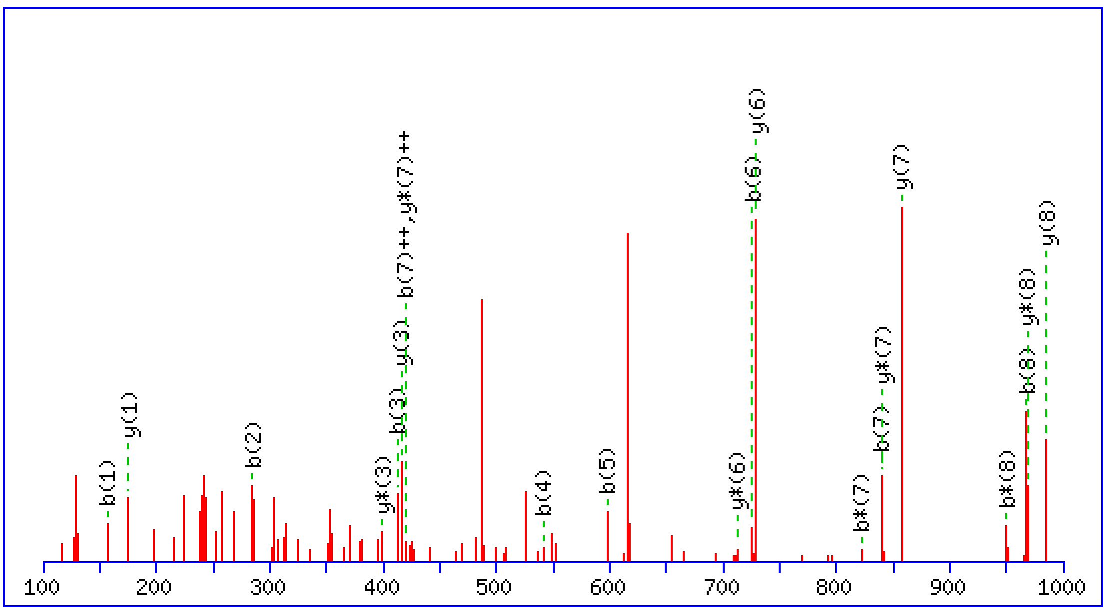
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **RQQQGQLQR**
Found in **KIF7_HUMAN**, Kinesin-like protein KIF7 OS=Homo sapiens GN=KIF7 PE=1 SV=2

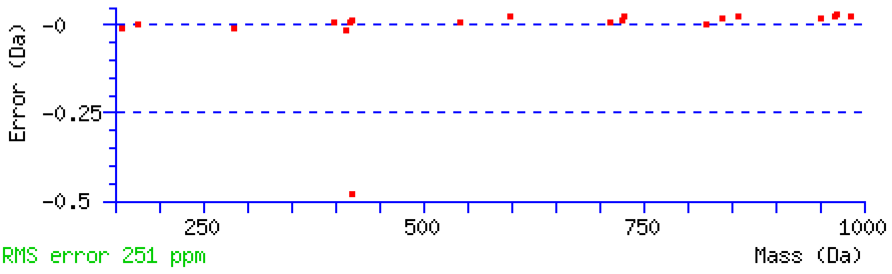
Match to Query 449027: 1140.622408 from(571.318480,2+) rtinseconds(3246) index(617584)
Title: Locus:1.1.1.1561.17
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

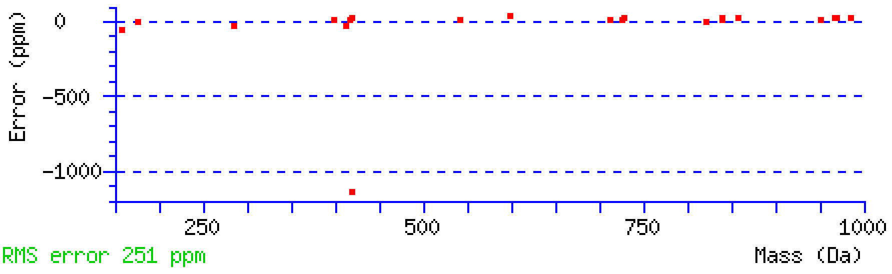
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1140.611191
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 44  Expect: 0.00047
Matches : 21/64 fragment ions using 45 most intense peaks   (help)
```

#	b	b^{++}	b^*	b^{*++}	Seq.	y	y^{++}	y^*	y^{*++}	#
1	*157.108387*	79.057831	140.081838	70.544557	**R**					9
2	*285.166965*	143.087121	268.140416	134.573846	**Q**	**985.517370**	493.262323	968.490821	484.749049	8
3	*413.225543*	207.116410	396.198994	198.603135	**Q**	**857.458792**	429.233034	840.432243	420.719760	7
4	*541.284121*	271.145699	524.257572	262.632424	**Q**	**729.400214**	365.203745	712.373665	356.690471	6
5	*598.305585*	299.656431	581.279036	291.143156	**G**	601.341636	301.174456	584.315087	292.661182	5
6	*726.364163*	363.685720	709.337614	355.172445	**Q**	544.320172	272.663724	527.293623	264.150450	4
7	*839.448227*	420.227752	822.421678	411.714477	**L**	**416.261594**	208.634435	399.235045	200.121160	3
8	*967.506805*	484.257041	950.480256	475.743766	**Q**	303.177530	152.092403	286.150981	143.579128	2
9					**R**	**175.118952**	88.063114	158.092403	79.549839	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.1	1140.611191	0.011217	RQQQGQLQR
33.1	1140.625107	-0.002699	KIQVEQPQR
16.9	1140.615219	0.007189	DVARHFIQR
12.4	1140.613861	0.008547	DLPALQEALR
12.4	1140.613861	0.008547	ELLGPPEAKR
11.8	1140.611191	0.011217	RPRTQAPGSR
10.4	1140.625092	-0.002684	KPEKNLQPR
9.3	1140.611191	0.011217	RPGDGARLQR
8.6	1140.625122	-0.002714	QPLVSQGQLR
8.0	1140.613876	0.008532	VGKIPDEEVR

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

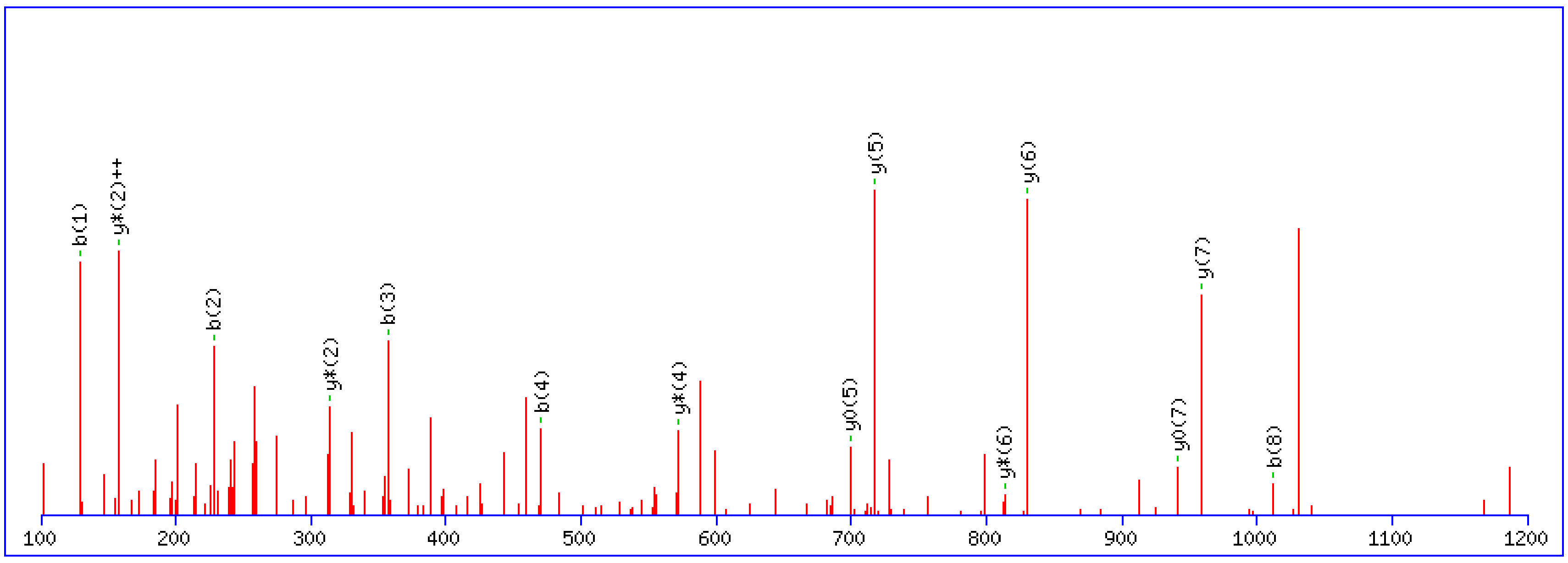
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QVELQEERR**
Found in **KIFC1_HUMAN**, Kinesin-like protein KIFC1 OS=Homo sapiens GN=KIFC1 PE=1 SV=2

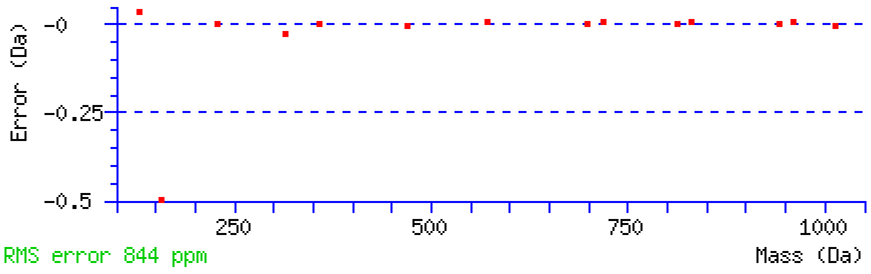
Match to Query 22567: 1185.618328 from(593.816440,2+) rtinseconds(4112) index(62280)
Title: Locus:1.1.1.2001.10
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 3.mgf

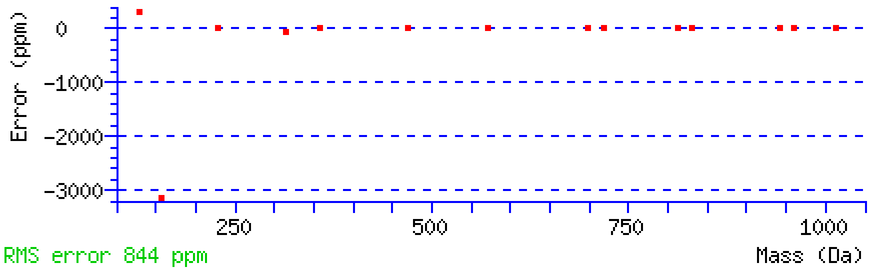
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1185.610168
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.0091
Matches : 14/88 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	***129.065854***	65.036565	112.039305	56.523291			Q							9
2	***228.134268***	114.570772	211.107719	106.057498			V	1058.558898	529.783087	1041.532349	521.269813	1040.548333	520.777805	8
3	***357.176861***	179.092069	340.150312	170.578794	339.166296	170.086786	E	**959.490484**	480.248880	942.463935	471.735606	941.479919	471.243598	7
4	***470.260925***	235.634101	453.234376	227.120826	452.250360	226.628818	L	**830.447891**	415.727584	813.421342	407.214309	812.437326	406.722301	6
5	598.319503	299.663390	581.292954	291.150115	580.308938	290.658107	Q	**717.363827**	359.185552	700.337278	350.672277	699.353262	350.180269	5
6	727.362096	364.184686	710.335547	355.671412	709.351531	355.179404	E	589.305249	295.156263	572.278700	286.642988	571.294684	286.150980	4
7	856.404689	428.705983	839.378140	420.192708	838.394124	419.700700	E	460.262656	230.634966	443.236107	222.121691	442.252091	221.629683	3
8	***1012.505800***	506.756538	995.479251	498.243264	994.495235	497.751256	R	331.220063	166.113669	314.193514	157.600395			2
9							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.5	1185.610168	0.008160	QVELQEERR
26.1	1185.610184	0.008144	VQELQQQSAR
25.5	1185.625443	-0.007115	RTVPWLENR
22.5	1185.610153	0.008175	RAEENALQQK
18.5	1185.614212	0.004116	QVIEELGGWR
17.3	1185.610168	0.008160	AESGNPSIRQK
16.5	1185.625427	-0.007099	RALEWLGADR
15.5	1185.628815	-0.010487	RLSPPACTLR
14.0	1185.624100	-0.005772	KDGSSPPLLEK
10.9	1185.612839	0.005489	AEEELLPLEK

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

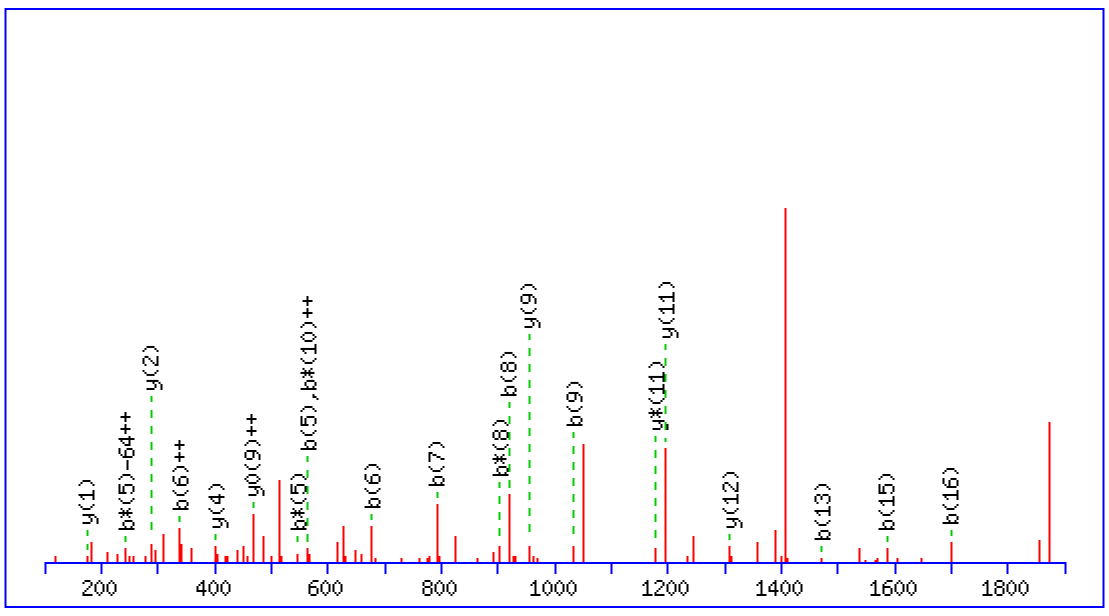
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MAKFALNQNLPDLGGPR**
Found in **KANK3_HUMAN**, KN motif and ankyrin repeat domain-containing protein 3 OS=Homo sapiens GN=KANK3 PE=2 SV=1

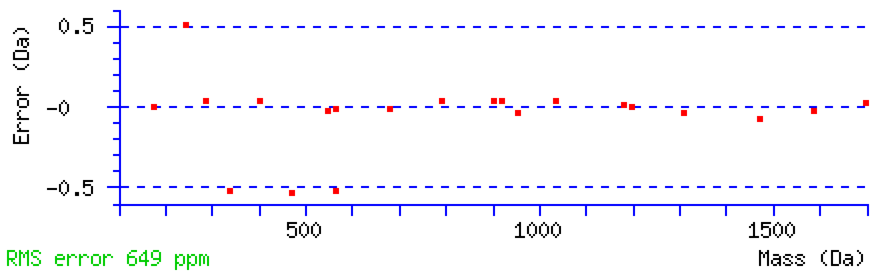
Match to Query 61245: 1872.943768 from(937.479160,2+) rtinseconds(4847) index(71802)
Title: Locus:1.1.1.3125.20
Data file 2011-11-12 - TFD - EP 6-4.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●

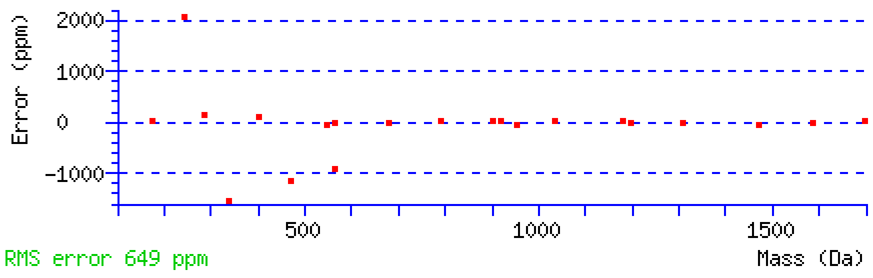


Monoisotopic mass of neutral peptide Mr(calc): 1872.951599
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
P16 : Oxidation (P)
Ions Score: 32 **Expect:** 0.0062
Matches : 21/226 fragment ions using 45 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	148.042676	74.524976					M							17
2	219.079790	110.043533					A	1726.923495	863.965385	1709.896946	855.452111	1708.912930	854.960103	16
3	347.174753	174.091014	330.148204	165.577740			K	1655.886381	828.446828	1638.859832	819.933554	1637.875816	819.441546	15
4	494.243167	247.625221	477.216618	239.111947			F	1527.791418	764.399347	1510.764869	755.886072	1509.780853	755.394064	14
5	***565.280281***	283.143779	548.253732	274.630504			A	1380.723004	690.865140	1363.696455	682.351865	1362.712439	681.859857	13
6	***678.364345***	339.685811	661.337796	331.172536			L	**1309.685890**	655.346583	1292.659341	646.833309	1291.675325	646.341300	12
7	***792.407272***	396.707274	775.380723	388.193999			N	**1196.601826**	598.804551	1179.575277	590.291276	1178.591261	589.799268	11
8	***920.465850***	460.736563	903.439301	452.223288			Q	1082.558899	541.783087	1065.532350	533.269813	1064.548334	532.777805	10
9	***1034.508777***	517.758027	1017.482228	509.244752			N	**954.500321**	477.753798	937.473772	469.240524	936.489756	468.748516	9
10	1147.592841	574.300058	1130.566292	565.786784			L	840.457394	420.732335	823.430845	412.219060	822.446829	411.727052	8
11	1244.645605	622.826440	1227.619056	614.313166			P	727.373330	364.190303	710.346781	355.677028	709.362765	355.185020	7
12	1359.672548	680.339912	1342.645999	671.826638	1341.661983	671.334630	D	630.320566	315.663921	613.294017	307.150646	612.310001	306.658638	6
13	***1472.756612***	736.881944	1455.730063	728.368670	1454.746047	727.876661	L	515.293623	258.150449	498.267074	249.637175			5
14	1529.778076	765.392676	1512.751527	756.879401	1511.767511	756.387393	G	**402.209559**	201.608417	385.183010	193.095143			4
15	***1586.799540***	793.903408	1569.772991	785.390133	1568.788975	784.898125	G	345.188095	173.097685	328.161546	164.584411			3
16	***1699.847219***	850.427247	1682.820670	841.913973	1681.836654	841.421965	P	**288.166631**	144.586953	271.140082	136.073679			2
17							R	**175.118952**	88.063114	158.092403	79.549839			1



RMS error 649 ppm



RMS error 649 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.1	1872.951599	-0.007831	MAKFALNQNLPDLGGPR
15.4	1872.951599	-0.007831	MAKFALNQNLPDLGGPR
8.2	1872.937012	0.006756	LPLPGPYDSRDDFPLR
8.1	1872.937195	0.006573	SPQECCLRVSLMPLR
5.6	1872.946915	-0.003147	SSPGPDTLVVLEFNPASK
4.8	1872.930466	0.013302	HIQWTPREMEVYIR
2.7	1872.951630	-0.007862	KVKPHPPPSGLPPCPR
2.6	1872.925110	0.018658	SSIMSITAEPPGNDSIVR
2.4	1872.946915	-0.003147	SSPGPDTLVVLEFNPASK
2.3	1872.951630	-0.007862	KVKPHPPPSGLPPCPR

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

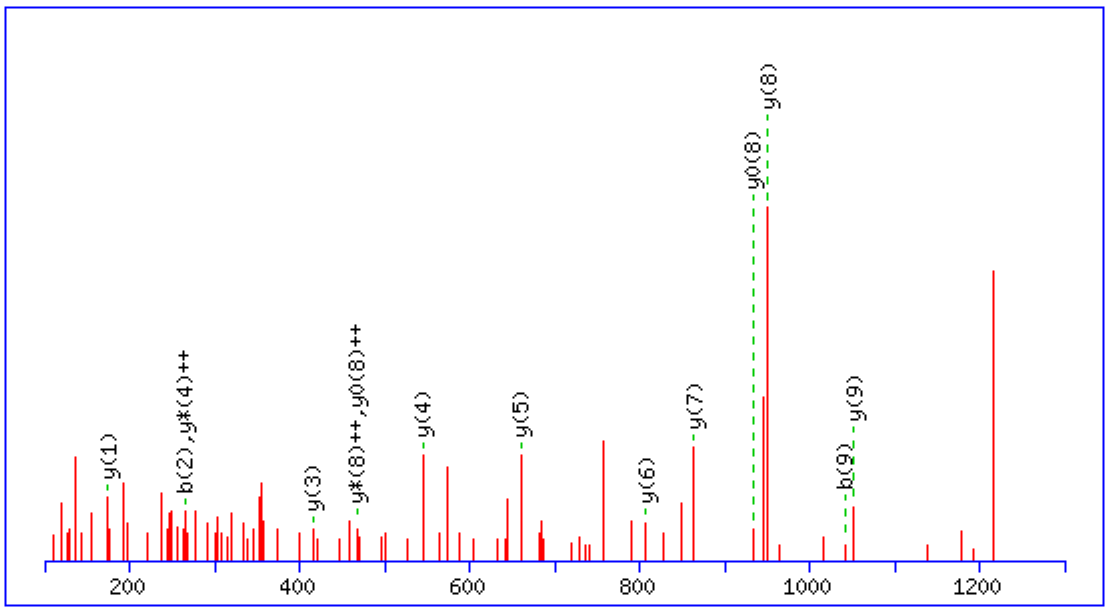
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YTSGFDELQR**
Found in **SPIT1_HUMAN**, Kunitz-type protease inhibitor 1 OS=Homo sapiens GN=SPINT1 PE=1 SV=2

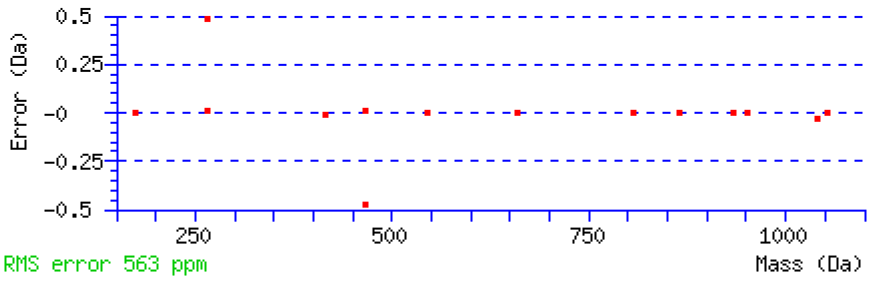
Match to Query 538090: 1214.552188 from(608.283370,2+) rtinseconds(2072) index(837646)
Title: Locus:1.1.1.1335.19
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

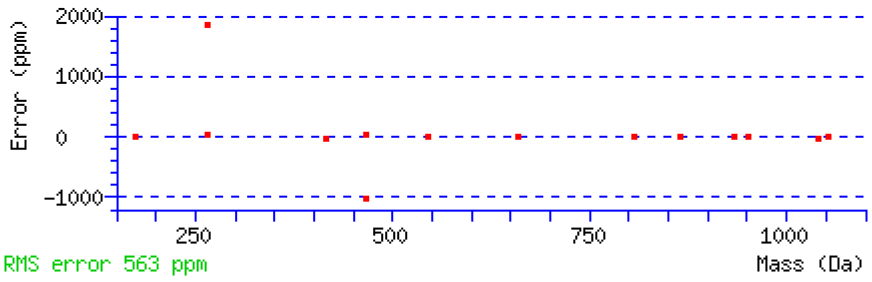
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1214.556763
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 42  Expect: 0.00026
Matches : 14/84 fragment ions using 33 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.070605	82.538940					Y							10
2	**265.118284**	133.062780			247.107719	124.057498	T	***1052.500715***	526.753995	1035.474166	518.240721	1034.490150	517.748713	9
3	352.150312	176.578794			334.139747	167.573512	S	***951.453036***	476.230156	934.426487	467.716881	933.442471	467.224873	8
4	409.171776	205.089526			391.161211	196.084244	G	***864.421008***	432.714142	847.394459	424.200867	846.410443	423.708859	7
5	556.240190	278.623733			538.229625	269.618451	F	***807.399544***	404.203410	790.372995	395.690135	789.388979	395.198127	6
6	671.267133	336.137205			653.256568	327.131922	D	***660.331130***	330.669203	643.304581	322.155928	642.320565	321.663920	5
7	800.309726	400.658501			782.299161	391.653219	E	***545.304187***	273.155732	528.277638	264.642457	527.293622	264.150449	4
8	913.393790	457.200533			895.383225	448.195251	L	***416.261594***	208.634435	399.235045	200.121160			3
9	**1041.452368**	521.229822	1024.425819	512.716548	1023.441803	512.224539	Q	303.177530	152.092403	286.150981	143.579128			2
10							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.6	1214.556763	-0.004575	YTSGFDELQR

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

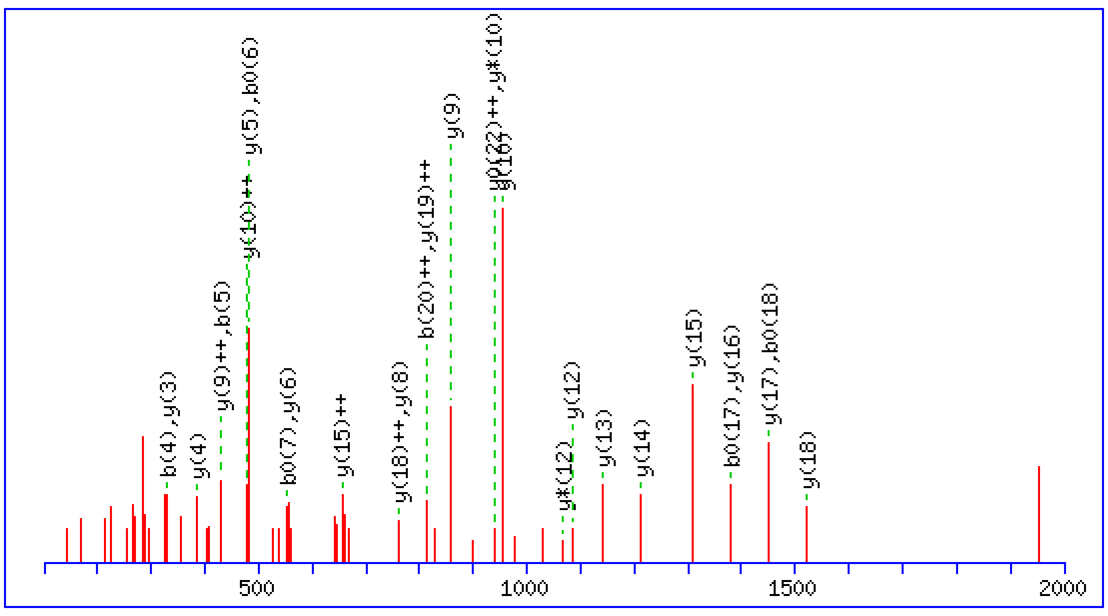
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GGVDTAAAPAGGAPPAHAPGPGR**
Found in **LAGE3_HUMAN**, L antigen family member 3 OS=Homo sapiens GN=LAGE3 PE=1 SV=2

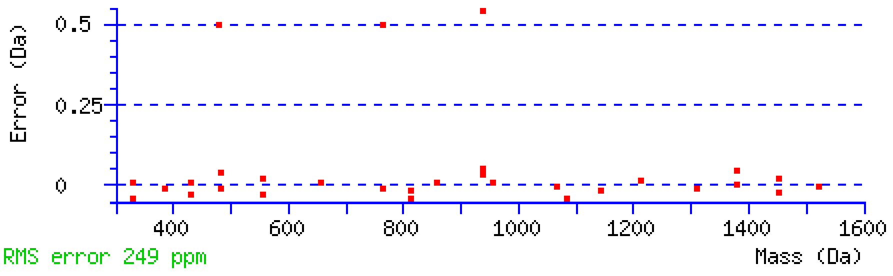
Match to Query 57052: 1950.957372 from(651.326400,3+) rtinseconds(1448) index(10539)
Title: Locus:1.1.1.1769.47
Data file 2011-11-12 - TFD - EP 5-6.mgf

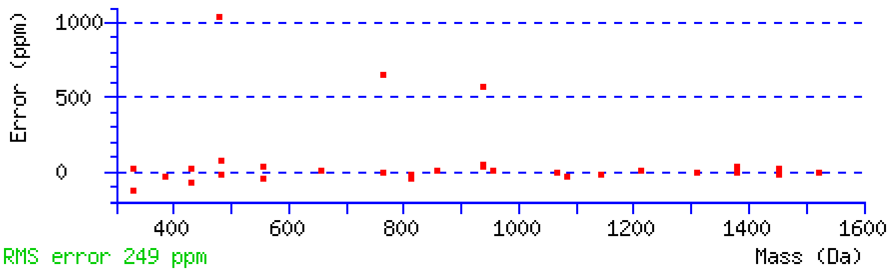
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1950.966034
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 116  Expect: 2.8e-011
Matches : 30/178 fragment ions using 27 most intense peaks   (help)
```

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	58.028740	29.518008			G							23
2	115.050204	58.028740			G	1894.951838	947.979557	1877.925289	939.466283	1876.941273	938.974274	22
3	214.118618	107.562947			V	1837.930374	919.468825	1820.903825	910.955550	1819.919809	910.463542	21
4	**329.145561**	165.076418	311.134996	156.071136	D	1738.861960	869.934618	1721.835411	861.421344	1720.851395	860.929335	20
5	**430.193240**	215.600258	412.182675	206.594976	T	1623.835017	812.421146	1606.808468	803.907872	1605.824452	803.415864	19
6	501.230354	251.118815	483.219789	242.113532	A	***1522.787338***	761.897307	1505.760789	753.384032			18
7	572.267468	286.637372	554.256903	277.632090	A	***1451.750224***	726.378750	1434.723675	717.865476			17
8	643.304582	322.155929	625.294017	313.150646	A	***1380.713110***	690.860193	1363.686561	682.346919			16
9	740.357346	370.682311	722.346781	361.677029	P	***1309.675996***	655.341636	1292.649447	646.828362			15
10	811.394460	406.200868	793.383895	397.195585	A	***1212.623232***	606.815254	1195.596683	598.301980			14
11	868.415924	434.711600	850.405359	425.706318	G	***1141.586118***	571.296697	1124.559569	562.783423			13
12	925.437388	463.222332	907.426823	454.217050	G	***1084.564654***	542.785965	1067.538105	534.272691			12
13	996.474502	498.740889	978.463937	489.735607	A	1027.543190	514.275233	1010.516641	505.761958			11
14	1093.527266	547.267271	1075.516701	538.261989	P	***956.506076***	478.756676	939.479527	470.243401			10
15	1190.580030	595.793653	1172.569465	586.788371	P	***859.453312***	430.230294	842.426763	421.717019			9
16	1261.617144	631.312210	1243.606579	622.306928	A	***762.400548***	381.703912	745.373999	373.190637			8
17	1398.676056	699.841666	1380.665491	690.836384	H	691.363434	346.185355	674.336885	337.672080			7
18	1469.713170	735.360223	1451.702605	726.354941	A	***554.304522***	277.655899	537.277973	269.142624			6
19	1566.765934	783.886605	1548.755369	774.881323	P	***483.267408***	242.137342	466.240859	233.624067			5
20	1623.787398	812.397337	1605.776833	803.392054	G	***386.214644***	193.610960	369.188095	185.097685			4
21	1720.840162	860.923719	1702.829597	851.918436	P	***329.193180***	165.100228	312.166631	156.586953			3
22	1777.861626	889.434451	1759.851061	880.429168	G	232.140416	116.573846	215.113867	108.060571			2
23					R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
116.4	1950.966034	-0.008662	GGVDTAAAPAGGAPPAHAPGPGR
3.6	1950.964691	-0.007319	AGQEPSPKPGTDVIPAAPR
1.1	1950.951614	0.005758	LITRAHVECSPAHTCR

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

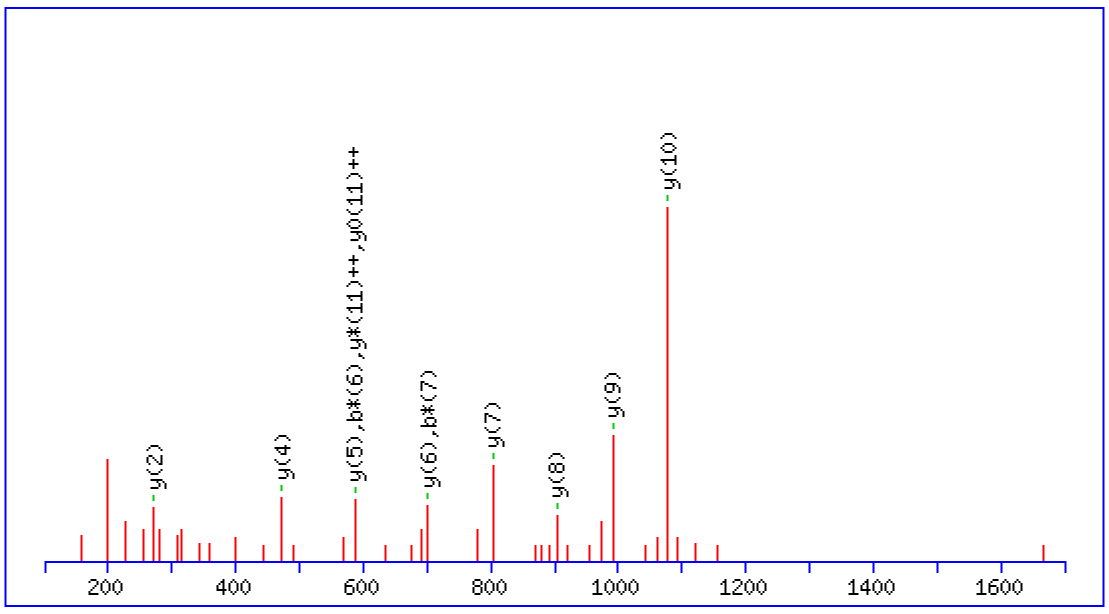
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NLSSTTDDEAPR**
Found in **LAD1_HUMAN**, Ladinin-1 OS=Homo sapiens GN=LAD1 PE=1 SV=2

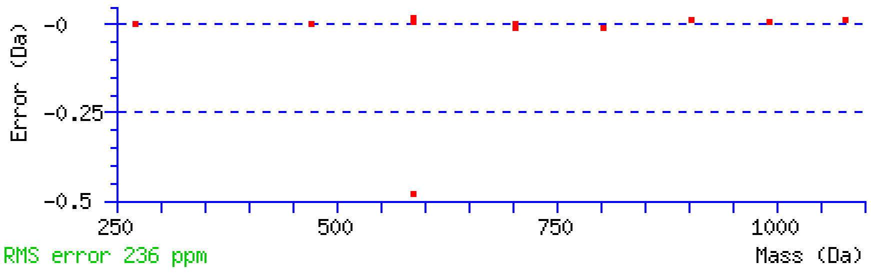
Match to Query 645164: 1304.586188 from(653.300370,2+) rtinseconds(1212) index(247803)
Title: Locus:1.1.1.904.37
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

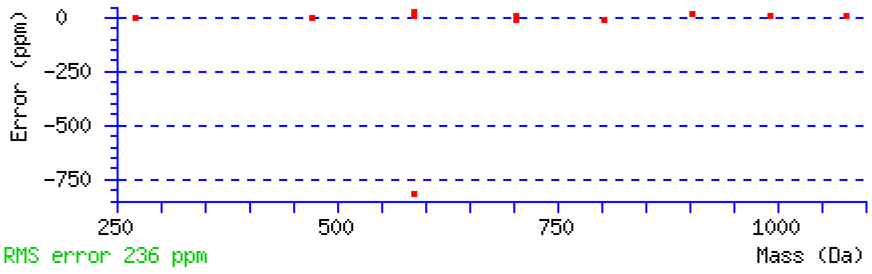
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1304.584427
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 76  Expect: 2e-007
Matches : 12/122 fragment ions using 10 most intense peaks   (help)
```

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			N							12
2	228.134267	114.570771	211.107718	106.057497			L	1191.548787	596.278032	1174.522238	587.764757	1173.538222	587.272749	11
3	315.166295	158.086785	298.139746	149.573511	297.155730	149.081503	S	***1078.464723***	539.736000	1061.438174	531.222725	1060.454158	530.730717	10
4	402.198323	201.602800	385.171774	193.089525	384.187758	192.597517	S	***991.432695***	496.219986	974.406146	487.706711	973.422130	487.214703	9
5	503.246002	252.126639	486.219453	243.613365	485.235437	243.121357	T	***904.400667***	452.703972	887.374118	444.190697	886.390102	443.698689	8
6	604.293681	302.650479	587.267132	294.137204	586.283116	293.645196	T	***803.352988***	402.180132	786.326439	393.666858	785.342423	393.174850	7
7	719.320624	360.163950	702.294075	351.650676	701.310059	351.158668	D	***702.305309***	351.656293	685.278760	343.143018	684.294744	342.651010	6
8	834.347567	417.677422	817.321018	409.164147	816.337002	408.672139	D	***587.278366***	294.142821	570.251817	285.629547	569.267801	285.137539	5
9	963.390160	482.198718	946.363611	473.685444	945.379595	473.193436	E	***472.251423***	236.629350	455.224874	228.116075	454.240858	227.624067	4
10	1034.427274	517.717275	1017.400725	509.204001	1016.416709	508.711993	A	343.208830	172.108053	326.182281	163.594779			3
11	1131.480038	566.243657	1114.453489	557.730383	1113.469473	557.238375	P	***272.171716***	136.589496	255.145167	128.076221			2
12							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
75.8	1304.584427	0.001761	NLSSTTDDEAPR
4.1	1304.595871	-0.009683	WIVLDGDIDPM
1.3	1304.593170	-0.006982	NLSGQPNFPCR
1.3	1304.593170	-0.006982	NLSGQPNFPCR
1.3	1304.593338	-0.007150	YSFQLWIAMM
1.3	1304.593338	-0.007150	YSFQLWIAMM

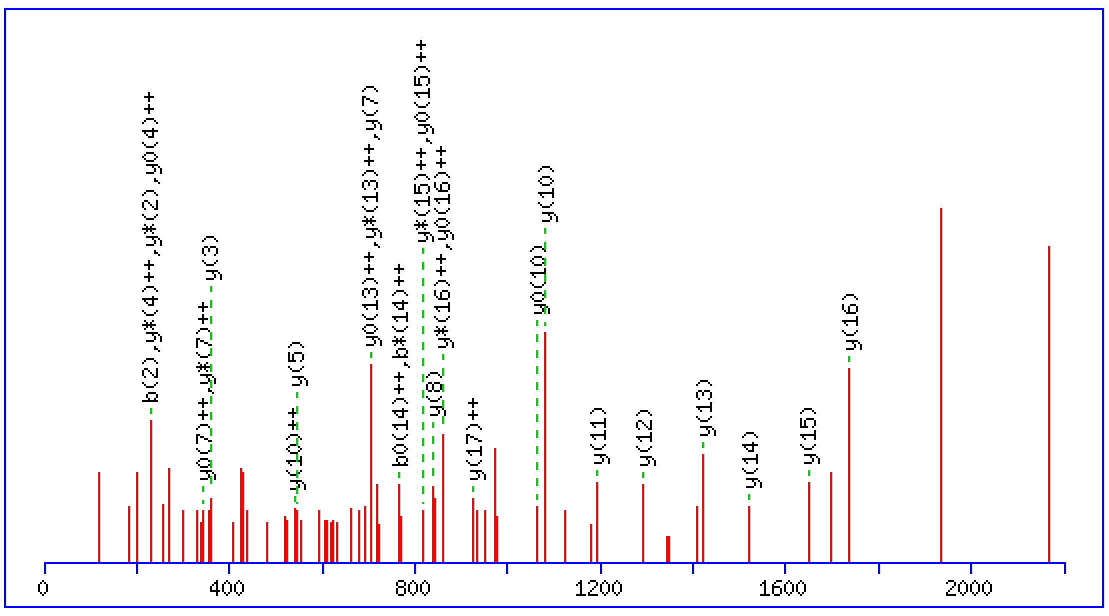
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VESLSQVEVILQHSAADIAR**
Found in **LAMB1_HUMAN**, Laminin subunit beta-1 OS=Homo sapiens GN=LAMB1 PE=1 SV=2

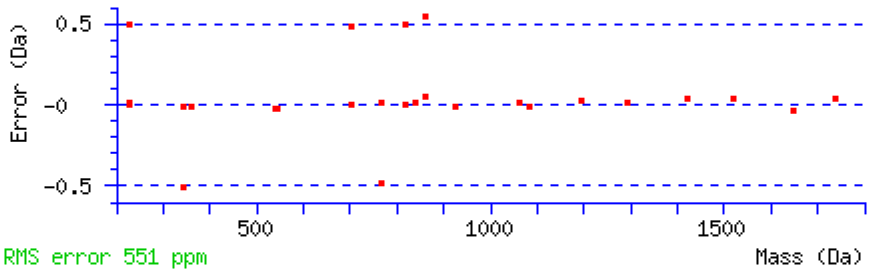
Match to Query 66829: 2164.130922 from(722.384250,3+) rtinseconds(3829) index(56921)
Title: Locus:1.1.1.2758.32
Data file 2011-11-12 - TFD - EP 6-1.mgf

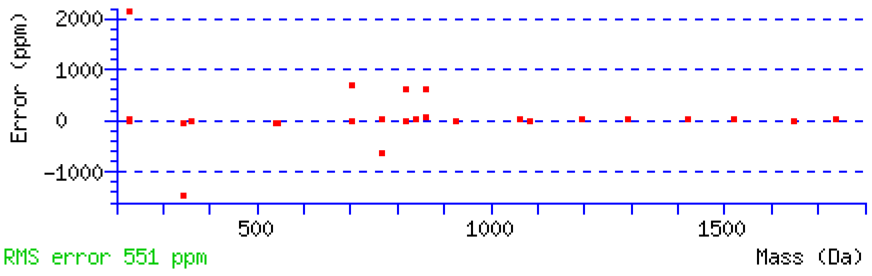
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [0] to [2200] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2164.148773
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 70  Expect: 9.8e-007
Matches : 28/210 fragment ions using 31 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	100.075690	50.541483					V							20
2	229.118283	115.062780			211.107718	106.057497	E	2066.087659	1033.547467	2049.061110	1025.034193	2048.077094	1024.542185	19
3	316.150311	158.578794			298.139746	149.573511	S	1937.045066	969.026171	1920.018517	960.512897	1919.034501	960.020888	18
4	429.234375	215.120826			411.223810	206.115543	L	1850.013038	925.510157	1832.986489	916.996882	1832.002473	916.504874	17
5	516.266403	258.636840			498.255838	249.631557	S	***1736.928974***	868.968125	1719.902425	860.454850	1718.918409	859.962842	16
6	644.324981	322.666129	627.298432	314.152854	626.314416	313.660846	Q	***1649.896946***	825.452111	1632.870397	816.938836	1631.886381	816.446828	15
7	743.393395	372.200336	726.366846	363.687061	725.382830	363.195053	V	***1521.838368***	761.422822	1504.811819	752.909548	1503.827803	752.417539	14
8	872.435988	436.721632	855.409439	428.208358	854.425423	427.716350	E	***1422.769954***	711.888615	1405.743405	703.375340	1404.759389	702.883332	13
9	971.504402	486.255839	954.477853	477.742565	953.493837	477.250557	V	***1293.727361***	647.367319	1276.700812	638.854044	1275.716796	638.362036	12
10	1084.588466	542.797871	1067.561917	534.284597	1066.577901	533.792588	I	***1194.658947***	597.833111	1177.632398	589.319837	1176.648382	588.827829	11
11	1197.672530	599.339903	1180.645981	590.826628	1179.661965	590.334620	L	***1081.574883***	541.291080	1064.548334	532.777805	1063.564318	532.285797	10
12	1325.731108	663.369192	1308.704559	654.855917	1307.720543	654.363909	Q	968.490819	484.749048	951.464270	476.235773	950.480254	475.743765	9
13	1462.790020	731.898648	1445.763471	723.385373	1444.779455	722.893365	H	***840.432241***	420.719759	823.405692	412.206484	822.421676	411.714476	8
14	1549.822048	775.414662	1532.795499	766.901387	1531.811483	766.409379	S	***703.373329***	352.190303	686.346780	343.677028	685.362764	343.185020	7
15	1620.859162	810.933219	1603.832613	802.419944	1602.848597	801.927936	A	616.341301	308.674289	599.314752	300.161014	598.330736	299.669006	6
16	1691.896276	846.451776	1674.869727	837.938501	1673.885711	837.446493	A	***545.304187***	273.155732	528.277638	264.642457	527.293622	264.150449	5
17	1806.923219	903.965247	1789.896670	895.451973	1788.912654	894.959965	D	474.267073	237.637175	457.240524	229.123900	456.256508	228.631892	4
18	1920.007283	960.507279	1902.980734	951.994005	1901.996718	951.501997	I	***359.240130***	180.123703	342.213581	171.610429			3
19	1991.044397	996.025836	1974.017848	987.512562	1973.033832	987.020554	A	246.156066	123.581671	229.129517	115.068397			2
20							R	175.118952	88.063114	158.092403	79.549840			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
69.9	2164.148773	-0.017851	VESLSQVEVILQHSAADIAR

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

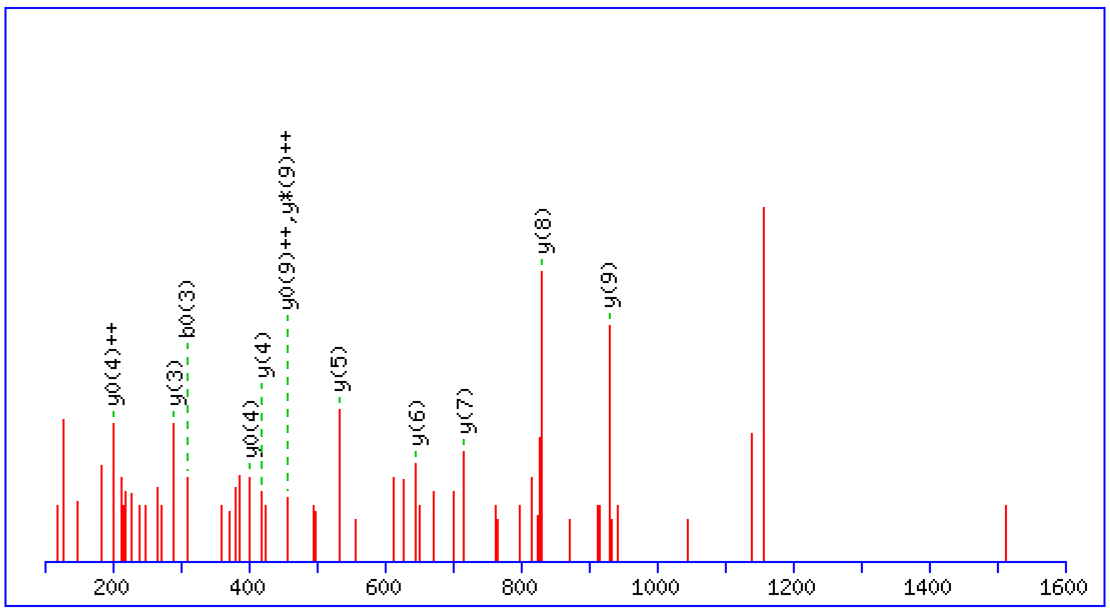
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EVVNAIIESGK**
Found in **LANC2_HUMAN**, LanC-like protein 2 OS=Homo sapiens GN=LANCL2 PE=1 SV=1

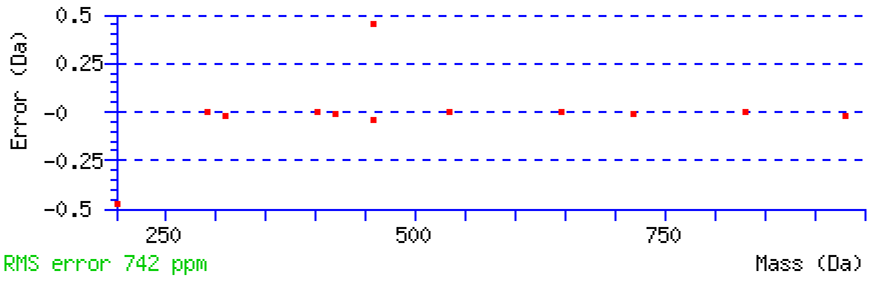
Match to Query 20025: 1157.618188 from(579.816370,2+) rtinseconds(1985) index(22490)
Title: Locus:1.1.1.2244.24
Data file 2011-11-10 - TFD - EP 4-3.mgf

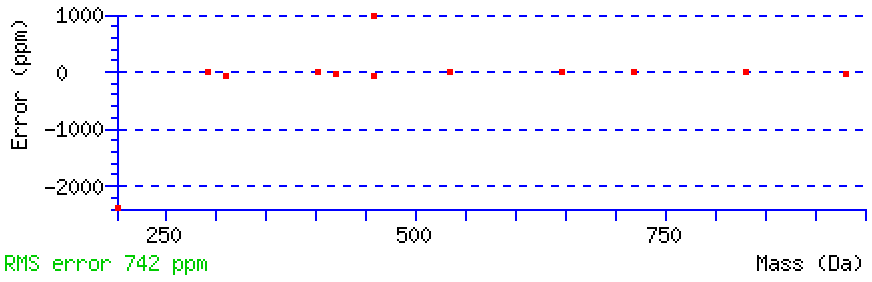
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1157.629181
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 44  Expect: 0.00057
Matches : 12/110 fragment ions using 21 most intense peaks   (help)
```

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	E							11
2	229.118283	115.062780			211.107718	106.057497	V	1029.593886	515.300581	1012.567337	506.787307	1011.583321	506.295299	10
3	328.186697	164.596987			310.176132	155.591704	V	***930.525472***	465.766374	913.498923	457.253100	912.514907	456.761092	9
4	442.229624	221.618450	425.203075	213.105176	424.219059	212.613168	N	***831.457058***	416.232167	814.430509	407.718893	813.446493	407.226885	8
5	513.266738	257.137007	496.240189	248.623733	495.256173	248.131725	A	***717.414131***	359.210704	700.387582	350.697429	699.403566	350.205421	7
6	626.350802	313.679039	609.324253	305.165765	608.340237	304.673757	I	***646.377017***	323.692147	629.350468	315.178872	628.366452	314.686864	6
7	739.434866	370.221071	722.408317	361.707797	721.424301	361.215789	I	***533.292953***	267.150115	516.266404	258.636840	515.282388	258.144832	5
8	868.477459	434.742368	851.450910	426.229093	850.466894	425.737085	E	***420.208889***	210.608082	403.182340	202.094808	402.198324	201.602800	4
9	955.509487	478.258382	938.482938	469.745107	937.498922	469.253099	S	***291.166296***	146.086786	274.139747	137.573512	273.155731	137.081504	3
10	1012.530951	506.769114	995.504402	498.255839	994.520386	497.763831	G	204.134268	102.570772	187.107719	94.057498			2
11							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.1	1157.629181	-0.010993	EVVNAIIESGK
15.0	1157.629181	-0.010993	IDIINAVESGK
6.6	1157.629181	-0.010993	VEVKEDAKPK
4.8	1157.608063	0.010125	KYQIFSGTSK

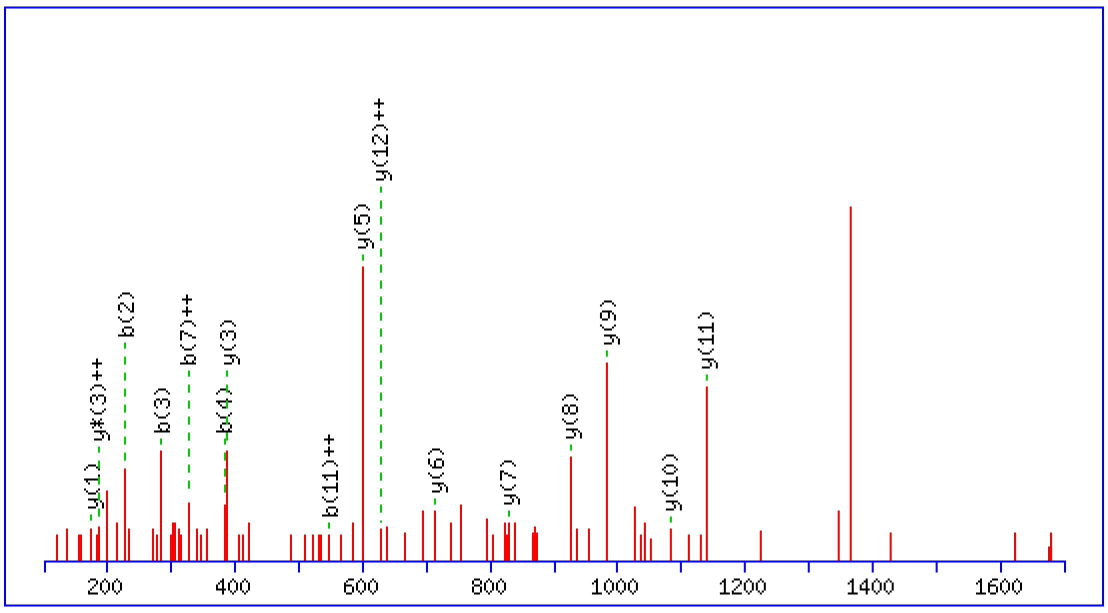
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILGVGPDDPDLVR**
Found in **ERG7_HUMAN**, Lanosterol synthase OS=Homo sapiens GN=LSS PE=1 SV=1

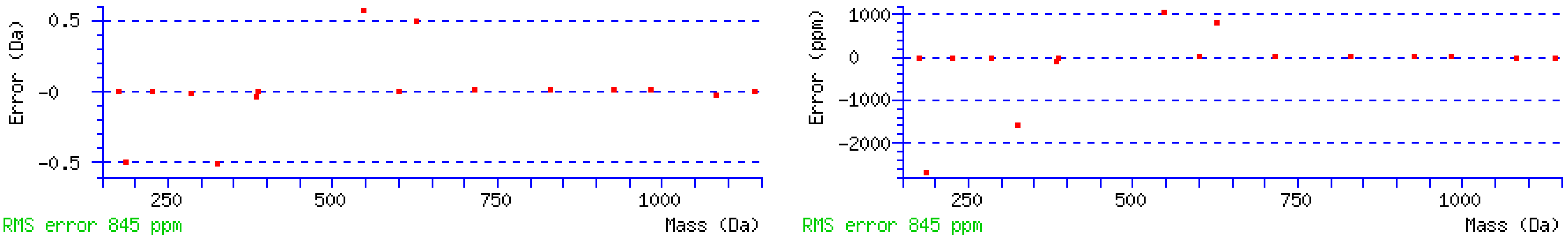
Match to Query 40435: 1364.728188 from(683.371370,2+) rtinseconds(2766) index(36757)
Title: Locus:1.1.1.2490.40
Data file 2011-11-10 - TFD - EP 3-2.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 1700 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1364.729996
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 36  Expect: 0.0026
Matches : 16/102 fragment ions using 51 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							13
2	**227.175404**	114.091340			L	1252.653193	626.830235	1235.626644	618.316960	1234.642628	617.824952	12
3	**284.196868**	142.602072			G	***1139.569129***	570.288203	1122.542580	561.774928	1121.558564	561.282920	11
4	**383.265282**	192.136279			V	***1082.547665***	541.777471	1065.521116	533.264196	1064.537100	532.772188	10
5	440.286746	220.647011			G	***983.479251***	492.243264	966.452702	483.729989	965.468686	483.237981	9
6	537.339510	269.173393			P	***926.457787***	463.732532	909.431238	455.219257	908.447222	454.727249	8
7	652.366453	326.686865	634.355888	317.681582	D	***829.405023***	415.206150	812.378474	406.692875	811.394458	406.200867	7
8	767.393396	384.200336	749.382831	375.195053	D	***714.378080***	357.692678	697.351531	349.179404	696.367515	348.687396	6
9	864.446160	432.726718	846.435595	423.721435	P	***599.351137***	300.179207	582.324588	291.665932	581.340572	291.173924	5
10	979.473103	490.240189	961.462538	481.234907	D	502.298373	251.652824	485.271824	243.139550	484.287808	242.647542	4
11	1092.557167	546.782221	1074.546602	537.776939	L	***387.271430***	194.139353	370.244881	185.626079			3
12	1191.625581	596.316429	1173.615016	587.311146	V	274.187366	137.597321	257.160817	129.084047			2
13					R	***175.118952***	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.6	1364.729996	-0.001808	ILGVGPDDPDLVR

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

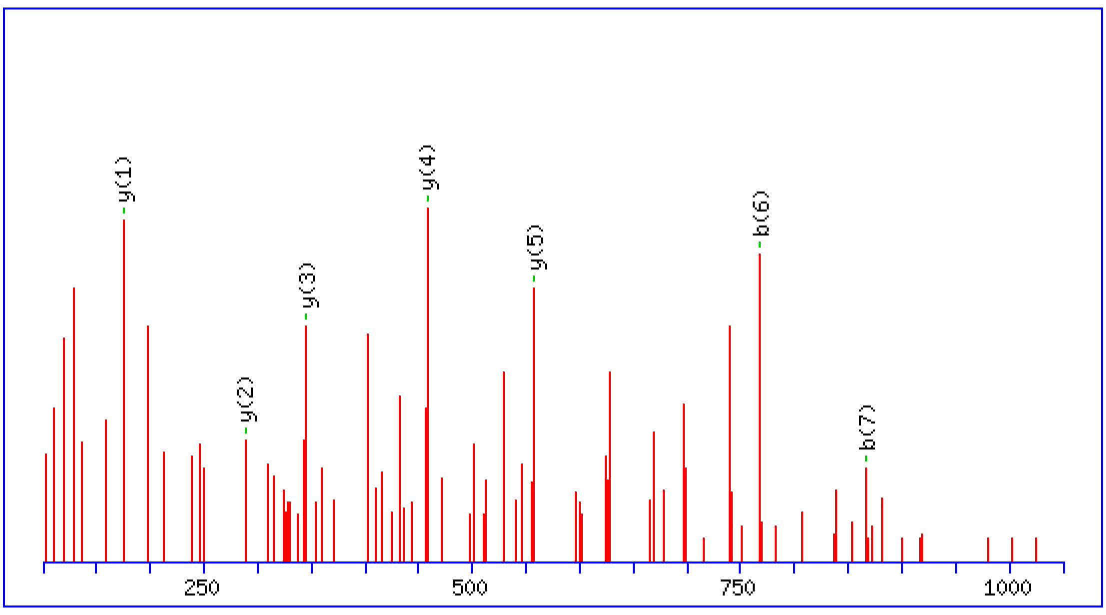
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **WPAQRPVPGIR**
Found in **LRFN1_HUMAN**, Leucine-rich repeat and fibronectin type III domain-containing protein 1 OS=Homo sapiens GN=LRFN1 PE=1 SV=2

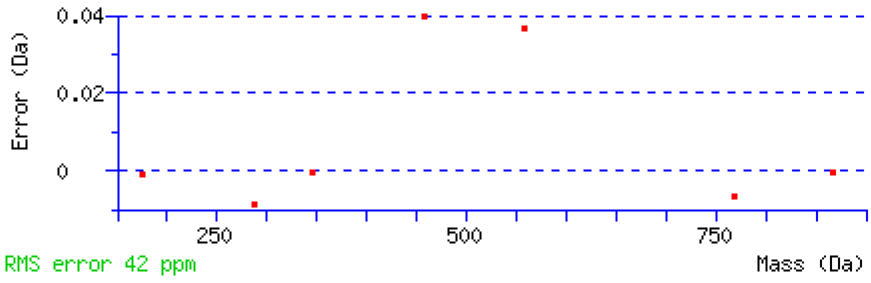
Match to Query 37167: 1323.710172 from(442.244000,3+) rtinseconds(1663) index(16084)
Title: Locus:1.1.1.2046.11
Data file 2011-11-14 - TFD - EP 8-1.mgf

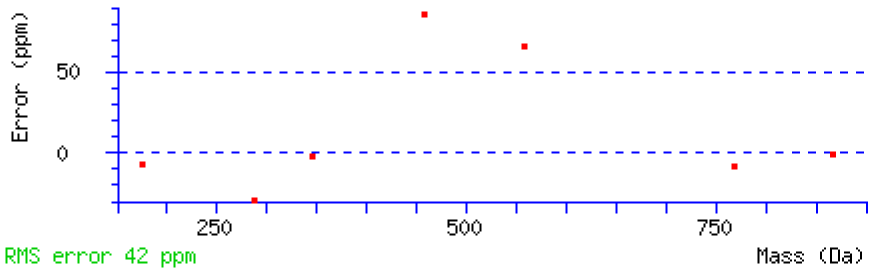
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1050] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1323.704773
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P2      : Oxidation (P)
P6      : Oxidation (P)
P8      : Oxidation (P)
Ions Score: 32  Expect: 0.0041
Matches : 7/74 fragment ions using 10 most intense peaks    (help)
```

#	b	b^{++}	b*	b*$^{++}$	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	187.086589	94.046932			W					11
2	300.134268	150.570772			P	1138.632734	569.820005	1121.606185	561.306731	10
3	371.171382	186.089329			A	1025.585055	513.296166	1008.558506	504.782891	9
4	499.229960	250.118618	482.203411	241.605343	Q	954.547941	477.777609	937.521392	469.264334	8
5	655.331071	328.169174	638.304522	319.655899	R	826.489363	413.748320	809.462814	405.235045	7
6	**768.378750**	384.693013	751.352201	376.179739	P	670.388252	335.697764	653.361703	327.184489	6
7	**867.447164**	434.227220	850.420615	425.713946	V	***557.340573***	279.173925	540.314024	270.660650	5
8	980.494843	490.751060	963.468294	482.237785	P	***458.272159***	229.639717	441.245610	221.126443	4
9	1037.516307	519.261792	1020.489758	510.748517	G	***345.224480***	173.115878	328.197931	164.602603	3
10	1150.600371	575.803824	1133.573822	567.290549	I	***288.203016***	144.605146	271.176467	136.091871	2
11					R	***175.118952***	88.063114	158.092403	79.549839	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.5	1323.704773	0.005399	WPAQRPVPGIR
9.3	1323.714645	-0.004473	DKTLESILHPR
4.5	1323.714645	-0.004473	SAEALGPGALVSPR
2.5	1323.698227	0.011945	IFTHHLCRAR
2.4	1323.722061	-0.011889	MPPPTILSTVPR
1.7	1323.700729	0.009443	SSAPRSPTPRPR
1.0	1323.714676	-0.004504	GGDGIKPPPIIGR
0.5	1323.704758	0.005414	LKDTHAGAGWLR
0.5	1323.715988	-0.005816	WHASQTRGLIR

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

{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EGGDGEEQDVGDAGR**
Found in **LRC47_HUMAN**, Leucine-rich repeat-containing protein 47 OS=Homo sapiens GN=LRRC47 PE=1 SV=1

Match to Query 830122: 1489.595328 from(745.804940,2+) rtinseconds(1054) index(244794)
Title: Locus:1.1.1.842.47
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1489.591721
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 62 **Expect:** 1.5e-006
Matches : 8/148 fragment ions using 12 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	130.049869	65.528572			112.039304	56.523290	E							15
2	187.071333	94.039305			169.060768	85.034022	G	1361.556393	681.281835	1344.529844	672.768560	1343.545828	672.276552	14
3	244.092797	122.550037			226.082232	113.544754	G	1304.534929	652.771102	1287.508380	644.257828	1286.524364	643.765820	13
4	359.119740	180.063508			341.109175	171.058226	D	1247.513465	624.260371	1230.486916	615.747096	1229.502900	615.255088	12
5	416.141204	208.574240			398.130639	199.568958	G	***1132.486522***	566.746899	1115.459973	558.233625	1114.475957	557.741616	11
6	545.183797	273.095537			527.173232	264.090254	E	***1075.465058***	538.236167	1058.438509	529.722893	1057.454493	529.230885	10
7	674.226390	337.616833			656.215825	328.611551	E	***946.422465***	473.714870	929.395916	465.201596	928.411900	464.709588	9
8	802.284968	401.646122	785.258419	393.132848	784.274403	392.640840	Q	***817.379872***	409.193574	800.353323	400.680299	799.369307	400.188291	8
9	917.311911	459.159594	900.285362	450.646319	899.301346	450.154311	D	***689.321294***	345.164285	672.294745	336.651010	671.310729	336.159002	7
10	1016.380325	508.693801	999.353776	500.180526	998.369760	499.688518	V	***574.294351***	287.650813	557.267802	279.137539	556.283786	278.645531	6
11	1073.401789	537.204533	1056.375240	528.691258	1055.391224	528.199250	G	***475.225937***	238.116606	458.199388	229.603332	457.215372	229.111324	5
12	1188.428732	594.718004	1171.402183	586.204730	1170.418167	585.712722	D	418.204473	209.605874	401.177924	201.092600	400.193908	200.600592	4
13	1259.465846	630.236561	1242.439297	621.723287	1241.455281	621.231279	A	***303.177530***	152.092403	286.150981	143.579128			3
14	1316.487310	658.747293	1299.460761	650.234019	1298.476745	649.742010	G	232.140416	116.573846	215.113867	108.060571			2
15							R	175.118952	88.063114	158.092403	79.549839			1

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
61.6	1489.591721	0.003607	EGGDGEEQDVGDAGR

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

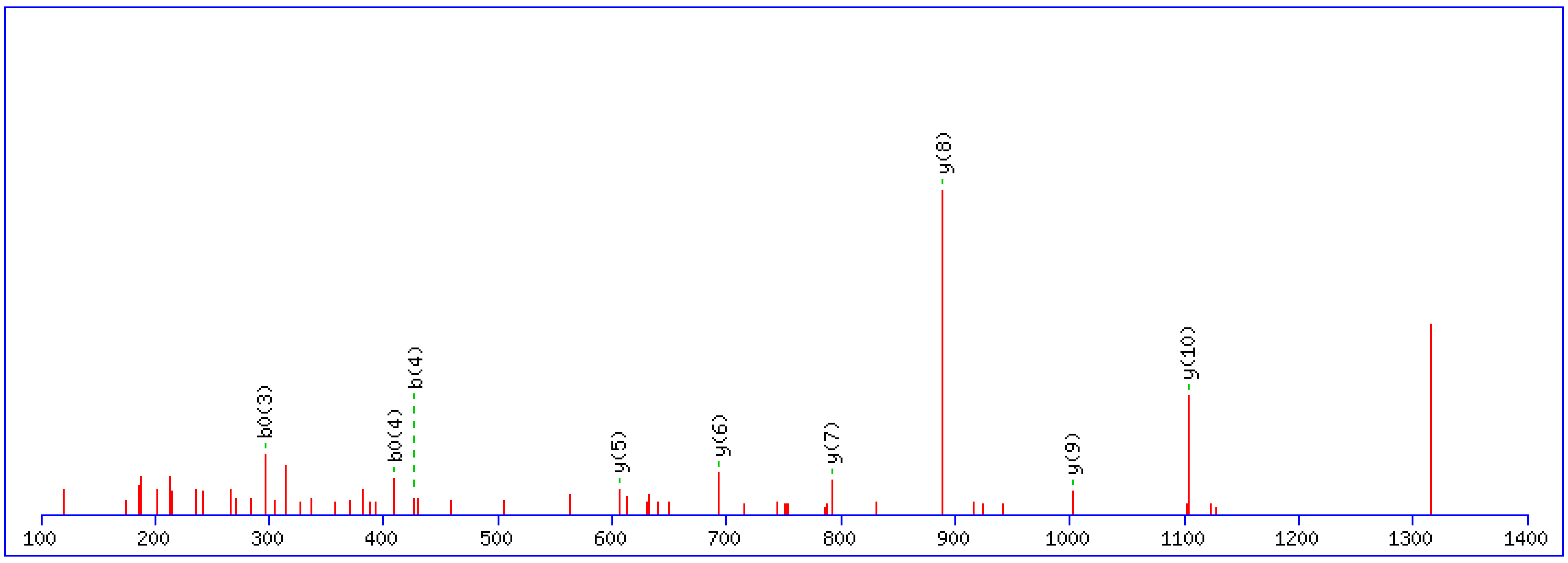
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LVTLPVSFAQLK**
Found in **LRC59_HUMAN**, Leucine-rich repeat-containing protein 59 OS=Homo sapiens GN=LRRC59 PE=1 SV=1

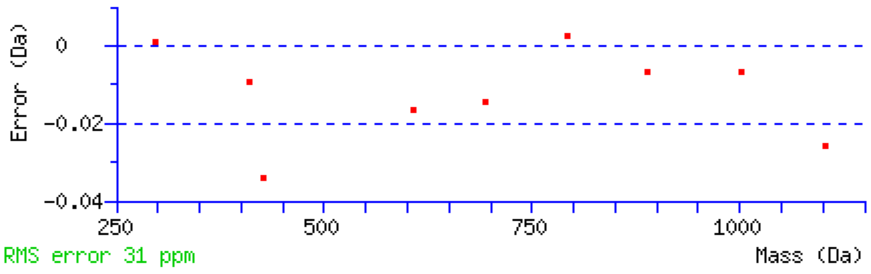
Match to Query 32487: 1314.780868 from(658.397710,2+) rtinseconds(3386) index(48645)
Title: Locus:1.1.1.1728.25
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 3.mgf

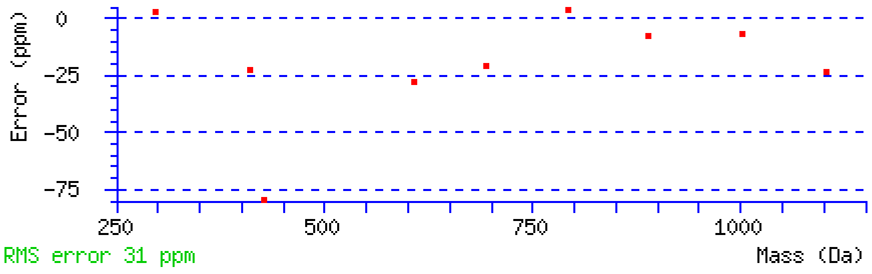
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 1400 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1314.791122
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 40  Expect: 0.00023
Matches : 9/100 fragment ions using 11 most intense peaks   (help)
```

#	b	b^{++}	b*	b*$^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^0	y^{0++}	#
1	114.091340	57.549308					L							12
2	213.159754	107.083515					V	1202.714337	601.860807	1185.687788	593.347532	1184.703772	592.855524	11
3	314.207433	157.607354			296.196868	148.602072	T	***1103.645923***	552.326600	1086.619374	543.813325	1085.635358	543.321317	10
4	427.291497	214.149386			409.280932	205.144104	L	***1002.598244***	501.802760	985.571695	493.289486	984.587679	492.797478	9
5	524.344261	262.675769			506.333696	253.670486	P	***889.514180***	445.260728	872.487631	436.747454	871.503615	436.255446	8
6	623.412675	312.209976			605.402110	303.204693	V	***792.461416***	396.734346	775.434867	388.221071	774.450851	387.729064	7
7	710.444703	355.725990			692.434138	346.720707	S	***693.393002***	347.200139	676.366453	338.686865	675.382437	338.194857	6
8	857.513117	429.260197			839.502552	420.254914	F	***606.360974***	303.684125	589.334425	295.170851			5
9	928.550231	464.778753			910.539666	455.773471	A	459.292560	230.149918	442.266011	221.636643			4
10	1056.608809	528.808043	1039.582260	520.294768	1038.598244	519.802760	Q	388.255446	194.631361	371.228897	186.118087			3
11	1169.692873	585.350075	1152.666324	576.836800	1151.682308	576.344792	L	260.196868	130.602072	243.170319	122.088797			2
12							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.9	1314.791122	-0.010254	LVTLPVSFAQLK
2.4	1314.775848	0.005020	LAVSLAETTGLIK
0.4	1314.791122	-0.010254	PTPVIKAFGILK

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

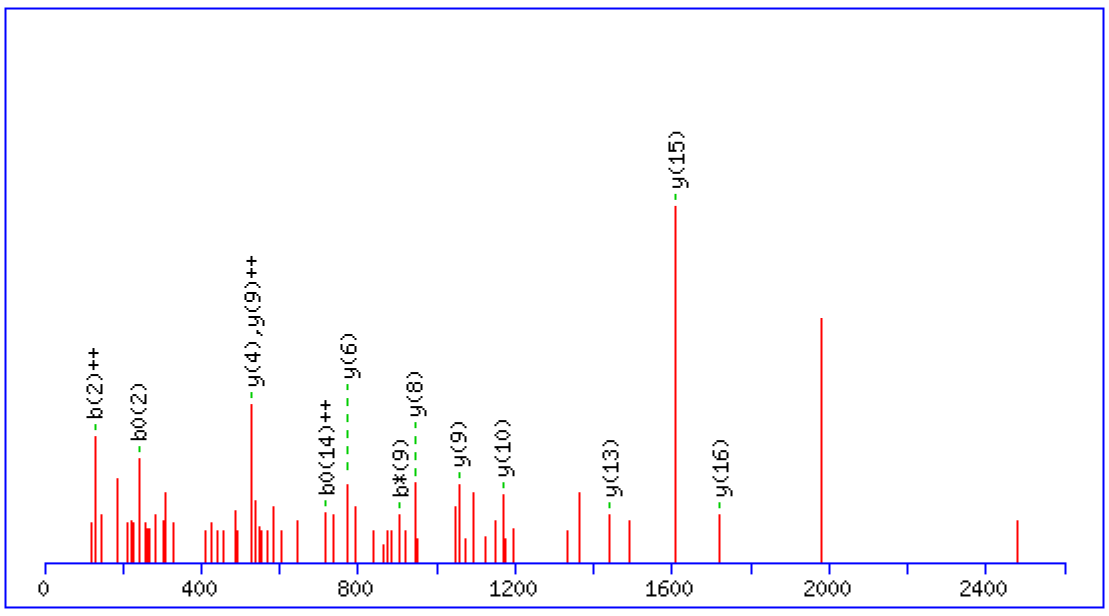
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EQIPAGTLLLAVEDPEKR**
Found in **FUK_HUMAN**, L-fucose kinase OS=Homo sapiens GN=FUK PE=2 SV=2

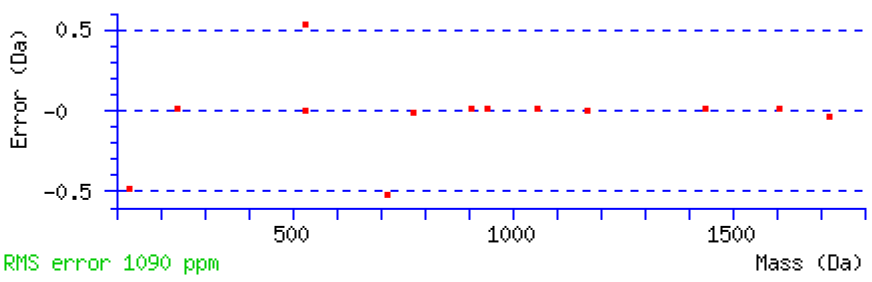
Match to Query 62585: 1978.073082 from(660.364970,3+) rtinseconds(3333) index(46687)
Title: Locus:1.1.1.2753.28
Data file 2011-11-10 - TFD - EP 4-2.mgf

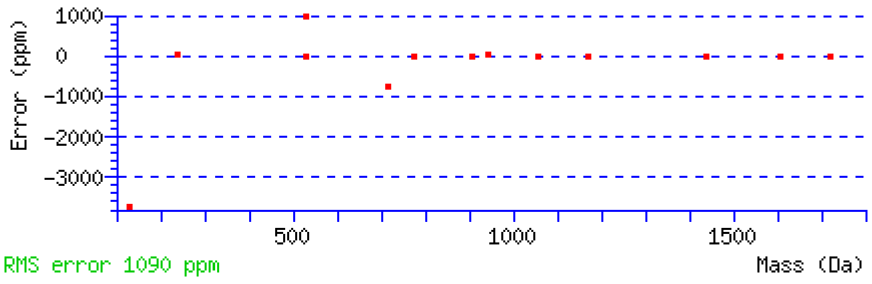
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1978.073471
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 48 **Expect:** 5.4e-005
Matches : 13/198 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	E							18
2	258.108447	129.557862	241.081898	121.044587	240.097882	120.552579	Q	1850.038191	925.522733	1833.011642	917.009459	1832.027626	916.517451	17
3	371.192511	186.099894	354.165962	177.586619	353.181946	177.094611	I	***1721.979613***	861.493445	1704.953064	852.980170	1703.969048	852.488162	16
4	468.245275	234.626276	451.218726	226.113001	450.234710	225.620993	P	***1608.895549***	804.951413	1591.869000	796.438138	1590.884984	795.946130	15
5	539.282389	270.144833	522.255840	261.631558	521.271824	261.139550	A	1511.842785	756.425031	1494.816236	747.911756	1493.832220	747.419748	14
6	596.303853	298.655565	579.277304	290.142290	578.293288	289.650282	G	***1440.805671***	720.906473	1423.779122	712.393199	1422.795106	711.901191	13
7	697.351532	349.179404	680.324983	340.666130	679.340967	340.174122	T	1383.784207	692.395741	1366.757658	683.882467	1365.773642	683.390459	12
8	810.435596	405.721436	793.409047	397.208162	792.425031	396.716154	L	1282.736528	641.871902	1265.709979	633.358628	1264.725963	632.866619	11
9	923.519660	462.263468	906.493111	453.750194	905.509095	453.258186	L	***1169.652464***	585.329870	1152.625915	576.816596	1151.641899	576.324588	10
10	1036.603724	518.805500	1019.577175	510.292226	1018.593159	509.800218	L	***1056.568400***	528.787838	1039.541851	520.274564	1038.557835	519.782555	9
11	1107.640838	554.324057	1090.614289	545.810783	1089.630273	545.318775	A	***943.484336***	472.245806	926.457787	463.732531	925.473771	463.240523	8
12	1206.709252	603.858264	1189.682703	595.344990	1188.698687	594.852982	V	872.447222	436.727249	855.420673	428.213975	854.436657	427.721967	7
13	1335.751845	668.379561	1318.725296	659.866286	1317.741280	659.374278	E	***773.378808***	387.193042	756.352259	378.679767	755.368243	378.187759	6
14	1450.778788	725.893032	1433.752239	717.379758	1432.768223	716.887750	D	644.336215	322.671746	627.309666	314.158471	626.325650	313.666463	5
15	1547.831552	774.419414	1530.805003	765.906140	1529.820987	765.414132	P	***529.309272***	265.158274	512.282723	256.644999	511.298707	256.152991	4
16	1676.874145	838.940711	1659.847596	830.427436	1658.863580	829.935428	E	432.256508	216.631892	415.229959	208.118617	414.245943	207.626609	3
17	1804.969108	902.988192	1787.942559	894.474918	1786.958543	893.982910	K	303.213915	152.110595	286.187366	143.597321			2
18							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.1	1978.073471	-0.000389	EQIPAGTLLLAVEDPEKR
2.6	1978.082230	-0.009148	QTLKAHMIVHSDVKPFK

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

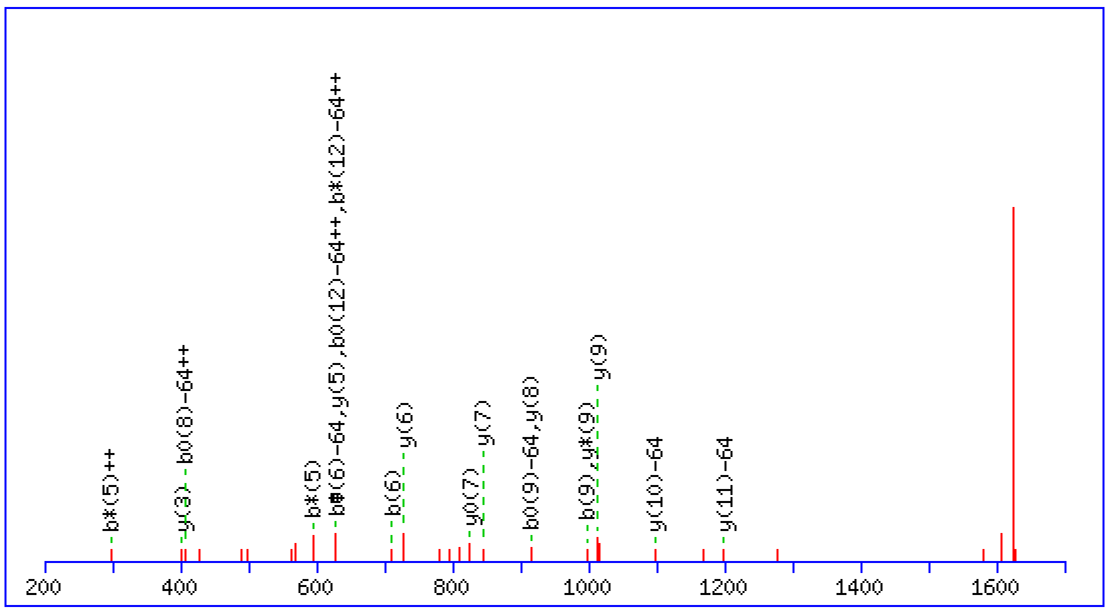
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QSFTMVADTPENLR**
Found in **LASP1_HUMAN**, LIM and SH3 domain protein 1 OS=Homo sapiens GN=LASP1 PE=1 SV=2

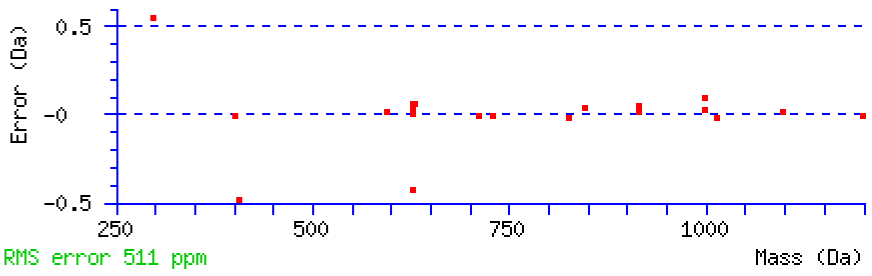
Match to Query 41049: 1623.768888 from(812.891720,2+) rtinseconds(2310) index(20531)
Title: Locus:1.1.1.2336.46
Data file 2011-11-10 - TFD - EP 4-7.mgf

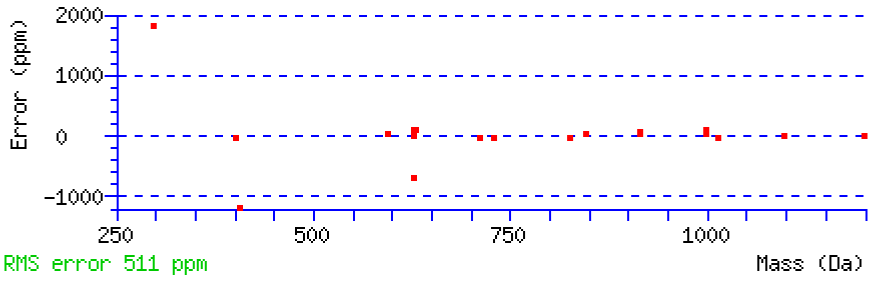
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1623.756271
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M5 : Oxidation (M), with neutral losses 63.998285(shown in table), 0.000000
Ions Score: 40 **Expect:** 0.0013
Matches : 20/226 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	129.065854	65.036565	112.039305	56.523291			Q							14
2	216.097882	108.552579	199.071333	100.039305	198.087317	99.547296	S	1432.706686	716.856981	1415.680137	708.343707	1414.696121	707.851699	13
3	363.166296	182.086786	346.139747	173.573512	345.155731	173.081504	F	1345.674658	673.340967	1328.648109	664.827693	1327.664093	664.335684	12
4	464.213975	232.610626	447.187426	224.097351	446.203410	223.605343	T	***1198.606244***	599.806760	1181.579695	591.293485	1180.595679	590.801477	11
5	547.251090	274.129183	530.224541	265.615909	529.240525	265.123901	M	***1097.558565***	549.282920	1080.532016	540.769646	1079.548000	540.277638	10
6	646.319504	323.663390	629.292955	315.150116	628.308939	314.658108	V	***1014.521450***	507.764363	997.494901	499.251088	996.510885	498.759080	9
7	717.356618	359.181947	700.330069	350.668673	699.346053	350.176665	A	***915.453036***	458.230156	898.426487	449.716881	897.442471	449.224873	8
8	832.383561	416.695419	815.357012	408.182144	814.372996	407.690136	D	***844.415922***	422.711599	827.389373	414.198324	826.405357	413.706316	7
9	933.431240	467.219258	916.404691	458.705984	915.420675	458.213976	T	***729.388979***	365.198127	712.362430	356.684853	711.378414	356.192845	6
10	1030.484004	515.745640	1013.457455	507.232366	1012.473439	506.740358	P	***628.341300***	314.674288	611.314751	306.161013	610.330735	305.669005	5
11	1159.526597	580.266937	1142.500048	571.753662	1141.516032	571.261654	E	531.288536	266.147906	514.261987	257.634631	513.277971	257.142623	4
12	1273.569524	637.288400	1256.542975	628.775126	1255.558959	628.283118	N	***402.245943***	201.626609	385.219394	193.113335			3
13	1386.653588	693.830432	1369.627039	685.317158	1368.643023	684.825149	L	288.203016	144.605146	271.176467	136.091871			2
14							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of QSFTMVADTPENLR
(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	1623.756271	0.012617	QSFTMVADTPENLR

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

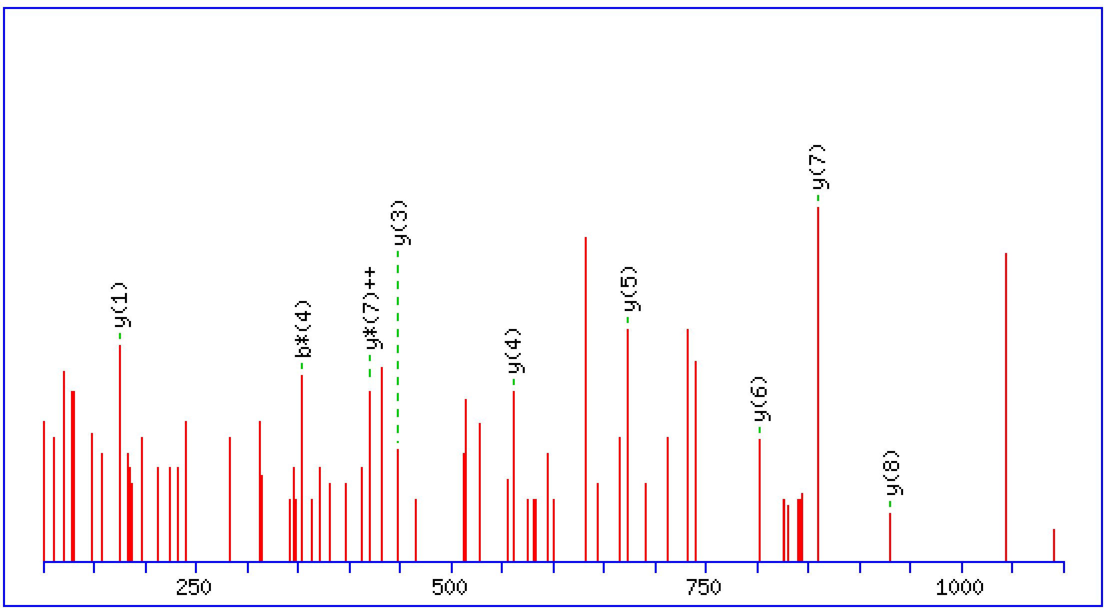
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NAGKLICVR**
Found in **ODB2_HUMAN**, Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial OS=Homo sapiens GN=DBT PE=1 SV=3

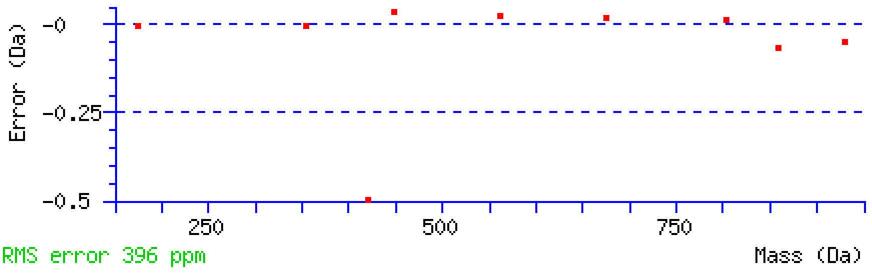
Match to Query 20027: 1043.582848 from(522.798700,2+) rtinseconds(2687) index(35281)
Title: Locus:1.1.1.2461.14
Data file 2011-11-10 - TFD - EP 3-2.mgf

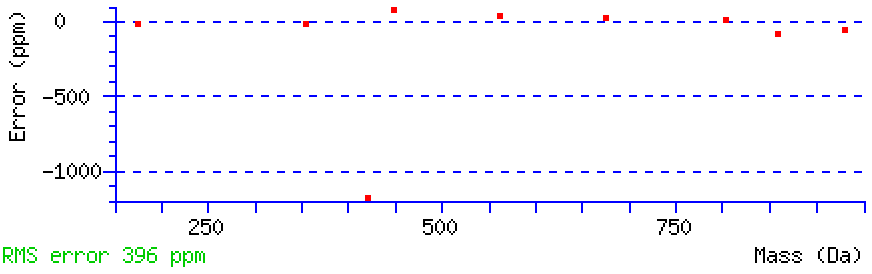
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1043.590958
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.0046
Matches : 9/64 fragment ions using 26 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	115.050203	58.028740	98.023654	49.515465	N					9
2	186.087317	93.547296	169.060768	85.034022	A	***930.555334***	465.781305	913.528785	457.268031	8
3	243.108781	122.058028	226.082232	113.544754	G	***859.518220***	430.262748	842.491671	421.749474	7
4	371.203744	186.105510	354.177195	177.592235	K	***802.496756***	401.752016	785.470207	393.238742	6
5	484.287808	242.647542	467.261259	234.134267	L	***674.401793***	337.704535	657.375244	329.191260	5
6	597.371872	299.189574	580.345323	290.676300	I	***561.317729***	281.162503	544.291180	272.649228	4
7	771.418171	386.212724	754.391622	377.699449	C	***448.233665***	224.620470	431.207116	216.107196	3
8	870.486585	435.746931	853.460036	427.233656	V	274.187366	137.597321	257.160817	129.084047	2
9					R	***175.118952***	88.063114	158.092403	79.549840	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.6	1043.590958	-0.008110	NAGKLICVR
7.3	1043.586258	-0.003410	QEIIVLDSK
3.3	1043.576370	0.006478	KGGADWLGLK
3.3	1043.576355	0.006493	LLSWLQER
2.8	1043.579727	0.003121	NKPKMVPSK
1.8	1043.579727	0.003121	NKPKMVPSK
1.6	1043.576370	0.006478	SYAGVAVIHK

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

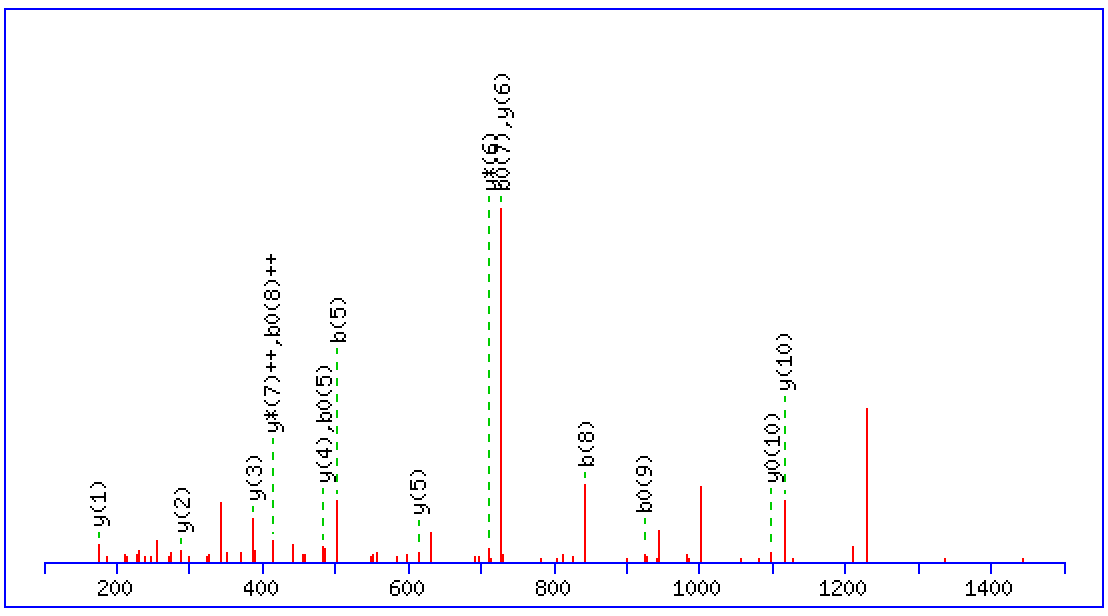
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSTSPDEPVPR**
Found in **S27A6_HUMAN**, Long-chain fatty acid transport protein 6 OS=Homo sapiens GN=SLC27A6 PE=1 SV=1

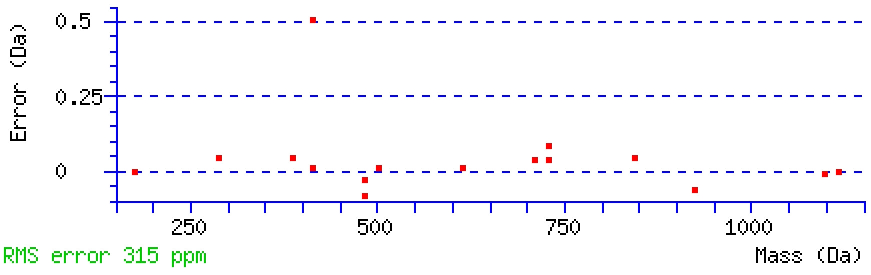
Match to Query 34659: 1228.591568 from(615.303060,2+) rtinseconds(2105) index(22945)
Title: Locus:1.1.1.2020.38
Data file 2011-11-12 - TFD - EP 5-6.mgf

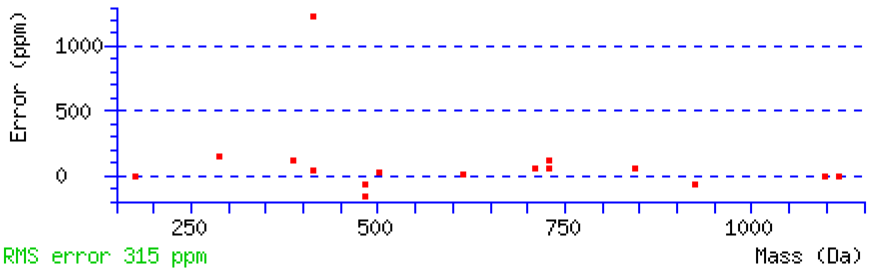
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1228.593552
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P5      : Oxidation (P)
P10     : Oxidation (P)
Ions Score: 51  Expect: 5.7e-005
Matches : 16/90 fragment ions using 21 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							11
2	201.123368	101.065322	183.112803	92.060039	S	***1116.516759***	558.762018	1099.490210	550.248743	1098.506194	549.756735	10
3	302.171047	151.589161	284.160482	142.583879	T	1029.484731	515.246004	1012.458182	506.732729	1011.474166	506.240721	9
4	389.203075	195.105175	371.192510	186.099893	S	928.437052	464.722164	911.410503	456.208890	910.426487	455.716882	8
5	**502.250754**	251.629015	484.240189	242.623732	P	841.405024	421.206150	824.378475	412.692876	823.394459	412.200868	7
6	617.277697	309.142487	599.267132	300.137204	D	***728.357345***	364.682311	711.330796	356.169036	710.346780	355.677028	6
7	746.320290	373.663783	728.309725	364.658501	E	***613.330402***	307.168839	596.303853	298.655565	595.319837	298.163557	5
8	**843.373054**	422.190165	825.362489	413.184883	P	***484.287809***	242.647542	467.261260	234.134268			4
9	942.441468	471.724372	924.430903	462.719090	V	***387.235045***	194.121160	370.208496	185.607886			3
10	1055.489147	528.248212	1037.478582	519.242929	P	***288.166631***	144.586953	271.140082	136.073679			2
11					R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.5	1228.593552	-0.001984	LSTSPDEPVPR
26.4	1228.593552	-0.001984	LSTSPDEPVPR
10.6	1228.593552	-0.001984	LSTSPDEPVPR
5.8	1228.587006	0.004562	EHLNSMVVER
4.7	1228.593521	-0.001953	VEAEPAEVTER
4.5	1228.598236	-0.006668	INVMNDRDPR
4.4	1228.582291	0.009277	LEAPDADELPK
2.0	1228.593521	-0.001953	EGSKDNPEPLK
1.1	1228.593521	-0.001953	DLEAESSPPLR
1.0	1228.580475	0.011093	LNCRPCPPR

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

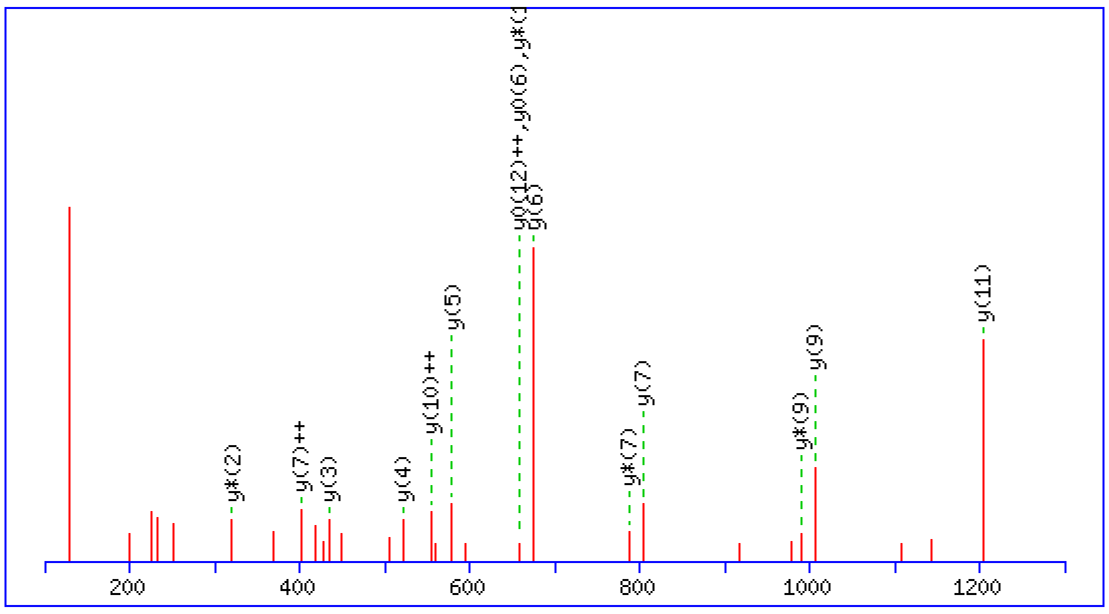
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AKPTSDKPGSPYR**
Found in **ACSL4_HUMAN**, Long-chain-fatty-acid--CoA ligase 4 OS=Homo sapiens GN=ACSL4 PE=1 SV=2

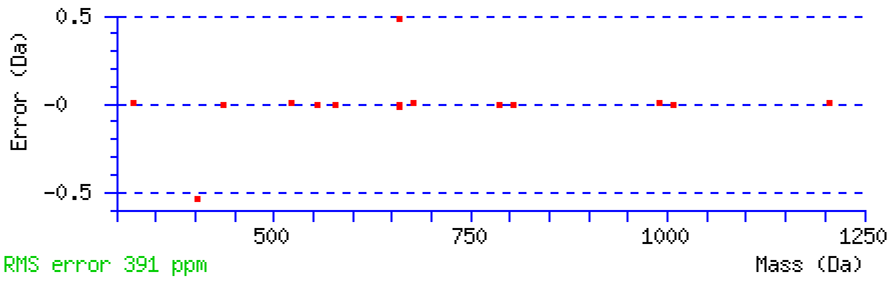
Match to Query 751243: 1402.718412 from(468.580080,3+) rtinseconds(777) index(656683)
Title: Locus:1.1.1.959.5
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

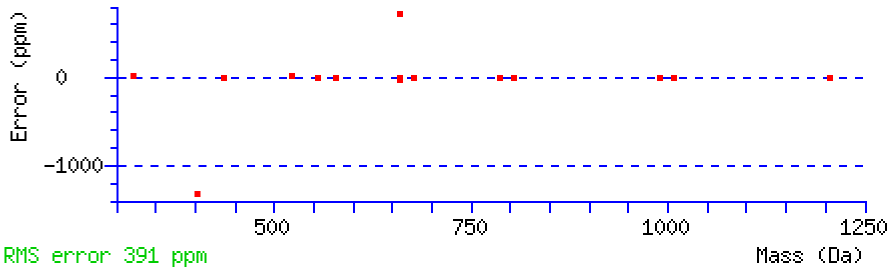
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1402.720459
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 49 **Expect:** 4.9e-005
Matches : 15/130 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.044390	36.525833					A							13
2	200.139353	100.573315	183.112804	92.060040			K	1332.690641	666.848959	1315.664092	658.335684	1314.680076	657.843676	12
3	297.192117	149.099696	280.165568	140.586422			P	***1204.595678***	602.801477	1187.569129	594.288203	1186.585113	593.796195	11
4	398.239796	199.623536	381.213247	191.110262	380.229231	190.618254	T	1107.542914	554.275095	1090.516365	545.761821	1089.532349	545.269813	10
5	485.271824	243.139550	468.245275	234.626275	467.261259	234.134267	S	***1006.495235***	503.751256	989.468686	495.237981	988.484670	494.745973	9
6	600.298767	300.653022	583.272218	292.139747	582.288202	291.647739	D	919.463207	460.235242	902.436658	451.721967	901.452642	451.229959	8
7	728.393730	364.700503	711.367181	356.187229	710.383165	355.695221	K	***804.436264***	402.721770	787.409715	394.208496	786.425699	393.716488	7
8	825.446494	413.226885	808.419945	404.713611	807.435929	404.221603	P	***676.341301***	338.674289	659.314752	330.161014	658.330736	329.669006	6
9	882.467958	441.737617	865.441409	433.224343	864.457393	432.732335	G	***579.288537***	290.147907	562.261988	281.634632	561.277972	281.142624	5
10	969.499986	485.253631	952.473437	476.740357	951.489421	476.248349	S	***522.267073***	261.637175	505.240524	253.123900	504.256508	252.631892	4
11	1066.552750	533.780013	1049.526201	525.266739	1048.542185	524.774731	P	***435.235045***	218.121161	418.208496	209.607886			3
12	1229.616079	615.311678	1212.589530	606.798403	1211.605514	606.306395	Y	338.182281	169.594778	321.155732	161.081504			2
13							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.3	1402.720459	-0.002047	AKPTSDKPGSPYR
3.2	1402.719147	-0.000735	TGPEDTTVLIETK
1.5	1402.723831	-0.005419	SLSGCPLADKSLR
0.6	1402.720459	-0.002047	QALNITPEQFSR

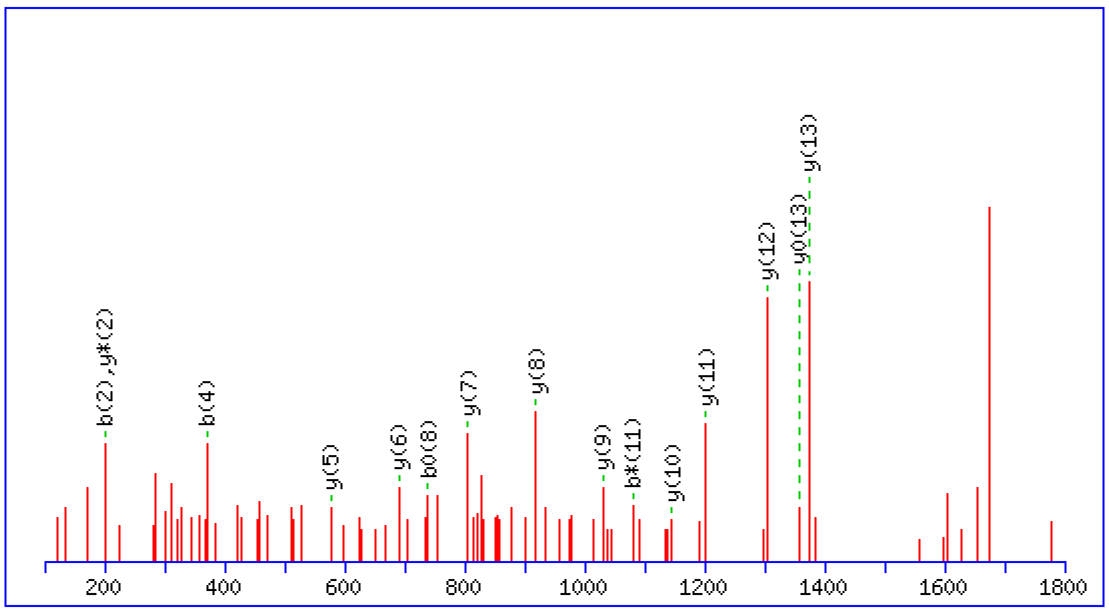
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SLVATGNLLDLEETAK**
Found in **ARH_HUMAN**, Low density lipoprotein receptor adapter protein 1 OS=Homo sapiens GN=LDLRAP1 PE=1 SV=3

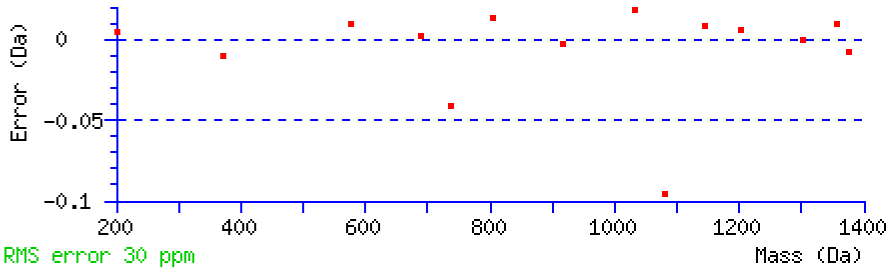
Match to Query 53740: 1672.893588 from(837.454070,2+) rtinseconds(3209) index(45465)
Title: Locus:1.1.1.2562.46
Data file 2011-11-10 - TFD - EP 3-4.mgf

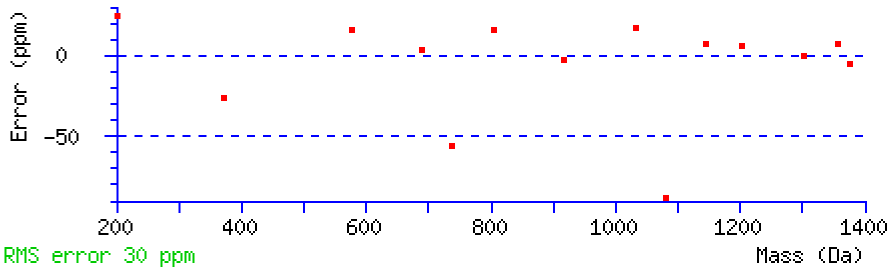
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1672.888306
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 53  Expect: 4.6e-005
Matches : 15/164 fragment ions using 30 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							16
2	**201.123368**	101.065322			183.112803	92.060039	L	1586.863580	793.935428	1569.837031	785.422154	1568.853015	784.930145	15
3	300.191782	150.599529			282.181217	141.594247	V	1473.779516	737.393396	1456.752967	728.880122	1455.768951	728.388114	14
4	**371.228896**	186.118086			353.218331	177.112804	A	***1374.711102***	687.859189	1357.684553	679.345915	1356.700537	678.853906	13
5	472.276575	236.641926			454.266010	227.636643	T	***1303.673988***	652.340632	1286.647439	643.827358	1285.663423	643.335350	12
6	529.298039	265.152658			511.287474	256.147375	G	***1202.626309***	601.816793	1185.599760	593.303518	1184.615744	592.811510	11
7	643.340966	322.174121	626.314417	313.660847	625.330401	313.168839	N	***1145.604845***	573.306061	1128.578296	564.792786	1127.594280	564.300778	10
8	756.425030	378.716153	739.398481	370.202879	738.414465	369.710871	L	***1031.561918***	516.284597	1014.535369	507.771323	1013.551353	507.279315	9
9	869.509094	435.258185	852.482545	426.744911	851.498529	426.252903	L	***918.477854***	459.742565	901.451305	451.229290	900.467289	450.737282	8
10	984.536037	492.771657	967.509488	484.258382	966.525472	483.766374	D	***805.393790***	403.200533	788.367241	394.687258	787.383225	394.195250	7
11	1097.620101	549.313689	1080.593552	540.800414	1079.609536	540.308406	L	***690.366847***	345.687062	673.340298	337.173787	672.356282	336.681779	6
12	1226.662694	613.834985	1209.636145	605.321710	1208.652129	604.829702	E	***577.282783***	289.145030	560.256234	280.631755	559.272218	280.139747	5
13	1355.705287	678.356282	1338.678738	669.843007	1337.694722	669.350999	E	448.240190	224.623733	431.213641	216.110459	430.229625	215.618451	4
14	1456.752966	728.880121	1439.726417	720.366847	1438.742401	719.874839	T	319.197597	160.102436	302.171048	151.589162	301.187032	151.097154	3
15	1527.790080	764.398678	1510.763531	755.885404	1509.779515	755.393396	A	218.149918	109.578597	201.123369	101.065322			2
16							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
53.3	1672.888306	0.005282	SLVATGNLLDLEETAK
7.4	1672.881790	0.011798	AIDATLMSPRGIAVDK
2.4	1672.881790	0.011798	AIDATLMSPRGIAVDK

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

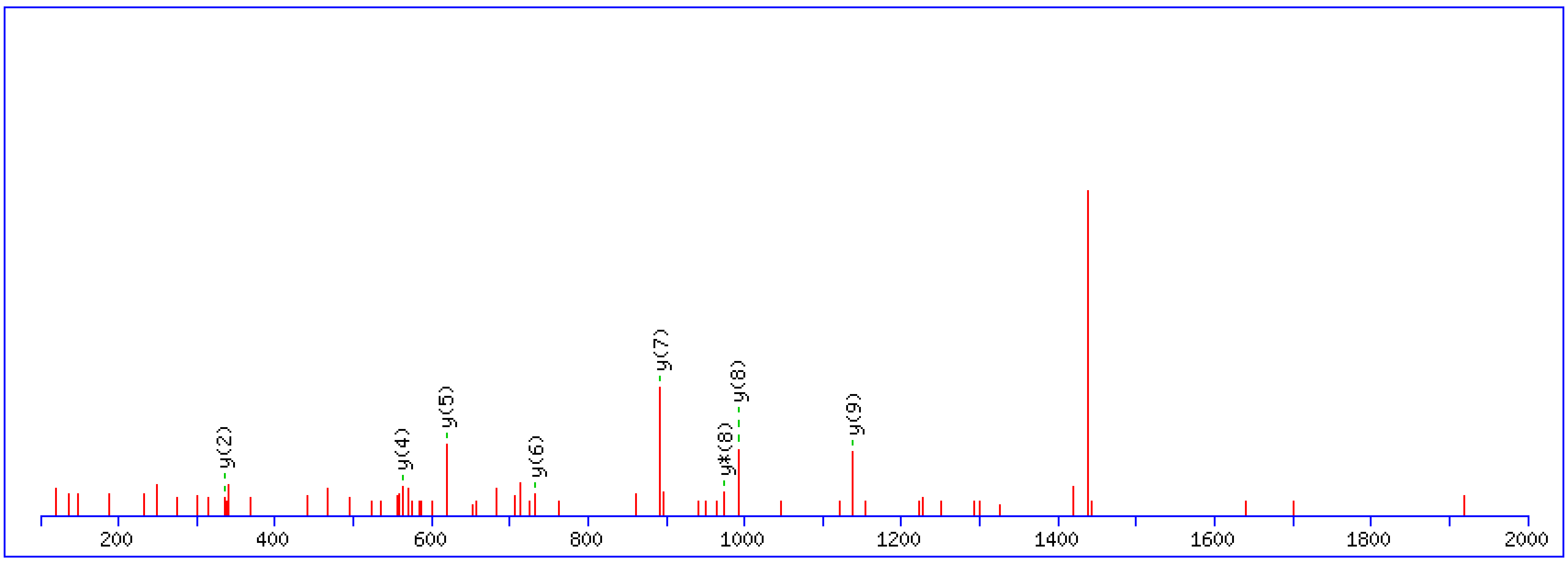
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SVLFVCLGNICR**
Found in **PPAC_HUMAN**, Low molecular weight phosphotyrosine protein phosphatase OS=Homo sapiens GN=ACP1 PE=1 SV=3

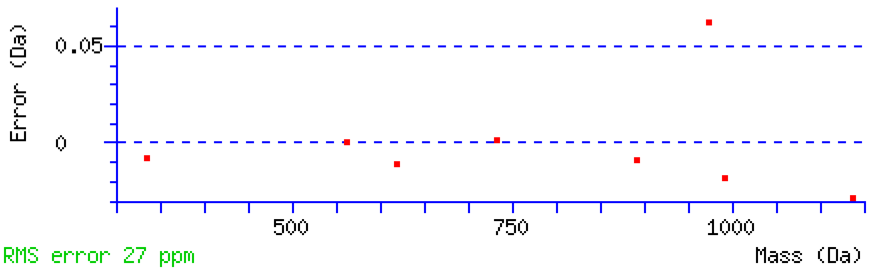
Match to Query 41240: 1436.713308 from(719.363930,2+) rtinseconds(3284) index(46745)
Title: Locus:1.1.1.1690.25
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 3.mgf

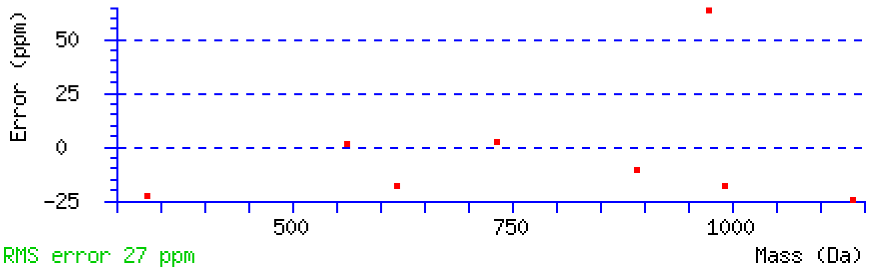
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1436.726837
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.0018
Matches : 8/94 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	88.039304	44.523290			70.028739	35.518008	S					12
2	187.107718	94.057497			169.097153	85.052214	V	1350.702075	675.854675	1333.675526	667.341401	11
3	300.191782	150.599529			282.181217	141.594247	L	1251.633661	626.320469	1234.607112	617.807194	10
4	447.260196	224.133736			429.249631	215.128454	F	*1138.549597*	569.778437	1121.523048	561.265162	9
5	546.328610	273.667943			528.318045	264.662661	V	*991.481183*	496.244230	974.454634	487.730955	8
6	706.359259	353.683268			688.348694	344.677985	C	*892.412769*	446.710023	875.386220	438.196748	7
7	819.443323	410.225300			801.432758	401.220017	L	*732.382120*	366.694698	715.355571	358.181423	6
8	876.464787	438.736032			858.454222	429.730749	G	*619.298056*	310.152666	602.271507	301.639391	5
9	990.507714	495.757495	973.481165	487.244221	972.497149	486.752213	N	*562.276592*	281.641934	545.250043	273.128659	4
10	1103.591778	552.299527	1086.565229	543.786253	1085.581213	543.294244	I	448.233665	224.620470	431.207116	216.107196	3
11	1263.622427	632.314852	1246.595878	623.801577	1245.611862	623.309569	C	*335.149601*	168.078438	318.123052	159.565164	2
12							R	175.118952	88.063114	158.092403	79.549839	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.1	1436.726837	-0.013529	SVLFVCLGNICR
1.8	1436.704376	0.008932	MPPGIGNTFLIVM
1.8	1436.704376	0.008932	MPPGIGNTFLIVM

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

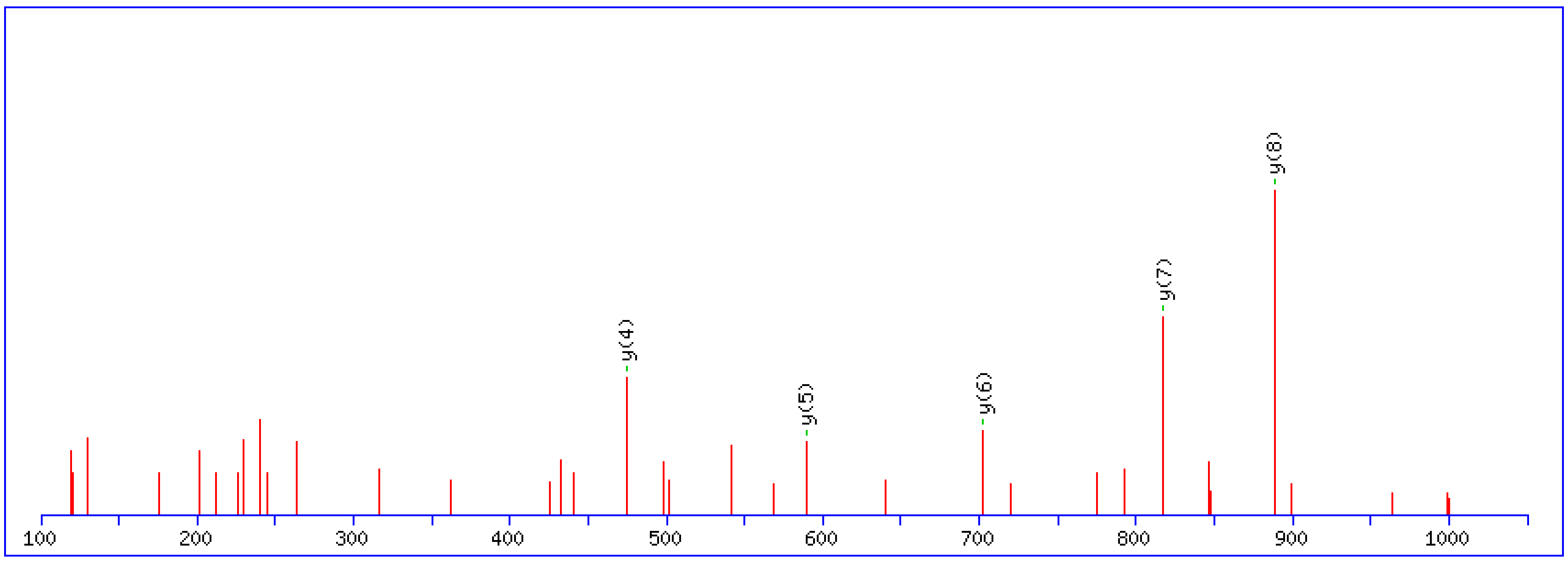
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TQADLDSLVR**
Found in **DCXR_HUMAN**, L-xylulose reductase OS=Homo sapiens GN=DCXR PE=1 SV=2

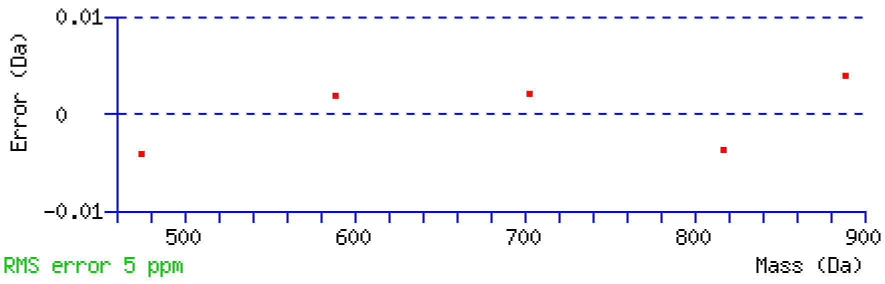
Match to Query 16208: 1116.587008 from(559.300780,2+) rtinseconds(2064) index(23922)
Title: Locus:1.1.1.1168.13
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 2.mgf

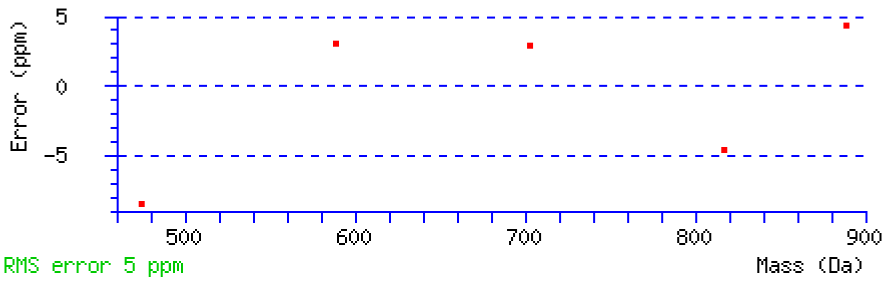
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1050] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1116.577499
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.005
Matches : 5/100 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							10
2	230.113533	115.560405	213.086984	107.047130	212.102968	106.555122	Q	1016.537100	508.772188	999.510551	500.258914	998.526535	499.766906	9
3	301.150647	151.078961	284.124098	142.565687	283.140082	142.073679	A	***888.478522***	444.742899	871.451973	436.229625	870.467957	435.737617	8
4	416.177590	208.592433	399.151041	200.079159	398.167025	199.587151	D	***817.441408***	409.224342	800.414859	400.711068	799.430843	400.219060	7
5	529.261654	265.134465	512.235105	256.621191	511.251089	256.129183	L	***702.414465***	351.710871	685.387916	343.197596	684.403900	342.705588	6
6	644.288597	322.647937	627.262048	314.134662	626.278032	313.642654	D	***589.330401***	295.168839	572.303852	286.655564	571.319836	286.163556	5
7	731.320625	366.163951	714.294076	357.650676	713.310060	357.158668	S	***474.303458***	237.655367	457.276909	229.142092	456.292893	228.650084	4
8	844.404689	422.705983	827.378140	414.192708	826.394124	413.700700	L	387.271430	194.139353	370.244881	185.626079			3
9	943.473103	472.240189	926.446554	463.726915	925.462538	463.234907	V	274.187366	137.597321	257.160817	129.084047			2
10							R	175.118952	88.063114	158.092403	79.549840			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.8	1116.577499	0.009509	TQADLDSLVR
6.8	1116.584885	0.002123	NGLMLPTDIK
4.7	1116.596115	-0.009107	ECVSILPRK
2.7	1116.584885	0.002123	QTLAPEVKTM
1.2	1116.584869	0.002139	EAASNGVLLLM
0.8	1116.592743	-0.005735	QTAFPNALQK

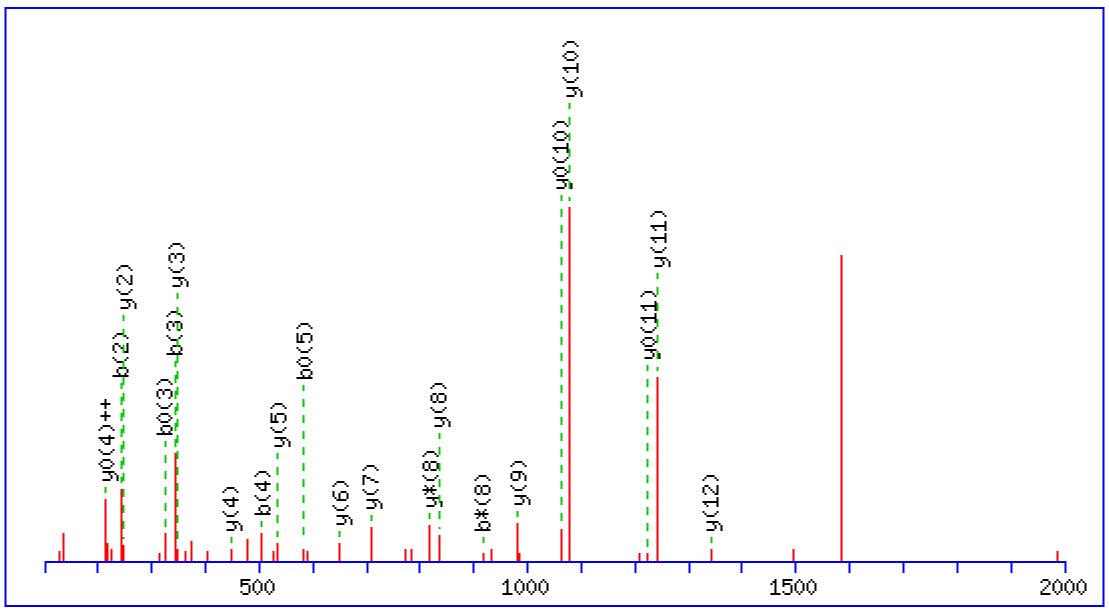
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EIVYPFQGDSTVTK**
Found in **LYPD2_HUMAN**, Ly6/PLAUR domain-containing protein 2 OS=Homo sapiens GN=LYPD2 PE=2 SV=1

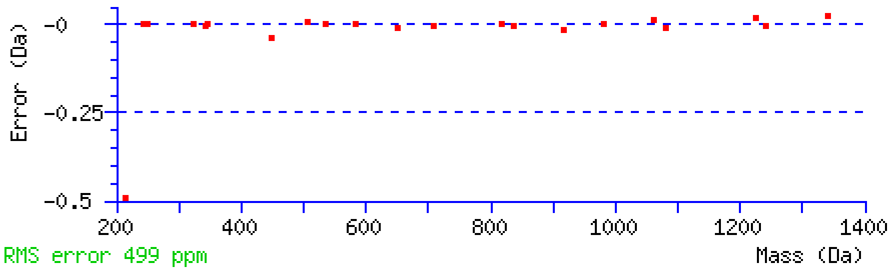
Match to Query 52743: 1582.786088 from(792.400320,2+) rtinseconds(2656) index(32976)
Title: Locus:1.1.1.2269.47
Data file 2011-11-10 - TFD - EP 4-6.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●

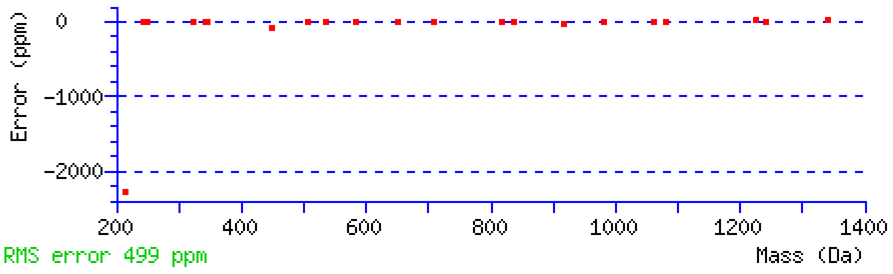


```
Monoisotopic mass of neutral peptide Mr(calc): 1582.787903
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 89  Expect: 1.7e-008
Matches : 21/142 fragment ions using 33 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	E							14
2	**243.133933**	122.070605			225.123368	113.065322	I	1454.752574	727.879925	1437.726025	719.366651	1436.742009	718.874643	13
3	**342.202347**	171.604812			324.191782	162.599529	V	***1341.668510***	671.337893	1324.641961	662.824619	1323.657945	662.332611	12
4	**505.265676**	253.136476			487.255111	244.131194	Y	***1242.600096***	621.803686	1225.573547	613.290412	1224.589531	612.798404	11
5	602.318440	301.662858			584.307875	292.657576	P	***1079.536767***	540.272022	1062.510218	531.758747	1061.526202	531.266739	10
6	749.386854	375.197065			731.376289	366.191783	F	***982.484003***	491.745640	965.457454	483.232365	964.473438	482.740357	9
7	877.445432	439.226354	860.418883	430.713080	859.434867	430.221072	Q	***835.415589***	418.211433	818.389040	409.698158	817.405024	409.206150	8
8	934.466896	467.737086	917.440347	459.223812	916.456331	458.731804	G	***707.357011***	354.182144	690.330462	345.668869	689.346446	345.176861	7
9	1049.493839	525.250558	1032.467290	516.737283	1031.483274	516.245275	D	***650.335547***	325.671412	633.308998	317.158137	632.324982	316.666129	6
10	1136.525867	568.766572	1119.499318	560.253297	1118.515302	559.761289	S	***535.308604***	268.157940	518.282055	259.644666	517.298039	259.152658	5
11	1237.573546	619.290411	1220.546997	610.777137	1219.562981	610.285129	T	***448.276576***	224.641926	431.250027	216.128652	430.266011	215.636644	4
12	1336.641960	668.824618	1319.615411	660.311344	1318.631395	659.819336	V	***347.228897***	174.118087	330.202348	165.604812	329.218332	165.112804	3
13	1437.689639	719.348458	1420.663090	710.835183	1419.679074	710.343175	T	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.578597	2
14							K	147.112804	74.060040	130.086255	65.546765			1



RMS error 499 ppm



RMS error 499 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
88.5	1582.787903	-0.001815	EIVYPFQGDSTVTK
12.4	1582.792603	-0.006515	KNTSAHFLPMVVHS
6.3	1582.789230	-0.003142	KYGVAVQDFAGSWR
5.4	1582.792603	-0.006515	KNTSAHFLPMVVHS
0.3	1582.788574	-0.002486	QAKLAVQMDVHDGR

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

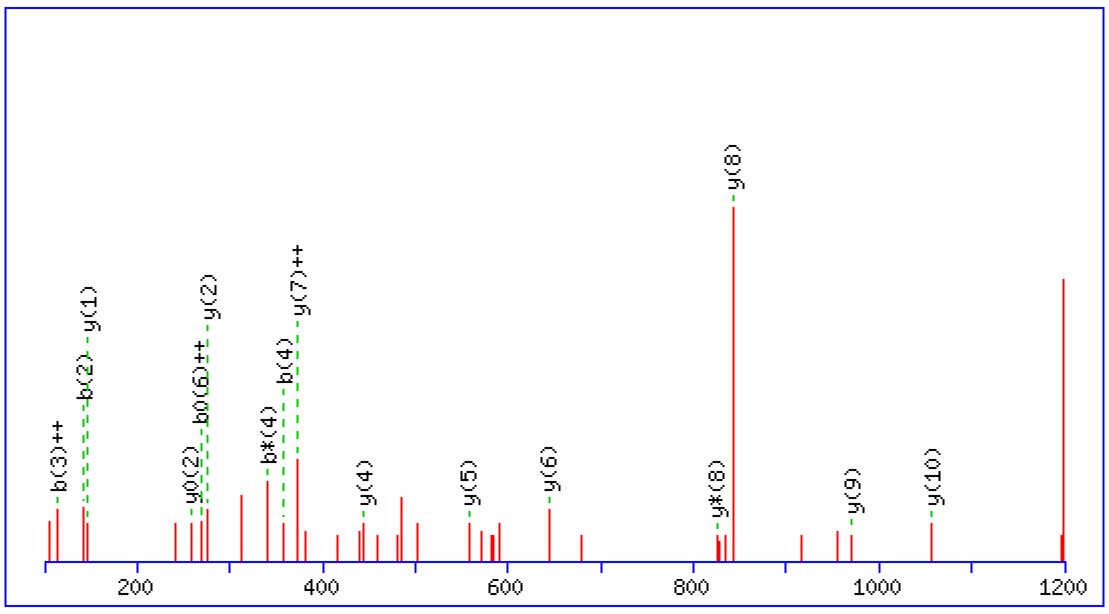
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AASQPTSLAPEK**
Found in **MBOA7_HUMAN**, Lysophospholipid acyltransferase 7 OS=Homo sapiens GN=MBOAT7 PE=1 SV=2

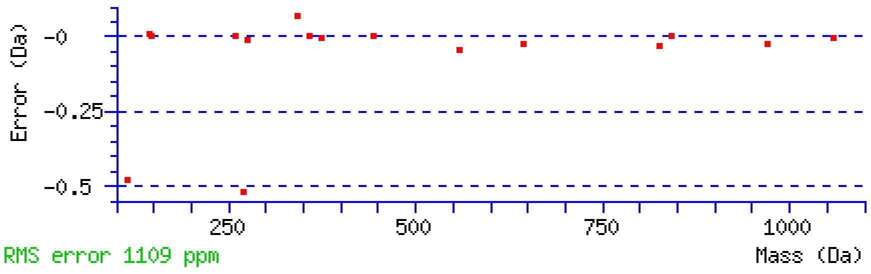
Match to Query 29169: 1198.622708 from(600.318630,2+) rtinseconds(1229) index(8583)
Title: Locus:1.1.1.1791.44
Data file 2011-11-12 - TFD - EP 6-1.mgf

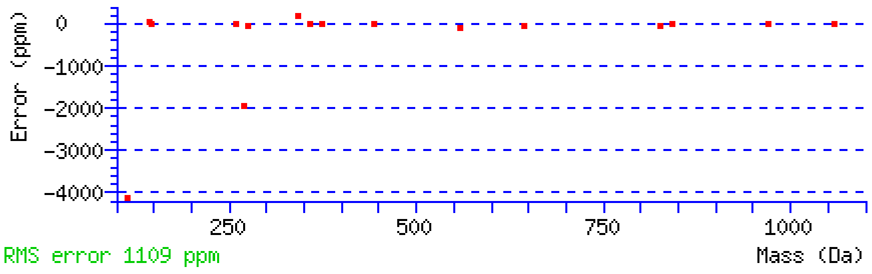
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1198.619339
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 64 **Expect:** 5.4e-006
Matches : 17/120 fragment ions using 31 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							12
2	**143.081504**	72.044390					A	1128.589530	564.798403	1111.562981	556.285129	1110.578965	555.793121	11
3	230.113532	115.560404			212.102967	106.555121	S	***1057.552416***	529.279846	1040.525867	520.766572	1039.541851	520.274564	10
4	**358.172110**	179.589693	341.145561	171.076419	340.161545	170.584411	Q	***970.520388***	485.763832	953.493839	477.250558	952.509823	476.758550	9
5	455.224874	228.116075	438.198325	219.602801	437.214309	219.110793	P	***842.461810***	421.734543	825.435261	413.221269	824.451245	412.729261	8
6	556.272553	278.639915	539.246004	270.126640	538.261988	269.634632	T	745.409046	373.208161	728.382497	364.694887	727.398481	364.202879	7
7	643.304581	322.155929	626.278032	313.642654	625.294016	313.150646	S	***644.361367***	322.684322	627.334818	314.171047	626.350802	313.679039	6
8	756.388645	378.697961	739.362096	370.184686	738.378080	369.692678	L	***557.329339***	279.168308	540.302790	270.655033	539.318774	270.163025	5
9	827.425759	414.216518	810.399210	405.703243	809.415194	405.211235	A	***444.245275***	222.626275	427.218726	214.113001	426.234710	213.620993	4
10	924.478523	462.742900	907.451974	454.229625	906.467958	453.737617	P	***373.208161***	187.107719	356.181612	178.594444	355.197596	178.102436	3
11	1053.521116	527.264196	1036.494567	518.750922	1035.510551	518.258914	E	***276.155397***	138.581336	259.128848	130.068062	258.144832	129.576054	2
12							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
63.5	1198.619339	0.003369	AASQPTSLAPEK
17.8	1198.630600	-0.007892	AASQTPSVVPSR
7.1	1198.612839	0.009869	DIGHLTRCTL
1.1	1198.619339	0.003369	DLQASLQEPAK

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

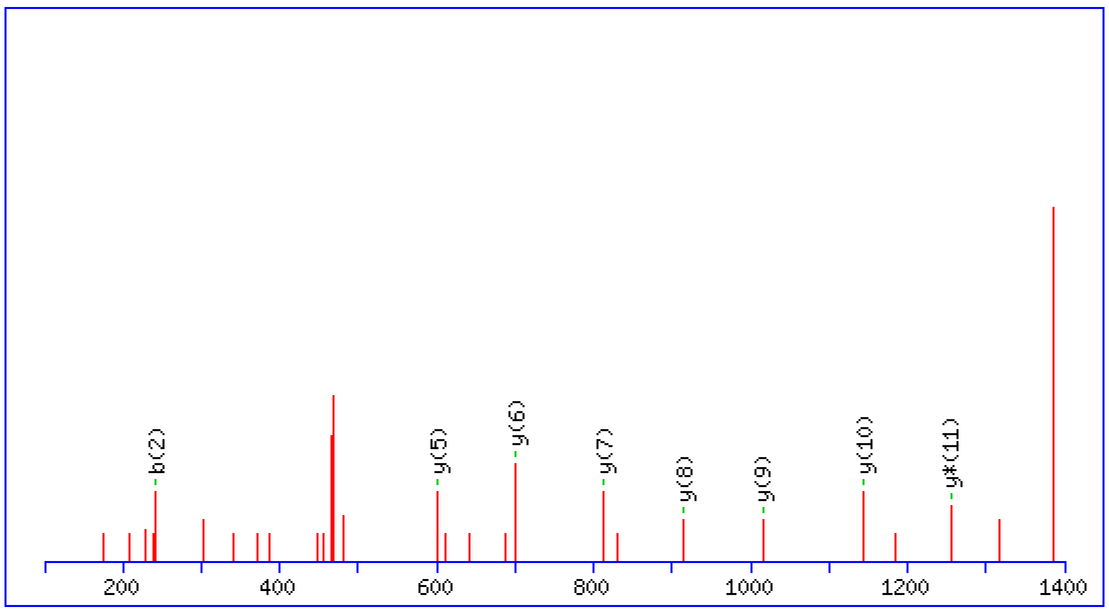
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LQETTLVANQLR**
Found in **MA2B1_HUMAN**, Lysosomal alpha-mannosidase OS=Homo sapiens GN=MAN2B1 PE=1 SV=3

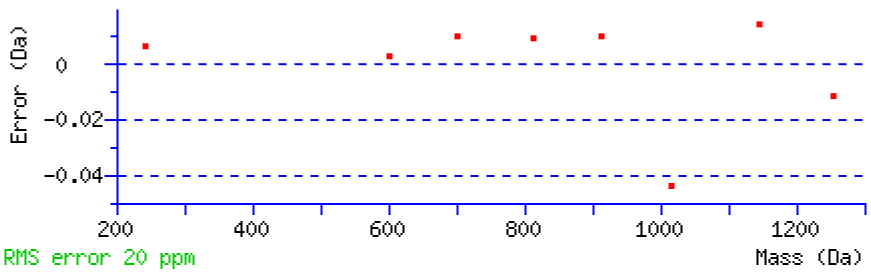
Match to Query 34616: 1384.767848 from(693.391200,2+) rtinseconds(2303) index(22381)
Title: Locus:1.1.1.2285.44
Data file 2011-11-10 - TFD - EP 3-7.mgf

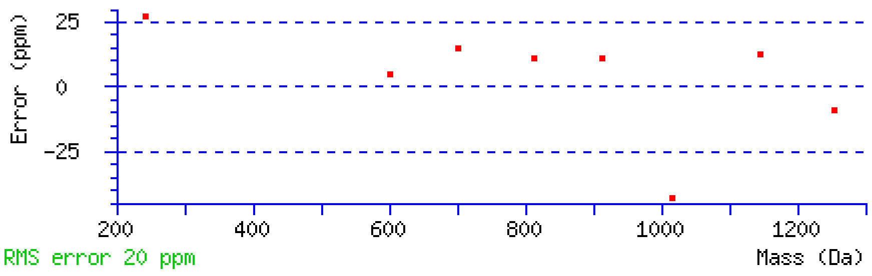
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1384.767410
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.0019
Matches : 8/112 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^0	y^{0++}	#
1	114.091340	57.549308					L							12
2	242.149918	121.578597	225.123369	113.065323			Q	1272.690642	636.848959	1255.664093	628.335685	1254.680077	627.843677	11
3	371.192511	186.099894	354.165962	177.586619	353.181946	177.094611	E	***1144.632064***	572.819670	1127.605515	564.306396	1126.621499	563.814387	10
4	472.240190	236.623733	455.213641	228.110459	454.229625	227.618451	T	***1015.589471***	508.298373	998.562922	499.785099	997.578906	499.293091	9
5	573.287869	287.147573	556.261320	278.634298	555.277304	278.142290	T	***914.541792***	457.774534	897.515243	449.261259	896.531227	448.769251	8
6	686.371933	343.689605	669.345384	335.176330	668.361368	334.684322	L	***813.494113***	407.250694	796.467564	398.737420			7
7	785.440347	393.223812	768.413798	384.710537	767.429782	384.218529	V	***700.410049***	350.708662	683.383500	342.195388			6
8	856.477461	428.742369	839.450912	420.229094	838.466896	419.737086	A	***601.341635***	301.174455	584.315086	292.661181			5
9	970.520388	485.763832	953.493839	477.250558	952.509823	476.758550	N	530.304521	265.655898	513.277972	257.142624			4
10	1098.578966	549.793121	1081.552417	541.279847	1080.568401	540.787839	Q	416.261594	208.634435	399.235045	200.121160			3
11	1211.663030	606.335153	1194.636481	597.821879	1193.652465	597.329870	L	288.203016	144.605146	271.176467	136.091871			2
12							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.7	1384.767410	0.000438	LQETTLVANQLR
9.8	1384.756180	0.011668	LKELPDTVGELR
4.4	1384.763550	0.004298	KIEVVMAEPLEK
1.3	1384.756195	0.011653	IQIVTAVDASGSPK
0.6	1384.756210	0.011638	TTPDIRITVPPK

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

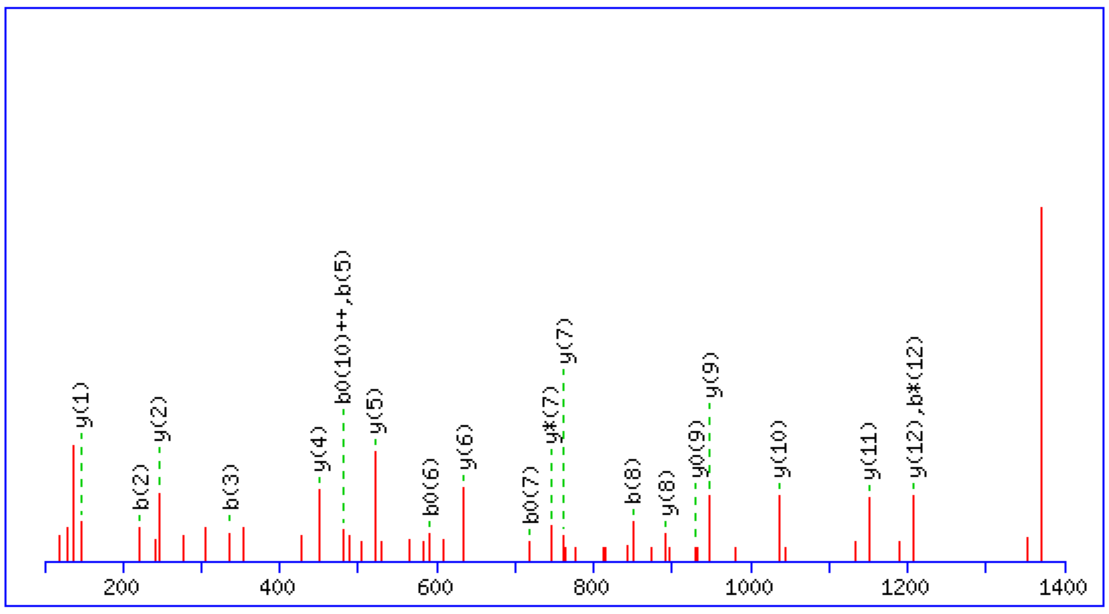
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YGDSGEQIAGFVK**
Found in **PPGB_HUMAN**, Lysosomal protective protein OS=Homo sapiens GN=CTSA PE=1 SV=2

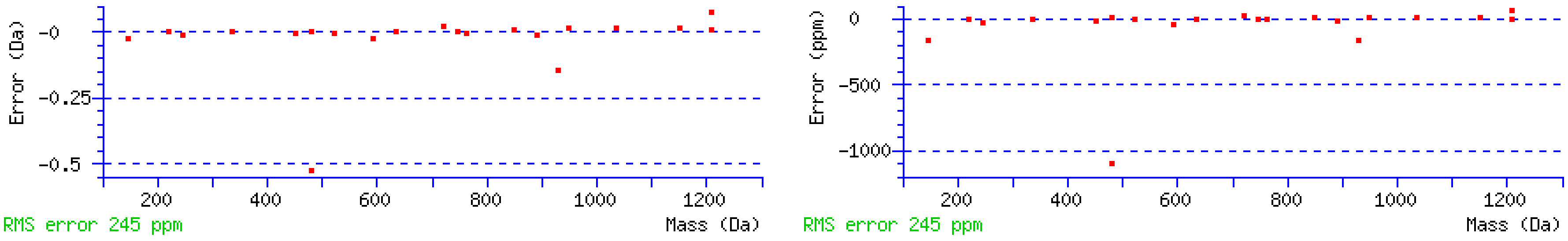
Match to Query 42734: 1369.649608 from(685.832080,2+) rtinseconds(2414) index(28853)
Title: Locus:1.1.1.2138.46
Data file 2011-11-12 - TFD - EP 5-6.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1369.651398
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 115 **Expect:** 3.5e-011
Matches : 21/114 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	164.070605	82.538940					Y							13
2	**221.092069**	111.049673					G	***1207.595344***	604.301310	1190.568795	595.788036	1189.584779	595.296028	12
3	**336.119012**	168.563144			318.108447	159.557862	D	***1150.573880***	575.790578	1133.547331	567.277304	1132.563315	566.785296	11
4	423.151040	212.079158			405.140475	203.073876	S	***1035.546937***	518.277107	1018.520388	509.763832	1017.536372	509.271824	10
5	**480.172504**	240.589890			462.161939	231.584608	G	***948.514909***	474.761093	931.488360	466.247818	930.504344	465.755810	9
6	609.215097	305.111187			591.204532	296.105904	E	***891.493445***	446.250361	874.466896	437.737086	873.482880	437.245078	8
7	737.273675	369.140476	720.247126	360.627201	719.263110	360.135193	Q	***762.450852***	381.729064	745.424303	373.215790			7
8	**850.357739**	425.682508	833.331190	417.169233	832.347174	416.677225	I	***634.392274***	317.699775	617.365725	309.186501			6
9	921.394853	461.201065	904.368304	452.687790	903.384288	452.195782	A	***521.308210***	261.157743	504.281661	252.644469			5
10	978.416317	489.711797	961.389768	481.198522	960.405752	480.706514	G	***450.271096***	225.639186	433.244547	217.125912			4
11	1125.484731	563.246004	1108.458182	554.732729	1107.474166	554.240721	F	393.249632	197.128454	376.223083	188.615180			3
12	1224.553145	612.780211	1207.526596	604.266936	1206.542580	603.774928	V	***246.181218***	123.594247	229.154669	115.080973			2
13							K	***147.112804***	74.060040	130.086255	65.546765			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
114.7	1369.651398	-0.001790	YGDSGEQIAGFVK
9.7	1369.640823	0.008785	YGRCDALTASSR
7.9	1369.662613	-0.013005	NFENTRESFVK

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

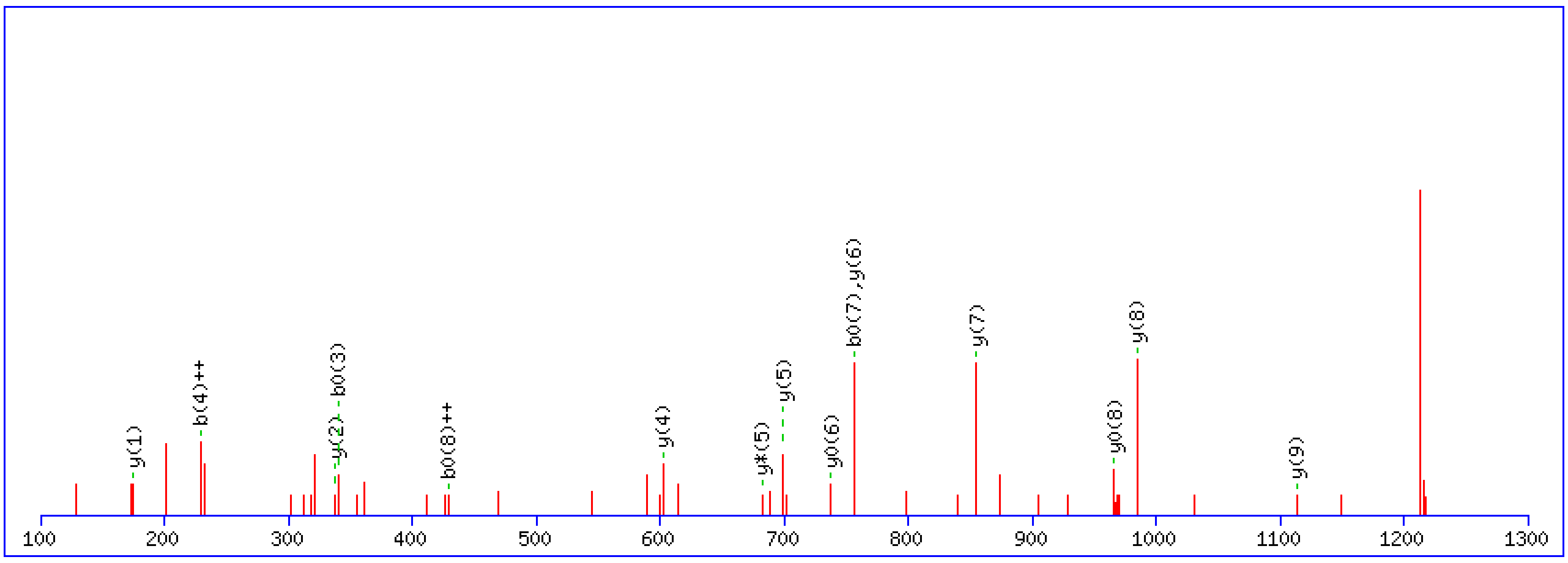
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VEEVGPYTYR**
Found in **SCRB2_HUMAN**, Lysosome membrane protein 2 OS=Homo sapiens GN=SCARB2 PE=1 SV=2

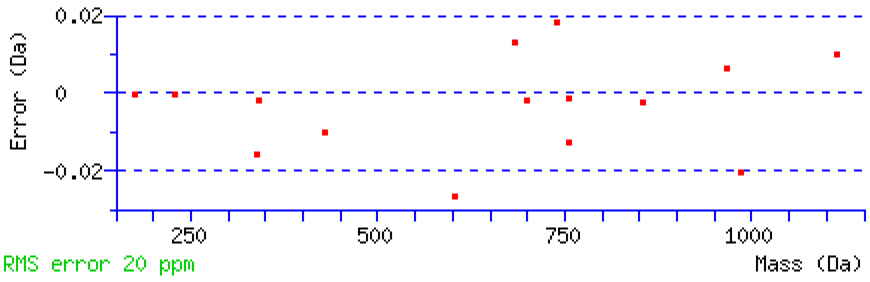
Match to Query 31847: 1211.582788 from(606.798670,2+) rtinseconds(1893) index(21169)
Title: Locus:1.1.1.1110.32
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 1.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1300] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●

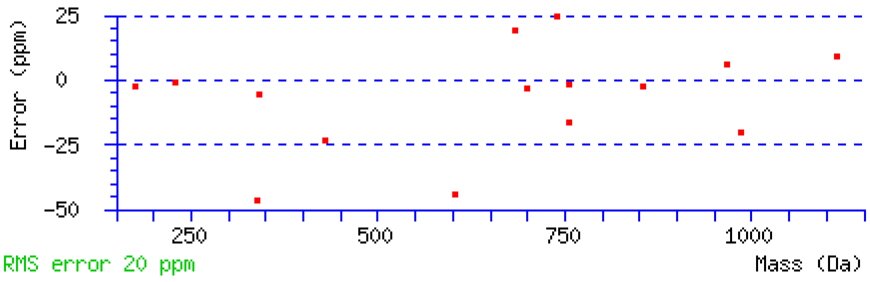


Monoisotopic mass of neutral peptide Mr(calc): 1211.582245
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 44 **Expect:** 0.00021
Matches : 16/84 fragment ions using 29 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483			V							10
2	229.118283	115.062780	211.107718	106.057497	E	***1113.521117***	557.264197	1096.494568	548.750922	1095.510552	548.258914	9
3	358.160876	179.584076	340.150311	170.578794	E	***984.478524***	492.742900	967.451975	484.229626	966.467959	483.737618	8
4	457.229290	229.118283	439.218725	220.113001	V	***855.435931***	428.221604	838.409382	419.708329	837.425366	419.216321	7
5	514.250754	257.629015	496.240189	248.623733	G	***756.367517***	378.687397	739.340968	370.174122	738.356952	369.682114	6
6	611.303518	306.155397	593.292953	297.150115	P	***699.346053***	350.176665	682.319504	341.663390	681.335488	341.171382	5
7	774.366847	387.687062	756.356282	378.681779	Y	***602.293289***	301.650283	585.266740	293.137008	584.282724	292.645000	4
8	875.414526	438.210901	857.403961	429.205619	T	439.229960	220.118618	422.203411	211.605344	421.219395	211.113336	3
9	1038.477855	519.742566	1020.467290	510.737283	Y	***338.182281***	169.594778	321.155732	161.081504			2
10					R	***175.118952***	88.063114	158.092403	79.549839			1



RMS error 20 ppm



RMS error 20 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.1	1211.582245	0.000543	VEEVGPYTYR
4.6	1211.571701	0.011087	KNPAPQCPPR
4.1	1211.578201	0.004587	DLEAHIDSANK
0.7	1211.585602	-0.002814	VENNMVSLYK

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

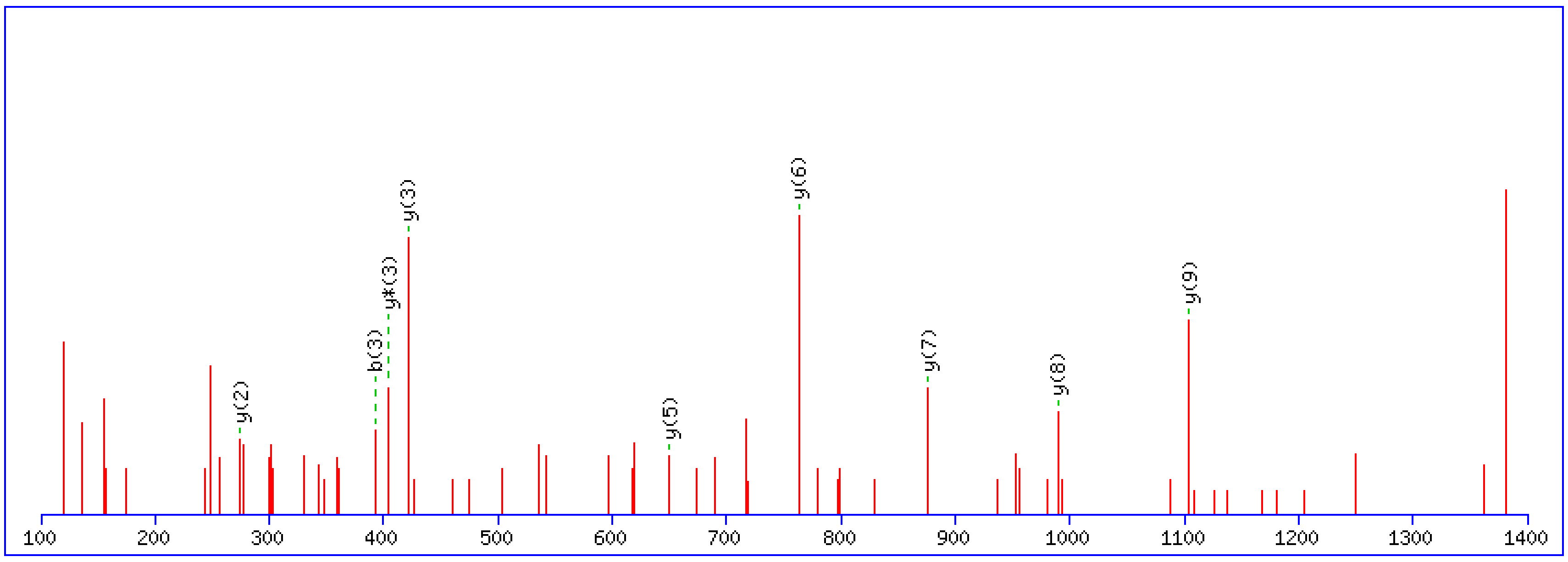
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YLDLILNDFVR**
Found in **SYK_HUMAN**, Lysyl-tRNA synthetase OS=Homo sapiens GN=KARS PE=1 SV=3

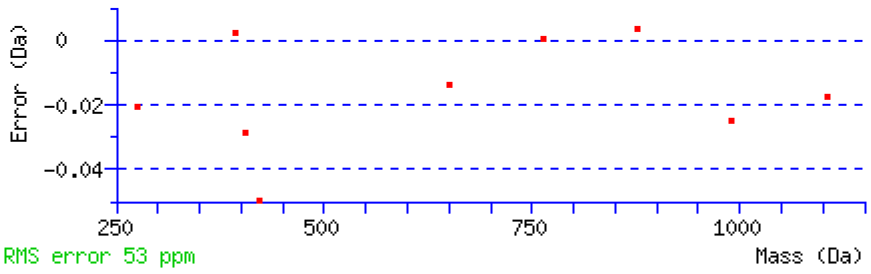
Match to Query 35076: 1379.751968 from(690.883260,2+) rtinseconds(3974) index(59781)
Title: Locus:1.1.1.1885.23
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 2.mgf

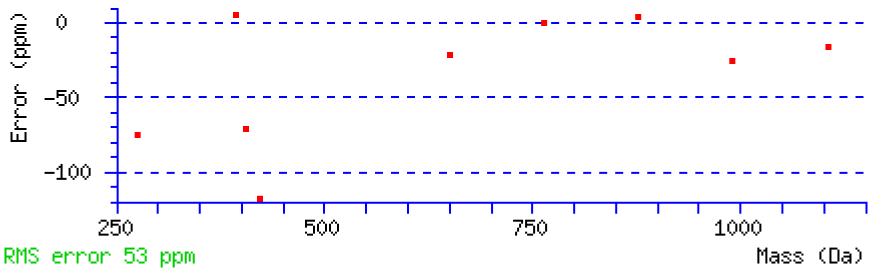
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1379.744888
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.0081
Matches : 9/98 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	164.070605	82.538940					**Y**							11
2	277.154669	139.080973					**L**	1217.688849	609.348063	1200.662300	600.834788	1199.678284	600.342780	10
3	392.181612	196.594444			374.171047	187.589162	**D**	***1104.604785***	552.806031	1087.578236	544.292756	1086.594220	543.800748	9
4	505.265676	253.136476			487.255111	244.131194	**L**	***989.577842***	495.292559	972.551293	486.779285	971.567277	486.287277	8
5	618.349740	309.678508			600.339175	300.673226	**I**	***876.493778***	438.750527	859.467229	430.237253	858.483213	429.745245	7
6	731.433804	366.220540			713.423239	357.215258	**L**	***763.409714***	382.208495	746.383165	373.695221	745.399149	373.203213	6
7	845.476731	423.242004	828.450182	414.728729	827.466166	414.236721	**N**	***650.325650***	325.666463	633.299101	317.153189	632.315085	316.661181	5
8	960.503674	480.755475	943.477125	472.242201	942.493109	471.750193	**D**	536.282723	268.645000	519.256174	260.131725	518.272158	259.639717	4
9	1107.572088	554.289682	1090.545539	545.776408	1089.561523	545.284400	**F**	***421.255780***	211.131528	404.229231	202.618254			3
10	1206.640502	603.823889	1189.613953	595.310615	1188.629937	594.818607	**V**	***274.187366***	137.597321	257.160817	129.084047			2
11							**R**	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.1	1379.744888	0.007080	YLDLILNDFVR
5.7	1379.755676	-0.003708	IFMLLVVGITSGM

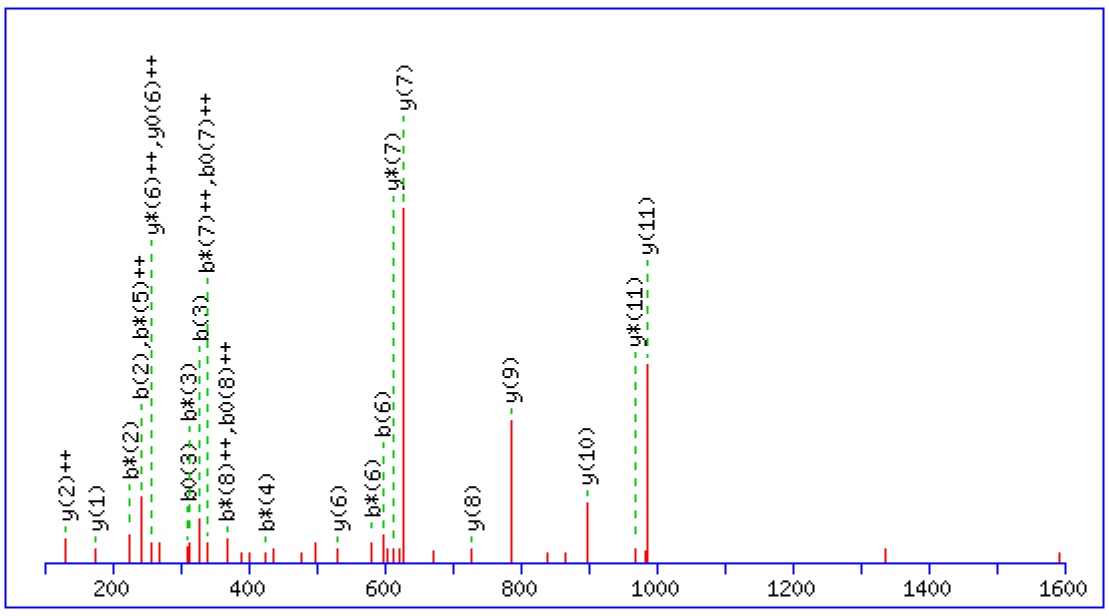
{MATRIX}{SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LQSLGVPGAAASR**
Found in **MGDP1_HUMAN**, Magnesium-dependent phosphatase 1 OS=Homo sapiens GN=MDP1 PE=1 SV=1

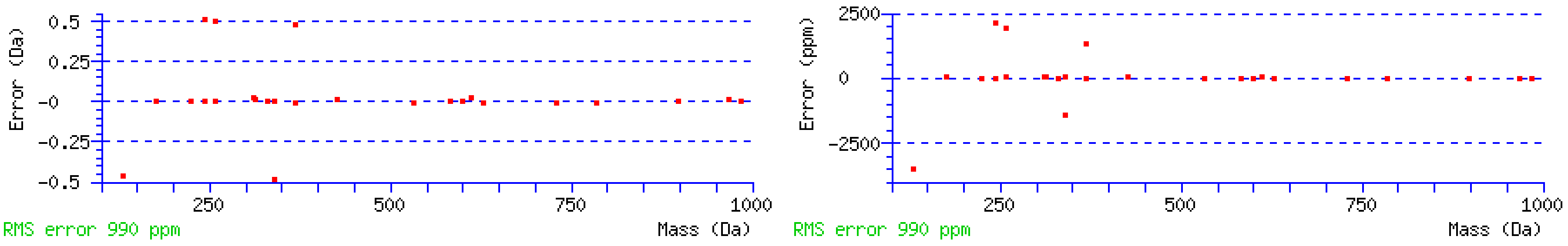
Match to Query 36747: 1225.677428 from(613.845990,2+) rtinseconds(1945) index(19783)
Title: Locus:1.1.1.1997.36
Data file 2011-11-10 - TFD - EP 4-6.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1225.677872
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.00075
Matches : 25/136 fragment ions using 37 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					L							13
2	**242.149918**	121.578597	225.123369	113.065323			Q	1113.601098	557.304187	1096.574549	548.790913	1095.590533	548.298905	12
3	**329.181946**	165.094611	312.155397	156.581336	311.171381	156.089328	S	***985.542520***	493.274898	968.515971	484.761623	967.531955	484.269615	11
4	442.266010	221.636643	425.239461	213.123369	424.255445	212.631361	L	***898.510492***	449.758884	881.483943	441.245610	880.499927	440.753602	10
5	499.287474	250.147375	482.260925	241.634100	481.276909	241.142092	G	***785.426428***	393.216852	768.399879	384.703577	767.415863	384.211570	9
6	**598.355888**	299.681582	581.329339	291.168308	580.345323	290.676300	V	***728.404964***	364.706120	711.378415	356.192846	710.394399	355.700838	8
7	695.408652	348.207964	678.382103	339.694690	677.398087	339.202682	P	***629.336550***	315.171913	612.310001	306.658639	611.325985	306.166631	7
8	752.430116	376.718696	735.403567	368.205422	734.419551	367.713414	G	***532.283786***	266.645531	515.257237	258.132256	514.273221	257.640248	6
9	823.467230	412.237253	806.440681	403.723979	805.456665	403.231971	A	475.262322	238.134799	458.235773	229.621524	457.251757	229.129516	5
10	894.504344	447.755810	877.477795	439.242536	876.493779	438.750528	A	404.225208	202.616242	387.198659	194.102967	386.214643	193.610959	4
11	965.541458	483.274367	948.514909	474.761093	947.530893	474.269085	A	333.188094	167.097685	316.161545	158.584410	315.177529	158.092402	3
12	1052.573486	526.790381	1035.546937	518.277107	1034.562921	517.785099	S	262.150980	131.579128	245.124431	123.065853	244.140415	122.573845	2
13							R	***175.118952***	88.063114	158.092403	79.549839			1



NCBI **BLAST** search of LQSLGVPGAAASR
(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	1225.677872	-0.000444	LQSLGVPGAAASR
26.2	1225.677841	-0.000413	EKALRPEVER
9.8	1225.666626	0.010802	AGLSPAEPLLSR
7.7	1225.666641	0.010787	SGPGLLPSEITR
7.7	1225.689087	-0.011659	EKARPRPTQK
0.8	1225.666626	0.010802	KPAEVEQPKGK
0.4	1225.666626	0.010802	AGLSPAEPLLSR
0.2	1225.666656	0.010772	SSLTPLGPPVSR

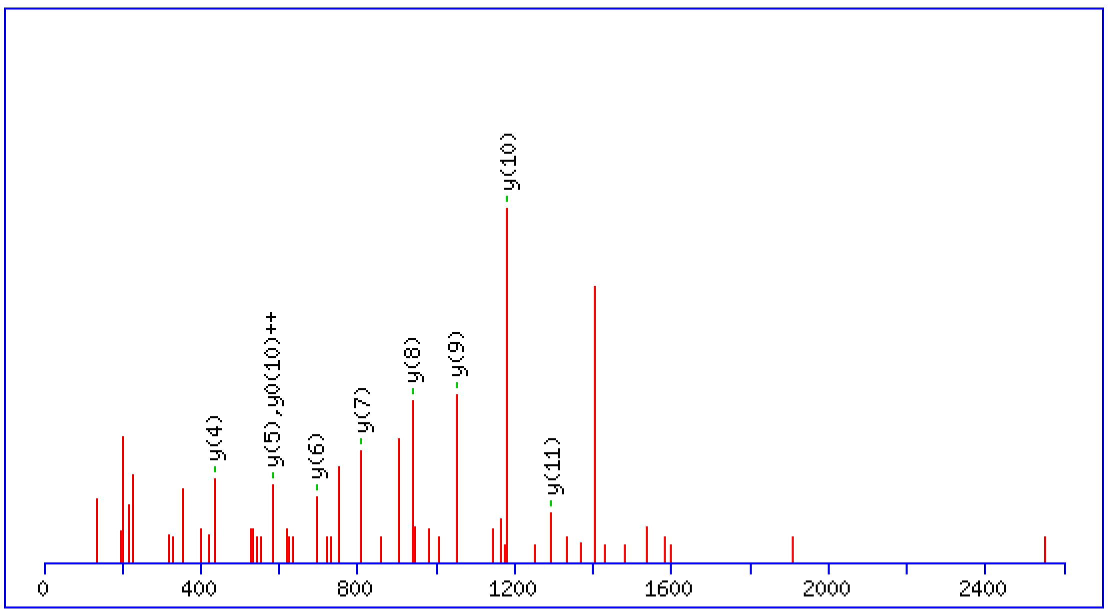
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILEIEDLFSSLK**
Found in **MPP5_HUMAN**, MAGUK p55 subfamily member 5 OS=Homo sapiens GN=MPP5 PE=1 SV=3

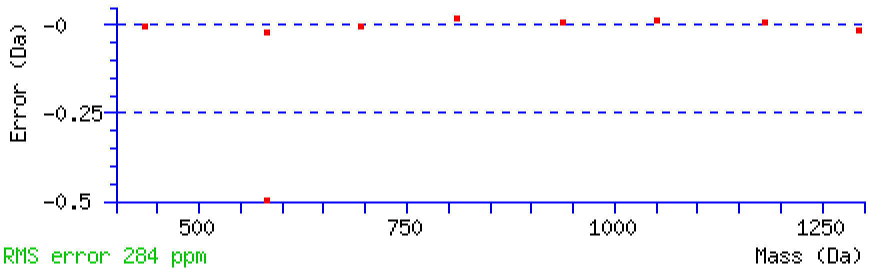
Match to Query 43399: 1405.770808 from(703.892680,2+) rtinseconds(4342) index(64249)
Title: Locus:1.1.1.3062.8
Data file 2011-11-14 - TFD - EP 8-2.mgf

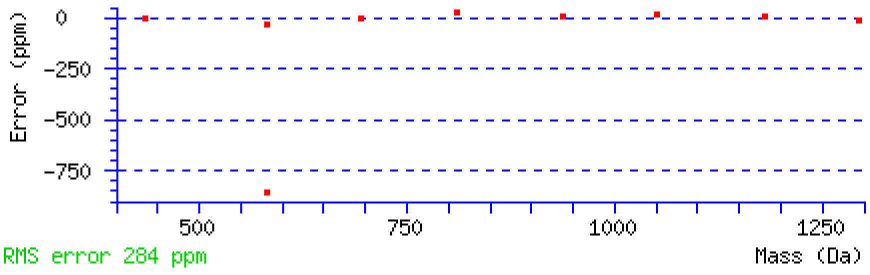
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1405.770416
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 62  Expect: 4.6e-006
Matches : 9/102 fragment ions using 13 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							12
2	227.175404	114.091340			L	*1293.693659*	647.350468	1276.667110	638.837193	1275.683094	638.345185	11
3	356.217997	178.612637	338.207432	169.607354	E	*1180.609595*	590.808436	1163.583046	582.295161	1162.599030	581.803153	10
4	469.302061	235.154669	451.291496	226.149386	I	*1051.567002*	526.287139	1034.540453	517.773865	1033.556437	517.281857	9
5	598.344654	299.675965	580.334089	290.670683	E	*938.482938*	469.745107	921.456389	461.231833	920.472373	460.739825	8
6	713.371597	357.189437	695.361032	348.184154	D	*809.440345*	405.223811	792.413796	396.710536	791.429780	396.218528	7
7	826.455661	413.731469	808.445096	404.726186	L	*694.413402*	347.710339	677.386853	339.197065	676.402837	338.705057	6
8	973.524075	487.265676	955.513510	478.260393	F	*581.329338*	291.168307	564.302789	282.655033	563.318773	282.163025	5
9	1060.556103	530.781690	1042.545538	521.776407	S	*434.260924*	217.634100	417.234375	209.120826	416.250359	208.628818	4
10	1147.588131	574.297704	1129.577566	565.292421	S	347.228896	174.118086	330.202347	165.604811	329.218331	165.112803	3
11	1260.672195	630.839736	1242.661630	621.834453	L	260.196868	130.602072	243.170319	122.088797			2
12					K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
61.9	1405.770416	0.000392	ILEIEDLFSSLK
9.4	1405.775146	-0.004338	LPQLMAPTPPGLR
8.8	1405.767761	0.003047	LLAPGVDPSPPRR
8.8	1405.767761	0.003047	LLAPGVDPSPPRR
8.3	1405.775146	-0.004338	LPQLMAPTPPGLR
4.3	1405.767761	0.003047	LLAPGVDPSPPRR
3.3	1405.757843	0.012965	IIAERHFDHLR
3.3	1405.767761	0.003047	LLAPGVDPSPPRR
3.3	1405.767761	0.003047	LLAPGVDPSPPRR
3.0	1405.767715	0.003093	LPPAAEPAERALR

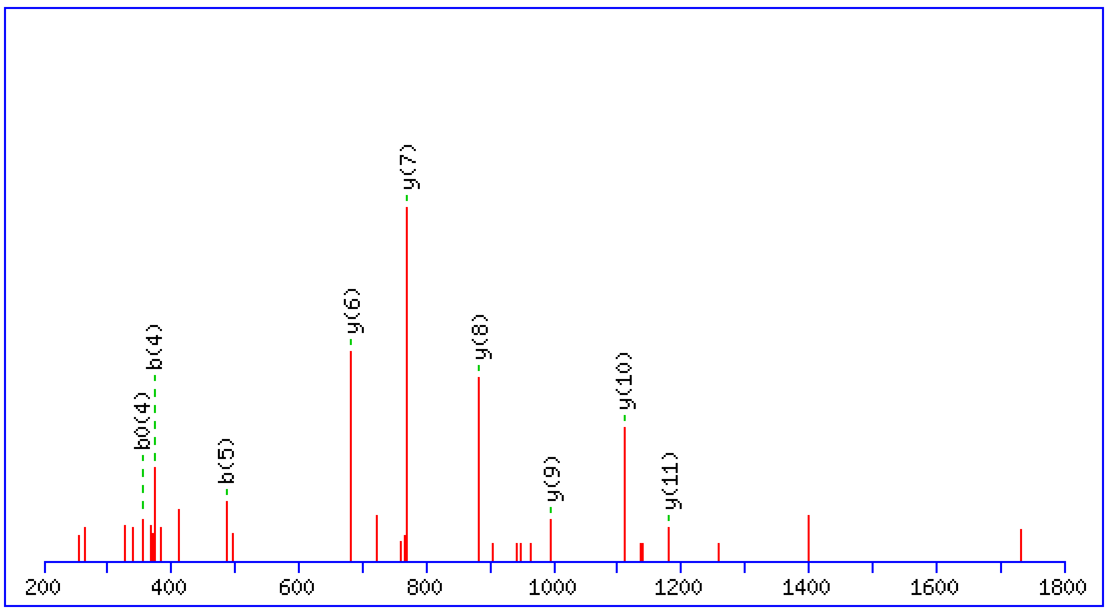
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DAADLLSPLALLR**
Found in **MFS10_HUMAN**, Major facilitator superfamily domain-containing protein 10 OS=Homo sapiens GN=MFSD10 PE=2 SV=1

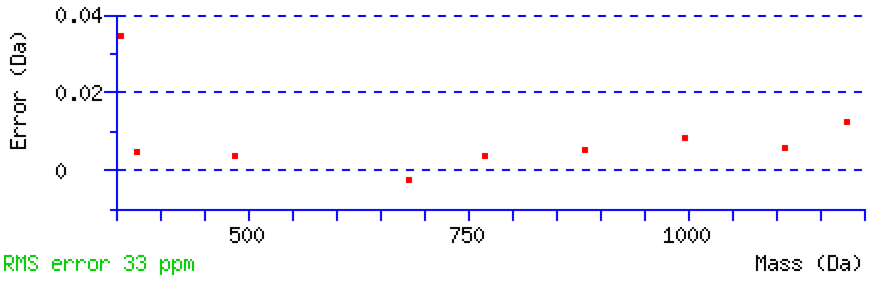
Match to Query 38467: 1366.786628 from(684.400590,2+) rtinseconds(4331) index(63086)
Title: Locus:1.1.1.3067.14
Data file 2011-11-14 - TFD - EP 7-1.mgf

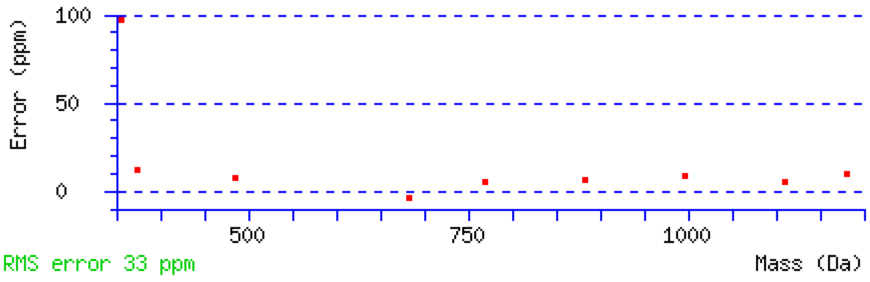
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1366.781982
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 55 **Expect:** 1.1e-005
Matches : 9/108 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.034219	58.520748	98.023654	49.515465	D							13
2	187.071333	94.039304	169.060768	85.034022	A	1252.762349	626.884812	1235.735800	618.371538	1234.751784	617.879530	12
3	258.108447	129.557862	240.097882	120.552579	A	***1181.725235***	591.366255	1164.698686	582.852981	1163.714670	582.360973	11
4	**373.135390**	187.071333	355.124825	178.066051	D	***1110.688121***	555.847698	1093.661572	547.334424	1092.677556	546.842416	10
5	**486.219454**	243.613365	468.208889	234.608083	L	***995.661178***	498.334227	978.634629	489.820952	977.650613	489.328944	9
6	599.303518	300.155397	581.292953	291.150115	L	***882.577114***	441.792195	865.550565	433.278920	864.566549	432.786912	8
7	686.335546	343.671411	668.324981	334.666129	S	***769.493050***	385.250163	752.466501	376.736888	751.482485	376.244880	7
8	783.388310	392.197793	765.377745	383.192511	P	***682.461022***	341.734149	665.434473	333.220874			6
9	896.472374	448.739825	878.461809	439.734543	L	585.408258	293.207767	568.381709	284.694492			5
10	967.509488	484.258382	949.498923	475.253100	A	472.324194	236.665735	455.297645	228.152460			4
11	1080.593552	540.800414	1062.582987	531.795132	L	401.287080	201.147178	384.260531	192.633903			3
12	1193.677616	597.342446	1175.667051	588.337163	L	288.203016	144.605146	271.176467	136.091871			2
13					R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.0	1366.781982	0.004646	DAADLLSPLALLR
6.8	1366.786011	0.000617	GEVWALLLEIPK
6.0	1366.797241	-0.010613	WQKVLNPELIK
1.9	1366.775467	0.011161	NHVRVMELLLK

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

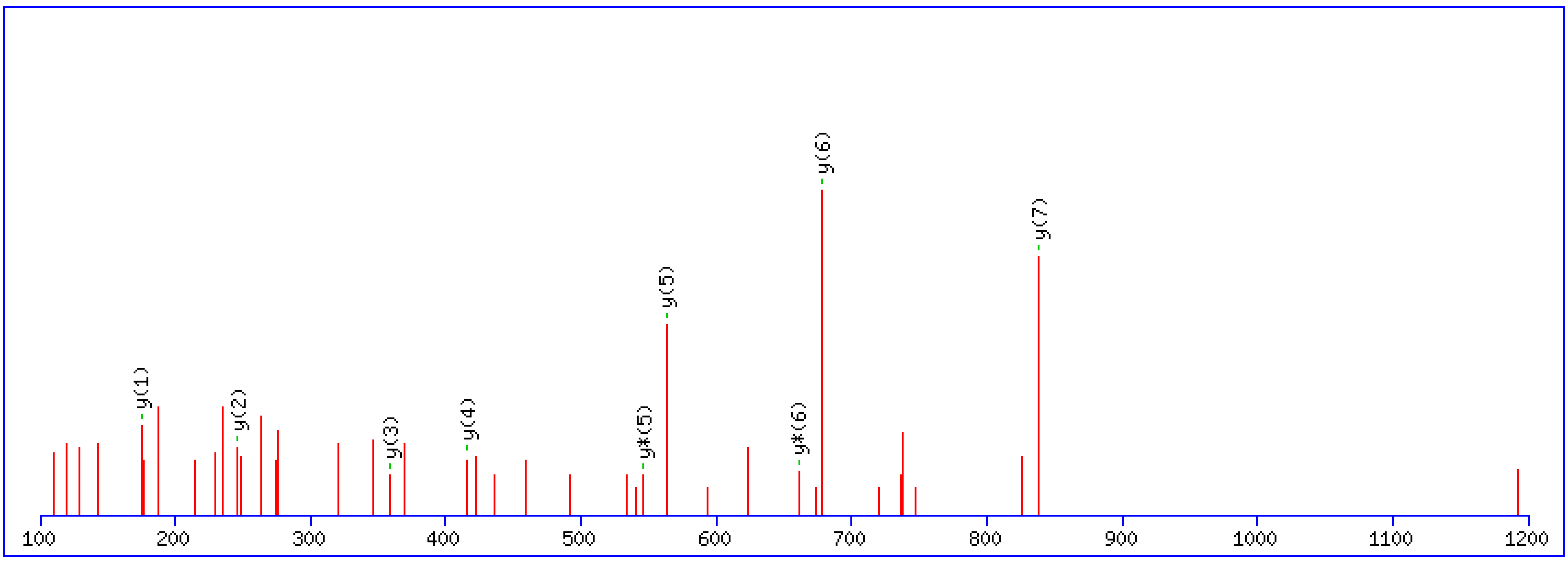
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ICDFGLAR**
Found in **FLT3_HUMAN**, Receptor-type tyrosine-protein kinase FLT3 OS=Homo sapiens GN=FLT3 PE=1 SV=2

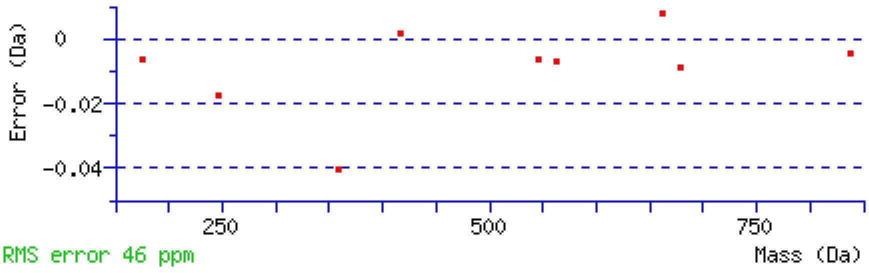
Match to Query 6962: 950.467508 from(476.241030,2+) rtinseconds(2069) index(23881)
Title: Locus:1.1.1.1233.11
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 3.mgf

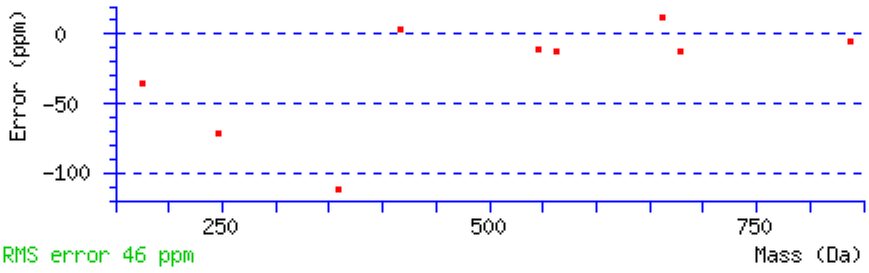
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 950.464386
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.0063
Matches : 9/56 fragment ions using 30 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							8
2	274.121989	137.564632			C	***838.387600***	419.697438	821.361051	411.184164	820.377035	410.692156	7
3	389.148932	195.078104	371.138367	186.072822	D	***678.356951***	339.682114	661.330402	331.168839	660.346386	330.676831	6
4	536.217346	268.612311	518.206781	259.607029	F	***563.330008***	282.168642	546.303459	273.655368			5
5	593.238810	297.123043	575.228245	288.117761	G	***416.261594***	208.634435	399.235045	200.121161			4
6	706.322874	353.665075	688.312309	344.659793	L	***359.240130***	180.123703	342.213581	171.610429			3
7	777.359988	389.183632	759.349423	380.178350	A	***246.156066***	123.581671	229.129517	115.068397			2
8					R	***175.118952***	88.063114	158.092403	79.549840			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.0	950.464386	0.003122	ICDFGLAR
33.0	950.464386	0.003122	LCDFGLAR
9.0	950.464386	0.003122	IQMTWTR
1.4	950.464386	0.003122	MKPGFSPR
0.5	950.474258	-0.006750	SSKPIMEK

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

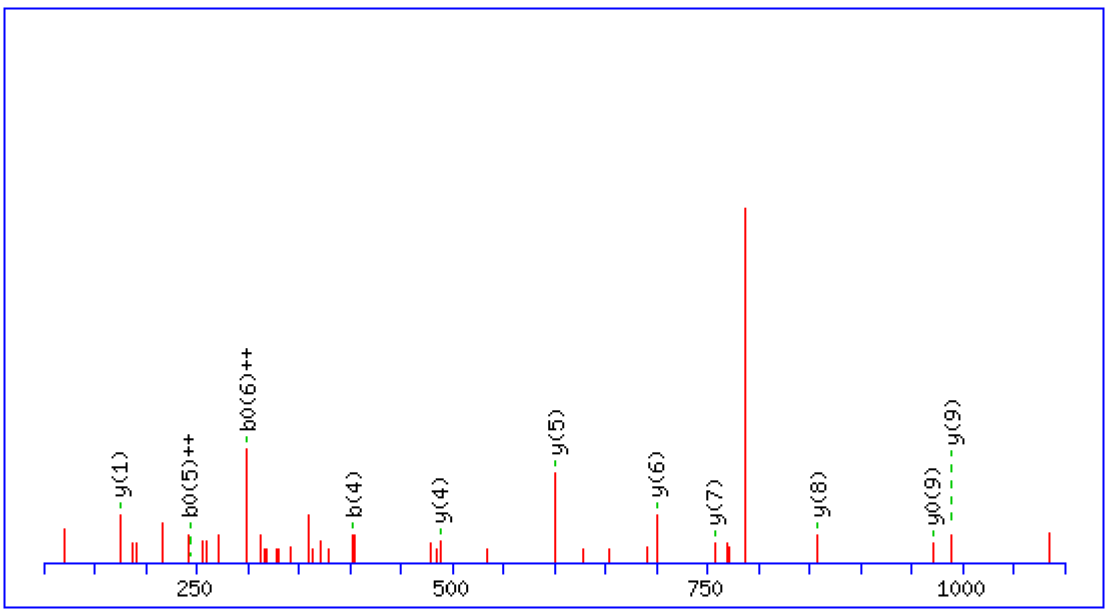
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LMTGVISPER**
Found in **MELK_HUMAN**, Maternal embryonic leucine zipper kinase OS=Homo sapiens GN=MELK PE=1 SV=3

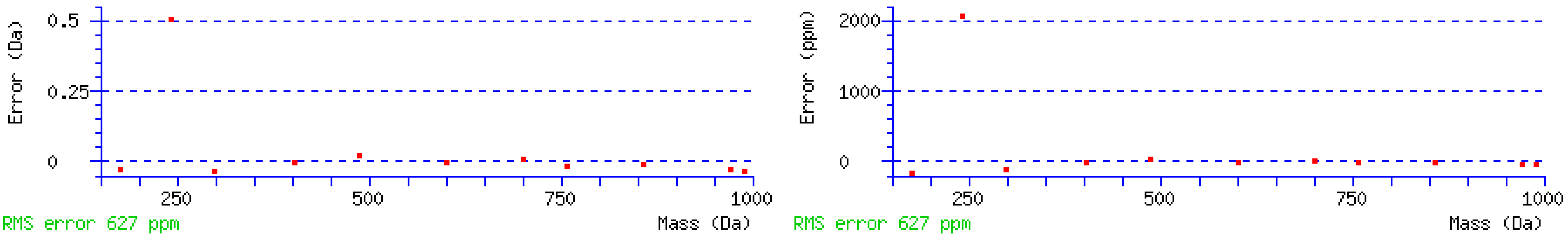
Match to Query 397083: 1101.581828 from(551.798190,2+) rtinseconds(2414) index(683820)
Title: Locus:1.1.1.1591.18
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1101.585220
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 45 **Expect:** 0.00055
Matches : 11/84 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							10
2	245.131825	123.069550			M	***989.508443***	495.257860	972.481894	486.744585	971.497878	486.252577	9
3	346.179504	173.593390	328.168939	164.588108	T	***858.467958***	429.737617	841.441409	421.224343	840.457393	420.732335	8
4	403.200968	202.104122	385.190403	193.098840	G	***757.420279***	379.213778	740.393730	370.700503	739.409714	370.208495	7
5	502.269382	251.638329	484.258817	242.633047	V	***700.398815***	350.703046	683.372266	342.189771	682.388250	341.697763	6
6	615.353446	308.180361	597.342881	299.175079	I	***601.330401***	301.168839	584.303852	292.655564	583.319836	292.163556	5
7	702.385474	351.696375	684.374909	342.691093	S	***488.246337***	244.626806	471.219788	236.113532	470.235772	235.621524	4
8	799.438238	400.222757	781.427673	391.217475	P	401.214309	201.110792	384.187760	192.597518	383.203744	192.105510	3
9	928.480831	464.744054	910.470266	455.738771	E	304.161545	152.584410	287.134996	144.071136	286.150980	143.579128	2
10					R	***175.118952***	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.9	1101.585220	-0.003392	LMTGVISPER
11.0	1101.581848	-0.000020	LLFNDPDLR
10.7	1101.577820	0.004008	LDSISGNLQR
9.6	1101.577820	0.004008	INANTITSPR
7.6	1101.571945	0.009883	LPSYHKWR
5.8	1101.585190	-0.003362	LAEEMLGLAR
5.5	1101.577805	0.004023	LDRTIAEER
5.2	1101.586563	-0.004735	LCVIHHPAR
4.5	1101.577835	0.003993	LASAGVDTNVR
3.1	1101.577835	0.003993	PSSVTALGQAR

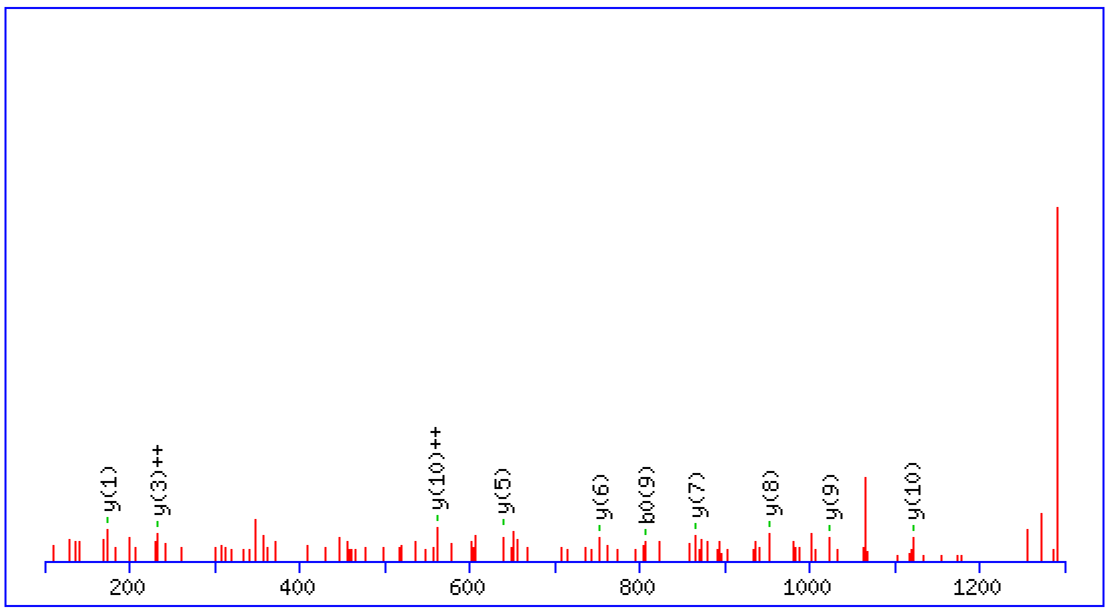
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLPASINTAYER**
Found in **MMP14_HUMAN**, Matrix metalloproteinase-14 OS=Homo sapiens GN=MMP14 PE=1 SV=3

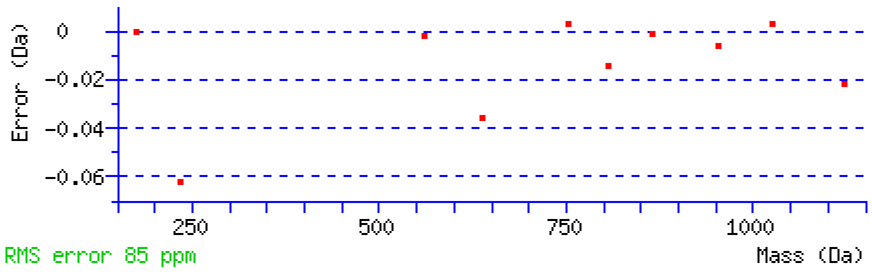
Match to Query 32740: 1290.651988 from(646.333270,2+) rtinseconds(2119) index(25536)
Title: Locus:1.1.1.2225.41
Data file 2011-11-10 - TFD - EP 3-3.mgf

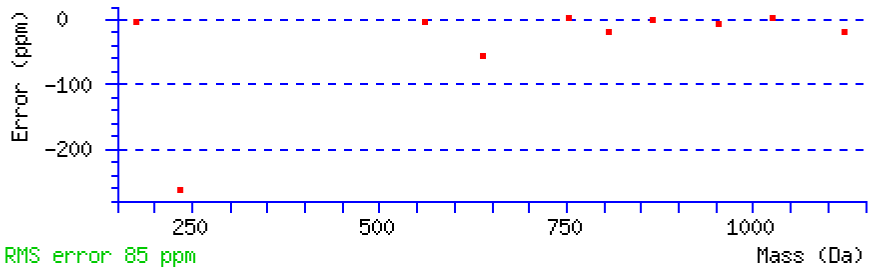
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1290.656784
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.0019
Matches : 10/110 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							12
2	171.112804	86.060040					L	1234.642628	617.824952	1217.616079	609.311677	1216.632063	608.819669	11
3	268.165568	134.586422					P	***1121.558564***	561.282920	1104.532015	552.769645	1103.547999	552.277637	10
4	339.202682	170.104979					A	***1024.505800***	512.756538	1007.479251	504.243263	1006.495235	503.751255	9
5	426.234710	213.620993			408.224145	204.615710	S	***953.468686***	477.237981	936.442137	468.724706	935.458121	468.232698	8
6	539.318774	270.163025			521.308209	261.157742	I	***866.436658***	433.721967	849.410109	425.208692	848.426093	424.716684	7
7	653.361701	327.184488	636.335152	318.671214	635.351136	318.179206	N	***753.352594***	377.179935	736.326045	368.666660	735.342029	368.174652	6
8	754.409380	377.708328	737.382831	369.195053	736.398815	368.703045	T	***639.309667***	320.158471	622.283118	311.645197	621.299102	311.153189	5
9	825.446494	413.226885	808.419945	404.713610	807.435929	404.221602	A	538.261988	269.634632	521.235439	261.121357	520.251423	260.629349	4
10	988.509823	494.758549	971.483274	486.245275	970.499258	485.753267	Y	467.224874	234.116075	450.198325	225.602800	449.214309	225.110792	3
11	1117.552416	559.279846	1100.525867	550.766571	1099.541851	550.274563	E	304.161545	152.584410	287.134996	144.071136	286.150980	143.579128	2
12							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.7	1290.656784	-0.004796	GLPASINTAYER
3.5	1290.660156	-0.008168	LIEERDTLMR
2.0	1290.656815	-0.004827	KPPSVFGSTAER
2.0	1290.656815	-0.004827	KPPSVFGSTAER

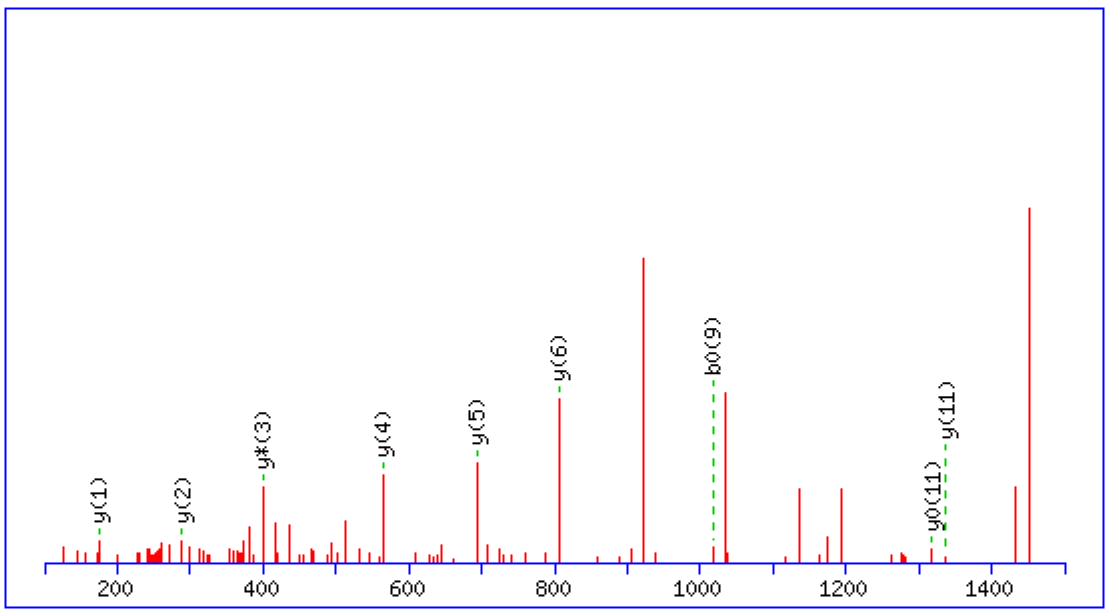
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DLKDSSIEMELR**
Found in **MGAP_HUMAN**, MAX gene-associated protein OS=Homo sapiens GN=MGA PE=1 SV=2

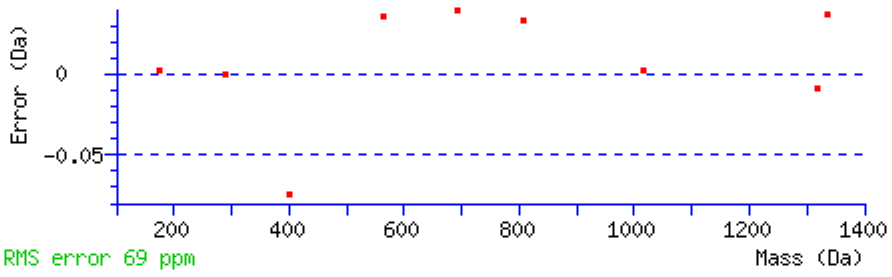
Match to Query 48438: 1450.692908 from(726.353730,2+) rtinseconds(3983) index(49902)
Title: Locus:1.1.1.2764.13
Data file 2011-11-10 - TFD - EP 4-6.mgf

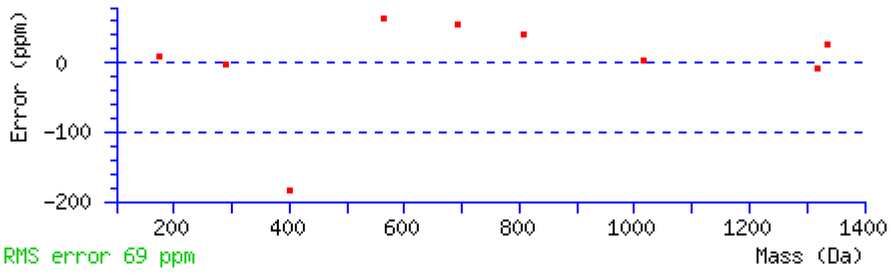
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1450.697327
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M9      : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 38  Expect: 0.0023
Matches : 9/190 fragment ions using 14 most intense peaks   (help)
```

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	116.034219	58.520748			98.023654	49.515465	D							12
2	229.118283	115.062779			211.107718	106.057497	L	***1336.677692***	668.842484	1319.651143	660.329210	1318.667127	659.837201	11
3	357.213246	179.110261	340.186697	170.596986	339.202681	170.104978	K	1223.593628	612.300452	1206.567079	603.787178	1205.583063	603.295170	10
4	472.240189	236.623732	455.213640	228.110458	454.229624	227.618450	D	1095.498665	548.252971	1078.472116	539.739696	1077.488100	539.247688	9
5	559.272217	280.139747	542.245668	271.626472	541.261652	271.134464	S	980.471722	490.739499	963.445173	482.226225	962.461157	481.734217	8
6	646.304245	323.655761	629.277696	315.142486	628.293680	314.650478	S	893.439694	447.223485	876.413145	438.710211	875.429129	438.218203	7
7	759.388309	380.197793	742.361760	371.684518	741.377744	371.192510	I	***806.407666***	403.707471	789.381117	395.194197	788.397101	394.702189	6
8	888.430902	444.719089	871.404353	436.205815	870.420337	435.713807	E	***693.323602***	347.165439	676.297053	338.652165	675.313037	338.160157	5
9	1035.466302	518.236789	1018.439753	509.723515	1017.455737	509.231507	M	***564.281009***	282.644143	547.254460	274.130868	546.270444	273.638860	4
10	1164.508895	582.758086	1147.482346	574.244811	1146.498330	573.752803	E	417.245609	209.126442	400.219060	200.613168	399.235044	200.121160	3
11	1277.592959	639.300118	1260.566410	630.786843	1259.582394	630.294835	L	***288.203016***	144.605146	271.176467	136.091871			2
12							R	***175.118952***	88.063114	158.092403	79.549839			1



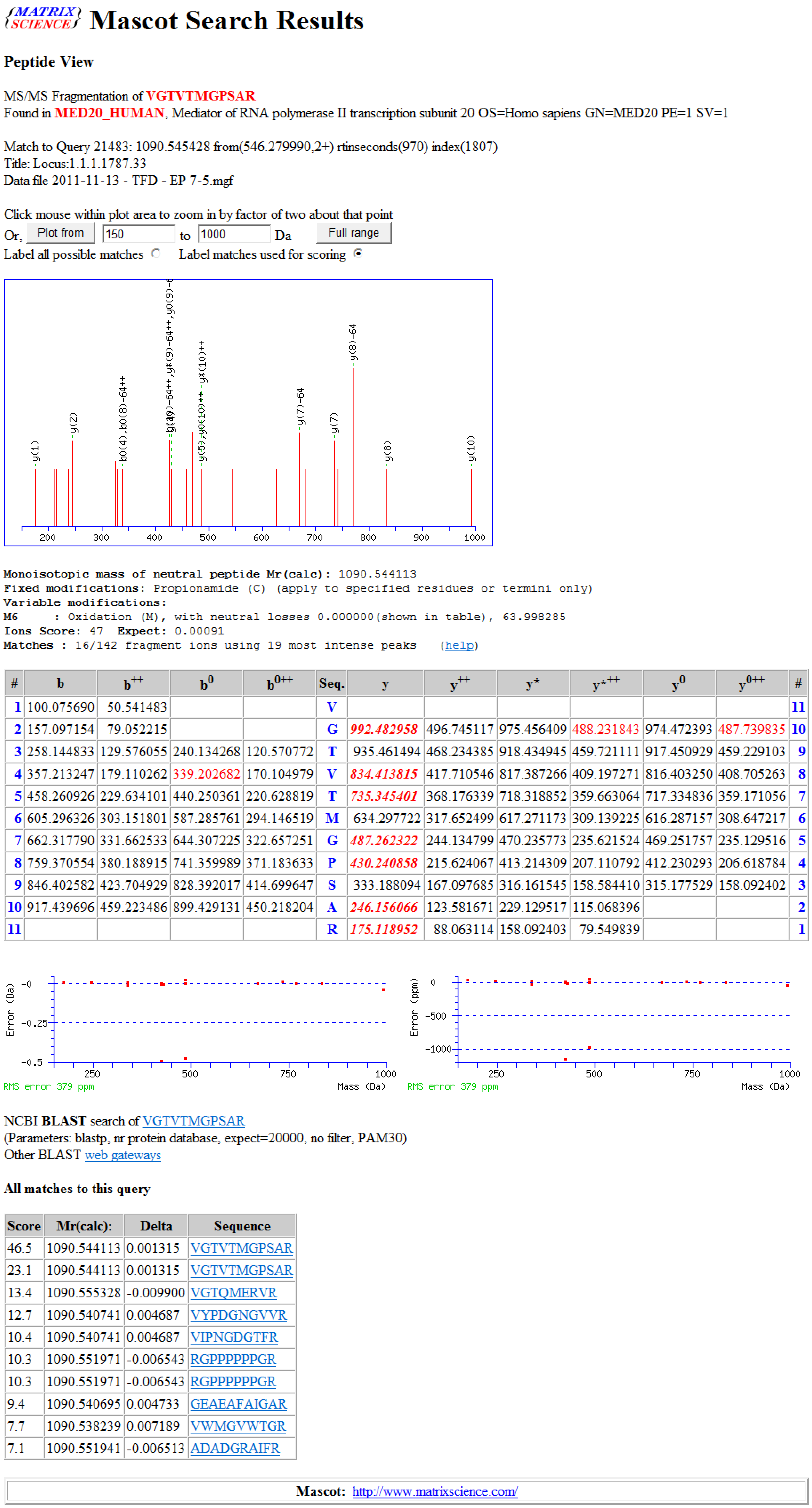


NCBI **BLAST** search of DLKDSSIEMELR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.7	1450.697327	-0.004419	DLKDSSIEMELR
16.8	1450.698685	-0.005777	NFQLMRDLDQR
15.1	1450.705231	-0.012323	SQTTSLENGVFPR
11.3	1450.695358	-0.002450	DGKVDGPHFGPPGR
11.3	1450.695358	-0.002450	DGKVDGPHFGPPGR
10.3	1450.691299	0.001609	SSQPTQPEPRHR
7.3	1450.706070	-0.013162	MNMPFVKGLENR
7.3	1450.706070	-0.013162	MNMPFVKGLENR
7.3	1450.706070	-0.013162	MNMPFVKGLENR
6.6	1450.697342	-0.004434	CLPKSDSSSSLPK

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



{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VGTVTMGPSAR**
Found in **MED20_HUMAN**, Mediator of RNA polymerase II transcription subunit 20 OS=Homo sapiens GN=MED20 PE=1 SV=1

Match to Query 21483: 1090.545428 from(546.279990,2+) rtinseconds(970) index(1807)
Title: Locus:1.1.1.1787.33
Data file 2011-11-13 - TFD - EP 7-5.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
Label all possible matches ○ Label matches used for scoring ●

```
Monoisotopic mass of neutral peptide Mr(calc): 1090.544113
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M6      : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 47  Expect: 0.00091
Matches : 16/142 fragment ions using 19 most intense peaks   (help)
```

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	100.075690	50.541483			V							11
2	157.097154	79.052215			G	992.482958	496.745117	975.456409	488.231843	974.472393	487.739835	10
3	258.144833	129.576055	240.134268	120.570772	T	935.461494	468.234385	918.434945	459.721111	917.450929	459.229103	9
4	357.213247	179.110262	339.202682	170.104979	V	834.413815	417.710546	817.387266	409.197271	816.403250	408.705263	8
5	458.260926	229.634101	440.250361	220.628819	T	735.345401	368.176339	718.318852	359.663064	717.334836	359.171056	7
6	605.296326	303.151801	587.285761	294.146519	M	634.297722	317.652499	617.271173	309.139225	616.287157	308.647217	6
7	662.317790	331.662533	644.307225	322.657251	G	487.262322	244.134799	470.235773	235.621524	469.251757	235.129516	5
8	759.370554	380.188915	741.359989	371.183633	P	430.240858	215.624067	413.214309	207.110792	412.230293	206.618784	4
9	846.402582	423.704929	828.392017	414.699647	S	333.188094	167.097685	316.161545	158.584410	315.177529	158.092402	3
10	917.439696	459.223486	899.429131	450.218204	A	246.156066	123.581671	229.129517	115.068396			2
11					R	175.118952	88.063114	158.092403	79.549839			1

NCBI **BLAST** search of VGTVTMGPSAR
(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	1090.544113	0.001315	VGTVTMGPSAR
23.1	1090.544113	0.001315	VGTVTMGPSAR
13.4	1090.555328	-0.009900	VGTQMERVR
12.7	1090.540741	0.004687	VYPDGNGVVR
10.4	1090.540741	0.004687	VIPNGDGTFR
10.3	1090.551971	-0.006543	RGPPPPPPGR
10.3	1090.551971	-0.006543	RGPPPPPPGR
9.4	1090.540695	0.004733	GEAEAFAIGAR
7.7	1090.538239	0.007189	VWMGVWTGR
7.1	1090.551941	-0.006513	ADADGRAIFR

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

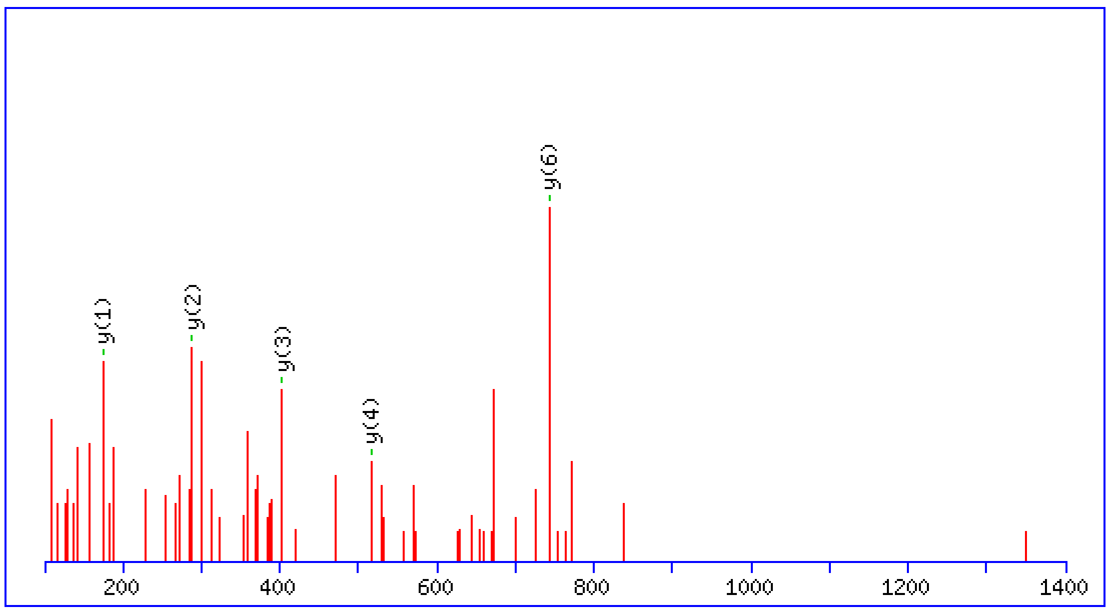
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LQVIDIR**
Found in **TXIP1_HUMAN**, Translin-associated factor X-interacting protein 1 OS=Homo sapiens GN=TSNAXIP1 PE=2 SV=1

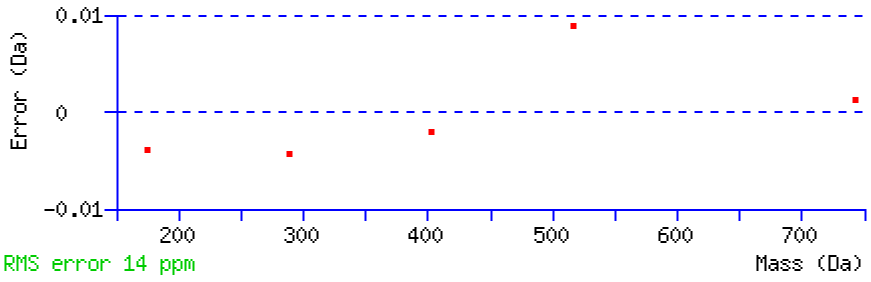
Match to Query 3665: 855.515228 from(428.764890,2+) rtinseconds(1858) index(16880)
Title: Locus:1.1.1.2267.7
Data file 2011-11-12 - TFD - EP 5-1.mgf

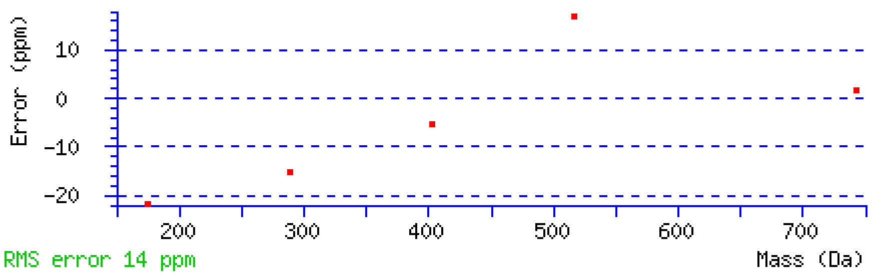
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 855.517792
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.0005
Matches : 5/58 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					L							7
2	242.149918	121.578597	225.123369	113.065323			Q	*743.441015*	372.224146	726.414466	363.710871	725.430450	363.218863	6
3	341.218332	171.112804	324.191783	162.599530			V	615.382437	308.194857	598.355888	299.681582	597.371872	299.189574	5
4	454.302396	227.654836	437.275847	219.141562			I	*516.314023*	258.660650	499.287474	250.147375	498.303458	249.655367	4
5	569.329339	285.168308	552.302790	276.655033	551.318774	276.163025	D	*403.229959*	202.118618	386.203410	193.605343	385.219394	193.113335	3
6	682.413403	341.710340	665.386854	333.197065	664.402838	332.705057	I	*288.203016*	144.605146	271.176467	136.091872			2
7							R	*175.118952*	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of LQVIDIR
(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	855.517792	-0.002564	LQVIDIR
41.0	855.517792	-0.002564	LQVLDLR
12.4	855.517792	-0.002564	LEVVAGLR
12.4	855.517792	-0.002564	LLGDLGLR
12.4	855.517792	-0.002564	LPTPKLR
12.4	855.517792	-0.002564	LQILTPR
12.4	855.517792	-0.002564	LVLDQLR
12.2	855.517792	-0.002564	ILVKPDR
10.8	855.517792	-0.002564	VLKDLPR
10.4	855.517792	-0.002564	KLVPVER

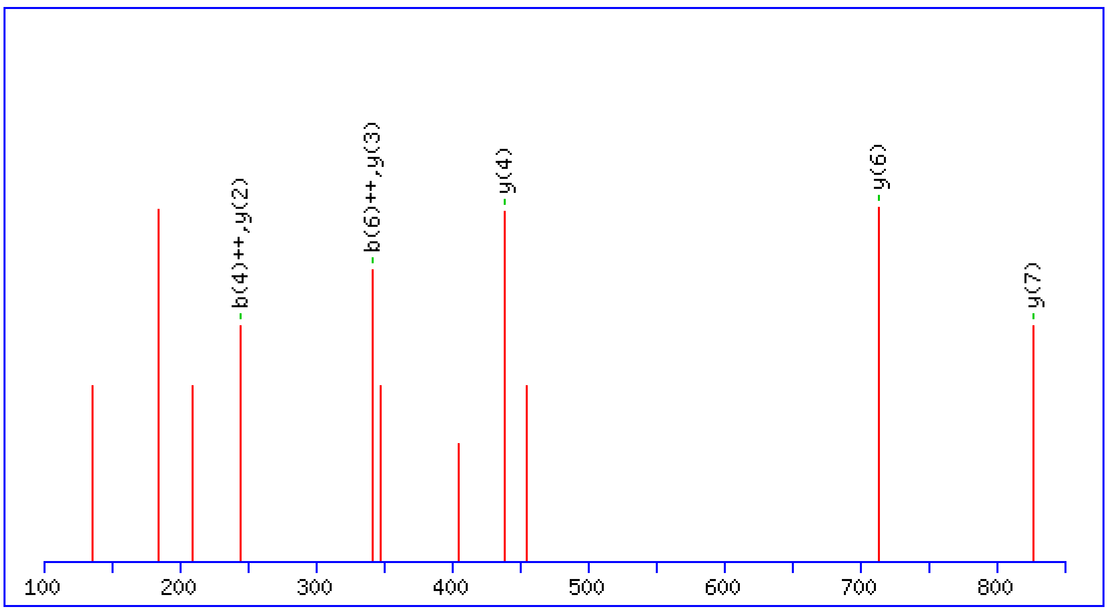
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLCTPPPK**
Found in **MCP_HUMAN**, Membrane cofactor protein OS=Homo sapiens GN=CD46 PE=1 SV=3

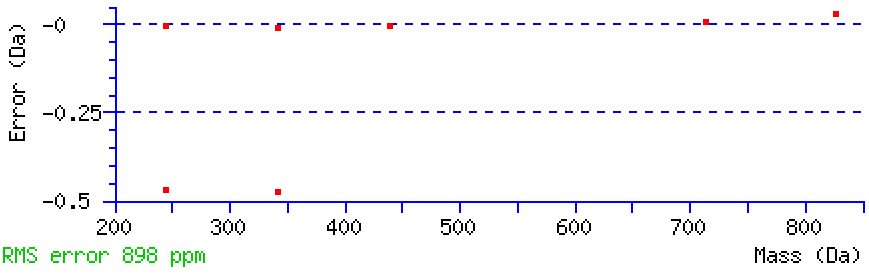
Match to Query 10119: 924.506568 from(463.260560,2+) rtinseconds(1085) index(4475)
Title: Locus:1.1.1.1909.15
Data file 2011-11-10 - TFD - EP 4-2.mgf

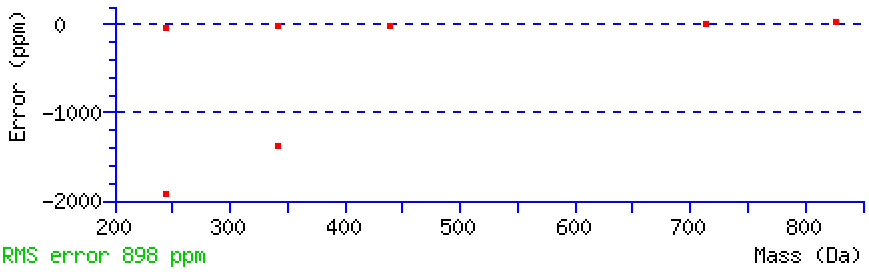
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 924.510269
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 46 **Expect:** 0.00018
Matches : 7/56 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	100.075690	50.541483			V							8
2	213.159754	107.083515			L	*826.449138*	413.728207	809.422589	405.214933	808.438573	404.722925	7
3	387.206053	194.106664			C	*713.365074*	357.186175	696.338525	348.672901	695.354509	348.180893	6
4	488.253732	**244.630504**	470.243167	235.625222	T	539.318775	270.163026	522.292226	261.649751	521.308210	261.157743	5
5	585.306496	293.156886	567.295931	284.151604	P	*438.271096*	219.639186	421.244547	211.125912			4
6	682.359260	**341.683268**	664.348695	332.677986	P	*341.218332*	171.112804	324.191783	162.599530			3
7	779.412024	390.209650	761.401459	381.204368	P	*244.165568*	122.586422	227.139019	114.073148			2
8					K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.3	924.510269	-0.003701	VLCTPPPK
10.1	924.500198	0.006370	RGGPRPGGR
10.1	924.502869	0.003699	LRDSPPPK
9.9	924.502884	0.003684	ATATPVPPR
9.4	924.502869	0.003699	TAAPPAPLR
7.2	924.502853	0.003715	LERADPPK
7.0	924.502869	0.003699	VLDLHSNK
3.1	924.502869	0.003699	LRDSPPPK
2.4	924.514114	-0.007546	VPPDGRLR
1.2	924.502869	0.003699	VIHEKDGK

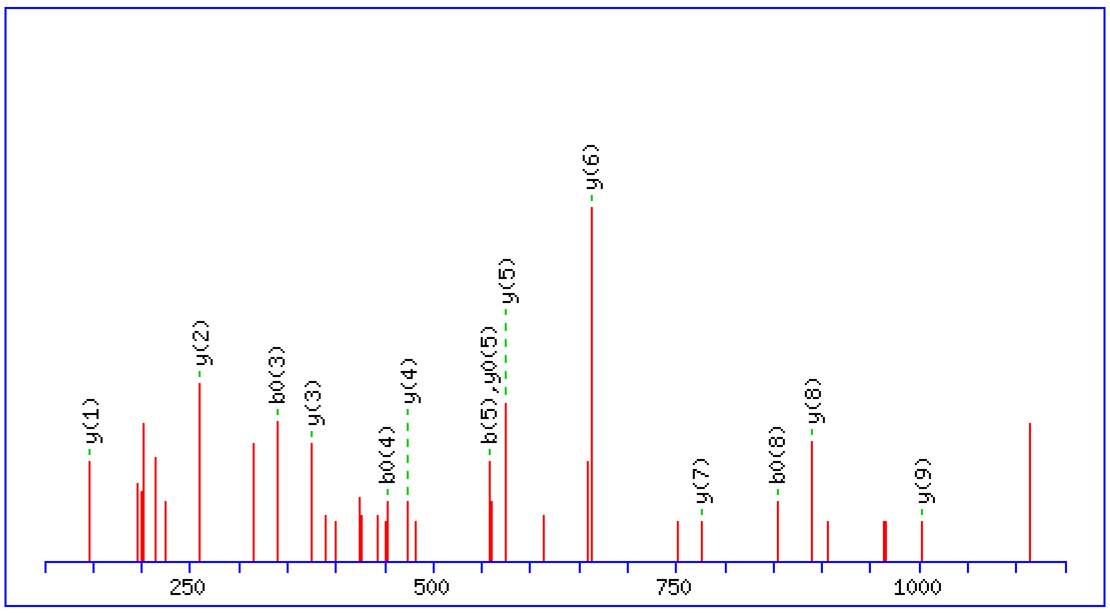
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QIDLSTVDLK**
Found in **MANF_HUMAN**, Mesencephalic astrocyte-derived neurotrophic factor OS=Homo sapiens GN=MANF PE=1 SV=3

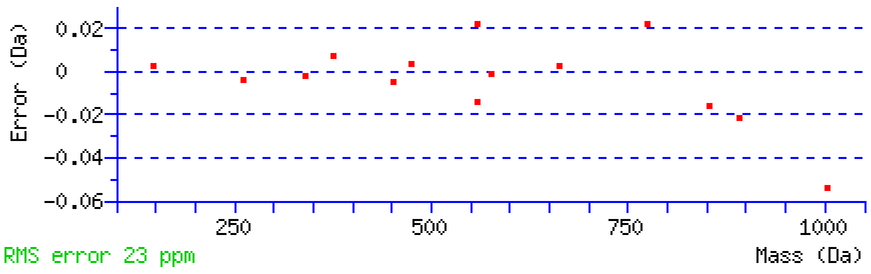
Match to Query 28275: 1130.616008 from(566.315280,2+) rtinseconds(2576) index(31852)
Title: Locus:1.1.1.2200.23
Data file 2011-11-12 - TFD - EP 5-6.mgf

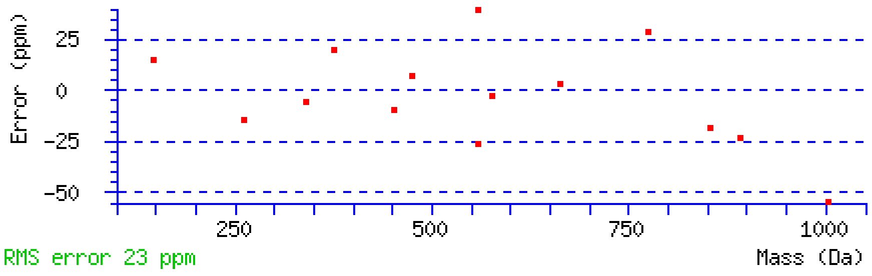
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1130.618301
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 59 **Expect:** 1.3e-005
Matches : 14/100 fragment ions using 26 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	129.065854	65.036565	112.039305	56.523291			**Q**							10
2	242.149918	121.578597	225.123369	113.065323			**I**	***1003.567003***	502.287140	986.540454	493.773865	985.556438	493.281857	9
3	357.176861	179.092069	340.150312	170.578794	339.166296	170.086786	**D**	***890.482939***	445.745108	873.456390	437.231833	872.472374	436.739825	8
4	470.260925	235.634101	453.234376	227.120826	452.250360	226.628818	**L**	***775.455996***	388.231636	758.429447	379.718361	757.445431	379.226353	7
5	557.292953	279.150115	540.266404	270.636840	539.282388	270.144832	**S**	***662.371932***	331.689604	645.345383	323.176330	644.361367	322.684322	6
6	658.340632	329.673954	641.314083	321.160680	640.330067	320.668672	**T**	***575.339904***	288.173590	558.313355	279.660315	557.329339	279.168307	5
7	757.409046	379.208161	740.382497	370.694887	739.398481	370.202879	**V**	***474.292225***	237.649750	457.265676	229.136476	456.281660	228.644468	4
8	872.435989	436.721633	855.409440	428.208358	854.425424	427.716350	**D**	***375.223811***	188.115543	358.197262	179.602269	357.213246	179.110261	3
9	985.520053	493.263665	968.493504	484.750390	967.509488	484.258382	**L**	***260.196868***	130.602072	243.170319	122.088797			2
10							**K**	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.8	1130.618301	-0.002293	QIDLSTVDLK
12.6	1130.618271	-0.002263	KLEADSLEVK
10.9	1130.618286	-0.002278	QLGETLTELK
8.8	1130.618271	-0.002263	KLSDLEEVAK
8.6	1130.608398	0.007610	APSPARPFLK
6.8	1130.618271	-0.002263	DIKSELAEVK

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

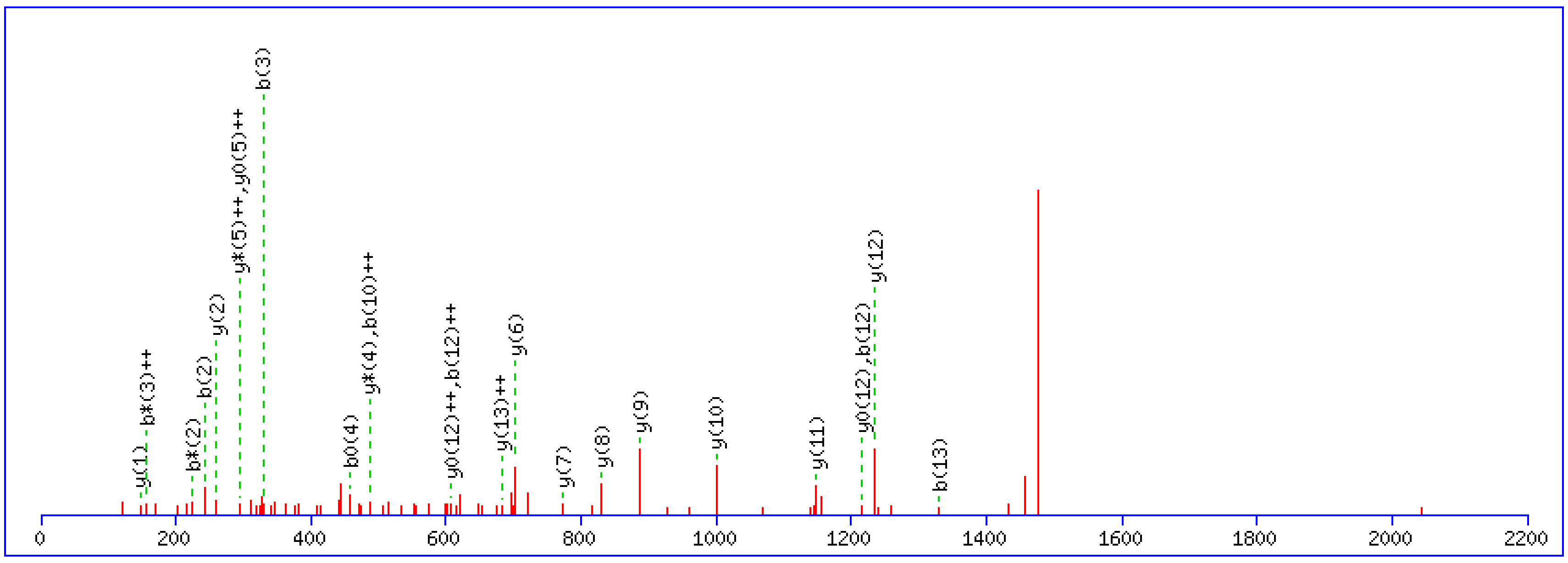
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **IQSFLGGAPTEDLK**
Found in **MSLN_HUMAN**, Mesothelin OS=Homo sapiens GN=MSLN PE=1 SV=2

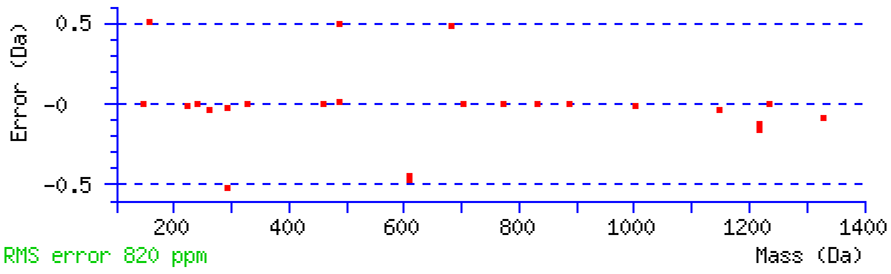
Match to Query 41405: 1474.760348 from(738.387450,2+) rtinseconds(2609) index(34197)
Title: Locus:1.1.1.1373.38
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 2.mgf

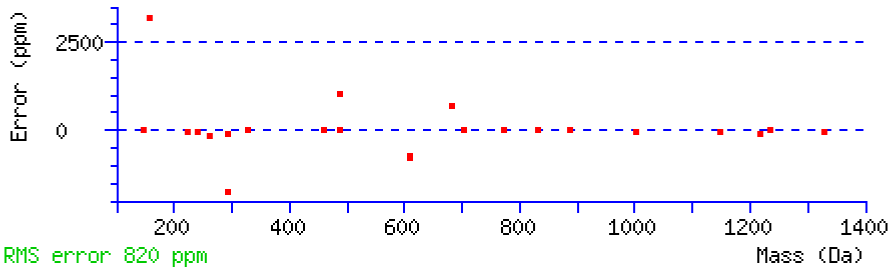
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1474.766754
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 43  Expect: 0.00039
Matches : 24/146 fragment ions using 51 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					I							14
2	**242.149918**	121.578597	225.123369	113.065323			Q	1362.689973	681.848625	1345.663424	673.335350	1344.679408	672.843342	13
3	**329.181946**	165.094611	312.155397	156.581336	311.171381	156.089328	S	***1234.631395***	617.819336	1217.604846	609.306061	1216.620830	608.814053	12
4	476.250360	238.628818	459.223811	230.115543	458.239795	229.623535	F	***1147.599367***	574.303322	1130.572818	565.790047	1129.588802	565.298039	11
5	589.334424	295.170850	572.307875	286.657576	571.323859	286.165568	L	***1000.530953***	500.769115	983.504404	492.255840	982.520388	491.763832	10
6	646.355888	323.681582	629.329339	315.168308	628.345323	314.676300	G	***887.446889***	444.227083	870.420340	435.713808	869.436324	435.221800	9
7	703.377352	352.192314	686.350803	343.679040	685.366787	343.187032	G	***830.425425***	415.716351	813.398876	407.203076	812.414860	406.711068	8
8	774.414466	387.710871	757.387917	379.197597	756.403901	378.705589	A	***773.403961***	387.205619	756.377412	378.692344	755.393396	378.200336	7
9	871.467230	436.237253	854.440681	427.723979	853.456665	427.231971	P	***702.366847***	351.687062	685.340298	343.173787	684.356282	342.681779	6
10	972.514909	486.761093	955.488360	478.247818	954.504344	477.755810	T	605.314083	303.160680	588.287534	294.647405	587.303518	294.155397	5
11	1101.557502	551.282389	1084.530953	542.769115	1083.546937	542.277107	E	504.266404	252.636840	487.239855	244.123565	486.255839	243.631557	4
12	**1216.584445**	608.795861	1199.557896	600.282586	1198.573880	599.790578	D	375.223811	188.115543	358.197262	179.602269	357.213246	179.110261	3
13	**1329.668509**	665.337893	1312.641960	656.824618	1311.657944	656.332610	L	***260.196868***	130.602072	243.170319	122.088797			2
14							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.6	1474.766754	-0.006406	IQSFLGGAPTEDLK
5.9	1474.762680	-0.002332	NRLSSAEELSEIK
1.6	1474.770096	-0.009748	SQIAAIVEMQELK
0.4	1474.768097	-0.007749	ALVRQFGQQDWK

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

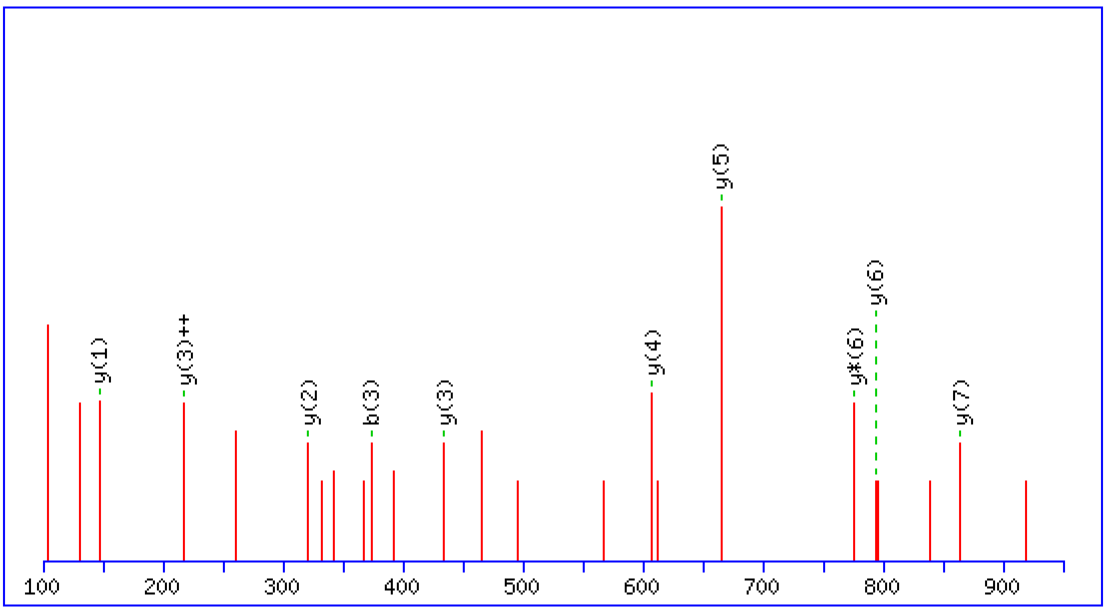
Mascot Search Results

Peptide View

MS/MS Fragmentation of **CAQGCICK**
Found in **MT1A_HUMAN**, Metallothionein-1A OS=Homo sapiens GN=MT1A PE=1 SV=2

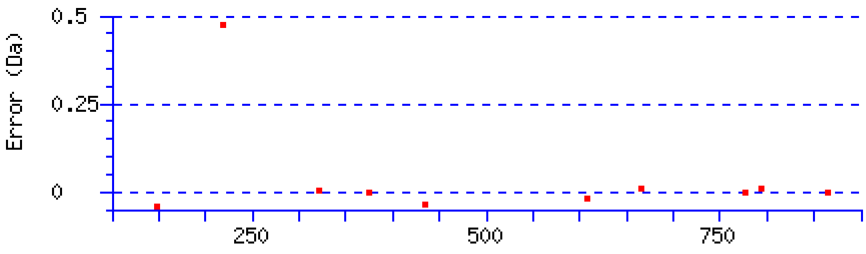
Match to Query 18708: 1037.444748 from(519.729650,2+) rtinseconds(872) index(882)
Title: Locus:1.1.1.1622.18
Data file 2011-11-12 - TFD - EP 6-5.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●

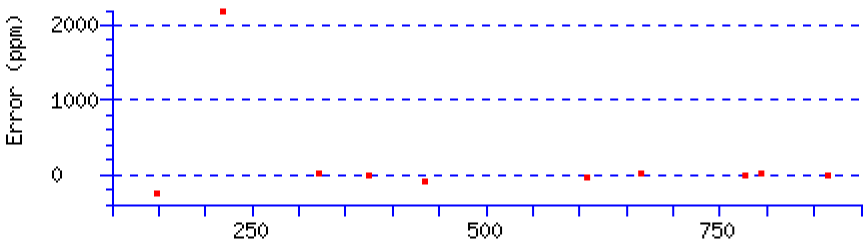


```
Monoisotopic mass of neutral peptide Mr(calc): 1037.445618
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 49  Expect: 5.2e-005
Matches : 10/52 fragment ions using 16 most intense peaks   (help)
```

#	b	b⁺⁺	b*	b*⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	#
1	175.053575	88.030425			C					8
2	246.090689	123.548982			A	*864.406622*	432.706949	847.380073	424.193675	7
3	374.149267	187.578272	357.122718	179.064997	Q	*793.369508*	397.188392	776.342959	388.675118	6
4	431.170731	216.089003	414.144182	207.575729	G	*665.310930*	333.159103	648.284381	324.645829	5
5	605.217030	303.112153	588.190481	294.598879	C	*608.289466*	304.648371	591.262917	296.135097	4
6	718.301094	359.654185	701.274545	351.140911	I	*434.243167*	217.625221	417.216618	209.111947	3
7	892.347393	446.677335	875.320844	438.164060	C	*321.159103*	161.083189	304.132554	152.569915	2
8					K	*147.112804*	74.060040	130.086255	65.546765	1



RMS error 694 ppm



RMS error 694 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.0	1037.445618	-0.000870	CAQGCICK
1.6	1037.452164	-0.007416	NPMDMGTIK
1.0	1037.440918	0.003830	MPLEMEPK
0.6	1037.448792	-0.004044	TPENFPCK

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

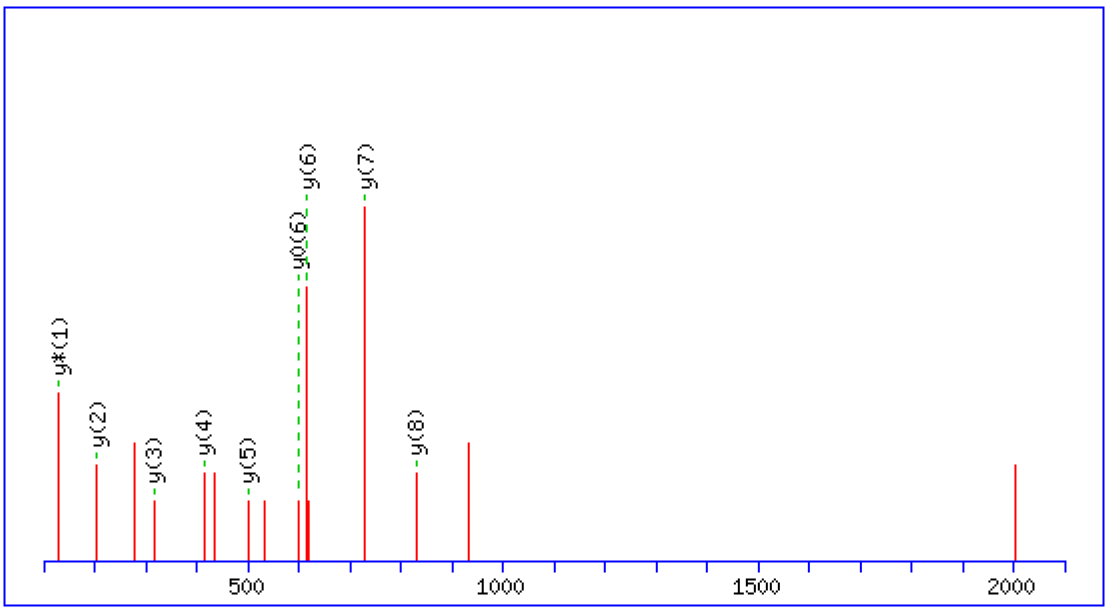
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TTLDSPLGK**
Found in **MGMT_HUMAN**, Methylated-DNA--protein-cysteine methyltransferase OS=Homo sapiens GN=MGMT PE=1 SV=1

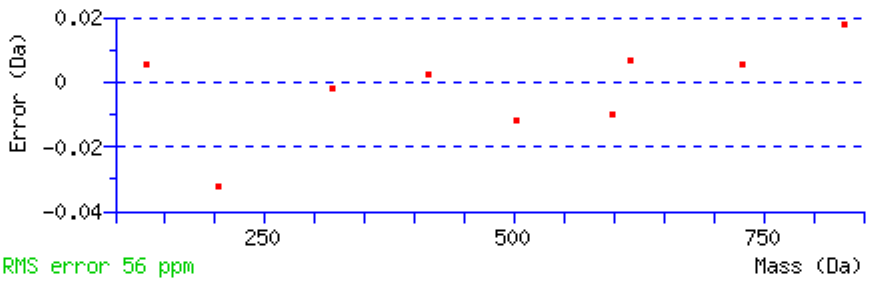
Match to Query 10963: 930.503028 from(466.258790,2+) rtinseconds(1711) index(14260)
Title: Locus:1.1.1.1918.21
Data file 2011-11-10 - TFD - EP 3-6.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ●

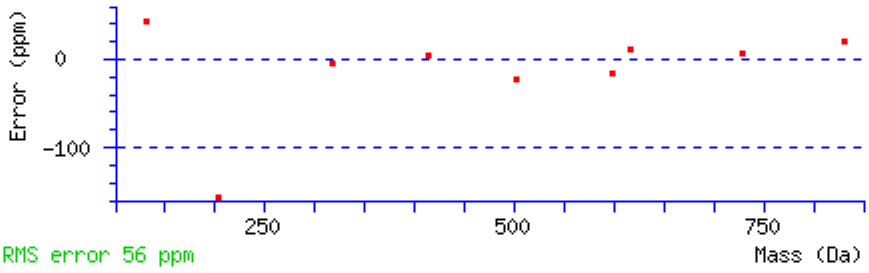


Monoisotopic mass of neutral peptide Mr(calc): 930.502213
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 64 **Expect:** 1.1e-006
Matches : 9/72 fragment ions using 13 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	102.054955	51.531116	84.044390	42.525833	T							9
2	203.102634	102.054955	185.092069	93.049672	T	*830.461810*	415.734543	813.435261	407.221269	812.451245	406.729261	8
3	316.186698	158.596987	298.176133	149.591704	L	*729.414131*	365.210704	712.387582	356.697429	711.403566	356.205421	7
4	431.213641	216.110458	413.203076	207.105176	D	*616.330067*	308.668672	599.303518	300.155397	598.319502	299.663389	6
5	518.245669	259.626473	500.235104	250.621190	S	*501.303124*	251.155200	484.276575	242.641926	483.292559	242.149918	5
6	615.298433	308.152855	597.287868	299.147572	P	*414.271096*	207.639186	397.244547	199.125912			4
7	728.382497	364.694887	710.371932	355.689604	L	*317.218332*	159.112804	300.191783	150.599530			3
8	785.403961	393.205619	767.393396	384.200336	G	*204.134268*	102.570772	187.107719	94.057498			2
9					K	147.112804	74.060040	130.086255	65.546765			1



RMS error 56 ppm



RMS error 56 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
63.9	930.502213	0.000815	TTLDSPLGK
0.2	930.503555	-0.000527	TPTWVRR
0.0	930.502182	0.000846	TSELPKEK

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

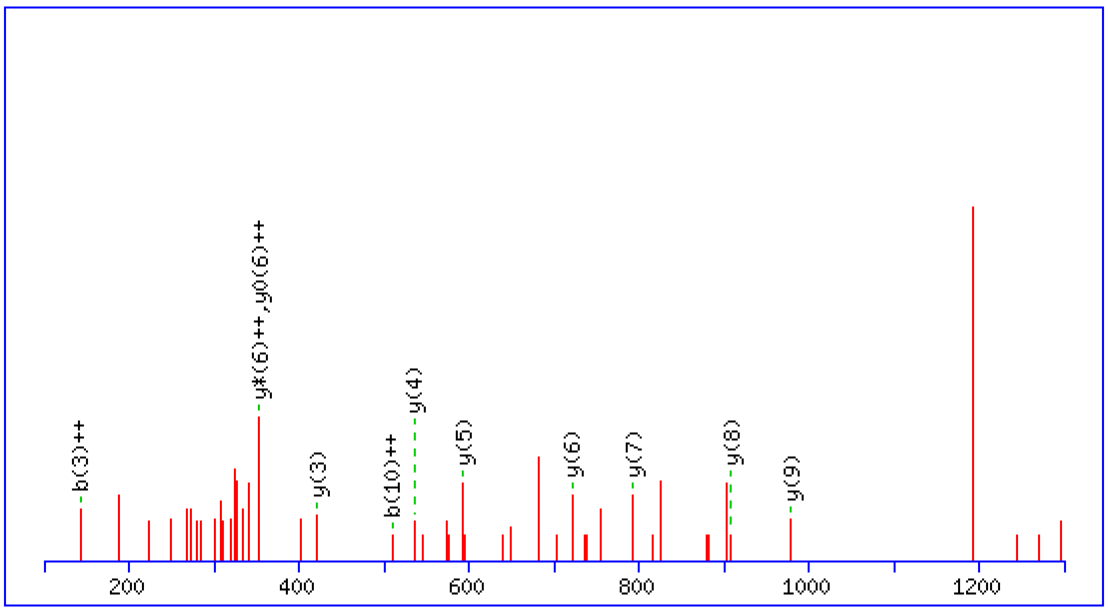
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLADAEGDVFR**
Found in **MMSA_HUMAN**, Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial OS=Homo sapiens GN=ALDH6A1 PE=1 SV=2

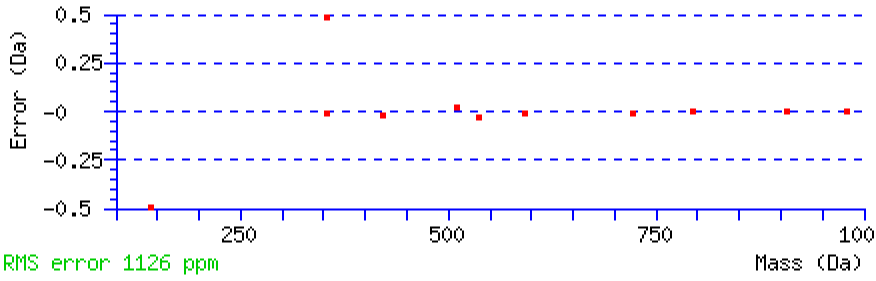
Match to Query 511962: 1192.574968 from(597.294760,2+) rtinseconds(2438) index(923988)
Title: Locus:1.1.1.1332.19
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

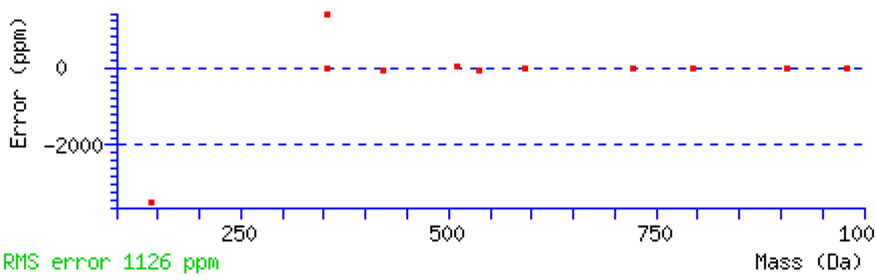
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 1300 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1192.572418
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 48 **Expect:** 0.00011
Matches : 11/94 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116	84.044390	42.525833	T							11
2	215.139019	108.073147	197.128454	99.067865	L	1092.532015	546.769646	1075.505466	538.256371	1074.521450	537.764363	10
3	286.176133	**143.591704**	268.165568	134.586422	A	***979.447951***	490.227614	962.421402	481.714339	961.437386	481.222331	9
4	401.203076	201.105176	383.192511	192.099894	D	***908.410837***	454.709057	891.384288	446.195782	890.400272	445.703774	8
5	472.240190	236.623733	454.229625	227.618451	A	***793.383894***	397.195585	776.357345	388.682311	775.373329	388.190303	7
6	601.282783	301.145030	583.272218	292.139747	E	***722.346780***	361.677028	705.320231	353.163753	704.336215	352.671745	6
7	658.304247	329.655762	640.293682	320.650479	G	***593.304187***	297.155732	576.277638	288.642457	575.293622	288.150449	5
8	773.331190	387.169233	755.320625	378.163951	D	***536.282723***	268.644999	519.256174	260.131725	518.272158	259.639717	4
9	872.399604	436.703440	854.389039	427.698158	V	***421.255780***	211.131528	404.229231	202.618253			3
10	1019.468018	**510.237647**	1001.457453	501.232365	F	322.187366	161.597321	305.160817	153.084046			2
11					R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.4	1192.572418	0.002550	TLADAEGDVFR

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

{MATRIX SCIENCE}

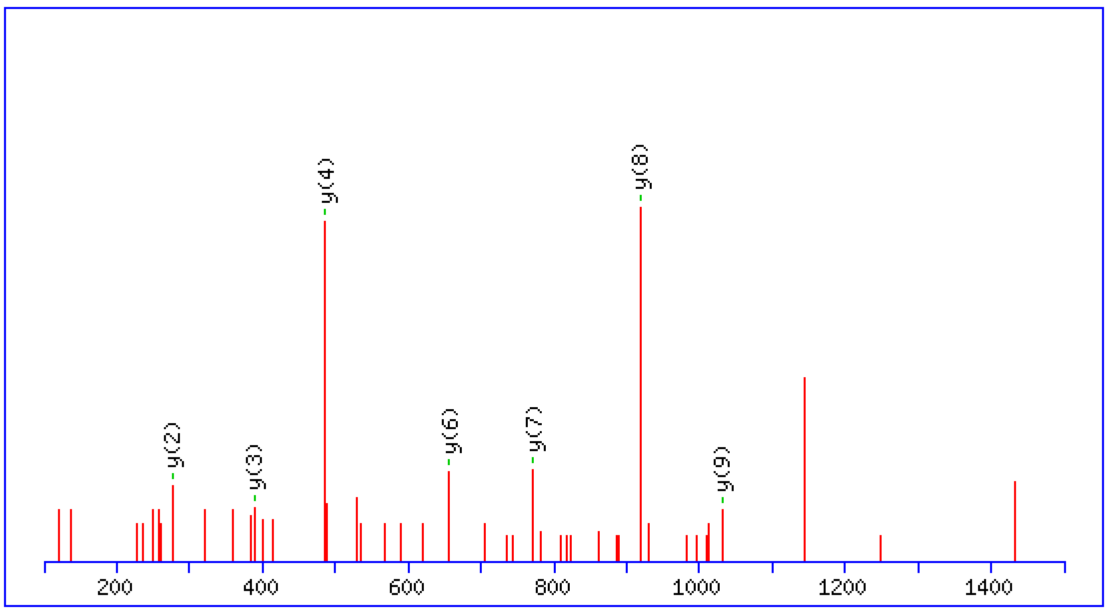
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILFDGIPLEK**
Found in **MUTA_HUMAN**, Methylmalonyl-CoA mutase, mitochondrial OS=Homo sapiens GN=MUT PE=1 SV=4

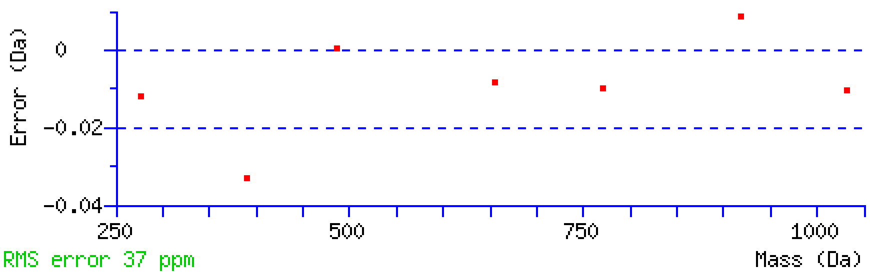
Match to Query 27751: 1143.652028 from(572.833290,2+) rtinseconds(3174) index(44112)
Title: Locus:1.1.1.2630.17
Data file 2011-11-14 - TFD - EP 8-2.mgf

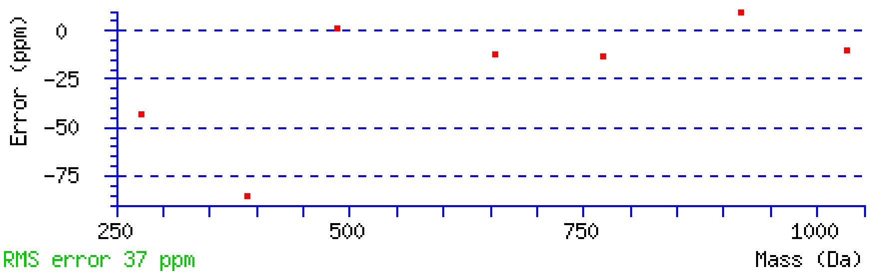
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 1500 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1143.653946
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 60 **Expect:** 8.2e-006
Matches : 7/82 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							10
2	227.175404	114.091340			L	*1031.577174*	516.292225	1014.550625	507.778951	1013.566609	507.286943	9
3	374.243818	187.625547			F	*918.493110*	459.750193	901.466561	451.236919	900.482545	450.744911	8
4	489.270761	245.139018	471.260196	236.133736	D	*771.424696*	386.215986	754.398147	377.702712	753.414131	377.210704	7
5	546.292225	273.649751	528.281660	264.644468	G	*656.397753*	328.702515	639.371204	320.189240	638.387188	319.697232	6
6	659.376289	330.191783	641.365724	321.186500	I	599.376289	300.191783	582.349740	291.678508	581.365724	291.186500	5
7	756.429053	378.718165	738.418488	369.712882	P	*486.292225*	243.649751	469.265676	235.136476	468.281660	234.644468	4
8	869.513117	435.260197	851.502552	426.254914	L	*389.239461*	195.123369	372.212912	186.610094	371.228896	186.118086	3
9	998.555710	499.781493	980.545145	490.776211	E	*276.155397*	138.581336	259.128848	130.068062	258.144832	129.576054	2
10					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of ILFDGIPLEK
(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	1143.653946	-0.001918	ILFDGIPLEK
9.1	1143.643387	0.008641	LLGCSPALKR
8.9	1143.661133	-0.009105	IIIAKENSTR
6.8	1143.647430	0.004598	IPMFIVHKK
2.8	1143.647232	0.004796	RRPSTASLTR
2.0	1143.643372	0.008656	LLKENQMLR
1.5	1143.661133	-0.009105	ILLTKSENAR
1.3	1143.643402	0.008626	LICGGKTLPR
1.0	1143.649933	0.002095	LPTTVLNATAK

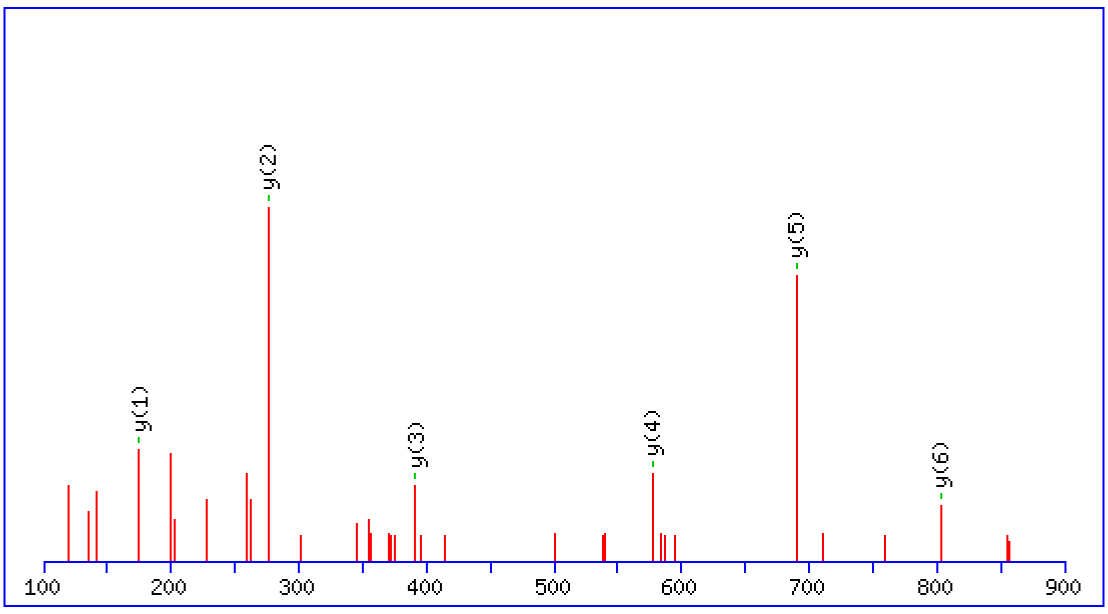
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILLWDTR**
Found in **MEP50_HUMAN**, Methylosome protein 50 OS=Homo sapiens GN=WDR77 PE=1 SV=1

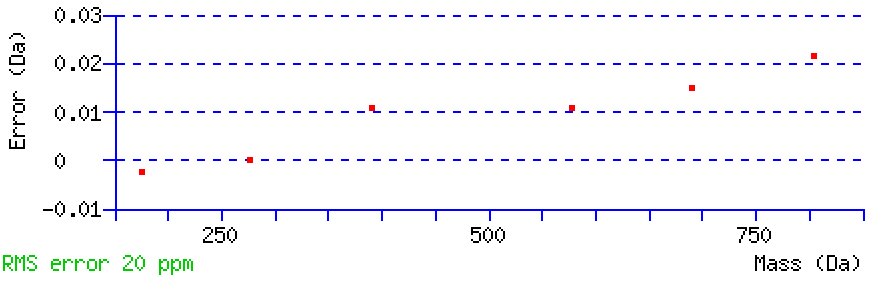
Match to Query 9318: 915.520188 from(458.767370,2+) rtinseconds(2877) index(39544)
Title: Locus:1.1.1.2391.4
Data file 2011-11-12 - TFD - EP 6-4.mgf

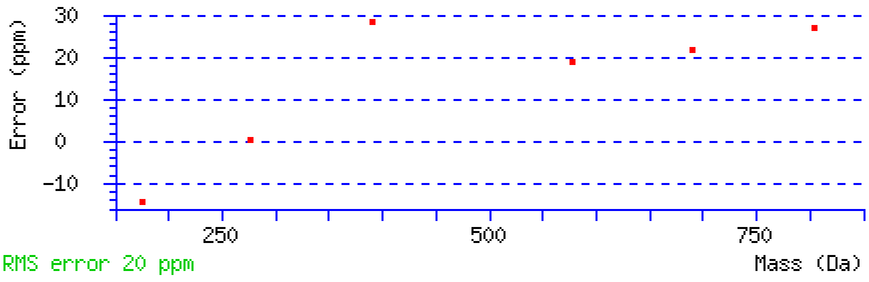
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 915.517792
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 54 **Expect:** 4.5e-005
Matches : 6/50 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308			I							7
2	227.175404	114.091340			L	*803.441015*	402.224146	786.414466	393.710871	785.430450	393.218863	6
3	340.259468	170.633372			L	*690.356951*	345.682114	673.330402	337.168839	672.346386	336.676831	5
4	526.338781	263.673029			W	*577.272887*	289.140082	560.246338	280.626807	559.262322	280.134799	4
5	641.365724	321.186500	623.355159	312.181218	D	*391.193574*	196.100425	374.167025	187.587150	373.183009	187.095142	3
6	742.413403	371.710340	724.402838	362.705057	T	*276.166631*	138.586953	259.140082	130.073679	258.156066	129.581671	2
7					R	*175.118952*	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.3	915.517792	0.002396	ILLWDTR
21.8	915.521149	-0.000961	LLLLDCR
13.1	915.513748	0.006440	IRELETR
10.6	915.513748	0.006440	LEKAAQTR
9.9	915.529007	-0.008819	ILSKYHR
6.4	915.527679	-0.007491	LLSIDLDK
6.3	915.529022	-0.008834	LFRLDPR
6.3	915.529022	-0.008834	LRFEPVR
5.5	915.524979	-0.004791	IRANSISR
0.7	915.513763	0.006425	SLAQQLTR

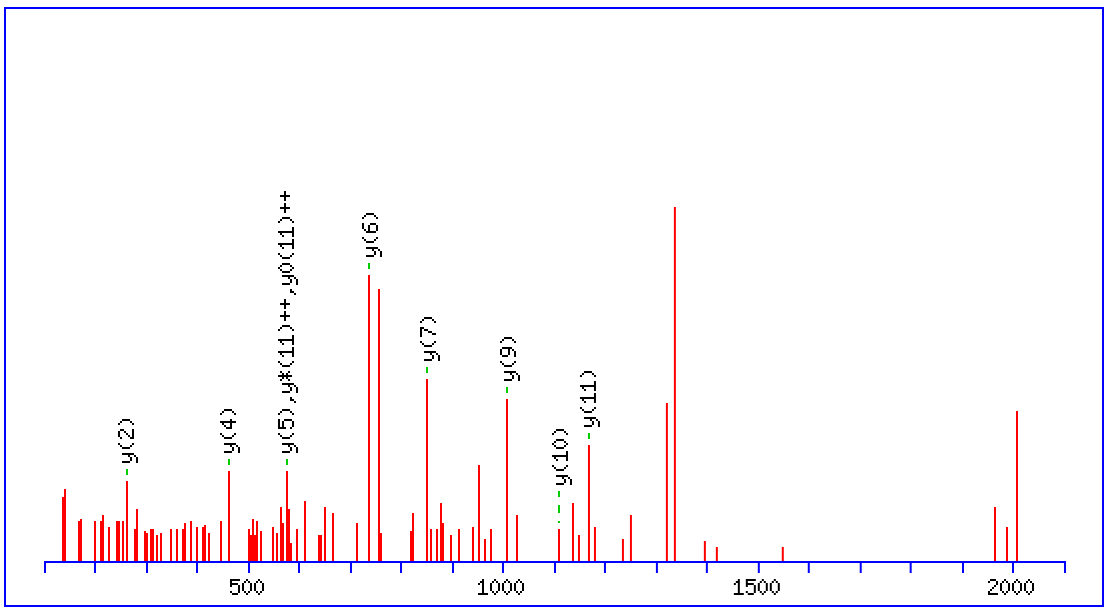
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLGTGTLYIAESR**
Found in **ICLN_HUMAN**, Methylosome subunit pICln OS=Homo sapiens GN=CLNS1A PE=1 SV=1

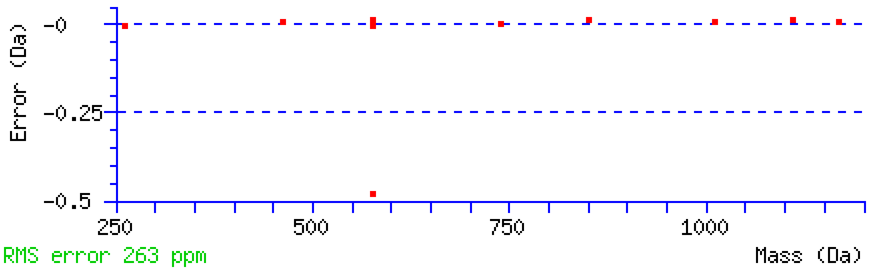
Match to Query 38362: 1336.693788 from(669.354170,2+) rtinseconds(2462) index(31728)
Title: Locus:1.1.1.2234.38
Data file 2011-11-12 - TFD - EP 6-4.mgf

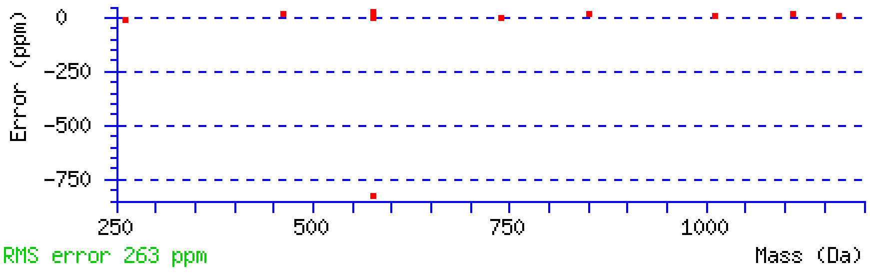
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1336.698669
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 67  Expect: 2.2e-006
Matches : 10/112 fragment ions using 12 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008			G							13
2	171.112804	86.060040			L	1280.684494	640.845885	1263.657945	632.332611	1262.673929	631.840603	12
3	228.134268	114.570772			G	***1167.600430***	584.303853	1150.573881	575.790579	1149.589865	575.298570	11
4	329.181947	165.094611	311.171382	156.089329	T	***1110.578966***	555.793121	1093.552417	547.279847	1092.568401	546.787839	10
5	386.203411	193.605343	368.192846	184.600061	G	***1009.531287***	505.269282	992.504738	496.756007	991.520722	496.263999	9
6	487.251090	244.129183	469.240525	235.123900	T	952.509823	476.758550	935.483274	468.245275	934.499258	467.753267	8
7	600.335154	300.671215	582.324589	291.665933	L	***851.462144***	426.234710	834.435595	417.721436	833.451579	417.229428	7
8	763.398483	382.202879	745.387918	373.197597	Y	***738.378080***	369.692678	721.351531	361.179404	720.367515	360.687396	6
9	876.482547	438.744912	858.471982	429.739629	I	***575.314751***	288.161014	558.288202	279.647739	557.304186	279.155731	5
10	947.519661	474.263468	929.509096	465.258186	A	***462.230687***	231.618981	445.204138	223.105707	444.220122	222.613699	4
11	1076.562254	538.784765	1058.551689	529.779482	E	391.193573	196.100425	374.167024	187.587150	373.183008	187.095142	3
12	1163.594282	582.300779	1145.583717	573.295497	S	***262.150980***	131.579128	245.124431	123.065854	244.140415	122.573846	2
13					R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
67.3	1336.698669	-0.004881	GLGTGTLYIAESR
7.0	1336.702042	-0.008254	LGSQTLTKTCSK
5.1	1336.706039	-0.012251	CALKLLYDSPK

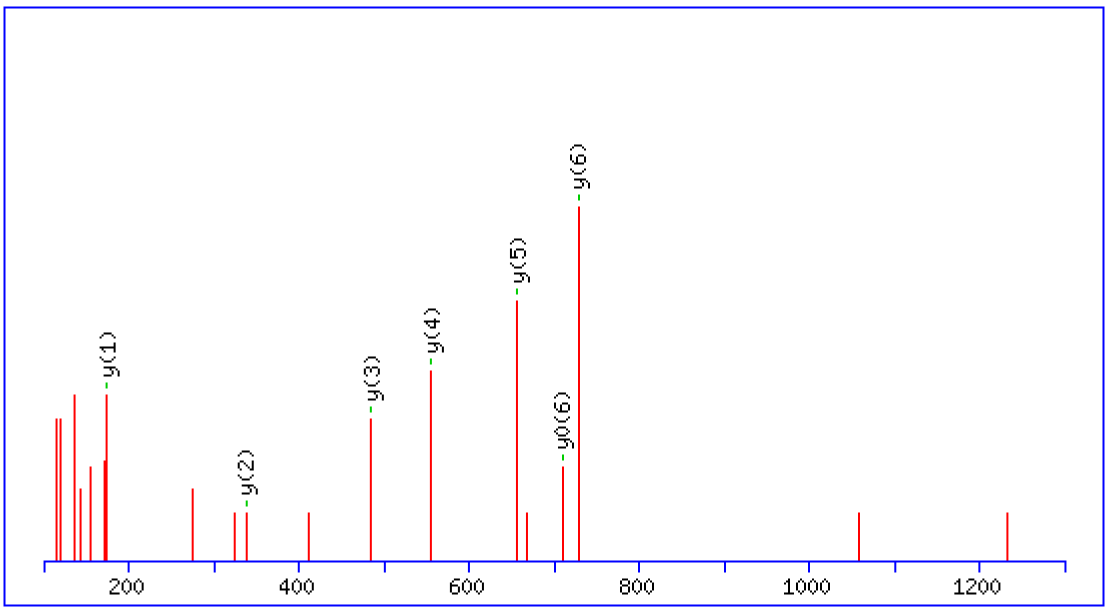
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **STATAFYR**
Found in **MGST1_HUMAN**, Microsomal glutathione S-transferase 1 OS=Homo sapiens GN=MGST1 PE=1 SV=1

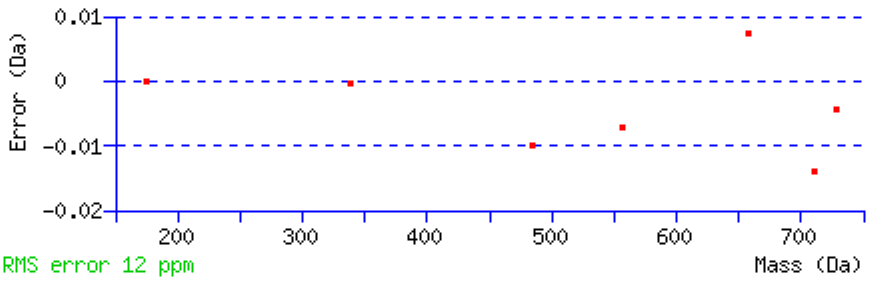
Match to Query 147542: 915.446808 from(458.730680,2+) rtinseconds(1551) index(668661)
Title: Locus:1.1.1.1257.11
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

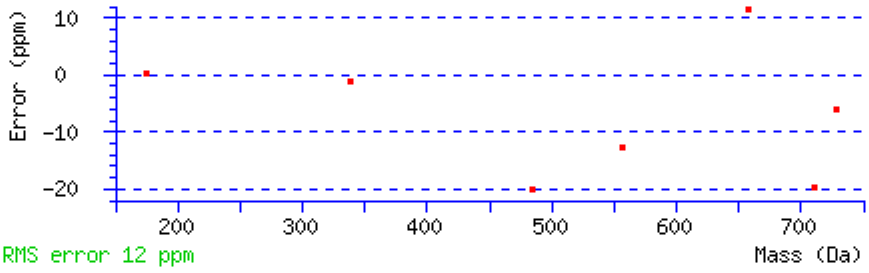
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 915.445023
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 44  Expect: 0.00045
Matches : 7/62 fragment ions using 13 most intense peaks   (help)
```

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	S							8
2	189.086983	95.047129	171.076418	86.041847	T	829.420281	415.213779	812.393732	406.700504	811.409716	406.208496	7
3	260.124097	130.565686	242.113532	121.560404	A	***728.372602***	364.689939	711.346053	356.176665	710.362037	355.684657	6
4	361.171776	181.089526	343.161211	172.084243	T	***657.335488***	329.171382	640.308939	320.658108	639.324923	320.166100	5
5	432.208890	216.608083	414.198325	207.602800	A	***556.287809***	278.647543	539.261260	270.134268			4
6	579.277304	290.142290	561.266739	281.137007	F	***485.250695***	243.128985	468.224146	234.615711			3
7	742.340633	371.673955	724.330068	362.668672	Y	***338.182281***	169.594778	321.155732	161.081504			2
8					R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
43.6	915.445023	0.001785	STATAFYR
7.8	915.441010	0.005798	DGSKPAGPR
5.8	915.452255	-0.005447	TSGRGPPGR

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

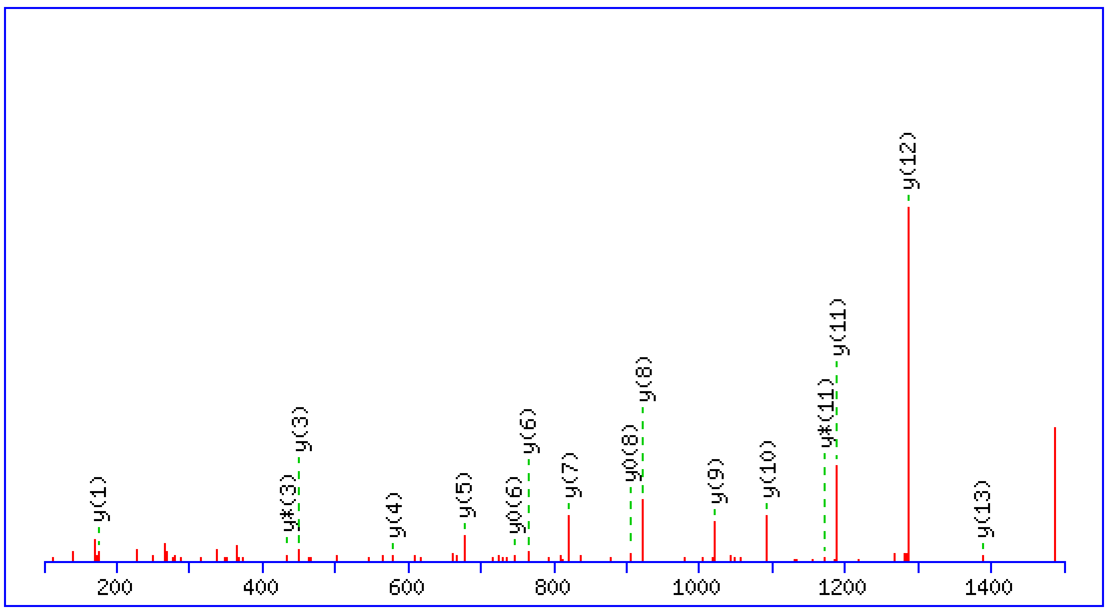
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VTPPAVTGSPEFER**
Found in **MGST2_HUMAN**, Microsomal glutathione S-transferase 2 OS=Homo sapiens GN=MGST2 PE=1 SV=1

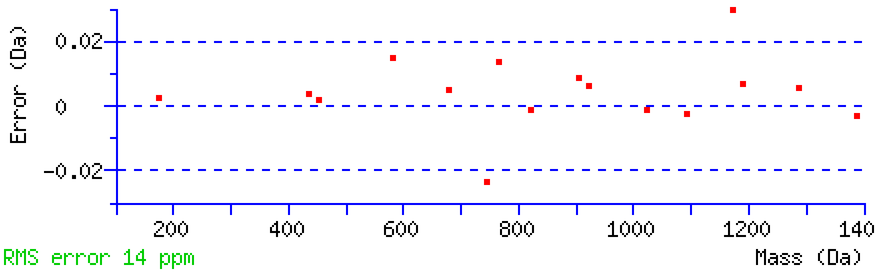
Match to Query 39107: 1485.748328 from(743.881440,2+) rtinseconds(2163) index(20819)
Title: Locus:1.1.1.2179.49
Data file 2011-11-14 - TFD - EP 8-7.mgf

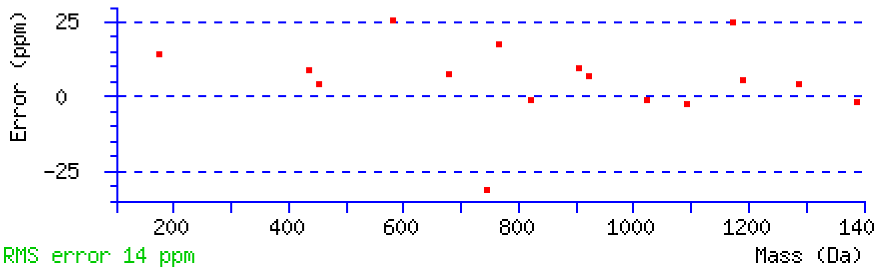
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1485.746368
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 106  Expect: 1.7e-010
Matches : 16/126 fragment ions using 25 most intense peaks   (help)
```

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	100.075690	50.541483			V							14
2	201.123369	101.065322	183.112804	92.060040	T	***1387.685222***	694.346249	1370.658673	685.832975	1369.674657	685.340967	13
3	298.176133	149.591704	280.165568	140.586422	P	***1286.637543***	643.822410	1269.610994	635.309135	1268.626978	634.817127	12
4	395.228897	198.118087	377.218332	189.112804	P	***1189.584779***	595.296028	1172.558230	586.782753	1171.574214	586.290745	11
5	466.266011	233.636643	448.255446	224.631361	A	***1092.532015***	546.769646	1075.505466	538.256371	1074.521450	537.764363	10
6	565.334425	283.170851	547.323860	274.165568	V	***1021.494901***	511.251089	1004.468352	502.737814	1003.484336	502.245806	9
7	666.382104	333.694690	648.371539	324.689408	T	***922.426487***	461.716882	905.399938	453.203607	904.415922	452.711599	8
8	723.403568	362.205422	705.393003	353.200140	G	***821.378808***	411.193042	804.352259	402.679768	803.368243	402.187760	7
9	810.435596	405.721436	792.425031	396.716154	S	***764.357344***	382.682310	747.330795	374.169036	746.346779	373.677028	6
10	907.488360	454.247818	889.477795	445.242536	P	***677.325316***	339.166296	660.298767	330.653022	659.314751	330.161014	5
11	1036.530953	518.769115	1018.520388	509.763832	E	***580.272552***	290.639914	563.246003	282.126640	562.261987	281.634632	4
12	1183.599367	592.303322	1165.588802	583.298039	F	***451.229959***	226.118617	434.203410	217.605343	433.219394	217.113335	3
13	1312.641960	656.824618	1294.631395	647.819336	E	304.161545	152.584410	287.134996	144.071136	286.150980	143.579128	2
14					R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
106.2	1485.746368	0.001960	VTPPAVTGSPEFER
1.9	1485.742340	0.005988	LSPSPTTEDPRVR
1.5	1485.736465	0.011863	SLAGPPPHFSSFSR
0.8	1485.757584	-0.009256	VIKLDHGSGEPYR

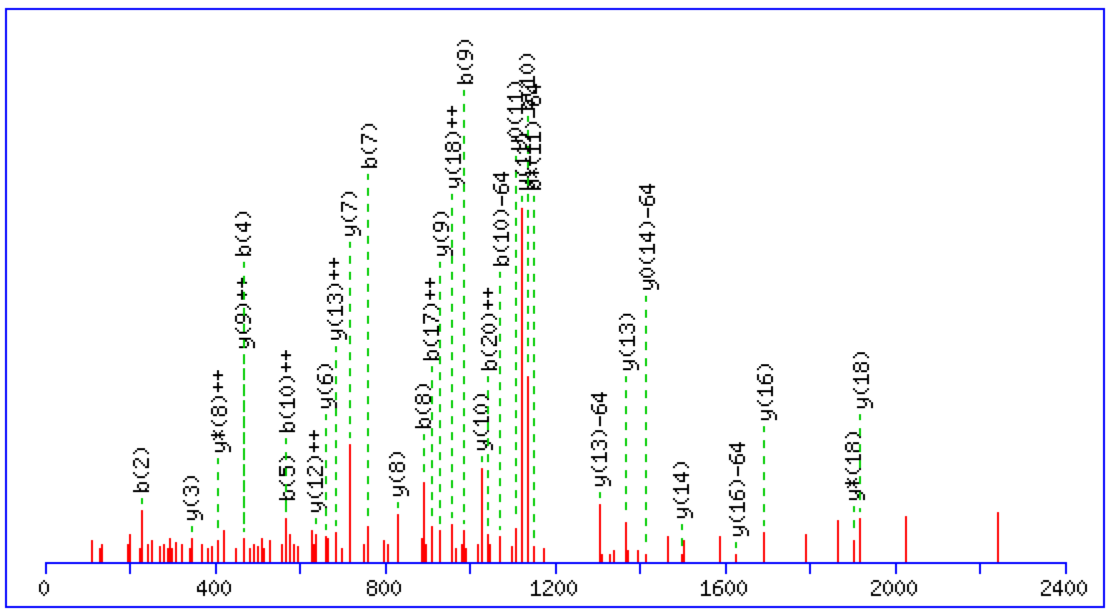
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLIQVGHEPMPPTLGTNVLGR**
Found in **MTCH1_HUMAN**, Mitochondrial carrier homolog 1 OS=Homo sapiens GN=MTCH1 PE=1 SV=1

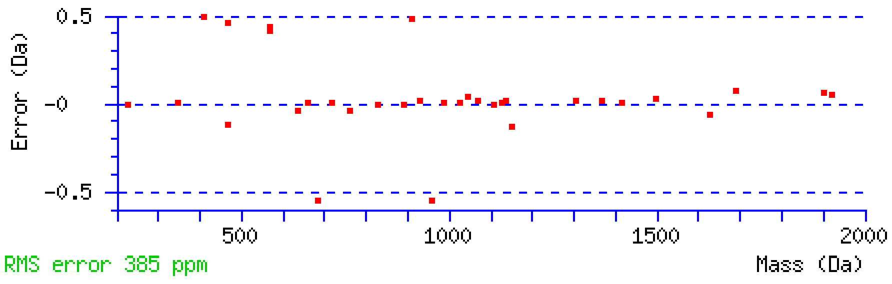
Match to Query 69829: 2257.223382 from(753.415070,3+) rtinseconds(3046) index(42728)
Title: Locus:1.1.1.2454.38
Data file 2011-11-12 - TFD - EP 6-4.mgf

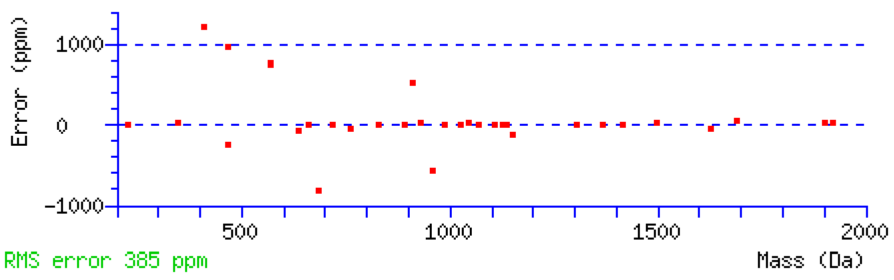
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2257.225281
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M10     : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 55  Expect: 1.7e-005
Matches : 33/330 fragment ions using 63 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							21
2	***227.175404***	114.091340					L	2145.148488	1073.077882	2128.121939	1064.564607	2127.137923	1064.072599	20
3	340.259468	170.633372					I	2032.064424	1016.535850	2015.037875	1008.022575	2014.053859	1007.530567	19
4	***468.318046***	234.662661	451.291497	226.149386			Q	***1918.980360***	959.993818	1901.953811	951.480543	1900.969795	950.988535	18
5	***567.386460***	284.196868	550.359911	275.683594			V	1790.921782	895.964529	1773.895233	887.451254	1772.911217	886.959246	17
6	624.407924	312.707600	607.381375	304.194326			G	***1691.853368***	846.430322	1674.826819	837.917047	1673.842803	837.425039	16
7	***761.466836***	381.237056	744.440287	372.723782			H	1634.831904	817.919590	1617.805355	809.406315	1616.821339	808.914307	15
8	***890.509429***	445.758353	873.482880	437.245078	872.498864	436.753070	E	***1497.772992***	749.390134	1480.746443	740.876859	1479.762427	740.384851	14
9	***987.562193***	494.284735	970.535644	485.771460	969.551628	485.279452	P	***1368.730399***	684.868837	1351.703850	676.355563	1350.719834	675.863555	13
10	***1134.597593***	**567.802435**	1117.571044	559.289160	1116.587028	558.797152	M	1271.677635	636.342455	1254.651086	627.829181	1253.667070	627.337173	12
11	1231.650357	616.328817	1214.623808	607.815542	1213.639792	607.323534	P	***1124.642235***	562.824755	1107.615686	554.311481	1106.631670	553.819473	11
12	1328.703121	664.855199	1311.676572	656.341924	1310.692556	655.849916	P	***1027.589471***	514.298373	1010.562922	505.785099	1009.578906	505.293091	10
13	1429.750800	715.379038	1412.724251	706.865764	1411.740235	706.373756	T	***930.536707***	465.771991	913.510158	457.258717	912.526142	456.766709	9
14	1542.834864	771.921070	1525.808315	763.407796	1524.824299	762.915787	L	***829.489028***	415.248152	812.462479	406.734877	811.478463	406.242869	8
15	1599.856328	800.431802	1582.829779	791.918527	1581.845763	791.426519	G	***716.404964***	358.706120	699.378415	350.192845	698.394399	349.700837	7
16	1700.904007	850.955641	1683.877458	842.442367	1682.893442	841.950359	T	***659.383500***	330.195388	642.356951	321.682113	641.372935	321.190105	6
17	1814.946934	**907.977105**	1797.920385	899.463830	1796.936369	898.971822	N	558.335821	279.671548	541.309272	271.158274			5
18	1914.015348	957.511312	1896.988799	948.998038	1896.004783	948.506029	V	444.292894	222.650085	427.266345	214.136810			4
19	2027.099412	1014.053344	2010.072863	1005.540070	2009.088847	1005.048061	L	***345.224480***	173.115878	328.197931	164.602603			3
20	2084.120876	**1042.564076**	2067.094327	1034.050801	2066.110311	1033.558793	G	232.140416	116.573846	215.113867	108.060571			2
21							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.6	2257.225281	-0.001899	LLIQVGHEPMPPTLGTNVLGR
46.8	2257.225281	-0.001899	LLIQVGHEPMPPTLGTNVLGR
34.6	2257.225281	-0.001899	LLIQVGHEPMPPTLGTNVLGR
28.6	2257.225281	-0.001899	LLIQVGHEPMPPTLGTNVLGR

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

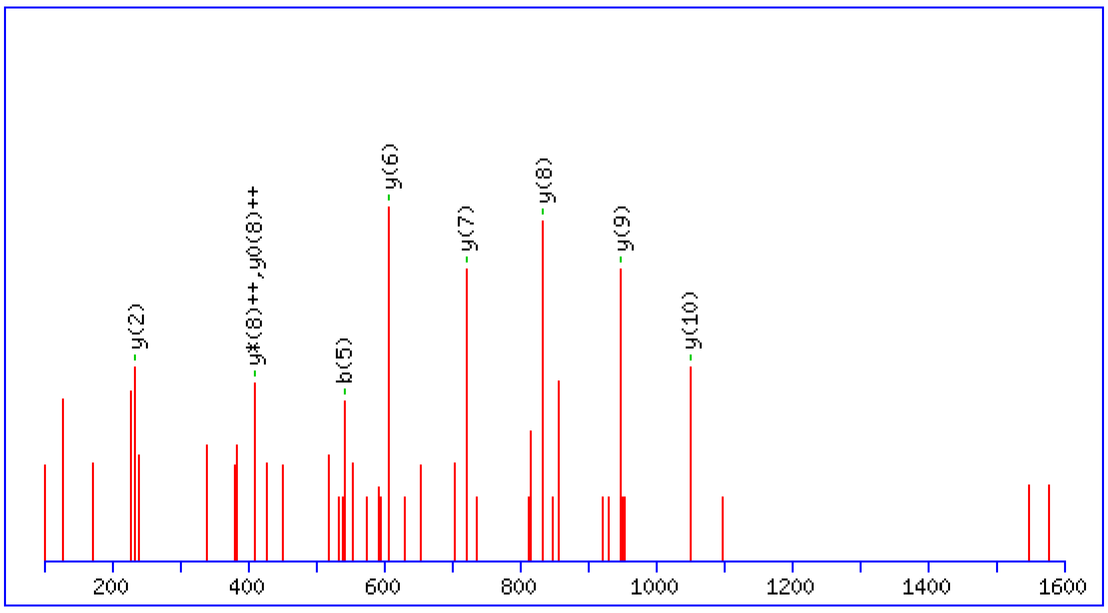
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VTDLLGGLFSK**
Found in **TIM44_HUMAN**, Mitochondrial import inner membrane translocase subunit TIM44 OS=Homo sapiens GN=TIMM44 PE=1 SV=2

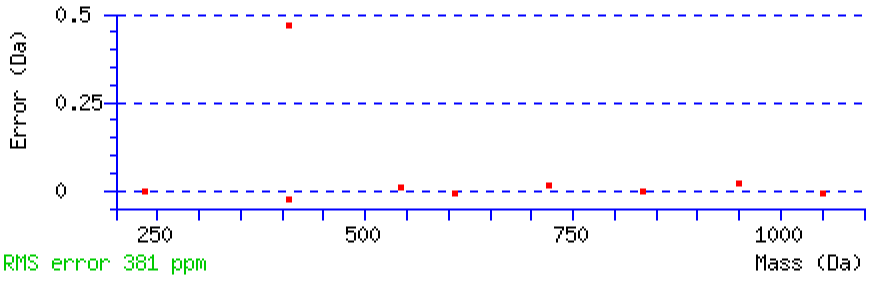
Match to Query 25512: 1148.646468 from(575.330510,2+) rtinseconds(3584) index(52249)
Title: Locus:1.1.1.2790.9
Data file 2011-11-13 - TFD - EP 7-4.mgf

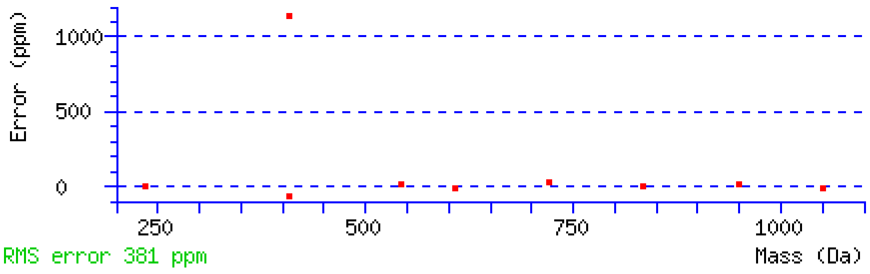
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1148.644135
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 47  Expect: 0.00013
Matches : 9/96 fragment ions using 10 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483			V							11
2	201.123369	101.065322	183.112804	92.060040	T	***1050.582988***	525.795132	1033.556439	517.281858	1032.572423	516.789850	10
3	316.150312	158.578794	298.139747	149.573512	D	***949.535309***	475.271293	932.508760	466.758018	931.524744	466.266010	9
4	429.234376	215.120826	411.223811	206.115544	L	***834.508366***	417.757821	817.481817	409.244547	816.497801	408.752539	8
5	542.318440	271.662858	524.307875	262.657576	L	***721.424302***	361.215789	704.397753	352.702515	703.413737	352.210507	7
6	599.339904	300.173590	581.329339	291.168308	G	***608.340238***	304.673757	591.313689	296.160483	590.329673	295.668475	6
7	656.361368	328.684322	638.350803	319.679040	G	551.318774	276.163025	534.292225	267.649751	533.308209	267.157743	5
8	769.445432	385.226354	751.434867	376.221072	L	494.297310	247.652293	477.270761	239.139019	476.286745	238.647011	4
9	916.513846	458.760561	898.503281	449.755279	F	381.213246	191.110261	364.186697	182.596987	363.202681	182.104979	3
10	1003.545874	502.276575	985.535309	493.271293	S	***234.144832***	117.576054	217.118283	109.062780	216.134267	108.570772	2
11					K	147.112804	74.060040	130.086255	65.546766			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.0	1148.644135	0.002333	VTDLLGGLFSK

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

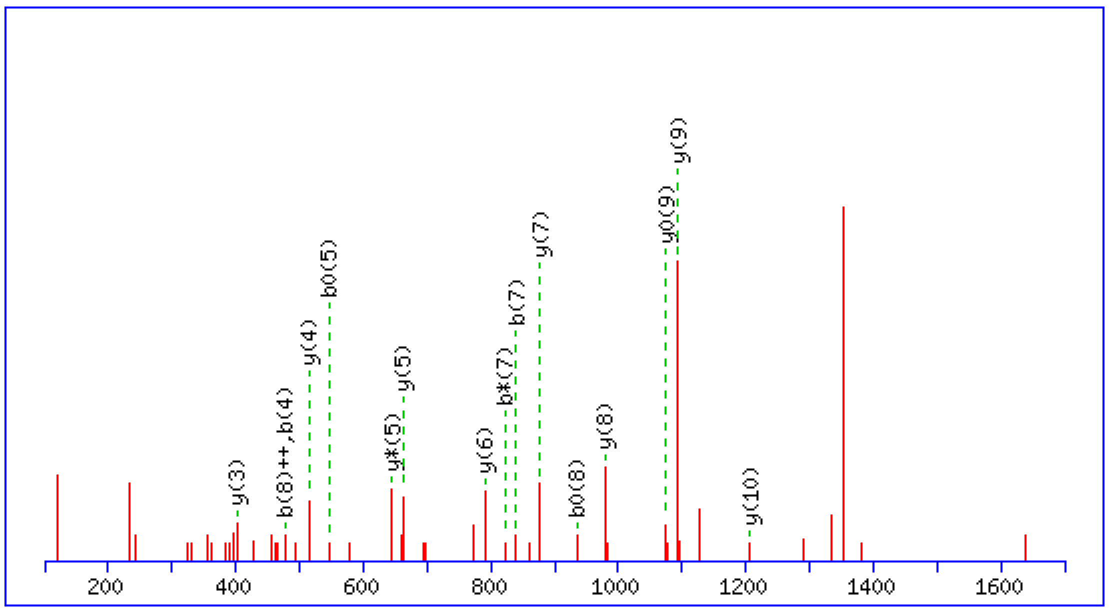
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FIDTSQFILNR**
Found in **TIM8A_HUMAN**, Mitochondrial import inner membrane translocase subunit Tim8 A OS=Homo sapiens GN=TIMM8A PE=1 SV=1

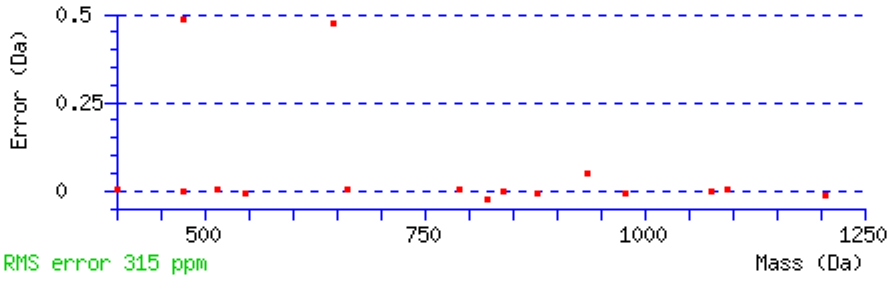
Match to Query 35026: 1352.699908 from(677.357230,2+) rtinseconds(3083) index(35483)
Title: Locus:1.1.1.2509.43
Data file 2011-11-12 - TFD - EP 6-7.mgf

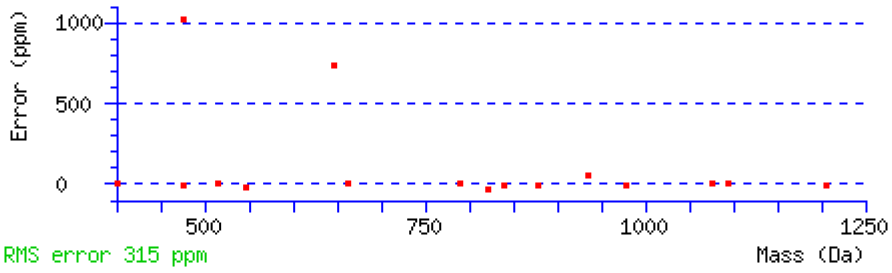
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1700] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1352.708847
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 53  Expect: 1.5e-005
Matches : 16/94 fragment ions using 29 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	148.075690	74.541483					F							11
2	261.159754	131.083515					I	***1206.647713***	603.827494	1189.621164	595.314220	1188.637148	594.822212	10
3	376.186697	188.596986			358.176132	179.591704	D	***1093.563649***	547.285462	1076.537100	538.772188	1075.553084	538.280180	9
4	**477.234376**	239.120826			459.223811	230.115544	T	***978.536706***	489.771991	961.510157	481.258716	960.526141	480.766708	8
5	564.266404	282.636840			546.255839	273.631558	S	***877.489027***	439.248151	860.462478	430.734877	859.478462	430.242869	7
6	692.324982	346.666129	675.298433	338.152855	674.314417	337.660847	Q	***790.456999***	395.732137	773.430450	387.218863			6
7	**839.393396**	420.200336	822.366847	411.687062	821.382831	411.195054	F	***662.398421***	331.702848	645.371872	323.189574			5
8	952.477460	476.742368	935.450911	468.229094	934.466895	467.737086	I	***515.330007***	258.168641	498.303458	249.655367			4
9	1065.561524	533.284400	1048.534975	524.771126	1047.550959	524.279117	L	***402.245943***	201.626609	385.219394	193.113335			3
10	1179.604451	590.305863	1162.577902	581.792589	1161.593886	581.300581	N	289.161879	145.084577	272.135330	136.571303			2
11							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
53.1	1352.708847	-0.008939	FIDTSQFILNR
1.6	1352.708847	-0.008939	FPSPHPSPAKLK
0.5	1352.708862	-0.008954	FPDFKSAGVTLR

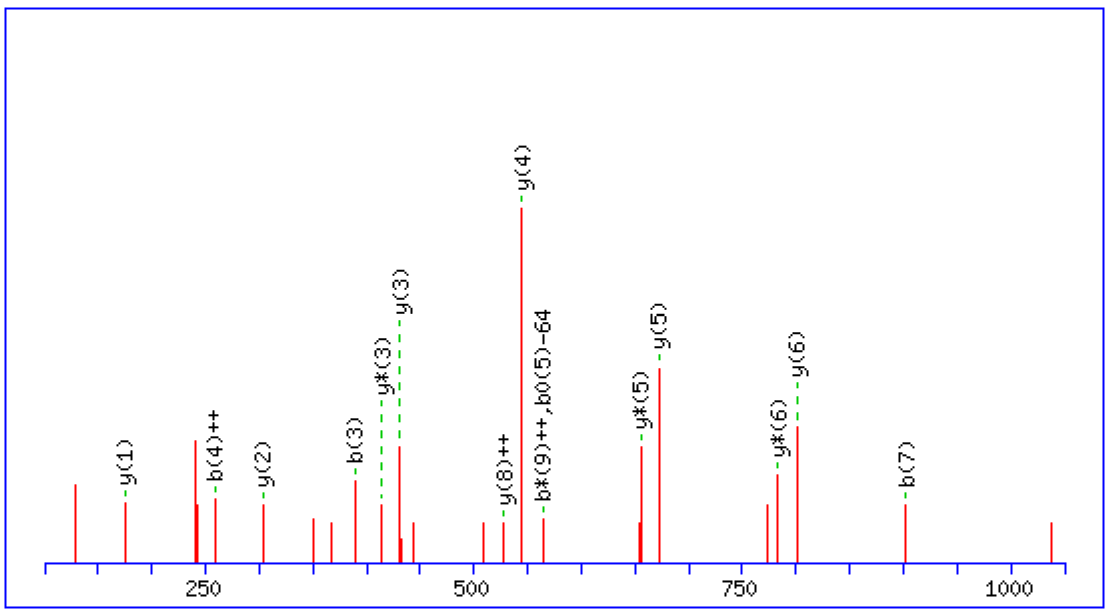
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LQMEQQQQLQQR**
Found in **TOM22_HUMAN**, Mitochondrial import receptor subunit TOM22 homolog OS=Homo sapiens GN=TOMM22 PE=1 SV=3

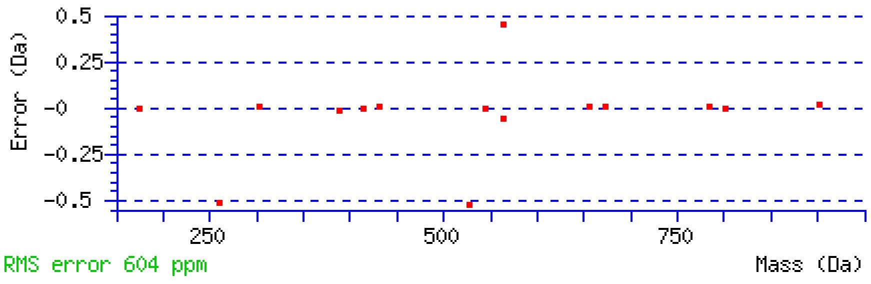
Match to Query 43499: 1572.771042 from(525.264290,3+) rtinseconds(1153) index(3856)
Title: Locus:1.1.1.1706.34
Data file 2011-11-10 - TFD - EP 3-6.mgf

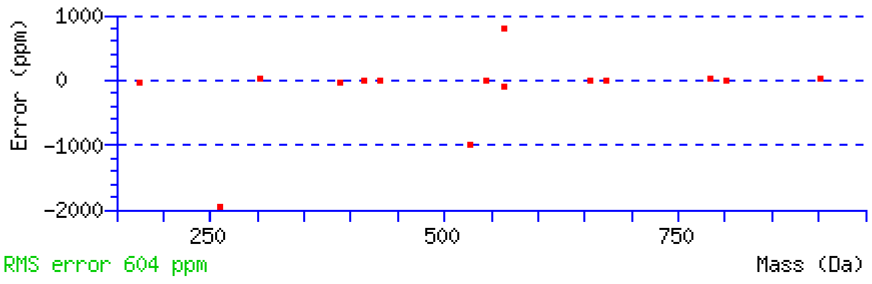
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1572.767822
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M3 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 35 **Expect:** 0.0047
Matches : 15/172 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							12
2	242.149918	121.578597	225.123369	113.065323			Q	1460.691055	730.849166	1443.664506	722.335891	1442.680490	721.843883	11
3	**389.185318**	195.096297	372.158769	186.583023			M	1332.632477	666.819877	1315.605928	658.306602	1314.621912	657.814594	10
4	518.227911	259.617594	501.201362	251.104319	500.217346	250.612311	E	1185.597077	593.302177	1168.570528	584.788902	1167.586512	584.296894	9
5	646.286489	323.646883	629.259940	315.133608	628.275924	314.641600	Q	1056.554484	528.780880	1039.527935	520.267606			8
6	774.345067	387.676172	757.318518	379.162897	756.334502	378.670889	Q	928.495906	464.751591	911.469357	456.238317			7
7	**902.403645**	451.705461	885.377096	443.192186	884.393080	442.700178	Q	***800.437328***	400.722302	783.410779	392.209028			6
8	1030.462223	515.734750	1013.435674	507.221475	1012.451658	506.729467	Q	***672.378750***	336.693013	655.352201	328.179739			5
9	1143.546287	572.276782	1126.519738	563.763507	1125.535722	563.271499	L	***544.320172***	272.663724	527.293623	264.150449			4
10	1271.604865	636.306071	1254.578316	627.792796	1253.594300	627.300788	Q	***431.236108***	216.121692	414.209559	207.608417			3
11	1399.663443	700.335360	1382.636894	691.822085	1381.652878	691.330077	Q	***303.177530***	152.092403	286.150981	143.579129			2
12							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.6	1572.767822	0.003220	LQMEQQQQLQQR
12.1	1572.756592	0.014450	CQQPASELLQDVR
7.2	1572.763123	0.007919	ALPTPSDSTLPAEAR
3.1	1572.785583	-0.014541	SRATSVGDQLEAPAR
2.0	1572.785599	-0.014557	NRAEDQTSPVVTTR
1.8	1572.767822	0.003220	MDAPRASAAKPPTGR
1.8	1572.767822	0.003220	MDAPRASAAKPPTGR
1.6	1572.783081	-0.012039	IRPSAVYVCGEHR
1.5	1572.768448	0.002594	VWEAWREEAELR
0.6	1572.781738	-0.010696	AGSLSPGQEQMVELK

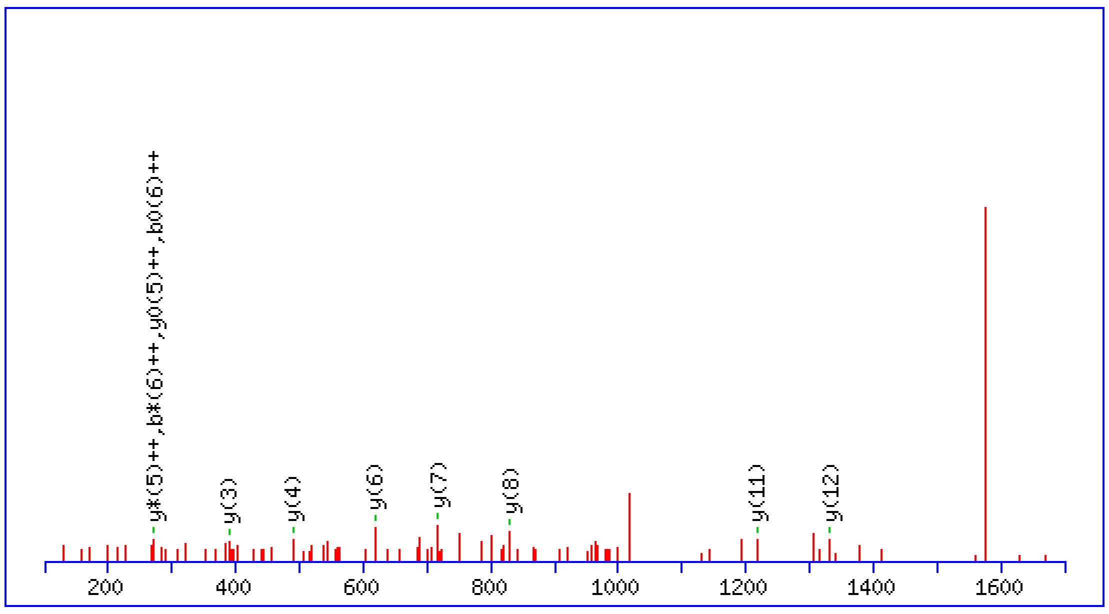
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GSVDSNWIVGATLEK**
Found in **TOM40_HUMAN**, Mitochondrial import receptor subunit TOM40 homolog OS=Homo sapiens GN=TOMM40 PE=1 SV=1

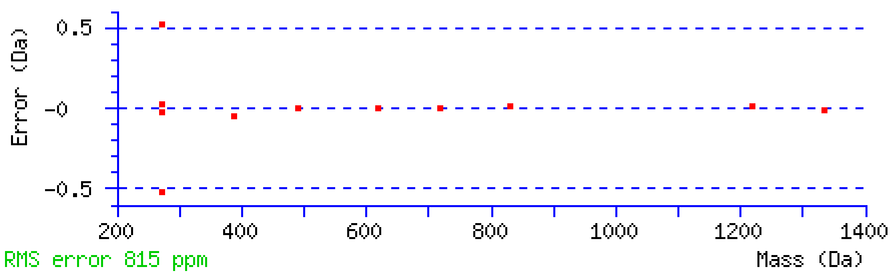
Match to Query 49639: 1574.790368 from(788.402460,2+) rtinseconds(3040) index(42661)
Title: Locus:1.1.1.2482.32
Data file 2011-11-10 - TFD - EP 4-4.mgf

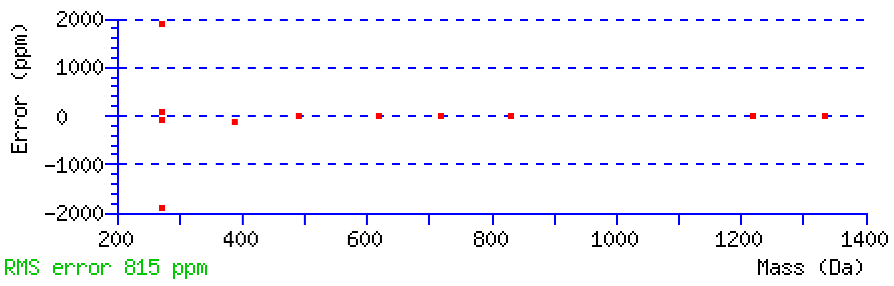
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1574.794037
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 44 **Expect:** 0.0014
Matches : 11/154 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							15
2	145.060768	73.034022			127.050203	64.028740	S	1518.779849	759.893563	1501.753300	751.380288	1500.769284	750.888280	14
3	244.129182	122.568229			226.118617	113.562947	V	1431.747821	716.377549	1414.721272	707.864274	1413.737256	707.372266	13
4	359.156125	180.081701			341.145560	171.076418	D	***1332.679407***	666.843342	1315.652858	658.330067	1314.668842	657.838059	12
5	446.188153	223.597715			428.177588	214.592432	S	***1217.652464***	609.329870	1200.625915	600.816596	1199.641899	600.324588	11
6	560.231080	280.619178	543.204531	272.105904	542.220515	271.613896	N	1130.620436	565.813856	1113.593887	557.300582	1112.609871	556.808574	10
7	746.310393	373.658835	729.283844	365.145560	728.299828	364.653552	W	1016.577509	508.792393	999.550960	500.279118	998.566944	499.787110	9
8	859.394457	430.200867	842.367908	421.687592	841.383892	421.195584	I	***830.498196***	415.752736	813.471647	407.239462	812.487631	406.747454	8
9	958.462871	479.735074	941.436322	471.221799	940.452306	470.729791	V	***717.414132***	359.210704	700.387583	350.697430	699.403567	350.205422	7
10	1015.484335	508.245806	998.457786	499.732531	997.473770	499.240523	G	***618.345718***	309.676497	601.319169	301.163223	600.335153	300.671215	6
11	1086.521449	543.764363	1069.494900	535.251088	1068.510884	534.759080	A	561.324254	281.165765	544.297705	272.652491	543.313689	272.160483	5
12	1187.569128	594.288202	1170.542579	585.774928	1169.558563	585.282920	T	***490.287140***	245.647208	473.260591	237.133934	472.276575	236.641926	4
13	1300.653192	650.830234	1283.626643	642.316960	1282.642627	641.824952	L	***389.239461***	195.123369	372.212912	186.610094	371.228896	186.118086	3
14	1429.695785	715.351531	1412.669236	706.838256	1411.685220	706.346248	E	276.155397	138.581337	259.128848	130.068062	258.144832	129.576054	2
15							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
43.9	1574.794037	-0.003669	GSVDSNWIVGATLEK
16.3	1574.776276	0.014092	TPADCPVIAIDSFR

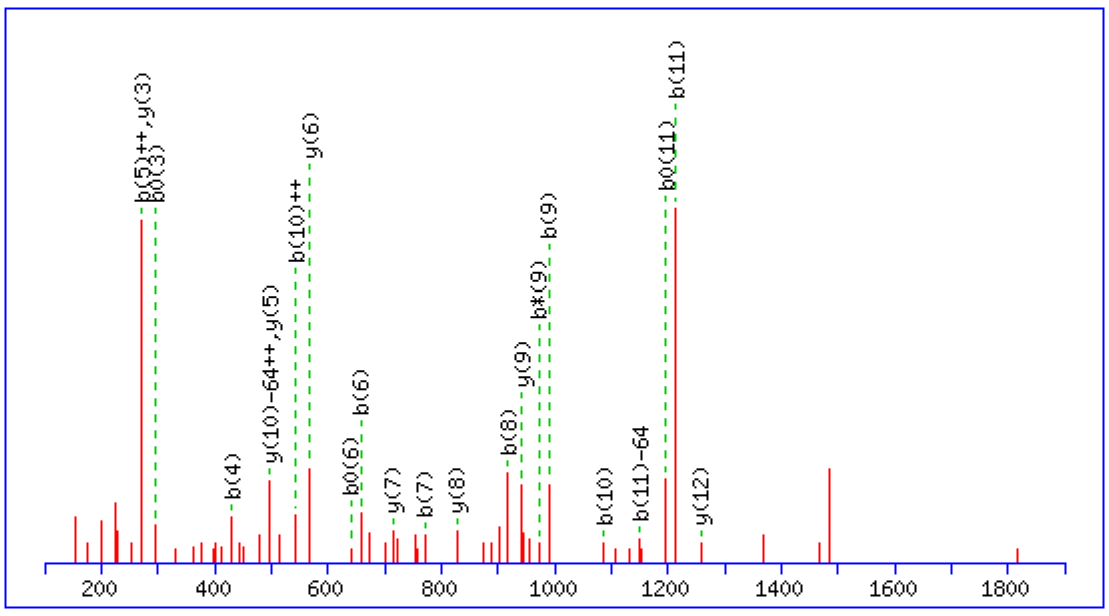
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NLSDIDLMAPQPGV**
Found in **TOM6_HUMAN**, Mitochondrial import receptor subunit TOM6 homolog OS=Homo sapiens GN=TOMM6 PE=1 SV=1

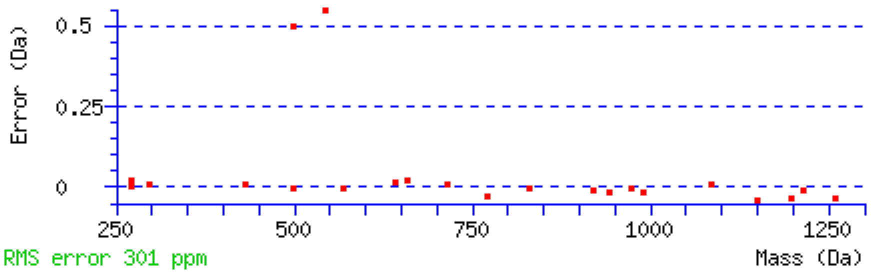
Match to Query 38793: 1484.714288 from(743.364420,2+) rtinseconds(3039) index(30848)
Title: Locus:1.1.1.2616.19
Data file 2011-11-10 - TFD - EP 4-7.mgf

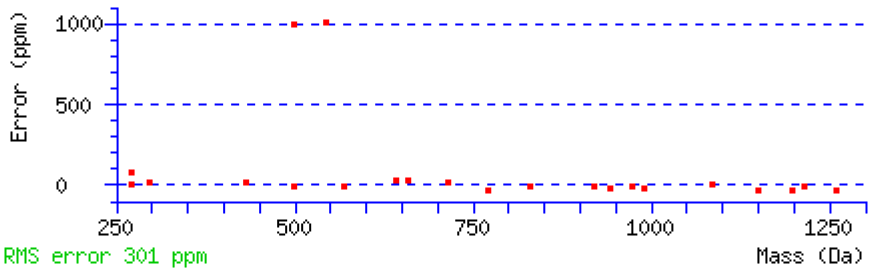
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1484.718094
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M8 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 68 **Expect:** 5.6e-007
Matches : 22/204 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			N							14
2	228.134267	114.570771	211.107718	106.057497			L	1371.682445	686.344860	1354.655896	677.831586	1353.671880	677.339578	13
3	315.166295	158.086785	298.139746	149.573511	297.155730	149.081503	S	***1258.598381***	629.802828	1241.571832	621.289554	1240.587816	620.797546	12
4	***430.193238***	215.600257	413.166689	207.086983	412.182673	206.594975	D	1171.566353	586.286814	1154.539804	577.773540	1153.555788	577.281532	11
5	543.277302	**272.142289**	526.250753	263.629015	525.266737	263.137007	I	1056.539410	528.773343	1039.512861	520.260068	1038.528845	519.768060	10
6	***658.304245***	329.655761	641.277696	321.142486	640.293680	320.650478	D	***943.455346***	472.231311	926.428797	463.718036	925.444781	463.226028	9
7	***771.388309***	386.197793	754.361760	377.684518	753.377744	377.192510	L	***828.428403***	414.717839	811.401854	406.204565			8
8	***918.423709***	459.715493	901.397160	451.202218	900.413144	450.710210	M	***715.344339***	358.175807	698.317790	349.662533			7
9	***989.460823***	495.234050	972.434274	486.720775	971.450258	486.228767	A	***568.308939***	284.658107	551.282390	276.144833			6
10	***1086.513587***	**543.760431**	1069.487038	535.247157	1068.503022	534.755149	P	***497.271825***	249.139550	480.245276	240.626276			5
11	***1214.572165***	607.789720	1197.545616	599.276446	1196.561600	598.784438	Q	400.219061	200.613168	383.192512	192.099894			4
12	1311.624929	656.316102	1294.598380	647.802828	1293.614364	647.310820	P	***272.160483***	136.583879					3
13	1368.646393	684.826834	1351.619844	676.313560	1350.635828	675.821552	G	175.107719	88.057497					2
14							V	118.086255	59.546766					1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
68.1	1484.718094	-0.003806	NLSDIDLMAPQPGV
34.6	1484.718094	-0.003806	NLSDIDLMAPQPGV
14.6	1484.718094	-0.003806	NLSDIDLMAPQPGV
1.4	1484.704163	0.010125	CPAGHKQSETTQK
1.0	1484.725937	-0.011649	LSDLEAQWAPSPR
0.8	1484.727295	-0.013007	ENRPPGTFHQFR

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

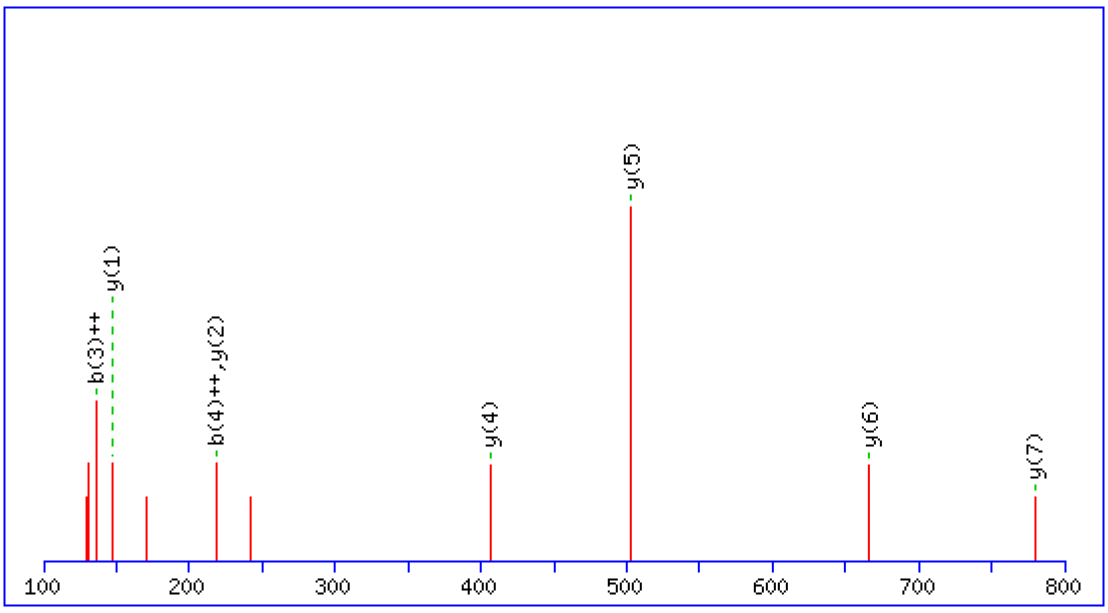
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **SAIYPTSAK**
Found in **MSRA_HUMAN**, Mitochondrial peptide methionine sulfoxide reductase OS=Homo sapiens GN=MSRA PE=1 SV=1

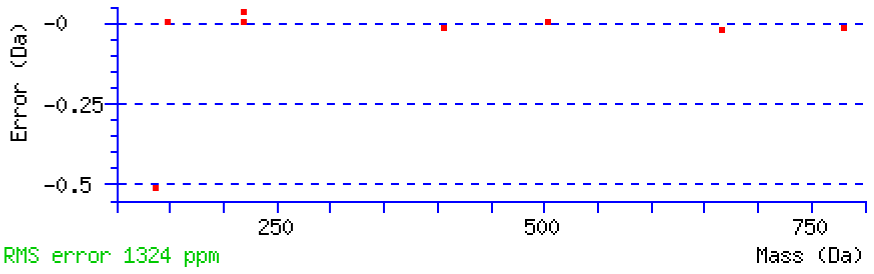
Match to Query 10647: 936.488168 from(469.251360,2+) rtinseconds(1238) index(3885)
Title: Locus:1.1.1.2056.15
Data file 2011-11-12 - TFD - EP 5-5.mgf

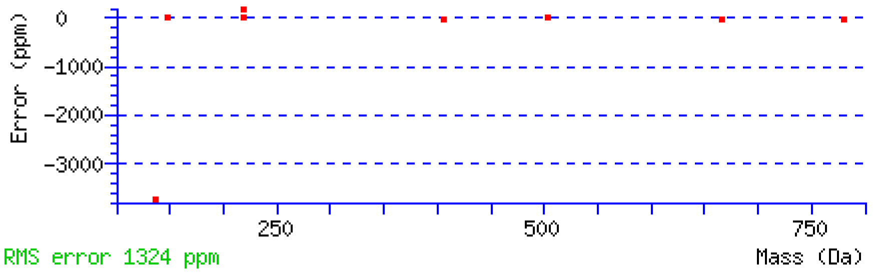
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 936.491623
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 57 **Expect:** 1.5e-005
Matches : 8/76 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	S							9
2	159.076418	80.041847	141.065853	71.036564	A	850.466896	425.737086	833.440347	417.223812	832.456331	416.731804	8
3	272.160482	**136.583879**	254.149917	127.578597	I	***779.429782***	390.218529	762.403233	381.705255	761.419217	381.213247	7
4	435.223811	**218.115544**	417.213246	209.110261	Y	***666.345718***	333.676497	649.319169	325.163223	648.335153	324.671215	6
5	532.276575	266.641926	514.266010	257.636643	P	***503.282389***	252.144832	486.255840	243.631558	485.271824	243.139550	5
6	633.324254	317.165765	615.313689	308.160483	T	***406.229625***	203.618450	389.203076	195.105176	388.219060	194.613168	4
7	720.356282	360.681779	702.345717	351.676497	S	305.181946	153.094611	288.155397	144.581336	287.171381	144.089328	3
8	791.393396	396.200336	773.382831	387.195054	A	***218.149918***	109.578597	201.123369	101.065322			2
9					K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.9	936.491623	-0.003455	SAIYPTSAK
21.6	936.491653	-0.003485	TGISDVFAK
14.9	936.485107	0.003061	ASLPHGPMK
1.6	936.488953	-0.000785	RGPQPNPR
1.1	936.488937	-0.000769	RDHRPEK

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

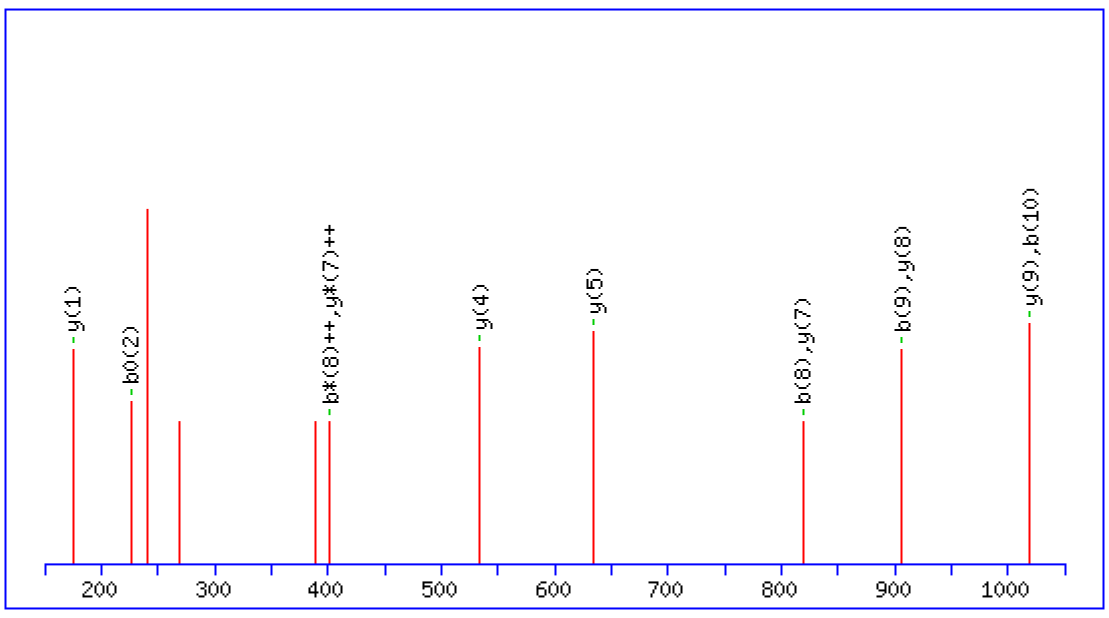
Mascot Search Results

Peptide View

MS/MS Fragmentation of **RSLNSSSSSPPSSPTMMPR**
Found in **M3KL4_HUMAN**, Mitogen-activated protein kinase kinase kinase MLK4 OS=Homo sapiens GN=MLK4 PE=1 SV=1

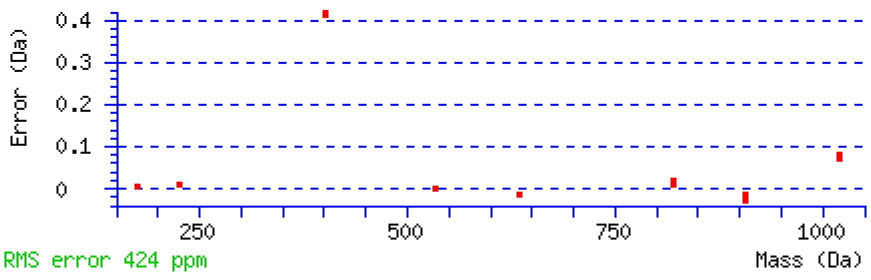
Match to Query 17731: 2036.944176 from(510.243320,4+) rtinseconds(1016) index(2805)
Title: Locus:1.1.1.1701.21
Data file 2011-11-10 - TFD - EP 4-5.mgf

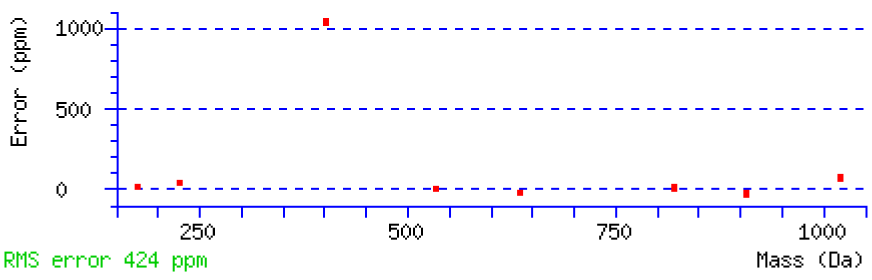
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2036.925522
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P10 : Oxidation (P)
P11 : Oxidation (P)
Ions Score: 46 **Expect:** 0.00071
Matches : 12/206 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	157.108387	79.057831	140.081838	70.544557			R							19
2	244.140415	122.573845	227.113866	114.060571	226.129850	113.568563	S	1881.831702	941.419489	1864.805153	932.906215	1863.821137	932.414207	18
3	357.224479	179.115877	340.197930	170.602603	339.213914	170.110595	L	1794.799674	897.903475	1777.773125	889.390201	1776.789109	888.898193	17
4	471.267406	236.137341	454.240857	227.624067	453.256841	227.132059	N	1681.715610	841.361443	1664.689061	832.848169	1663.705045	832.356161	16
5	558.299434	279.653355	541.272885	271.140081	540.288869	270.648073	S	1567.672683	784.339980	1550.646134	775.826705	1549.662118	775.334697	15
6	645.331462	323.169369	628.304913	314.656094	627.320897	314.164087	S	1480.640655	740.823966	1463.614106	732.310691	1462.630090	731.818683	14
7	732.363490	366.685383	715.336941	358.172108	714.352925	357.680100	S	1393.608627	697.307952	1376.582078	688.794677	1375.598062	688.302669	13
8	**819.395518**	410.201397	802.368969	401.688122	801.384953	401.196114	S	1306.576599	653.791938	1289.550050	645.278663	1288.566034	644.786655	12
9	**906.427546**	453.717411	889.400997	445.204136	888.416981	444.712128	S	1219.544571	610.275924	1202.518022	601.762649	1201.534006	601.270641	11
10	**1019.475225**	510.241250	1002.448676	501.727976	1001.464660	501.235968	P	1132.512543	566.759910	1115.485994	558.246635	1114.501978	557.754627	10
11	1132.522904	566.765090	1115.496355	558.251816	1114.512339	557.759807	P	***1019.464864***	510.236070	1002.438315	501.722796	1001.454299	501.230788	9
12	1219.554932	610.281104	1202.528383	601.767830	1201.544367	601.275822	S	***906.417185***	453.712231	889.390636	445.198956	888.406620	444.706948	8
13	1306.586960	653.797118	1289.560411	645.283844	1288.576395	644.791836	S	***819.385157***	410.196217	802.358608	401.682942	801.374592	401.190934	7
14	1403.639724	702.323500	1386.613175	693.810226	1385.629159	693.318218	P	732.353129	366.680203	715.326580	358.166928	714.342564	357.674920	6
15	1504.687403	752.847340	1487.660854	744.334065	1486.676838	743.842057	T	***635.300365***	318.153821	618.273816	309.640546	617.289800	309.148538	5
16	1635.727888	818.367582	1618.701339	809.854308	1617.717323	809.362300	M	***534.252686***	267.629981	517.226137	259.116707			4
17	1766.768373	883.887825	1749.741824	875.374550	1748.757808	874.882542	M	403.212201	202.109738	386.185652	193.596464			3
18	1863.821137	932.414207	1846.794588	923.900932	1845.810572	923.408924	P	272.171716	136.589496	255.145167	128.076221			2
19							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.8	2036.925522	0.018654	RSLNSSSSSPPSSPTMMPR
32.0	2036.925522	0.018654	RSLNSSSSSPPSSPTMMPR
19.7	2036.925522	0.018654	RSLNSSSSSPPSSPTMMPR
16.9	2036.925522	0.018654	RSLNSSSSSPPSSPTMMPR
16.9	2036.925522	0.018654	RSLNSSSSSPPSSPTMMPR
16.1	2036.951309	-0.007133	YSSMEDHLEILEWTLR
14.3	2036.925522	0.018654	RSLNSSSSSPPSSPTMMPR
13.0	2036.930054	0.014122	GDARGAQLWPPGSDPDGGPR
11.2	2036.930054	0.014122	GDARGAQLWPPGSDPDGGPR
11.2	2036.930054	0.014122	GDARGAQLWPPGSDPDGGPR

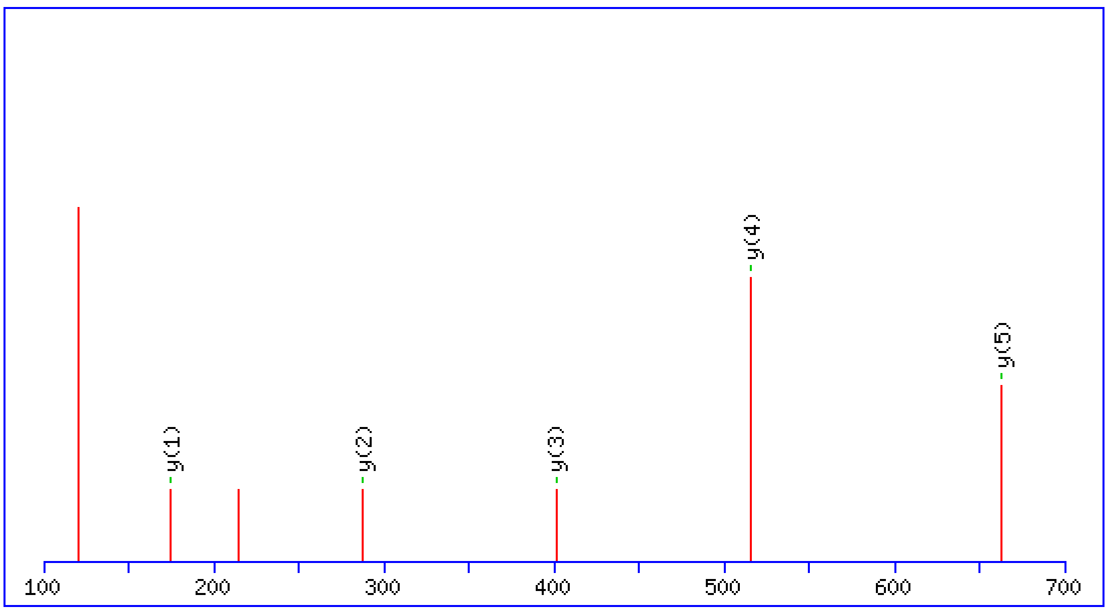
(MATRIX SCIENCE) Mascot Search Results

Peptide View

MS/MS Fragmentation of **EIFDLIR**
Found in **MIP18_HUMAN**, Mitotic spindle-associated MMXD complex subunit MIP18 OS=Homo sapiens GN=FAM96B PE=1 SV=1

Match to Query 8267: 904.504328 from(453.259440,2+) rtinseconds(3128) index(34932)
Title: Locus:1.1.1.2647.10
Data file 2011-11-13 - TFD - EP 7-7.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
Label all possible matches ○ Label matches used for scoring ●



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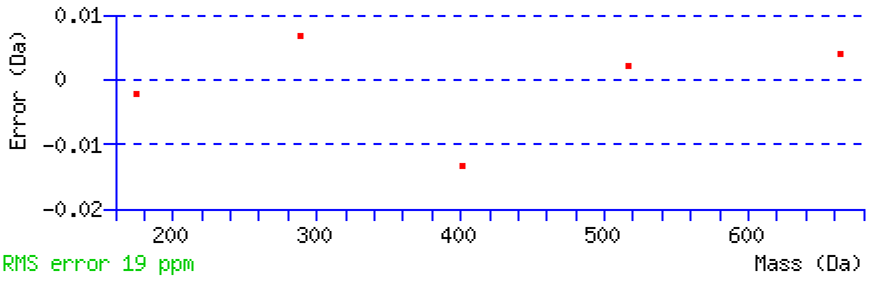
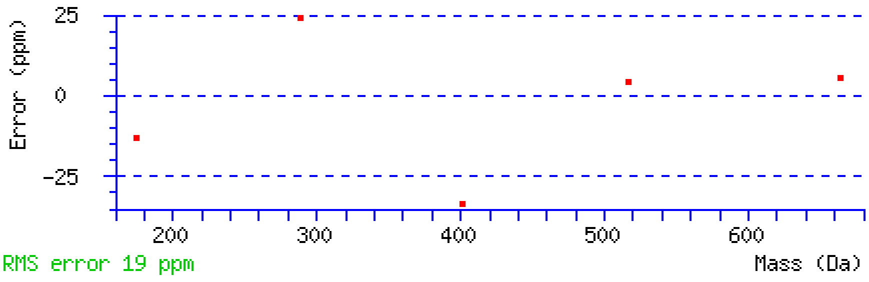
Monoisotopic mass of neutral peptide Mr(calc): 904.501801
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 47  Expect: 0.00023
Matches : 5/54 fragment ions using 6 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572	112.039304	56.523290	E							7
2	243.133933	122.070605	225.123368	113.065322	I	776.466501	388.736889	759.439952	380.223614	758.455936	379.731606	6
3	390.202347	195.604811	372.191782	186.599529	F	***663.382437***	332.194857	646.355888	323.681582	645.371872	323.189574	5
4	505.229290	253.118283	487.218725	244.113001	D	***516.314023***	258.660650	499.287474	250.147375	498.303458	249.655367	4
5	618.313354	309.660315	600.302789	300.655033	L	***401.287080***	201.147178	384.260531	192.633903			3
6	731.397418	366.202347	713.386853	357.197065	I	***288.203016***	144.605146	271.176467	136.091871			2
7					R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of EIFDLIR
(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	904.501801	0.002527	EIFDLIR
30.2	904.513031	-0.008703	NKFIDLR
12.7	904.513031	-0.008703	AAGAFSLLR
4.9	904.497803	0.006525	SVVGTSSLR
4.5	904.501801	0.002527	IEFLQQK
2.6	904.501801	0.002527	IYLLPDR
2.6	904.501801	0.002527	YLPLLDR
1.0	904.513031	-0.008703	EIKNVFR

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

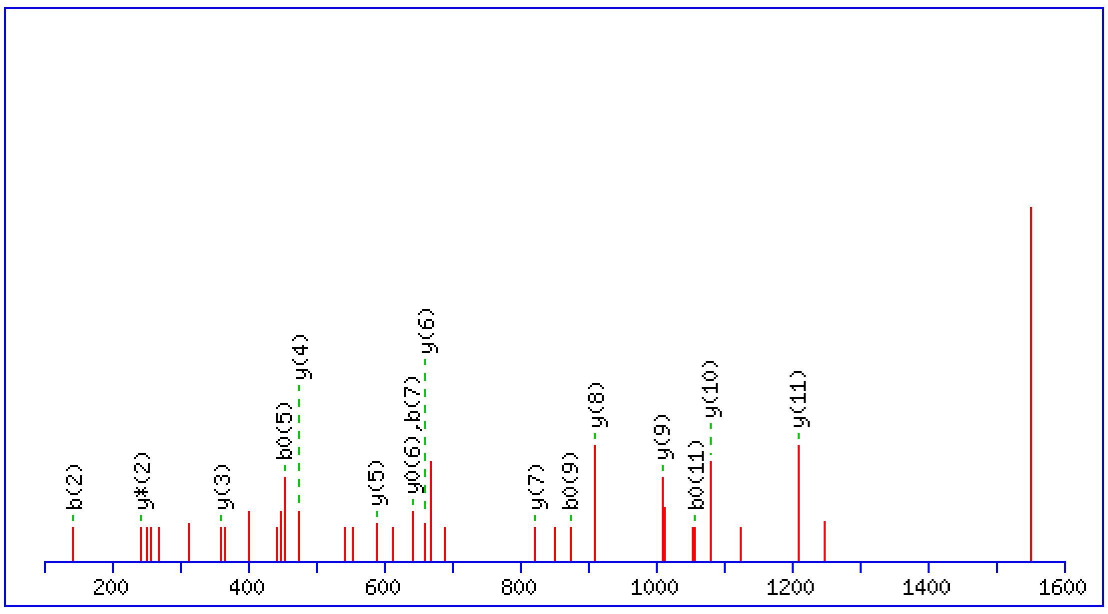
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **AASLEAVSYAIDTLK**
Found in **MOC2B_HUMAN**, Molybdopterin synthase catalytic subunit OS=Homo sapiens GN=MOCS2 PE=1 SV=1

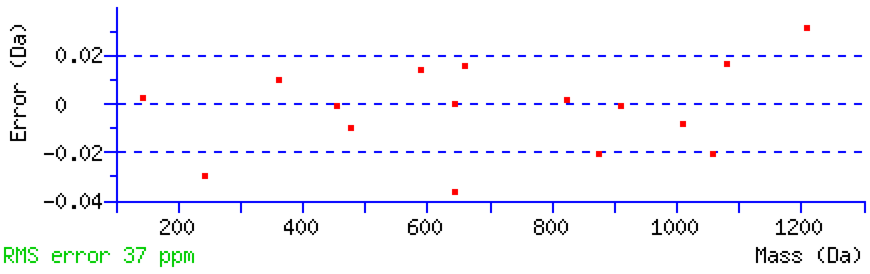
Match to Query 45342: 1550.819008 from(776.416780,2+) rtinseconds(3646) index(49256)
Title: Locus:1.1.1.2972.37
Data file 2011-11-12 - TFD - EP 5-5.mgf

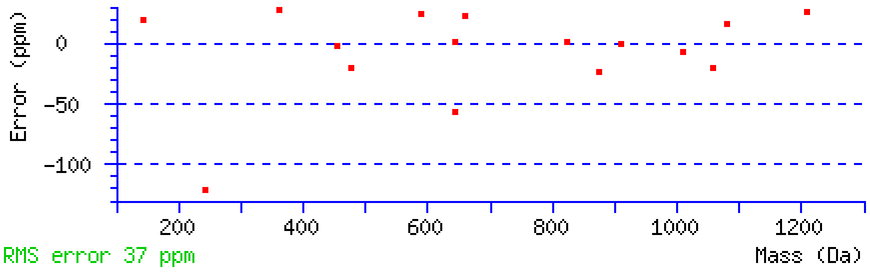
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1600] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1550.819153
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 59  Expect: 1.4e-005
Matches : 16/132 fragment ions using 27 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			A							15
2	**143.081504**	72.044390			A	1480.789352	740.898314	1463.762803	732.385040	1462.778787	731.893032	14
3	230.113532	115.560404	212.102967	106.555121	S	1409.752238	705.379757	1392.725689	696.866483	1391.741673	696.374475	13
4	343.197596	172.102436	325.187031	163.097153	L	1322.720210	661.863743	1305.693661	653.350469	1304.709645	652.858460	12
5	472.240189	236.623732	454.229624	227.618450	E	***1209.636146***	605.321711	1192.609597	596.808437	1191.625581	596.316429	11
6	543.277303	272.142290	525.266738	263.137007	A	***1080.593553***	540.800414	1063.567004	532.287140	1062.582988	531.795132	10
7	**642.345717**	321.676497	624.335152	312.671214	V	***1009.556439***	505.281858	992.529890	496.768583	991.545874	496.276575	9
8	729.377745	365.192511	711.367180	356.187228	S	***910.488025***	455.747651	893.461476	447.234376	892.477460	446.742368	8
9	892.441074	446.724175	874.430509	437.718893	Y	***823.455997***	412.231637	806.429448	403.718362	805.445432	403.226354	7
10	963.478188	482.242732	945.467623	473.237450	A	***660.392668***	330.699972	643.366119	322.186697	642.382103	321.694689	6
11	1076.562252	538.784764	1058.551687	529.779481	I	***589.355554***	295.181415	572.329005	286.668140	571.344989	286.176132	5
12	1191.589195	596.298236	1173.578630	587.292953	D	***476.271490***	238.639383	459.244941	230.126108	458.260925	229.634100	4
13	1292.636874	646.822075	1274.626309	637.816793	T	***361.244547***	181.125911	344.217998	172.612637	343.233982	172.120629	3
14	1405.720938	703.364107	1387.710373	694.358824	L	260.196868	130.602072	243.170319	122.088797			2
15					K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.7	1550.819153	-0.000145	AASLEAVSYAIDTLK

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

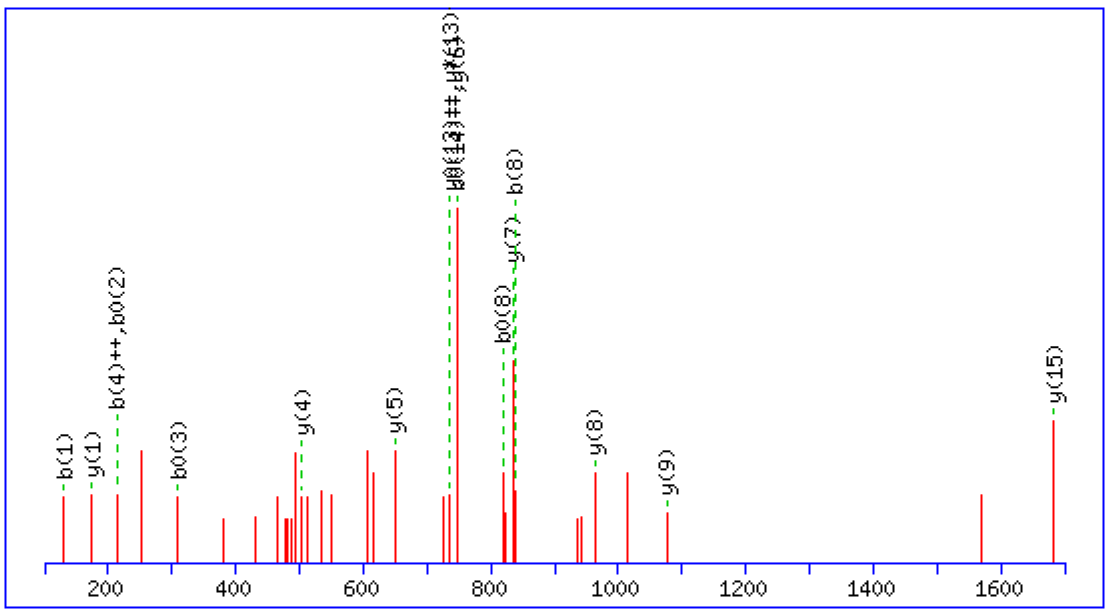
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ETPPDALILESPFTNIR**
Found in **ABD12_HUMAN**, Monoacylglycerol lipase ABHD12 OS=Homo sapiens GN=ABHD12 PE=2 SV=2

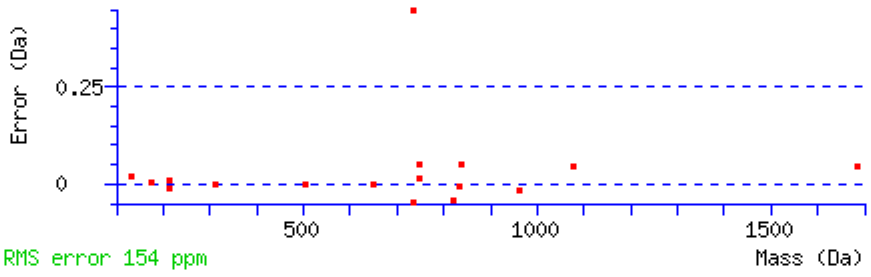
Match to Query 61309: 1912.007292 from(638.343040,3+) rtinseconds(3851) index(57435)
Title: Locus:1.1.1.2802.17
Data file 2011-11-10 - TFD - EP 3-4.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●

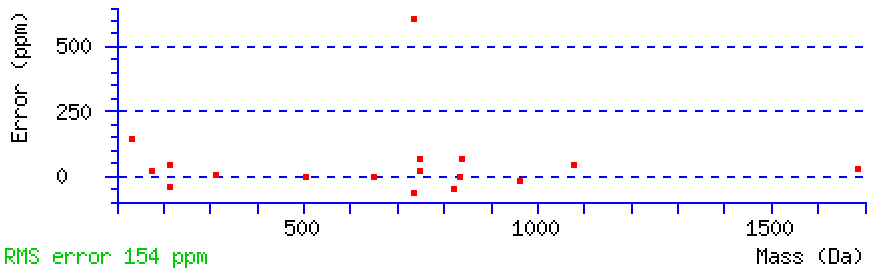


Monoisotopic mass of neutral peptide Mr(calc): 1911.994171
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 44 **Expect:** 0.0001
Matches : 17/158 fragment ions using 26 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	**130.049869**	65.528572			112.039304	56.523290	E							17
2	231.097548	116.052412			213.086983	107.047130	T	1783.958877	892.483077	1766.932328	883.969802	1765.948312	883.477794	16
3	328.150312	164.578794			310.139747	155.573512	P	***1682.911198***	841.959237	1665.884649	833.445963	1664.900633	832.953955	15
4	425.203076	213.105176			407.192511	204.099894	P	1585.858434	793.432855	1568.831885	784.919581	1567.847869	784.427573	14
5	540.230019	270.618648			522.219454	261.613365	D	1488.805670	744.906473	1471.779121	736.393199	1470.795105	735.901190	13
6	611.267133	306.137205			593.256568	297.131922	A	1373.778727	687.393002	1356.752178	678.879727	1355.768162	678.387719	12
7	724.351197	362.679237			706.340632	353.673954	L	1302.741613	651.874445	1285.715064	643.361170	1284.731048	642.869162	11
8	**837.435261**	419.221269			819.424696	410.215986	I	1189.657549	595.332413	1172.631000	586.819138	1171.646984	586.327130	10
9	950.519325	475.763301			932.508760	466.758018	L	***1076.573485***	538.790381	1059.546936	530.277106	1058.562920	529.785098	9
10	1079.561918	540.284597			1061.551353	531.279315	E	***963.489421***	482.248349	946.462872	473.735074	945.478856	473.243066	8
11	1166.593946	583.800611			1148.583381	574.795329	S	***834.446828***	417.727052	817.420279	409.213778	816.436263	408.721770	7
12	1263.646710	632.326993			1245.636145	623.321711	P	***747.414800***	374.211038	730.388251	365.697764	729.404235	365.205756	6
13	1410.715124	705.861200			1392.704559	696.855918	F	***650.362036***	325.684656	633.335487	317.171382	632.351471	316.679374	5
14	1511.762803	756.385040			1493.752238	747.379757	T	***503.293622***	252.150449	486.267073	243.637174	485.283057	243.145166	4
15	1625.805730	813.406503	1608.779181	804.893229	1607.795165	804.401221	N	402.245943	201.626609	385.219394	193.113335			3
16	1738.889794	869.948535	1721.863245	861.435261	1720.879229	860.943253	I	288.203016	144.605146	271.176467	136.091871			2
17							R	***175.118952***	88.063114	158.092403	79.549839			1



RMS error 154 ppm



RMS error 154 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.3	1911.994171	0.013121	ETPPDALILESPFTNIR
1.7	1912.024048	-0.016756	MVPIIPGGNSIPLTFSNR
1.0	1911.994171	0.013121	VFPALAGQAPEEQGEIIK
0.9	1911.998917	0.008375	QDVMVHFIVPVKNQAR
0.0	1912.020004	-0.012712	KINQNVAALPVASSVMDR
0.0	1911.994858	0.012434	AGPAQTLIRPQDMKGASR

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

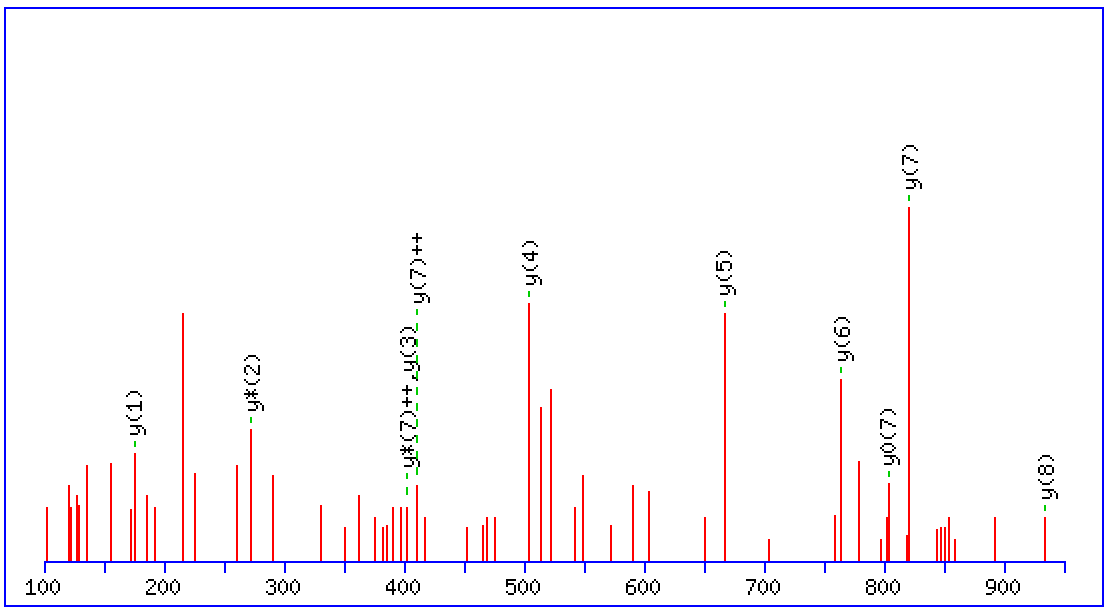
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELGPYTLDR**
Found in **MUC16_HUMAN**, Mucin-16 OS=Homo sapiens GN=MUC16 PE=1 SV=2

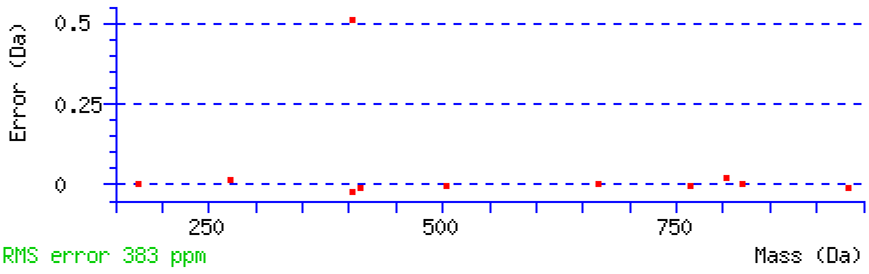
Match to Query 346279: 1062.541088 from(532.277820,2+) rtinseconds(2168) index(918962)
Title: Locus:1.1.1.1227.23
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

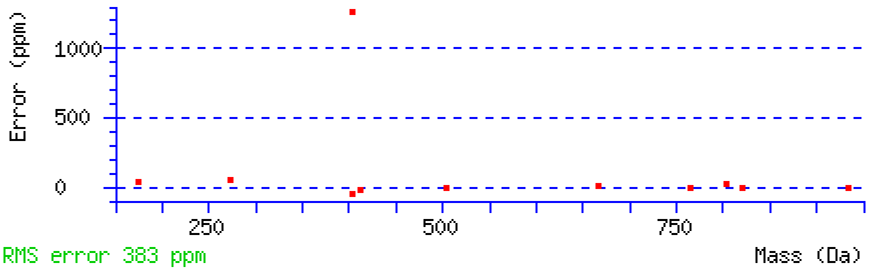
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1062.534561
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 48 **Expect:** 0.00017
Matches : 11/78 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	130.049869	65.528572	112.039304	56.523290	E							9
2	243.133933	122.070605	225.123368	113.065322	L	***934.499259***	467.753268	917.472710	459.239993	916.488694	458.747985	8
3	300.155397	150.581336	282.144832	141.576054	G	***821.415195***	411.211236	804.388646	402.697961	803.404630	402.205953	7
4	397.208161	199.107718	379.197596	190.102436	P	***764.393731***	382.700504	747.367182	374.187229	746.383166	373.695221	6
5	560.271490	280.639383	542.260925	271.634101	Y	***667.340967***	334.174122	650.314418	325.660847	649.330402	325.168839	5
6	661.319169	331.163223	643.308604	322.157940	T	***504.277638***	252.642457	487.251089	244.129182	486.267073	243.637174	4
7	774.403233	387.705255	756.392668	378.699972	L	***403.229959***	202.118617	386.203410	193.605343	385.219394	193.113335	3
8	889.430176	445.218726	871.419611	436.213444	D	290.145895	145.576585	273.119346	137.063311	272.135330	136.571303	2
9					R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.3	1062.534561	0.006527	ELGPYTLDR
7.6	1062.534561	0.006527	EPGDLKFNK
7.1	1062.545776	-0.004688	EIFQNEKR
6.0	1062.537918	0.003170	EISDLMLAR
6.0	1062.545776	-0.004688	ELALGQYNR
6.0	1062.545776	-0.004688	ELNEQFKR
6.0	1062.534546	0.006542	EPEKYPLR
4.3	1062.545807	-0.004719	GEGGAPPLPPR
4.3	1062.545792	-0.004704	EPSGLRFNK
2.3	1062.534546	0.006542	IPSAEYLDR

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

{MATRIX SCIENCE}

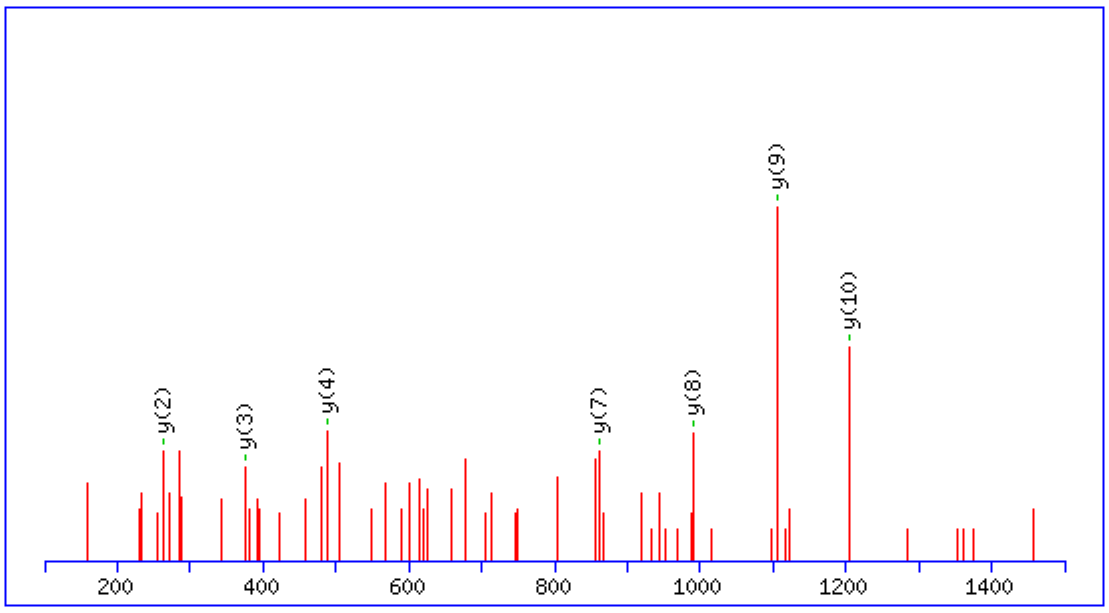
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NAVDEFLLLLDK**
Found in **MALT1_HUMAN**, Mucosa-associated lymphoid tissue lymphoma translocation protein 1 OS=Homo sapiens GN=MALT1 PE=1 SV=1

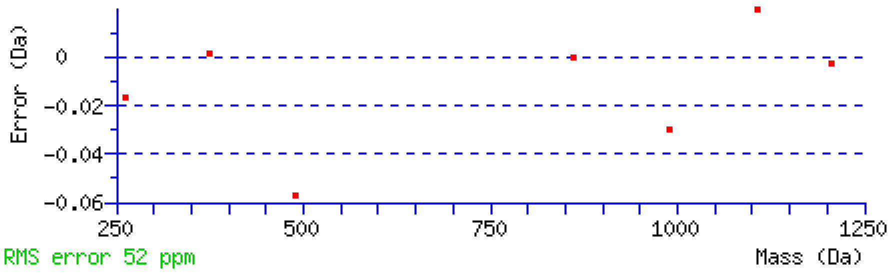
Match to Query 40867: 1388.760328 from(695.387440,2+) rtinseconds(4565) index(67812)
Title: Locus:1.1.1.3212.14
Data file 2011-11-10 - TFD - EP 4-2.mgf

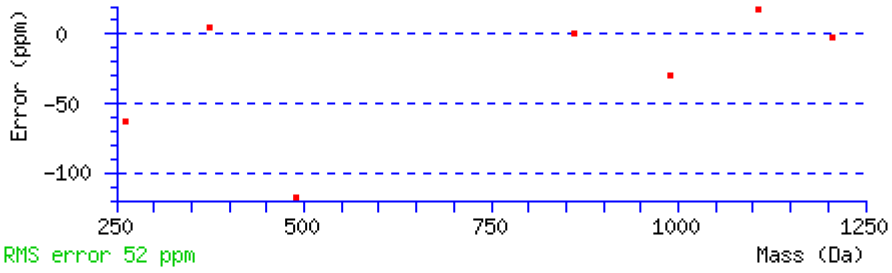
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1388.755112
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 46 **Expect:** 0.00025
Matches : 7/124 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			N							12
2	186.087317	93.547296	169.060768	85.034022			A	1275.719481	638.363379	1258.692932	629.850104	1257.708916	629.358096	11
3	285.155731	143.081504	268.129182	134.568229			V	***1204.682367***	602.844822	1187.655818	594.331547	1186.671802	593.839539	10
4	400.182674	200.594975	383.156125	192.081701	382.172109	191.589693	D	***1105.613953***	553.310615	1088.587404	544.797340	1087.603388	544.305332	9
5	529.225267	265.116272	512.198718	256.602997	511.214702	256.110989	E	***990.587010***	495.797143	973.560461	487.283868	972.576445	486.791860	8
6	676.293681	338.650479	659.267132	330.137204	658.283116	329.645196	F	***861.544417***	431.275847	844.517868	422.762572	843.533852	422.270564	7
7	789.377745	395.192511	772.351196	386.679236	771.367180	386.187228	L	714.476003	357.741640	697.449454	349.228365	696.465438	348.736357	6
8	902.461809	451.734543	885.435260	443.221268	884.451244	442.729260	L	601.391939	301.199608	584.365390	292.686333	583.381374	292.194325	5
9	1015.545873	508.276575	998.519324	499.763300	997.535308	499.271292	L	***488.307875***	244.657575	471.281326	236.144301	470.297310	235.652293	4
10	1128.629937	564.818606	1111.603388	556.305332	1110.619372	555.813324	L	***375.223811***	188.115543	358.197262	179.602269	357.213246	179.110261	3
11	1243.656880	622.332078	1226.630331	613.818804	1225.646315	613.326796	D	***262.139747***	131.573512	245.113198	123.060237	244.129182	122.568229	2
12							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.5	1388.755112	0.005216	NAVDEFLLLLDK

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

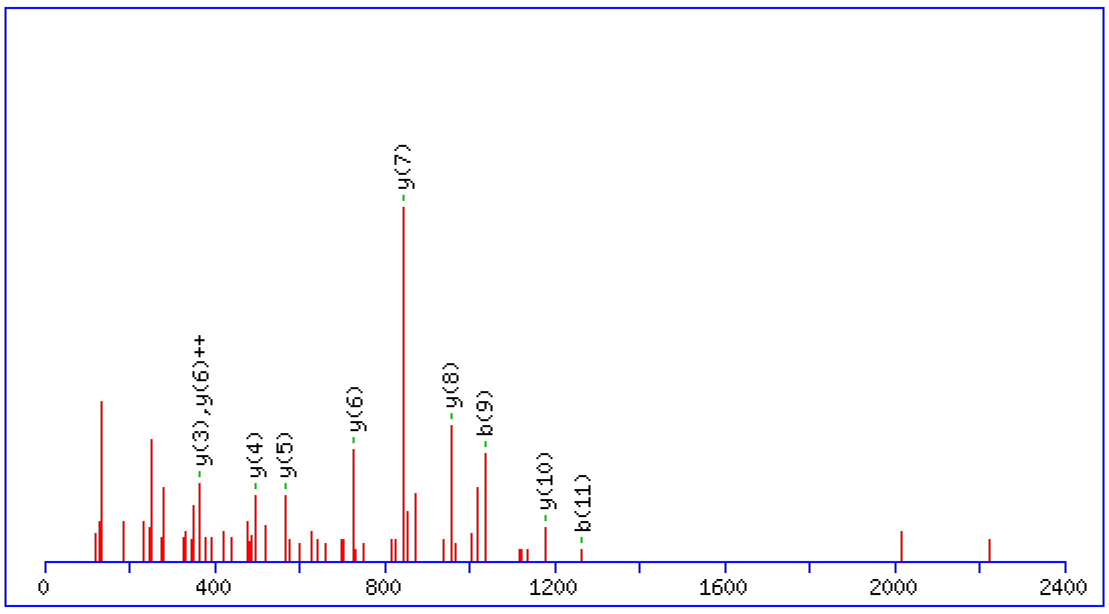
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DDDKNNDGYIDYAEFAK**
Found in **MCFD2_HUMAN**, Multiple coagulation factor deficiency protein 2 OS=Homo sapiens GN=MCFD2 PE=1 SV=1

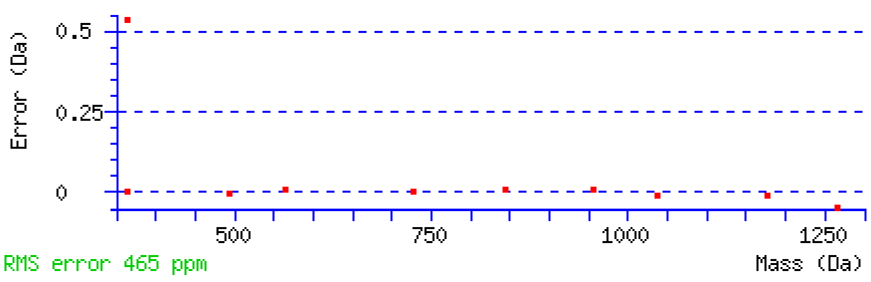
Match to Query 56158: 1991.834262 from(664.952030,3+) rtinseconds(2689) index(31524)
Title: Locus:1.1.1.2609.36
Data file 2011-11-12 - TFD - EP 5-5.mgf

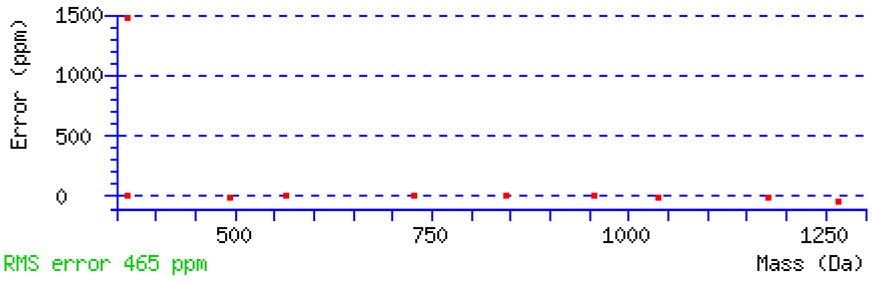
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1991.838455
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 51  Expect: 1.5e-005
Matches : 10/180 fragment ions using 12 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.034219	58.520748			98.023654	49.515465	D							17
2	231.061162	116.034219			213.050597	107.028936	D	1877.818814	939.413045	1860.792265	930.899771	1859.808249	930.407763	16
3	346.088105	173.547690			328.077540	164.542408	D	1762.791871	881.899574	1745.765322	873.386299	1744.781306	872.894291	15
4	474.183068	237.595172	457.156519	229.081898	456.172503	228.589890	K	1647.764928	824.386102	1630.738379	815.872828	1629.754363	815.380820	14
5	588.225995	294.616636	571.199446	286.103361	570.215430	285.611353	N	1519.669965	760.338621	1502.643416	751.825346	1501.659400	751.333338	13
6	702.268922	351.638099	685.242373	343.124824	684.258357	342.632816	N	1405.627038	703.317157	1388.600489	694.803883	1387.616473	694.311875	12
7	817.295865	409.151570	800.269316	400.638296	799.285300	400.146288	D	1291.584111	646.295694	1274.557562	637.782419	1273.573546	637.290411	11
8	874.317329	437.662303	857.290780	429.149028	856.306764	428.657020	G	***1176.557168***	588.782222	1159.530619	580.268948	1158.546603	579.776940	10
9	**1037.380658**	519.193967	1020.354109	510.680693	1019.370093	510.188685	Y	1119.535704	560.271490	1102.509155	551.758216	1101.525139	551.266208	9
10	1150.464722	575.735999	1133.438173	567.222725	1132.454157	566.730716	I	***956.472375***	478.739826	939.445826	470.226551	938.461810	469.734543	8
11	**1265.491665**	633.249471	1248.465116	624.736196	1247.481100	624.244188	D	***843.388311***	422.197794	826.361762	413.684519	825.377746	413.192511	7
12	1428.554994	714.781135	1411.528445	706.267861	1410.544429	705.775853	Y	***728.361368***	364.684322	711.334819	356.171048	710.350803	355.679040	6
13	1499.592108	750.299692	1482.565559	741.786418	1481.581543	741.294410	A	***565.298039***	283.152658	548.271490	274.639383	547.287474	274.147375	5
14	1628.634701	814.820989	1611.608152	806.307714	1610.624136	805.815706	E	***494.260925***	247.634101	477.234376	239.120826	476.250360	238.628818	4
15	1775.703115	888.355196	1758.676566	879.841921	1757.692550	879.349913	F	***365.218332***	183.112804	348.191783	174.599530			3
16	1846.740229	923.873753	1829.713680	915.360478	1828.729664	914.868470	A	218.149918	109.578597	201.123369	101.065322			2
17							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
50.8	1991.838455	-0.004193	DDDKNNDGYIDYAEFAK

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

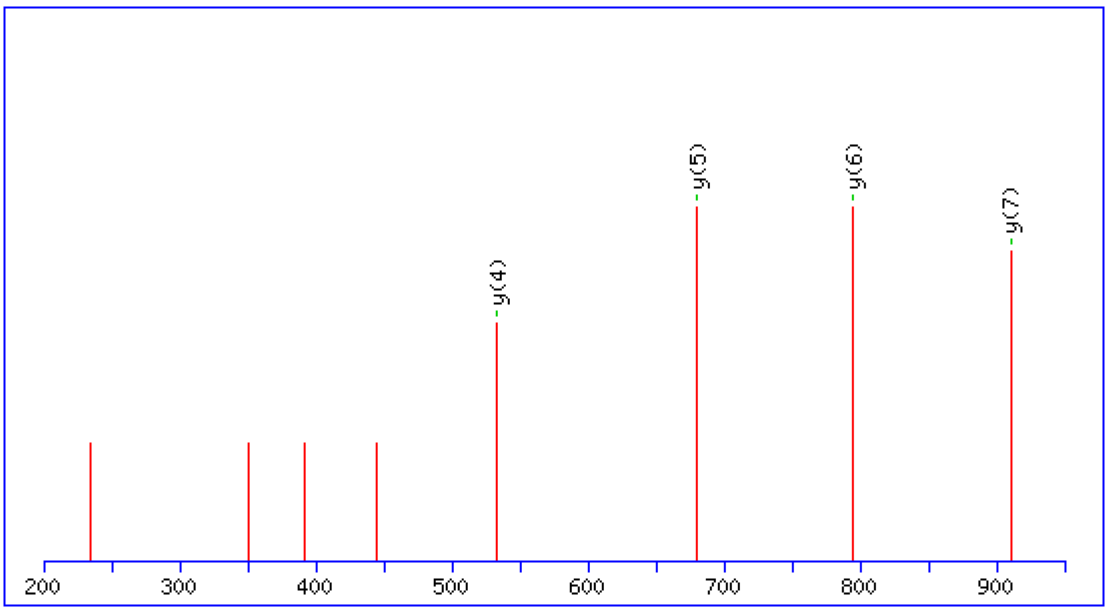
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LDDFWSLK**
Found in **MKLN1_HUMAN**, Muskelin OS=Homo sapiens GN=MKLN1 PE=1 SV=2

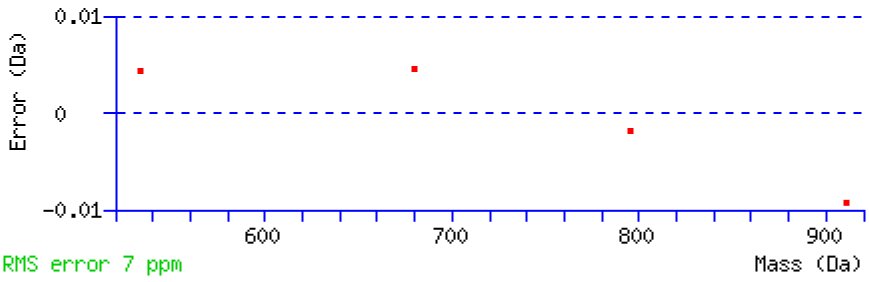
Match to Query 16934: 1022.509928 from(512.262240,2+) rtinseconds(1963) index(16309)
Title: Locus:1.1.1.2155.20
Data file 2011-11-10 - TFD - EP 3-7.mgf

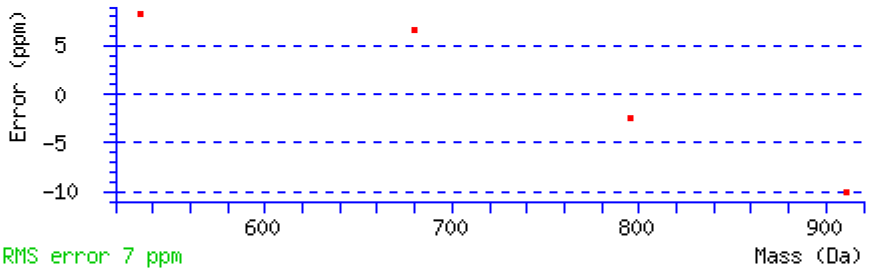
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1022.507294
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.0046
Matches : 4/64 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			**L**							8
2	229.118283	115.062779	211.107718	106.057497	**D**	***910.430509***	455.718893	893.403960	447.205618	892.419944	446.713610	7
3	344.145226	172.576251	326.134661	163.570968	**D**	***795.403566***	398.205421	778.377017	389.692147	777.393001	389.200139	6
4	491.213640	246.110458	473.203075	237.105176	**F**	***680.376623***	340.691950	663.350074	332.178675	662.366058	331.686667	5
5	677.292953	339.150115	659.282388	330.144832	**W**	***533.308209***	267.157743	516.281660	258.644468	515.297644	258.152460	4
6	764.324981	382.666129	746.314416	373.660846	**S**	347.228896	174.118086	330.202347	165.604811	329.218331	165.112803	3
7	877.409045	439.208161	859.398480	430.202878	**L**	260.196868	130.602072	243.170319	122.088798			2
8					**K**	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.5	1022.507294	0.002634	LDDFWSLK
5.4	1022.514008	-0.004080	LMVEMEKK
2.8	1022.507294	0.002634	EVVYWSPK
2.5	1022.503265	0.006663	IYDVEQTR

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

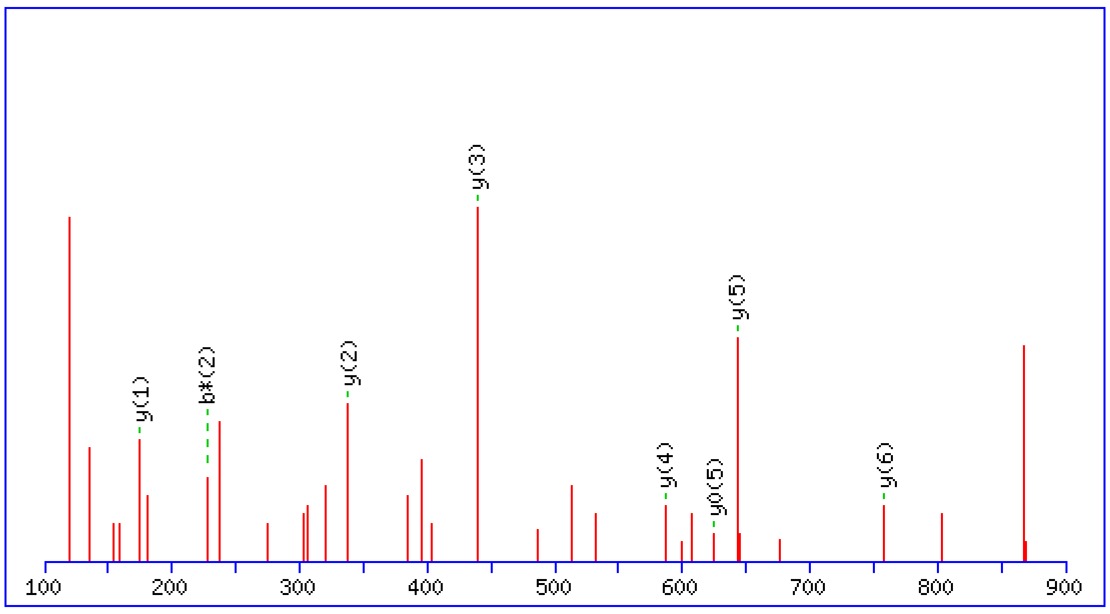
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QDGFTYR**
Found in **MAL_HUMAN**, Myelin and lymphocyte protein OS=Homo sapiens GN=MAL PE=2 SV=1

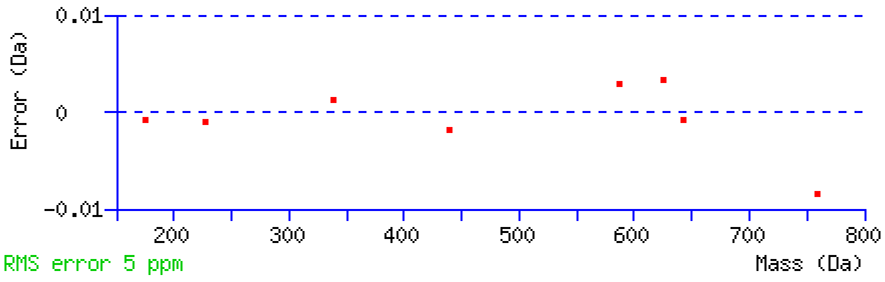
Match to Query 109438: 885.400448 from(443.707500,2+) rtinseconds(1505) index(667941)
Title: Locus:1.1.1.1239.8
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

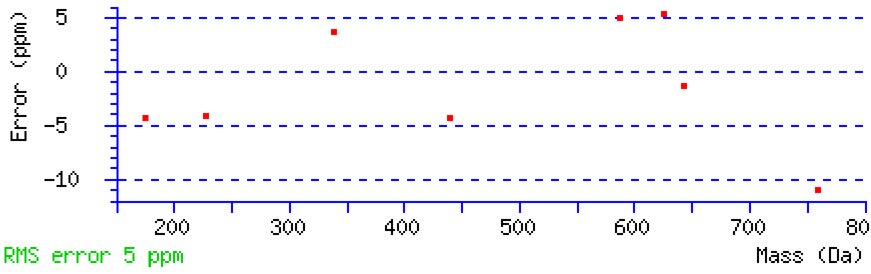
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 885.398087
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 44 **Expect:** 0.00023
Matches : 8/66 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	129.065854	65.036565	112.039305	56.523291			**Q**							7
2	244.092797	122.550037	227.066248	114.036762	226.082232	113.544754	**D**	***758.346781***	379.677029	741.320232	371.163754	740.336216	370.671746	6
3	301.114261	151.060768	284.087712	142.547494	283.103696	142.055486	**G**	***643.319838***	322.163557	626.293289	313.650283	625.309273	313.158275	5
4	448.182675	224.594975	431.156126	216.081701	430.172110	215.589693	**F**	***586.298374***	293.652825	569.271825	285.139551	568.287809	284.647543	4
5	549.230354	275.118815	532.203805	266.605541	531.219789	266.113533	**T**	***439.229960***	220.118618	422.203411	211.605344	421.219395	211.113336	3
6	712.293683	356.650480	695.267134	348.137205	694.283118	347.645197	**Y**	***338.182281***	169.594778	321.155732	161.081504			2
7							**R**	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.2	885.398087	0.002361	QDGFTYR
12.4	885.408844	-0.008396	KCFLTAM
6.2	885.398056	0.002392	YQAEGYR
4.4	885.394043	0.006405	EPAGENGGR
3.5	885.394058	0.006390	SSSHSPPR
3.3	885.401443	-0.000995	QEMPPPR
3.3	885.401443	-0.000995	QEMPPPR
2.8	885.394043	0.006405	NEPNPQR
2.5	885.401443	-0.000995	QEMPPPR
2.5	885.401443	-0.000995	QEMPPPR

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

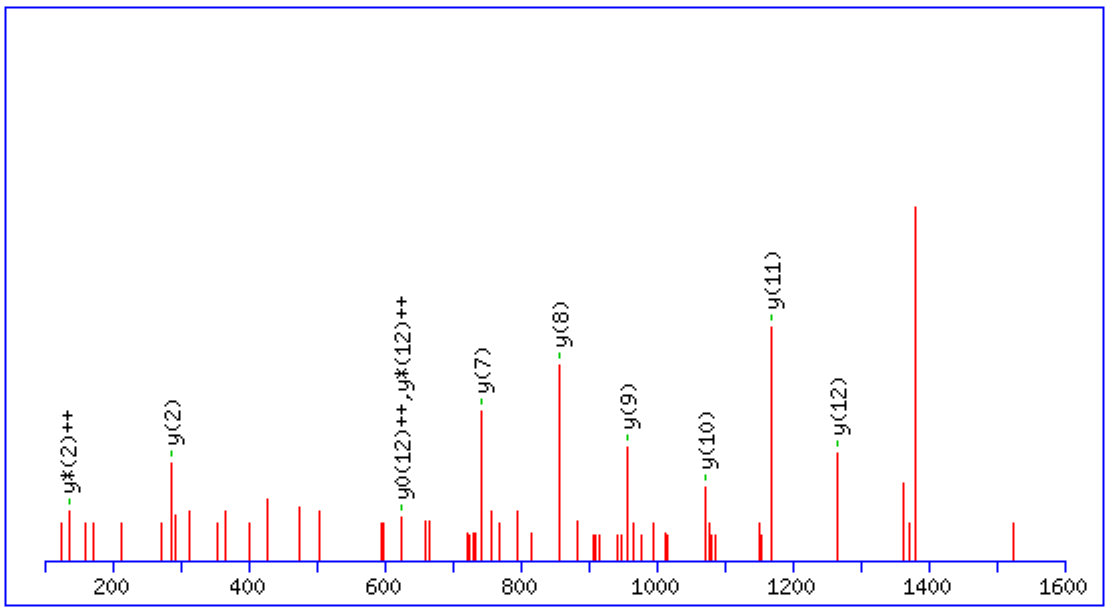
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NPPDVDGVIGEIR**
Found in **MPZL2_HUMAN**, Myelin protein zero-like protein 2 OS=Homo sapiens GN=MPZL2 PE=1 SV=1

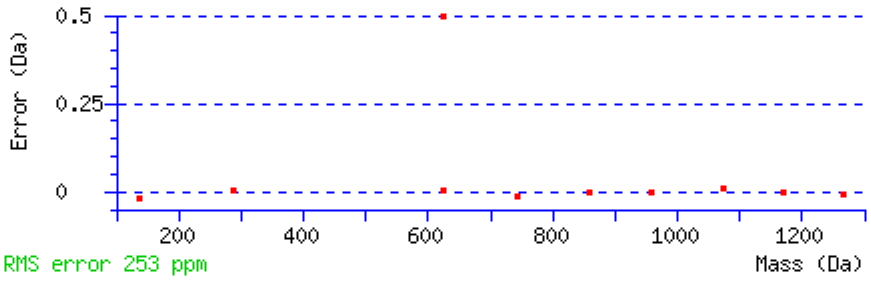
Match to Query 40189: 1379.696328 from(690.855440,2+) rtinseconds(2847) index(37072)
Title: Locus:1.1.1.2398.41
Data file 2011-11-10 - TFD - EP 4-5.mgf

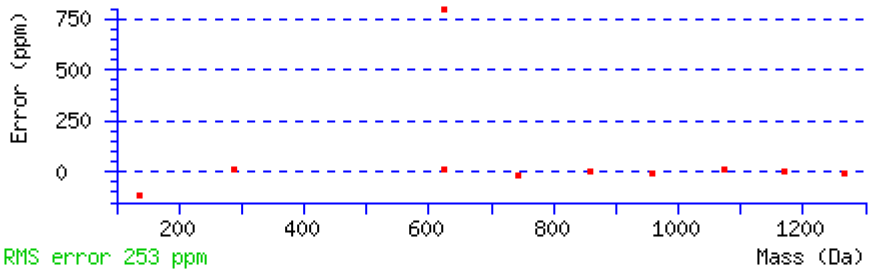
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1600] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1379.704498
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 57  Expect: 2.2e-005
Matches : 10/134 fragment ions using 13 most intense peaks   (help)
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			N							13
2	212.102967	106.555121	195.076418	98.041847			P	***1266.668843***	633.838059	1249.642294	625.324785	1248.658278	624.832777	12
3	309.155731	155.081504	292.129182	146.568229			P	***1169.616079***	585.311677	1152.589530	576.798403	1151.605514	576.306395	11
4	424.182674	212.594975	407.156125	204.081701	406.172109	203.589693	D	***1072.563315***	536.785295	1055.536766	528.272021	1054.552750	527.780013	10
5	523.251088	262.129182	506.224539	253.615908	505.240523	253.123900	V	***957.536372***	479.271824	940.509823	470.758549	939.525807	470.266541	9
6	638.278031	319.642654	621.251482	311.129379	620.267466	310.637371	D	***858.467958***	429.737617	841.441409	421.224342	840.457393	420.732334	8
7	695.299495	348.153386	678.272946	339.640111	677.288930	339.148103	G	***743.441015***	372.224145	726.414466	363.710871	725.430450	363.218863	7
8	794.367909	397.687593	777.341360	389.174318	776.357344	388.682310	V	686.419551	343.713413	669.393002	335.200139	668.408986	334.708131	6
9	907.451973	454.229625	890.425424	445.716350	889.441408	445.224342	I	587.351137	294.179206	570.324588	285.665932	569.340572	285.173924	5
10	964.473437	482.740357	947.446888	474.227082	946.462872	473.735074	G	474.267073	237.637174	457.240524	229.123900	456.256508	228.631892	4
11	1093.516030	547.261653	1076.489481	538.748379	1075.505465	538.256371	E	417.245609	209.126442	400.219060	200.613168	399.235044	200.121160	3
12	1206.600094	603.803685	1189.573545	595.290411	1188.589529	594.798402	I	***288.203016***	144.605146	271.176467	136.091871			2
13							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
57.4	1379.704498	-0.008170	NPPDVDGVIGEIR

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

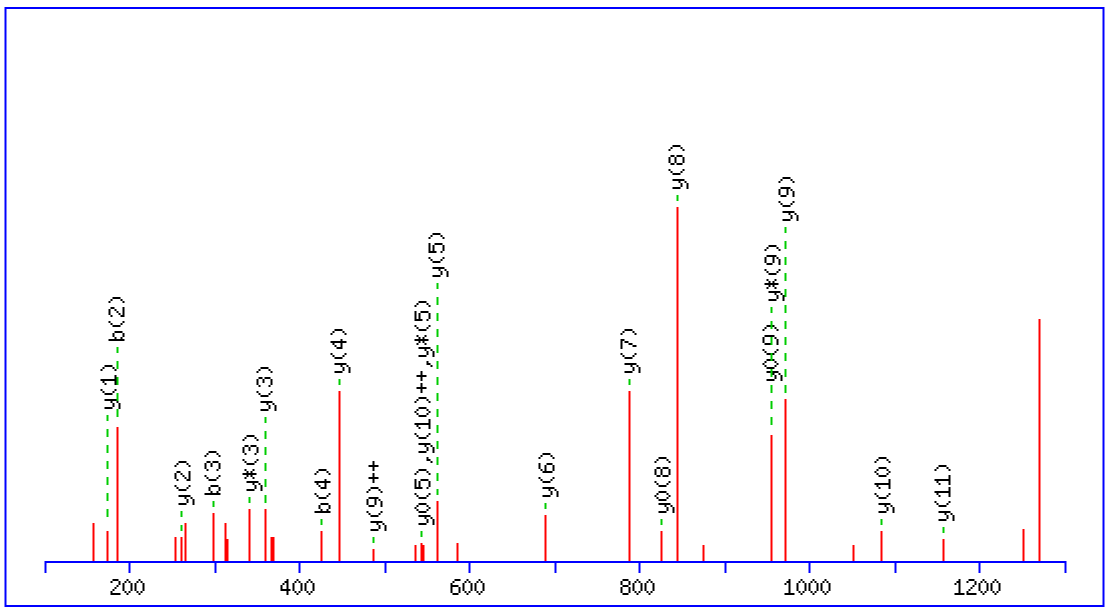
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LAIQGPEDSPSR**
Found in **MLF2_HUMAN**, Myeloid leukemia factor 2 OS=Homo sapiens GN=MLF2 PE=1 SV=1

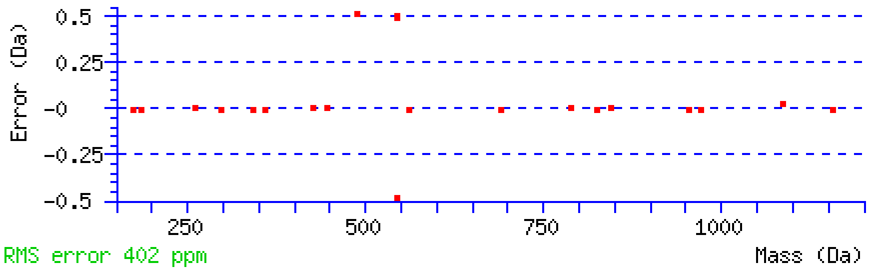
Match to Query 33121: 1268.631588 from(635.323070,2+) rtinseconds(1693) index(12606)
Title: Locus:1.1.1.2230.40
Data file 2011-11-12 - TFD - EP 5-5.mgf

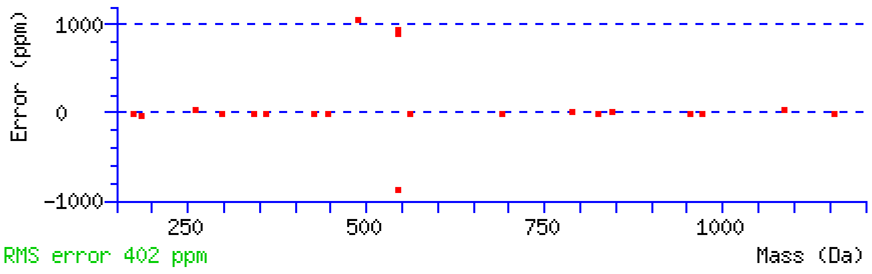
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1268.636063
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 94 **Expect:** 1.4e-008
Matches : 22/112 fragment ions using 35 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							12
2	**185.128454**	93.067865					A	***1156.559292***	578.783284	1139.532743	570.270010	1138.548727	569.778002	11
3	**298.212518**	149.609897					I	***1085.522178***	543.264727	1068.495629	534.751453	1067.511613	534.259444	10
4	**426.271096**	213.639186	409.244547	205.125912			Q	***972.438114***	486.722695	955.411565	478.209421	954.427549	477.717413	9
5	483.292560	242.149918	466.266011	233.636643			G	***844.379536***	422.693406	827.352987	414.180132	826.368971	413.688124	8
6	580.345324	290.676300	563.318775	282.163026			P	***787.358072***	394.182674	770.331523	385.669400	769.347507	385.177392	7
7	709.387917	355.197597	692.361368	346.684322	691.377352	346.192314	E	***690.305308***	345.656292	673.278759	337.143018	672.294743	336.651010	6
8	824.414860	412.711068	807.388311	404.197793	806.404295	403.705785	D	***561.262715***	281.134996	544.236166	272.621721	543.252150	272.129713	5
9	911.446888	456.227082	894.420339	447.713807	893.436323	447.221799	S	***446.235772***	223.621524	429.209223	215.108250	428.225207	214.616242	4
10	1008.499652	504.753464	991.473103	496.240189	990.489087	495.748181	P	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.100228	3
11	1095.531680	548.269478	1078.505131	539.756204	1077.521115	539.264196	S	***262.150980***	131.579128	245.124431	123.065854	244.140415	122.573846	2
12							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
94.4	1268.636063	-0.004475	LAIQGPEDSPSR
8.2	1268.636063	-0.004475	ALDKDSPPPSSR
1.9	1268.643448	-0.011860	LSPSCPDALAPK
0.2	1268.633392	-0.001804	TGSKPRSGGNHR

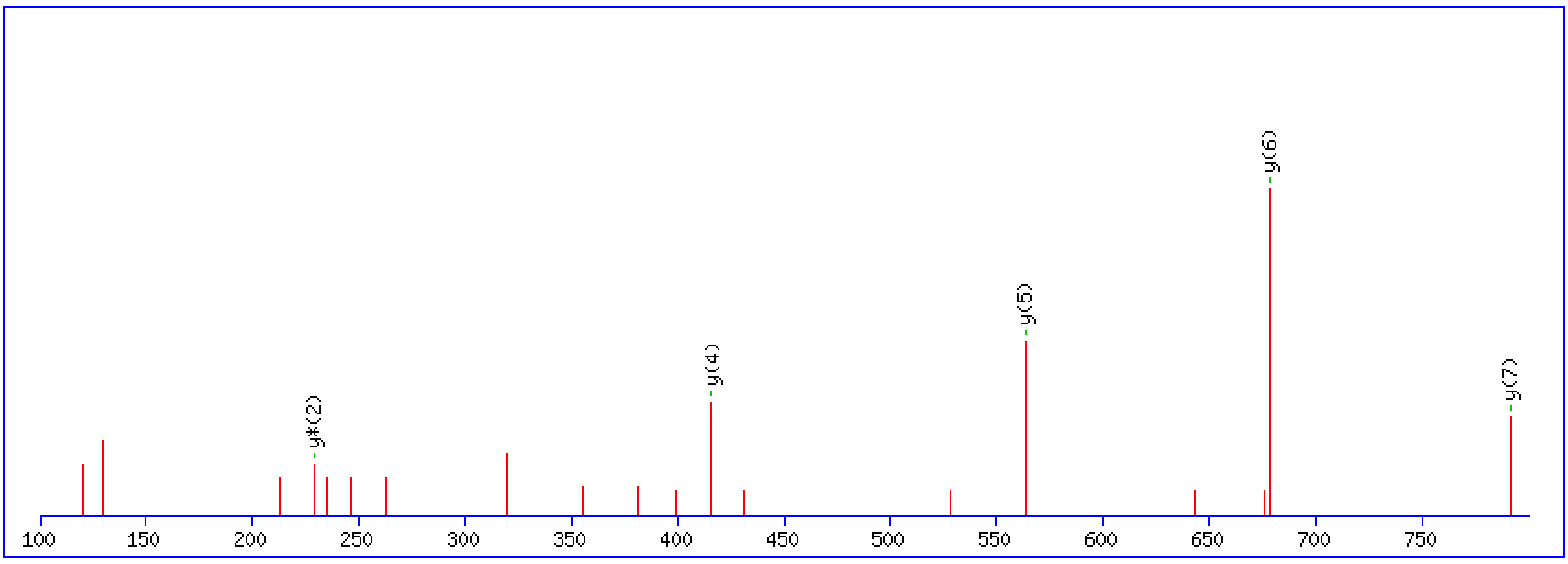
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IIDFGLAR**
Found in **MYLK2_HUMAN**, Myosin light chain kinase 2, skeletal/cardiac muscle OS=Homo sapiens GN=MYLK2 PE=1 SV=3

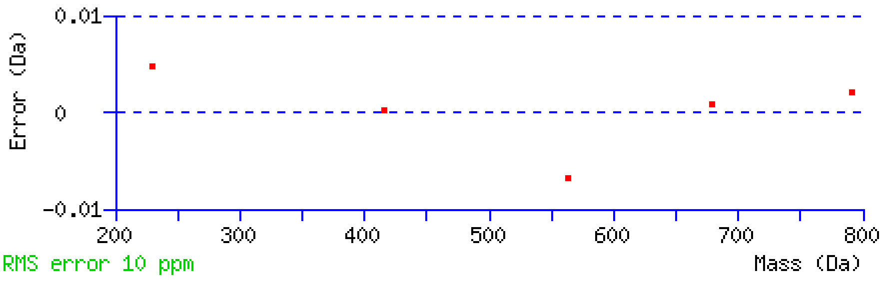
Match to Query 4187: 903.514908 from(452.764730,2+) rtinseconds(2733) index(36512)
Title: Locus:1.1.1.1420.3
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 2.mgf

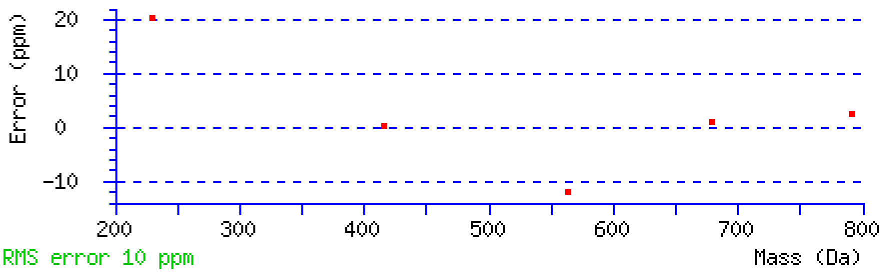
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 903.517792
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.005
Matches : 5/56 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			**I**							8
2	227.175404	114.091340			**I**	***791.441015***	396.224146	774.414466	387.710871	773.430450	387.218863	7
3	342.202347	171.604811	324.191782	162.599529	**D**	***678.356951***	339.682114	661.330402	331.168839	660.346386	330.676831	6
4	489.270761	245.139018	471.260196	236.133736	**F**	***563.330008***	282.168642	546.303459	273.655368			5
5	546.292225	273.649751	528.281660	264.644468	**G**	***416.261594***	208.634435	399.235045	200.121160			4
6	659.376289	330.191783	641.365724	321.186500	**L**	359.240130	180.123703	342.213581	171.610428			3
7	730.413403	365.710340	712.402838	356.705057	**A**	246.156066	123.581671	229.129517	115.068396			2
8					**R**	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.1	903.517792	-0.002884	IIDFGLAR
31.1	903.517792	-0.002884	ILDFGLAR
31.1	903.517792	-0.002884	LIDFGLAR
6.3	903.517792	-0.002884	IDIRPFK
5.2	903.517807	-0.002899	LVSVFPAR
3.8	903.509949	0.004959	VASVLGLVM
3.4	903.509918	0.004990	LLTKVAEM
3.4	903.509903	0.005005	IIEMSAIK
3.4	903.506561	0.008347	IPAVTYPK
3.4	903.509903	0.005005	LIALEMAK

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

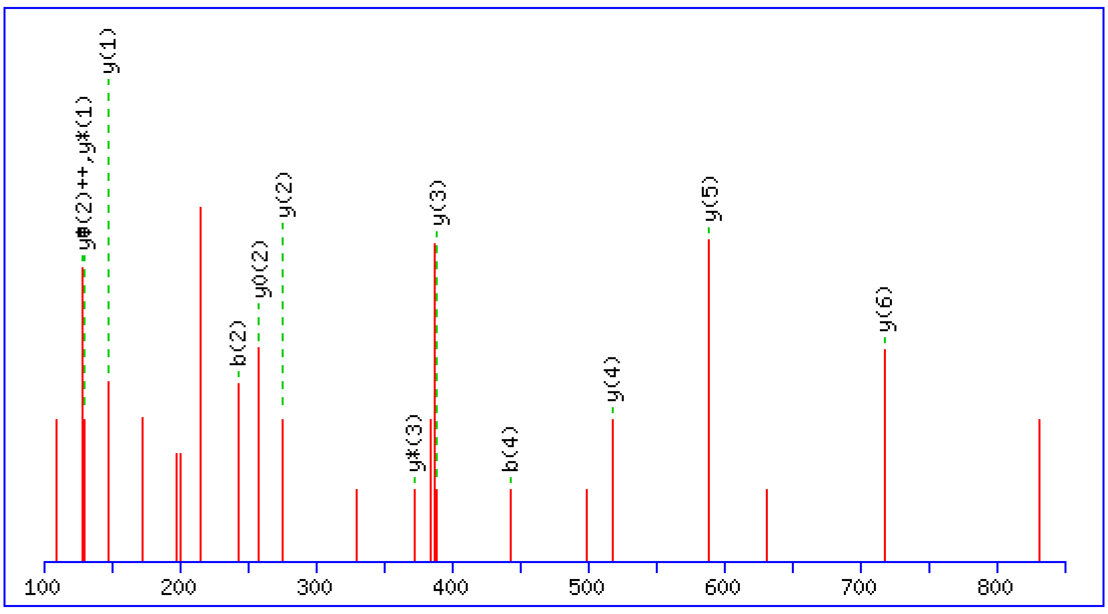
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LEAELEK**
Found in **MYO5C_HUMAN**, Myosin-Vc OS=Homo sapiens GN=MYO5C PE=1 SV=2

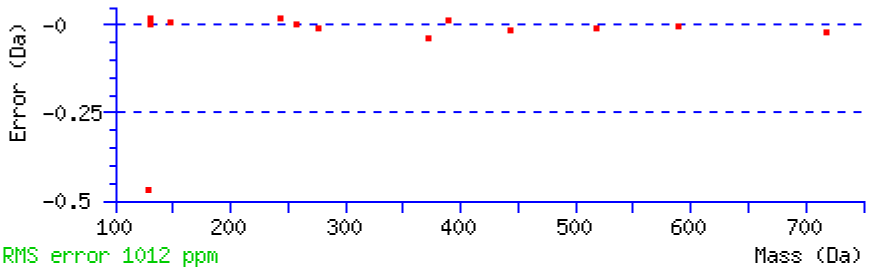
Match to Query 40552: 830.441548 from(416.228050,2+) rtinseconds(1222) index(332762)
Title: Locus:1.1.1.800.4
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

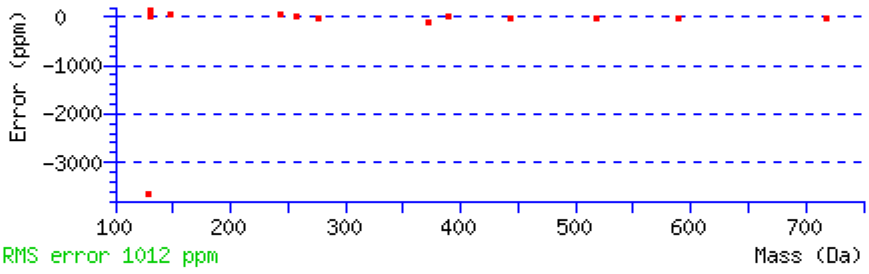
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 830.438507
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 45 **Expect:** 0.00072
Matches : 13/56 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							7
2	**243.133933**	122.070605	225.123368	113.065322	E	***718.361761***	359.684519	701.335212	351.171244	700.351196	350.679236	6
3	314.171047	157.589161	296.160482	148.583879	A	***589.319168***	295.163222	572.292619	286.649948	571.308603	286.157940	5
4	**443.213640**	222.110458	425.203075	213.105176	E	***518.282054***	259.644665	501.255505	251.131391	500.271489	250.639383	4
5	556.297704	278.652490	538.287139	269.647208	L	***389.239461***	195.123369	372.212912	186.610094	371.228896	186.118086	3
6	685.340297	343.173787	667.329732	334.168504	E	***276.155397***	138.581336	259.128848	130.068062	258.144832	129.576054	2
7					K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.0	830.438507	0.003041	LEAELEK
29.1	830.438507	0.003041	LEALEEK
28.7	830.438507	0.003041	EALEIEK
28.3	830.438522	0.003026	SILEPEK
28.3	830.438538	0.003010	TVPEIEK
21.7	830.438507	0.003041	AEEILEK
21.4	830.449753	-0.008205	IEEAITR
21.3	830.449738	-0.008190	ELAENKK
19.6	830.449738	-0.008190	ELEANKK
19.4	830.449738	-0.008190	KNAEELK

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

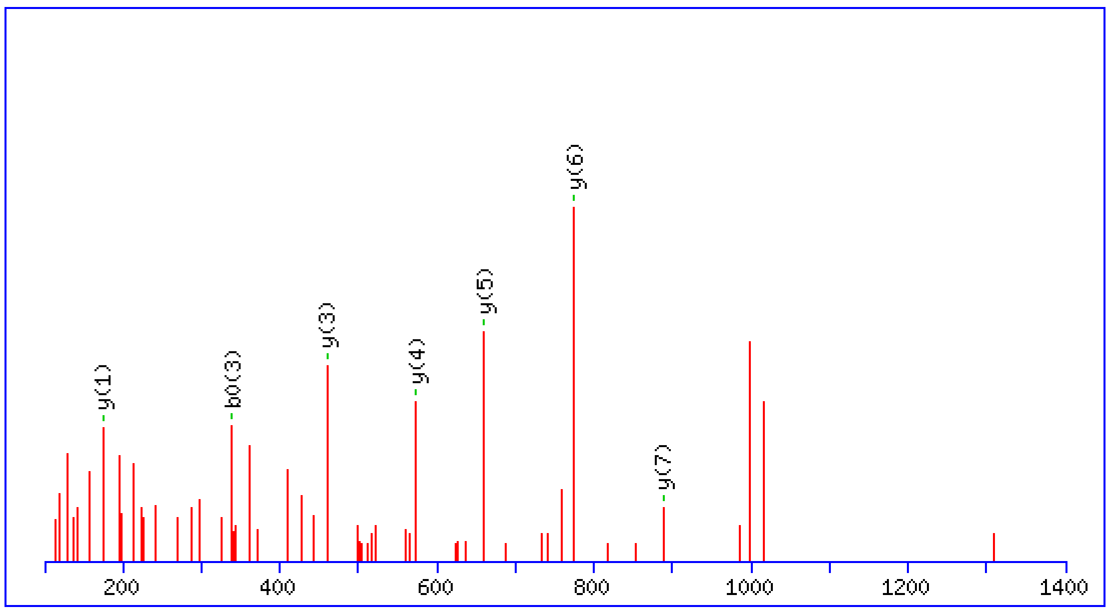
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QLDSLRER**
Found in **MTA70_HUMAN**, N6-adenosine-methyltransferase 70 kDa subunit OS=Homo sapiens GN=METTL3 PE=1 SV=2

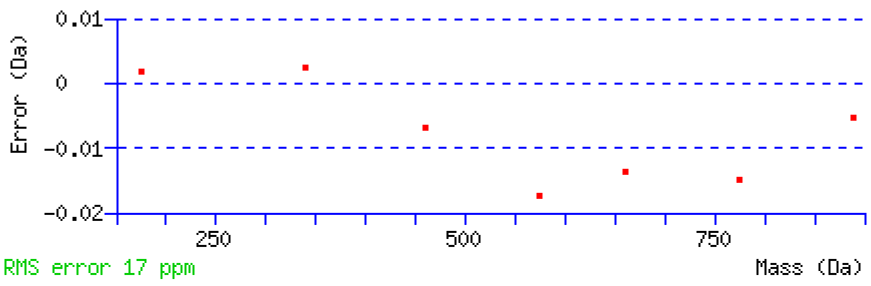
Match to Query 11472: 1015.532048 from(508.773300,2+) rtinseconds(1532) index(13786)
Title: Locus:1.1.1.2070.20
Data file 2011-11-10 - TFD - EP 4-3.mgf

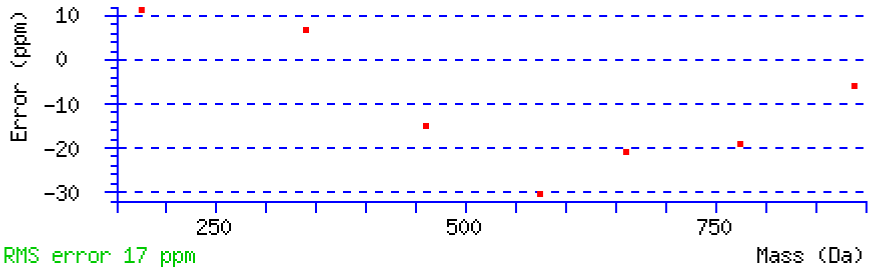
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1015.541031
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 53 **Expect:** 9.4e-005
Matches : 7/78 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	129.065854	65.036565	112.039305	56.523291			Q							8
2	242.149918	121.578597	225.123369	113.065323			L	***888.489755***	444.748516	871.463206	436.235241	870.479190	435.743233	7
3	357.176861	179.092069	340.150312	170.578794	339.166296	170.086786	D	***775.405691***	388.206484	758.379142	379.693209	757.395126	379.201201	6
4	444.208889	222.608083	427.182340	214.094808	426.198324	213.602800	S	***660.378748***	330.693012	643.352199	322.179738	642.368183	321.687730	5
5	557.292953	279.150115	540.266404	270.636840	539.282388	270.144832	L	***573.346720***	287.176998	556.320171	278.663724	555.336155	278.171716	4
6	713.394064	357.200670	696.367515	348.687396	695.383499	348.195388	R	***460.262656***	230.634966	443.236107	222.121692	442.252091	221.629684	3
7	842.436657	421.721967	825.410108	413.208692	824.426092	412.716684	E	304.161545	152.584411	287.134996	144.071136	286.150980	143.579128	2
8							R	***175.118952***	88.063114	158.092403	79.549840			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
59.0	1015.529816	0.002232	QLDSIVGER
52.5	1015.541031	-0.008983	QLDSLRER
16.4	1015.529800	0.002248	KLVEGEEGR
13.2	1015.533829	-0.001781	QPPEALAFK
11.4	1015.533859	-0.001811	GAPDPFLGVK
11.4	1015.529800	0.002248	QIDEIRDK
11.4	1015.537216	-0.005168	QIDQMVGLI
11.1	1015.541046	-0.008998	LQDERTVR
10.2	1015.541046	-0.008998	KPRETDVR
10.2	1015.529800	0.002248	QLTEEIQR

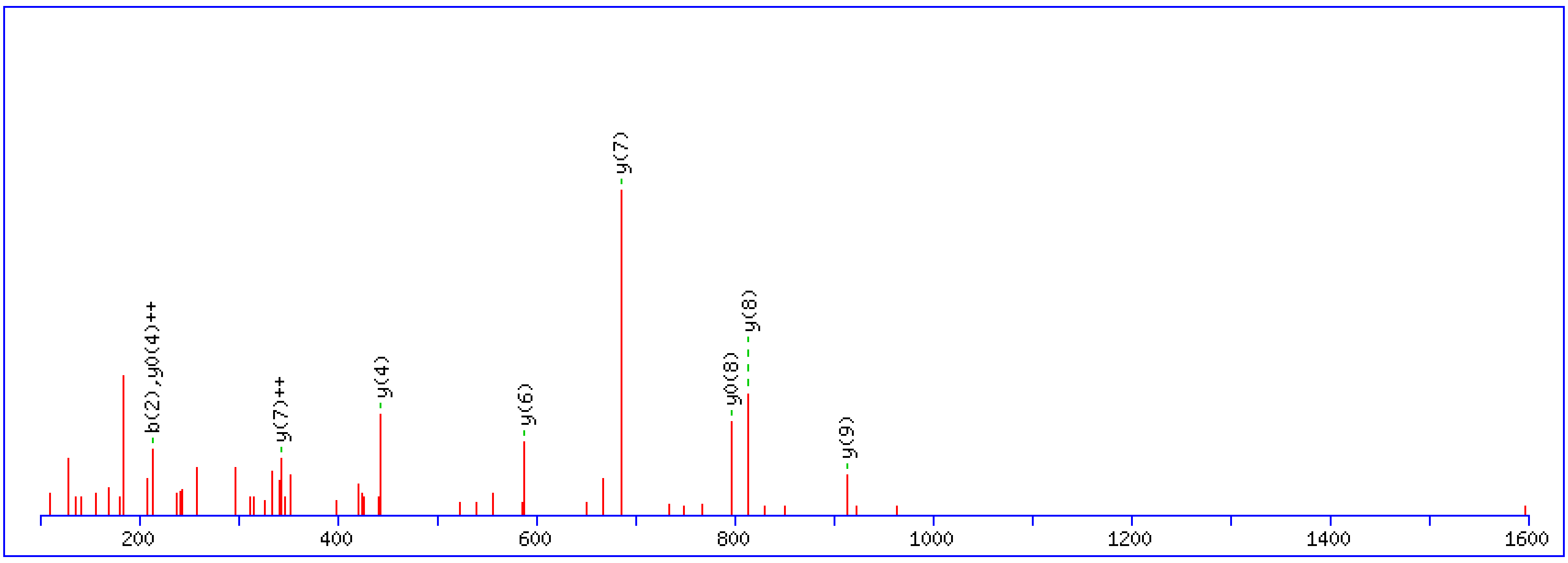
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LVEPGSPAEK**
Found in **NHRF1_HUMAN**, Na(+)/H(+) exchange regulatory cofactor NHE-RF1 OS=Homo sapiens GN=SLC9A3R1 PE=1 SV=4

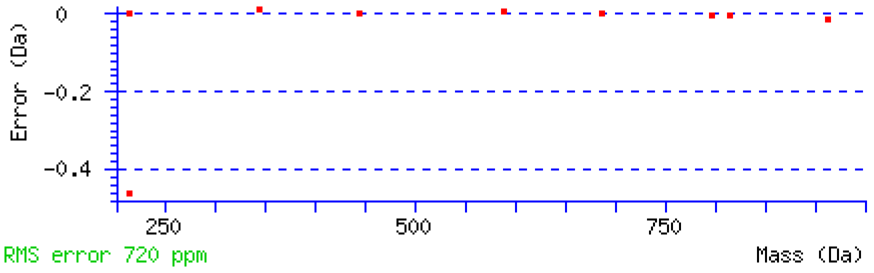
Match to Query 11261: 1025.538188 from(513.776370,2+) rtinseconds(1030) index(4140)
Title: Locus:1.1.1.838.20
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 3.mgf

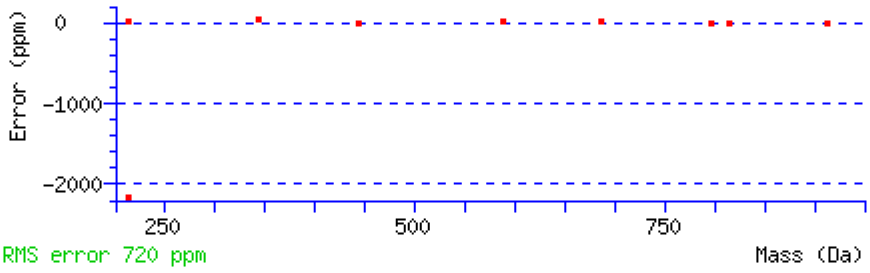
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1025.539307
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.00033
Matches : 9/84 fragment ions using 9 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.091340	57.549308			L							10
2	213.159754	107.083515			V	***913.462538***	457.234907	896.435989	448.721633	895.451973	448.229625	9
3	342.202347	171.604811	324.191782	162.599529	E	***814.394124***	407.700700	797.367575	399.187426	796.383559	398.695418	8
4	439.255111	220.131193	421.244546	211.125911	P	***685.351531***	343.179404	668.324982	334.666129	667.340966	334.174121	7
5	496.276575	248.641925	478.266010	239.636643	G	***588.298767***	294.653022	571.272218	286.139747	570.288202	285.647739	6
6	583.308603	292.157940	565.298038	283.152657	S	531.277303	266.142290	514.250754	257.629015	513.266738	257.137007	5
7	680.361367	340.684322	662.350802	331.679039	P	***444.245275***	222.626275	427.218726	214.113001	426.234710	213.620993	4
8	751.398481	376.202879	733.387916	367.197596	A	347.192511	174.099893	330.165962	165.586619	329.181946	165.094611	3
9	880.441074	440.724175	862.430509	431.718893	E	276.155397	138.581336	259.128848	130.068062	258.144832	129.576054	2
10					K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.8	1025.539307	-0.001119	LVEPGSPAEK
3.7	1025.543335	-0.005147	LVFDEYLK

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

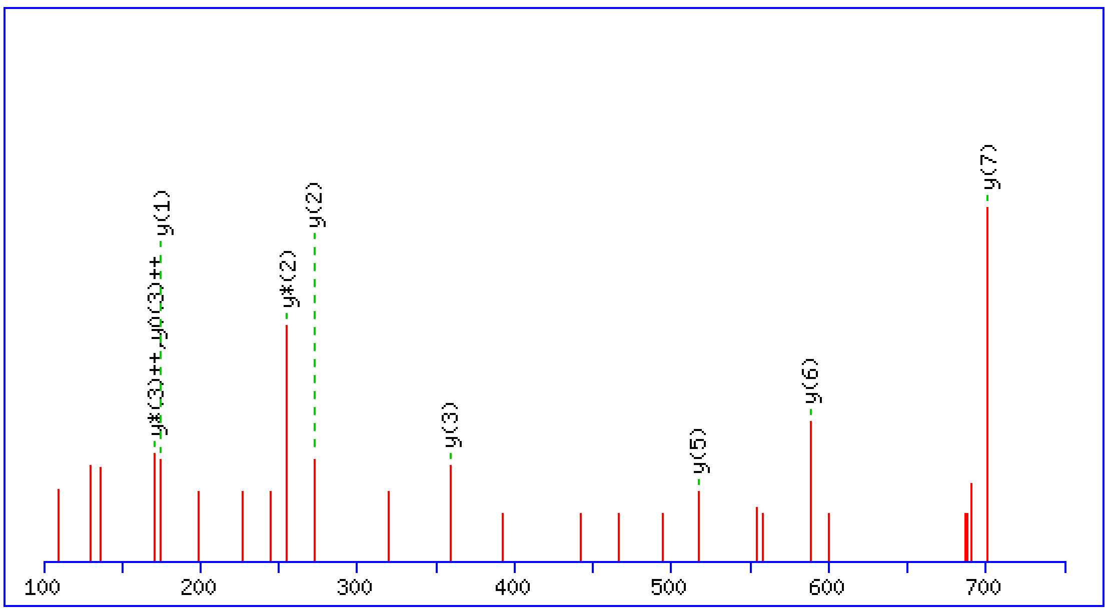
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVLASASPR**
Found in **ASML_HUMAN**, N-acetylserotonin O-methyltransferase-like protein OS=Homo sapiens GN=ASMTL PE=1 SV=3

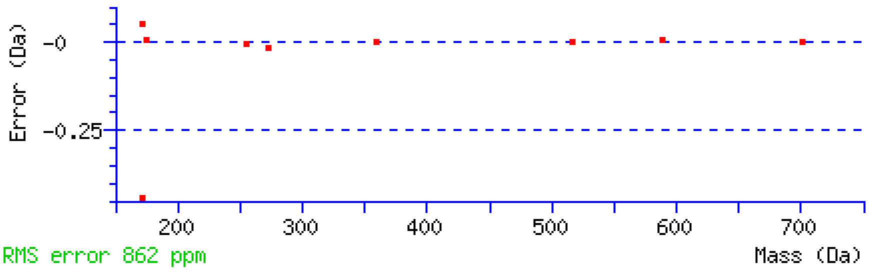
Match to Query 8822: 898.523728 from(450.269140,2+) rtinseconds(1256) index(8159)
Title: Locus:1.1.1.1911.14
Data file 2011-11-14 - TFD - EP 8-2.mgf

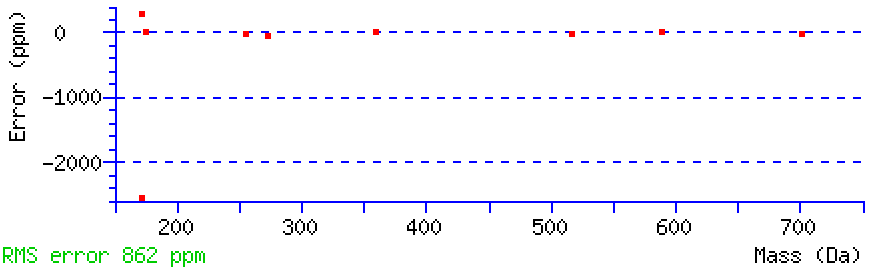
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [750] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 898.523605
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 53 **Expect:** 3.8e-005
Matches : 9/68 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483			V							9
2	199.144104	100.075690			V	800.462478	400.734877	783.435929	392.221603	782.451913	391.729595	8
3	312.228168	156.617722			L	***701.394064***	351.200670	684.367515	342.687395	683.383499	342.195387	7
4	383.265282	192.136279			A	***588.310000***	294.658638	571.283451	286.145363	570.299435	285.653355	6
5	470.297310	235.652293	452.286745	226.647010	S	***517.272886***	259.140081	500.246337	250.626806	499.262321	250.134798	5
6	541.334424	271.170850	523.323859	262.165568	A	430.240858	215.624067	413.214309	207.110792	412.230293	206.618784	4
7	628.366452	314.686864	610.355887	305.681581	S	***359.203744***	180.105510	342.177195	171.592235	341.193179	171.100227	3
8	725.419216	363.213246	707.408651	354.207964	P	***272.171716***	136.589496	255.145167	128.076221			2
9					R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.6	898.523605	0.000123	VVLASASPR
8.4	898.523621	0.000107	VVPEGVKR
6.0	898.523590	0.000138	DQLLAAIR
4.0	898.523621	0.000107	SPVKTVPR
3.5	898.523605	0.000123	LVAASVPAR
3.4	898.523605	0.000123	VLVGNLER
2.4	898.523605	0.000123	APTLALGTR

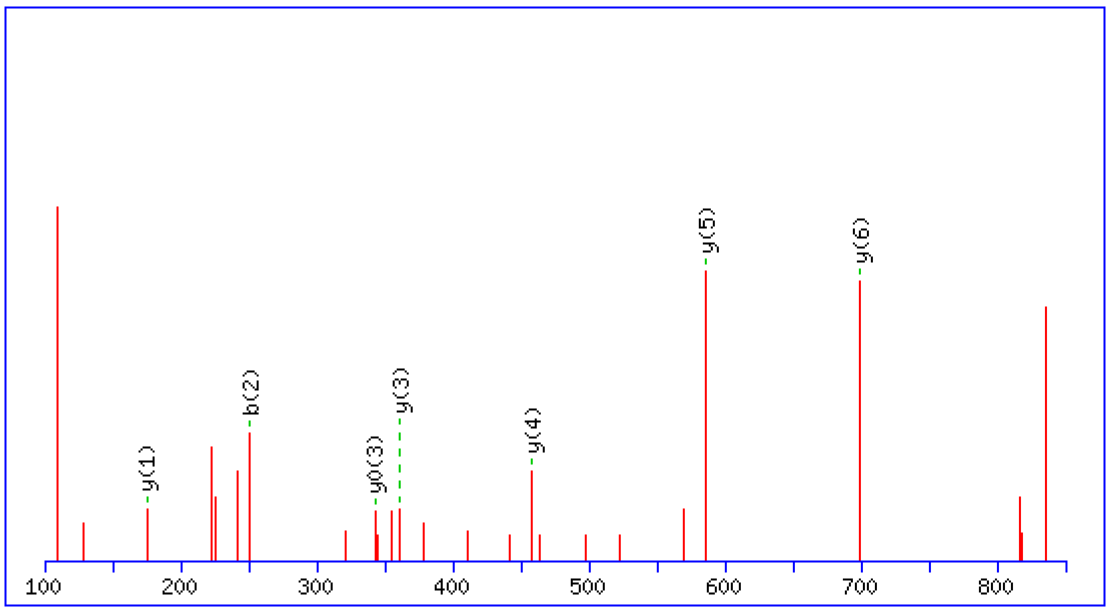
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **HIKPVSR**
Found in **ESCO2_HUMAN**, N-acetyltransferase ESCO2 OS=Homo sapiens GN=ESCO2 PE=1 SV=1

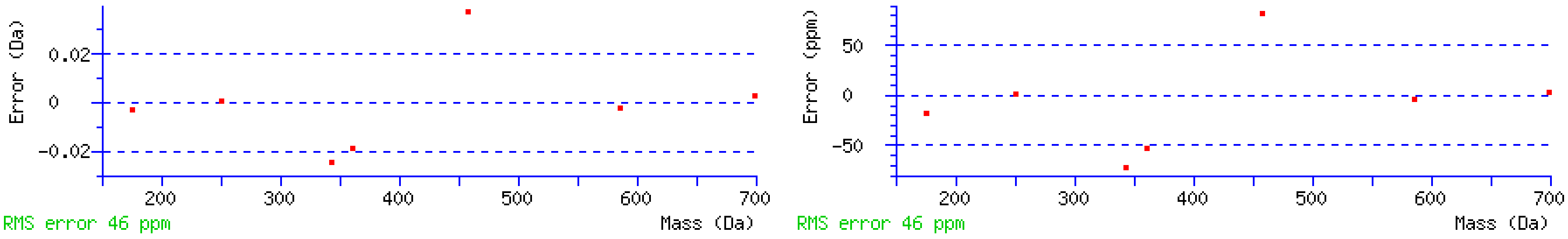
Match to Query 2997: 835.504408 from(418.759480,2+) rtinseconds(1401) index(6057)
Title: Locus:1.1.1.1864.3
Data file 2011-11-12 - TFD - EP 6-7.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 835.502808
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 37 **Expect:** 0.00025
Matches : 7/56 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	138.066188	69.536732					**H**							7
2	251.150252	126.078764					**I**	***699.451185***	350.229231	682.424636	341.715956	681.440620	341.223948	6
3	379.245215	190.126245	362.218666	181.612971			**K**	***586.367121***	293.687199	569.340572	285.173924	568.356556	284.681916	5
4	476.297979	238.652627	459.271430	230.139353			**P**	***458.272158***	229.639717	441.245609	221.126443	440.261593	220.634435	4
5	575.366393	288.186835	558.339844	279.673560			**V**	***361.219394***	181.113335	344.192845	172.600060	343.208829	172.108052	3
6	662.398421	331.702849	645.371872	323.189574	644.387856	322.697566	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
7							**R**	***175.118952***	88.063114	158.092403	79.549840			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.6	835.502808	0.001600	HIKPVSR
27.0	835.502808	0.001600	HLQLAVR
21.4	835.502808	0.001600	HLKSPVR
9.8	835.502808	0.001600	HLPKLGR

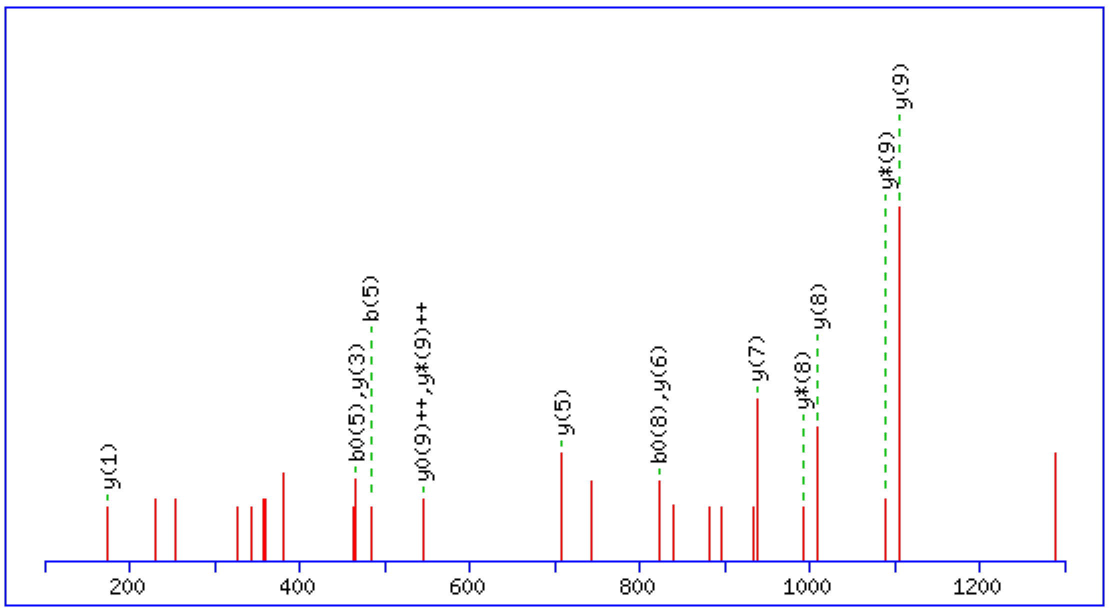
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSPADDELYQR**
Found in **NDUF3_HUMAN**, NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 3 OS=Homo sapiens GN=NDUFAF3 PE=1 SV=1

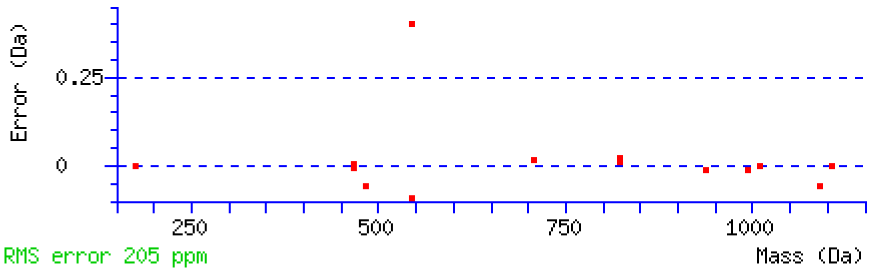
Match to Query 32305: 1305.617488 from(653.816020,2+) rtinseconds(1967) index(16573)
Title: Locus:1.1.1.2080.42
Data file 2011-11-12 - TFD - EP 6-7.mgf

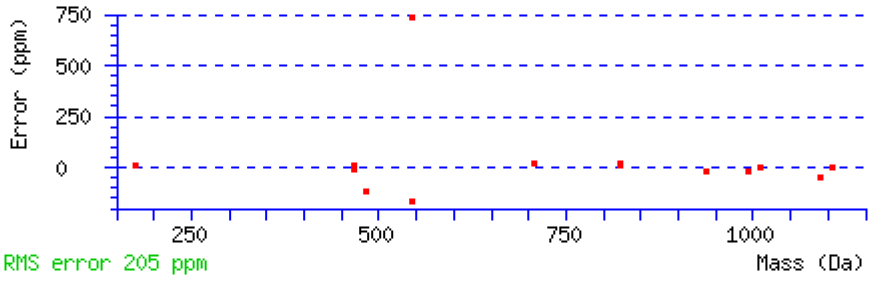
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1305.620071
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 40 **Expect:** 0.0008
Matches : 14/92 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							11
2	201.123368	101.065322			183.112803	92.060039	S	1193.543308	597.275292	1176.516759	588.762018	1175.532743	588.270010	10
3	298.176132	149.591704			280.165567	140.586422	P	***1106.511280***	553.759278	1089.484731	545.246004	1088.500715	544.753996	9
4	369.213246	185.110261			351.202681	176.104978	A	***1009.458516***	505.232896	992.431967	496.719622	991.447951	496.227614	8
5	484.240189	242.623732			466.229624	233.618450	D	***938.421402***	469.714339	921.394853	461.201065	920.410837	460.709057	7
6	599.267132	300.137204			581.256567	291.131922	D	***823.394459***	412.200868	806.367910	403.687593	805.383894	403.195585	6
7	728.309725	364.658501			710.299160	355.653218	E	***708.367516***	354.687396	691.340967	346.174122	690.356951	345.682114	5
8	841.393789	421.200533			823.383224	412.195250	L	579.324923	290.166100	562.298374	281.652825			4
9	1004.457118	502.732197			986.446553	493.726915	Y	***466.240859***	233.624068	449.214310	225.110793			3
10	1132.515696	566.761486	1115.489147	558.248212	1114.505131	557.756204	Q	303.177530	152.092403	286.150981	143.579129			2
11							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.1	1305.620071	-0.002583	LSPADDELYQR

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

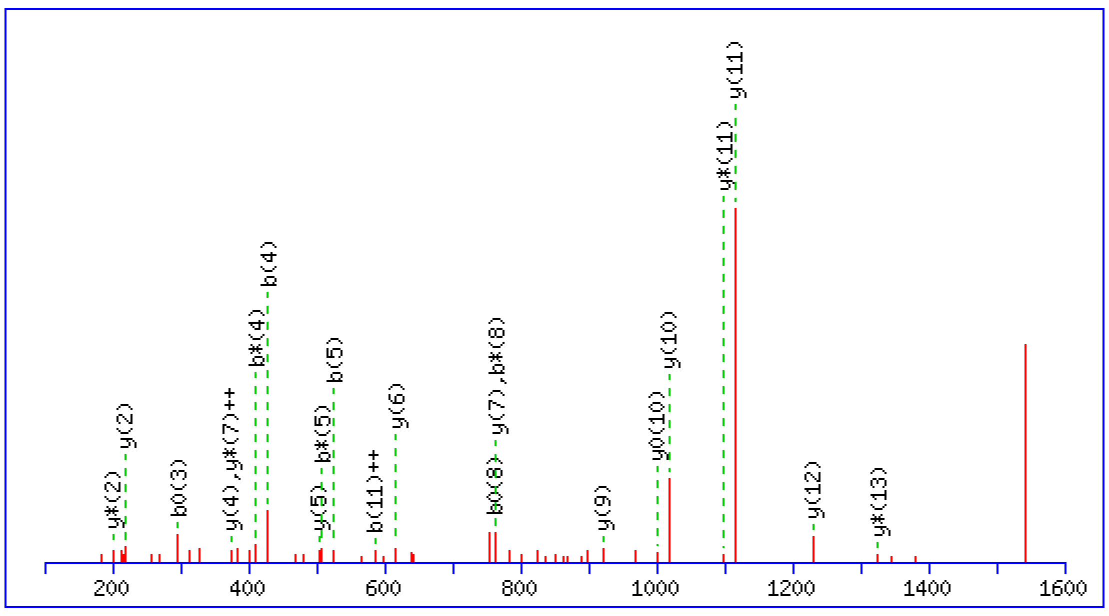
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VTLNPPGTFLEGVAK**
Found in **NDUAB_HUMAN**, NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11 OS=Homo sapiens GN=NDUFA11 PE=1 SV=3

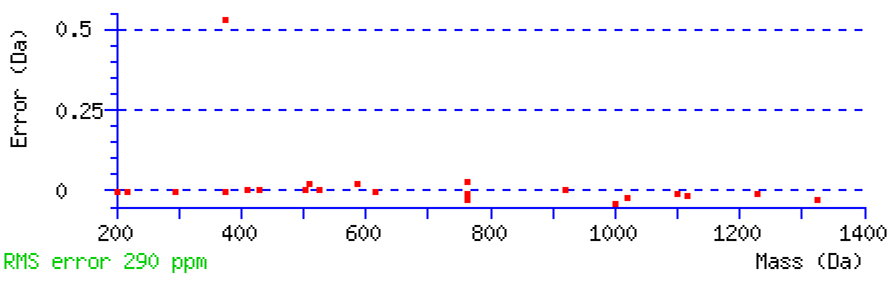
Match to Query 41354: 1541.846548 from(771.930550,2+) rtinseconds(3149) index(36700)
Title: Locus:1.1.1.2534.48
Data file 2011-11-12 - TFD - EP 6-7.mgf

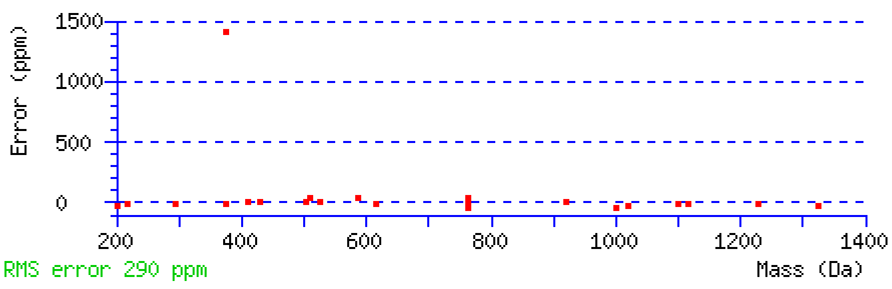
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1541.845352
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 61  Expect: 8.2e-006
Matches : 24/152 fragment ions using 33 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	100.075690	50.541483					V							15
2	**201.123369**	101.065322			183.112804	92.060040	T	1443.784208	722.395742	1426.757659	713.882468	1425.773643	713.390460	14
3	314.207433	157.607354			296.196868	148.602072	L	1342.736529	671.871903	1325.709980	663.358628	1324.725964	662.866620	13
4	**428.250360**	214.628818	411.223811	206.115544	410.239795	205.623536	N	***1229.652465***	615.329871	1212.625916	606.816596	1211.641900	606.324588	12
5	**525.303124**	263.155200	508.276575	254.641926	507.292559	254.149918	P	***1115.609538***	558.308407	1098.582989	549.795133	1097.598973	549.303125	11
6	622.355888	311.681582	605.329339	303.168308	604.345323	302.676300	P	***1018.556774***	509.782025	1001.530225	501.268751	1000.546209	500.776743	10
7	679.377352	340.192314	662.350803	331.679040	661.366787	331.187032	G	***921.504010***	461.255643	904.477461	452.742369	903.493445	452.250361	9
8	780.425031	390.716154	763.398482	382.202879	762.414466	381.710871	T	864.482546	432.744911	847.455997	424.231637	846.471981	423.739629	8
9	927.493445	464.250361	910.466896	455.737086	909.482880	455.245078	F	***763.434867***	382.221072	746.408318	373.707797	745.424302	373.215789	7
10	1040.577509	520.792393	1023.550960	512.279118	1022.566944	511.787110	L	***616.366453***	308.686865	599.339904	300.173590	598.355888	299.681582	6
11	1169.620102	585.313689	1152.593553	576.800415	1151.609537	576.308407	E	***503.282389***	252.144833	486.255840	243.631558	485.271824	243.139550	5
12	1226.641566	613.824421	1209.615017	605.311147	1208.631001	604.819139	G	***374.239796***	187.623536	357.213247	179.110261			4
13	**1325.709980**	663.358628	1308.683431	654.845354	1307.699415	654.353346	V	317.218332	159.112804	300.191783	150.599530			3
14	1396.747094	698.877185	1379.720545	690.363911	1378.736529	689.871903	A	***218.149918***	109.578597	201.123369	101.065322			2
15							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
60.9	1541.845352	0.001196	VTLNPPGTFLEGVAK
6.6	1541.859924	-0.013376	SLIEPISMIVPRR
6.5	1541.841293	0.005255	AEPLLTASRTEQVK
5.9	1541.831406	0.015142	QSPDVAPYLRPKR
5.8	1541.860611	-0.014063	TVLKYSPFVVSFR
4.7	1541.841324	0.005224	GQLEVQIQTVTQAK
4.6	1541.856552	-0.010004	FLEQNGQLGKPLAK
2.3	1541.852524	-0.005976	QNADNLSGTLLLKR
1.9	1541.831406	0.015142	QSPDVAPYLRPKR
1.4	1541.856583	-0.010035	QEGLGRLGLPFPVK

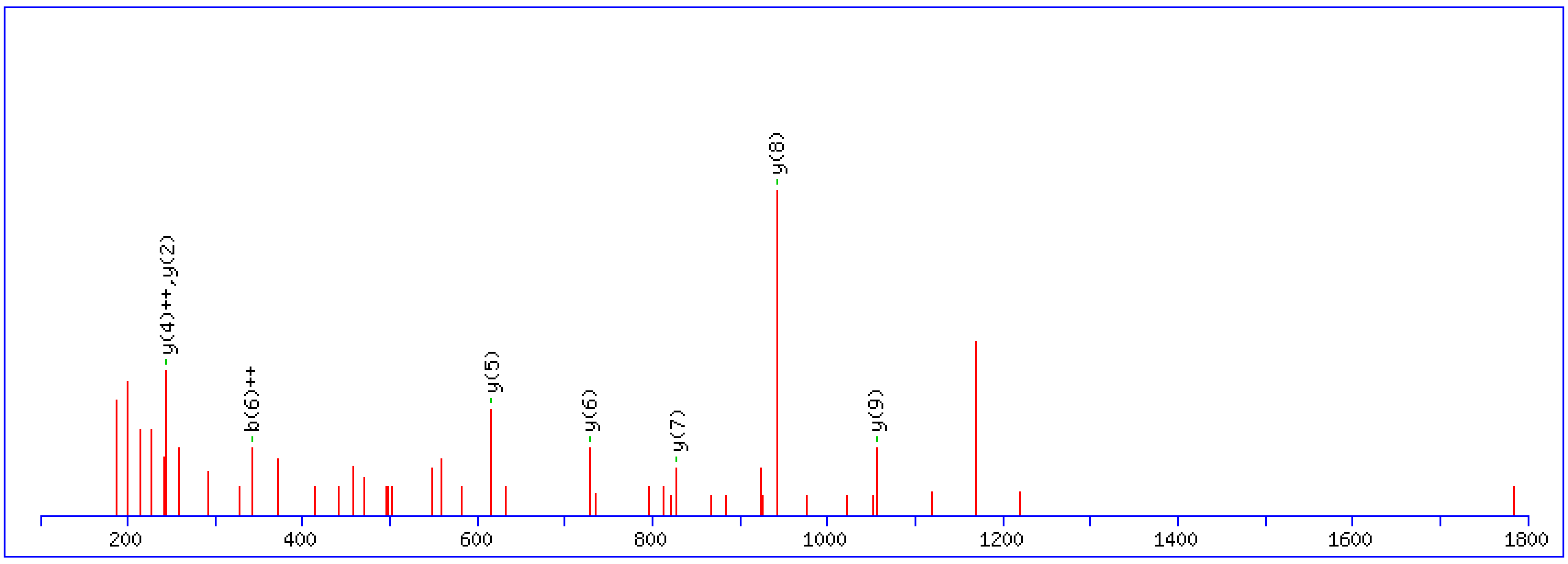
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILDVLEEIPK**
Found in **NDUA5_HUMAN**, NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 OS=Homo sapiens GN=NDUFA5 PE=1 SV=3

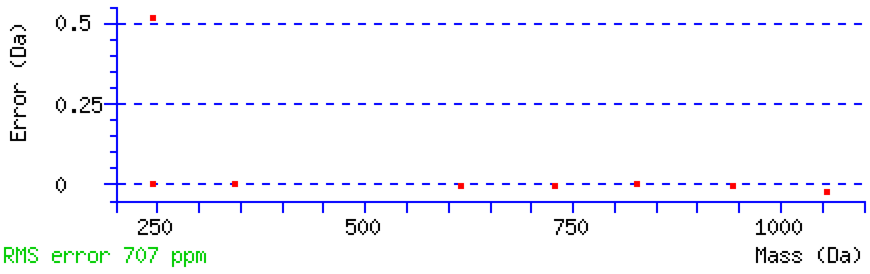
Match to Query 21219: 1167.668768 from(584.841660,2+) rtinseconds(3315) index(47331)
Title: Locus:1.1.1.1702.11
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 3.mgf

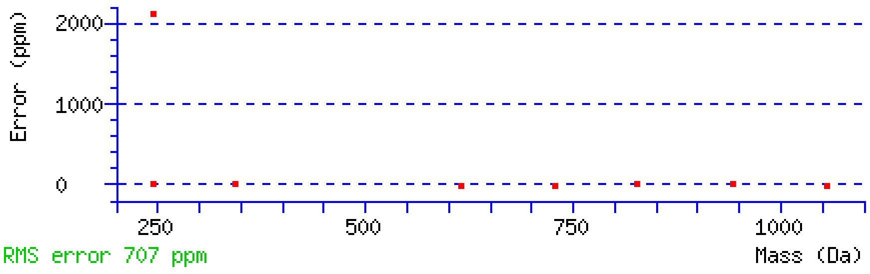
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1167.675064
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 43 **Expect:** 0.00034
Matches : 9/80 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							10
2	227.175404	114.091340			L	***1055.598303***	528.302790	1038.571754	519.789515	1037.587738	519.297507	9
3	342.202347	171.604811	324.191782	162.599529	D	***942.514239***	471.760758	925.487690	463.247483	924.503674	462.755475	8
4	441.270761	221.139018	423.260196	212.133736	V	***827.487296***	414.247286	810.460747	405.734012	809.476731	405.242004	7
5	554.354825	277.681051	536.344260	268.675768	L	***728.418882***	364.713079	711.392333	356.199805	710.408317	355.707797	6
6	683.397418	342.202347	665.386853	333.197065	E	***615.334818***	308.171047	598.308269	299.657773	597.324253	299.165765	5
7	812.440011	406.723644	794.429446	397.718361	E	486.292225	243.649751	469.265676	235.136476	468.281660	234.644468	4
8	925.524075	463.265676	907.513510	454.260393	I	357.249632	179.128454	340.223083	170.615180			3
9	1022.576839	511.792058	1004.566274	502.786775	P	***244.165568***	122.586422	227.139019	114.073148			2
10					K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.9	1167.675064	-0.006296	ILDVLEEIPK
9.1	1167.668564	0.000204	ILVPMNTPGVK
4.5	1167.661163	0.007605	SDLLGKPLGPR
2.5	1167.672379	-0.003611	IPAEGRVALAR
0.5	1167.657318	0.011450	PLPLLPMDLK
0.2	1167.661148	0.007620	LIGPQLDEKR

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

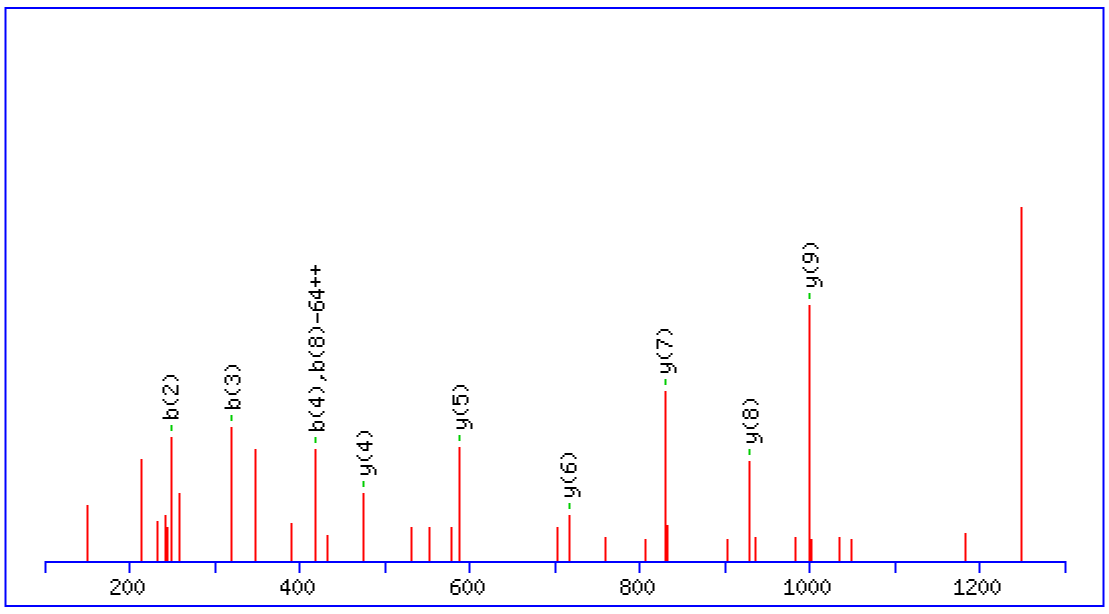
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TMAVLQIEAEK**
Found in **NDUB5_HUMAN**, NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial OS=Homo sapiens GN=NDUFB5 PE=1 SV=1

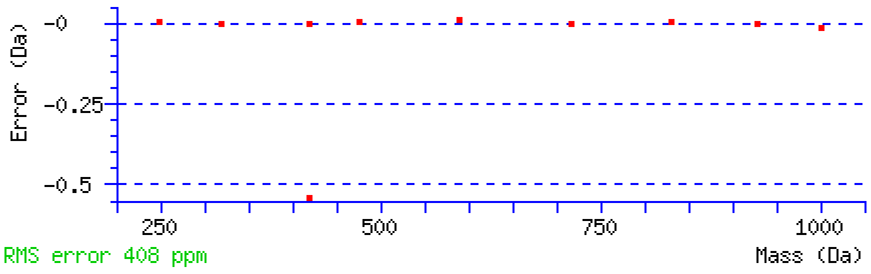
Match to Query 35922: 1247.640808 from(624.827680,2+) rtinseconds(2013) index(21200)
Title: Locus:1.1.1.1985.43
Data file 2011-11-12 - TFD - EP 5-6.mgf

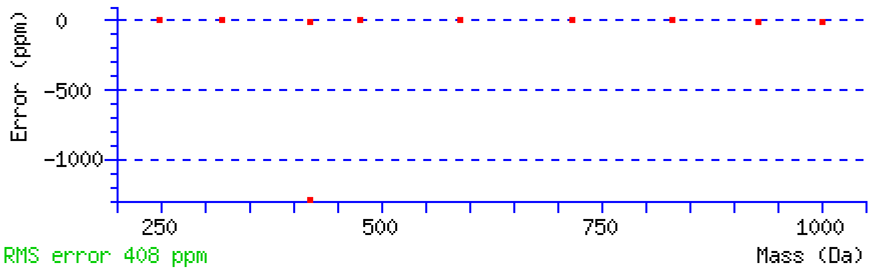
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1247.643112
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M2 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 61 **Expect:** 2.6e-006
Matches : 10/160 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							11
2	**249.090355**	125.048815			231.079790	116.043533	M	1147.602738	574.305007	1130.576189	565.791733	1129.592173	565.299725	10
3	**320.127469**	160.567372			302.116904	151.562090	A	***1000.567338***	500.787307	983.540789	492.274033	982.556773	491.782025	9
4	**419.195883**	210.101579			401.185318	201.096297	V	***929.530224***	465.268750	912.503675	456.755476	911.519659	456.263468	8
5	532.279947	266.643612			514.269382	257.638329	L	***830.461810***	415.734543	813.435261	407.221269	812.451245	406.729261	7
6	660.338525	330.672901	643.311976	322.159626	642.327960	321.667618	Q	***717.377746***	359.192511	700.351197	350.679237	699.367181	350.187229	6
7	773.422589	387.214933	756.396040	378.701658	755.412024	378.209650	I	***589.319168***	295.163222	572.292619	286.649948	571.308603	286.157940	5
8	902.465182	451.736229	885.438633	443.222955	884.454617	442.730947	E	***476.235104***	238.621190	459.208555	230.107915	458.224539	229.615907	4
9	973.502296	487.254786	956.475747	478.741512	955.491731	478.249504	A	347.192511	174.099893	330.165962	165.586619	329.181946	165.094611	3
10	1102.544889	551.776083	1085.518340	543.262808	1084.534324	542.770800	E	276.155397	138.581336	259.128848	130.068062	258.144832	129.576054	2
11							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
60.5	1247.643112	-0.002304	TMAVLQIEAEK
1.1	1247.633224	0.007584	APQNLTFMAAGK

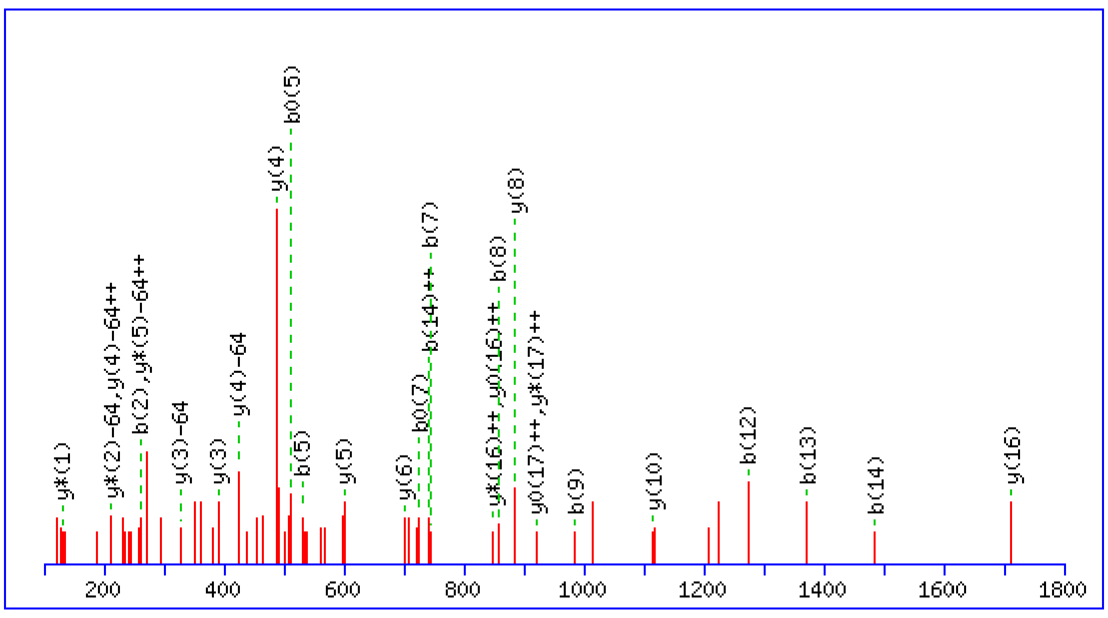
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IFPGDTILETGEVIPPMK**
Found in **NDUB6_HUMAN**, NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 6 OS=Homo sapiens GN=NDUFB6 PE=1 SV=3

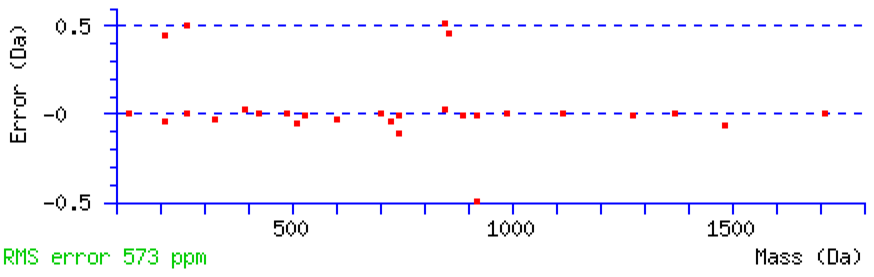
Match to Query 56321: 1972.013652 from(658.345160,3+) rtinseconds(3336) index(46114)
Title: Locus:1.1.1.2421.18
Data file 2011-11-12 - TFD - EP 6-6.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1800] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●

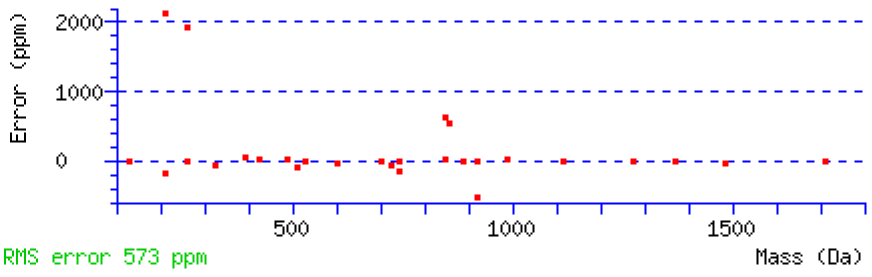


Monoisotopic mass of neutral peptide Mr(calc): 1972.022720
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M17 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 44 **Expect:** 0.00041
Matches : 28/240 fragment ions using 42 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							18
2	***261.159754***	131.083515			F	1859.945931	930.476604	1842.919382	921.963329	1841.935366	921.471321	17
3	358.212518	179.609897			P	***1712.877517***	856.942396	1695.850968	848.429122	1694.866952	847.937114	16
4	415.233982	208.120629			G	1615.824753	808.416014	1598.798204	799.902740	1597.814188	799.410732	15
5	***530.260925***	265.634101	512.250360	256.628818	D	1558.803289	779.905283	1541.776740	771.392008	1540.792724	770.900000	14
6	631.308604	316.157940	613.298039	307.152658	T	1443.776346	722.391811	1426.749797	713.878537	1425.765781	713.386528	13
7	***744.392668***	372.699972	726.382103	363.694690	I	1342.728667	671.867971	1325.702118	663.354697	1324.718102	662.862689	12
8	***857.476732***	429.242004	839.466167	420.236722	L	1229.644603	615.325940	1212.618054	606.812665	1211.634038	606.320657	11
9	***986.519325***	493.763301	968.508760	484.758018	E	***1116.560539***	558.783907	1099.533990	550.270633	1098.549974	549.778625	10
10	1087.567004	544.287140	1069.556439	535.281858	T	987.517946	494.262611	970.491397	485.749336	969.507381	485.257328	9
11	1144.588468	572.797872	1126.577903	563.792589	G	***886.470267***	443.738771	869.443718	435.225497	868.459702	434.733489	8
12	***1273.631061***	637.319168	1255.620496	628.313886	E	829.448803	415.228040	812.422254	406.714765	811.438238	406.222757	7
13	***1372.699475***	686.853375	1354.688910	677.848093	V	***700.406210***	350.706743	683.379661	342.193469			6
14	***1485.783539***	743.395407	1467.772974	734.390125	I	***601.337796***	301.172536	584.311247	292.659262			5
15	1582.836303	791.921789	1564.825738	782.916507	P	***488.253732***	244.630504	471.227183	236.117230			4
16	1679.889067	840.448171	1661.878502	831.442889	P	***391.200968***	196.104122	374.174419	187.590848			3
17	1826.924467	913.965871	1808.913902	904.960589	M	294.148204	147.577740	277.121655	139.064465			2
18					K	147.112804	74.060040	130.086255	65.546765			1



RMS error 573 ppm



RMS error 573 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
43.9	1972.022720	-0.009068	IFPGDTILETGEVIPPMK
39.3	1972.022720	-0.009068	IFPGDTILETGEVIPPMK
33.3	1972.022720	-0.009068	IFPGDTILETGEVIPPMK
7.3	1972.001389	0.012263	ERPGYRAGVAAPDLLDPK
5.2	1972.026566	-0.012914	LVGPAFLDGPQSLDDKLR
3.9	1972.022491	-0.008839	NGDEISKLSQLVNSNNLK
3.1	1972.011307	0.002345	QVPDTSVQETDRILVEK
0.8	1972.002289	0.011363	GTPIGMPPPGMRPPPPGIR
0.2	1972.001419	0.012233	GLPPPLQQQQQPPPQQK
0.2	1972.001419	0.012233	GLPPPLQQQQQPPPQQK

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

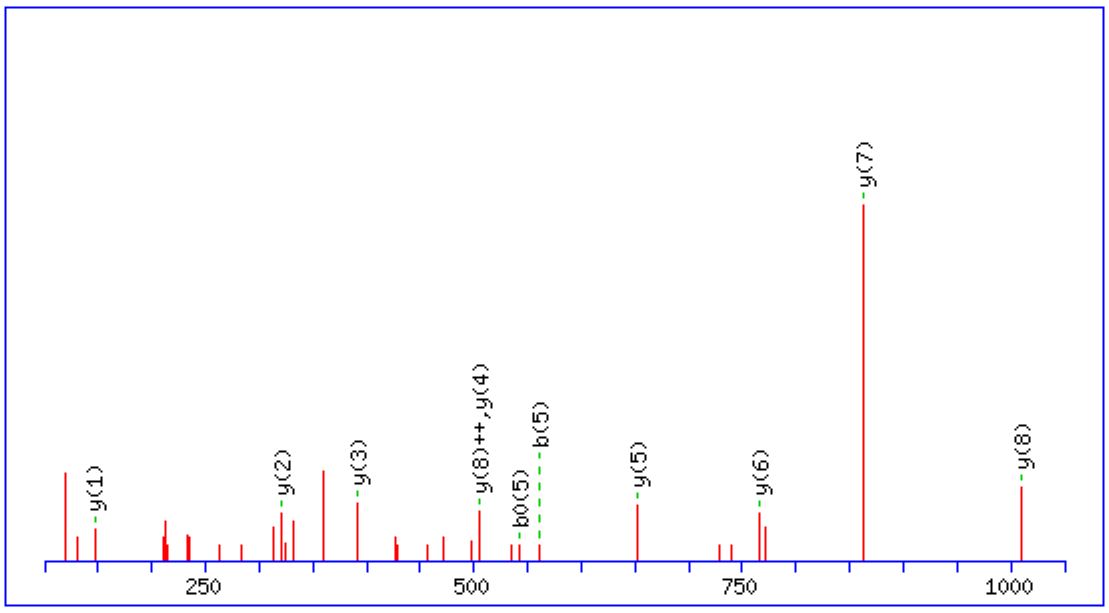
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DSFPNFLACK**
Found in **NDUB7_HUMAN**, NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7 OS=Homo sapiens GN=NDUFB7 PE=1 SV=4

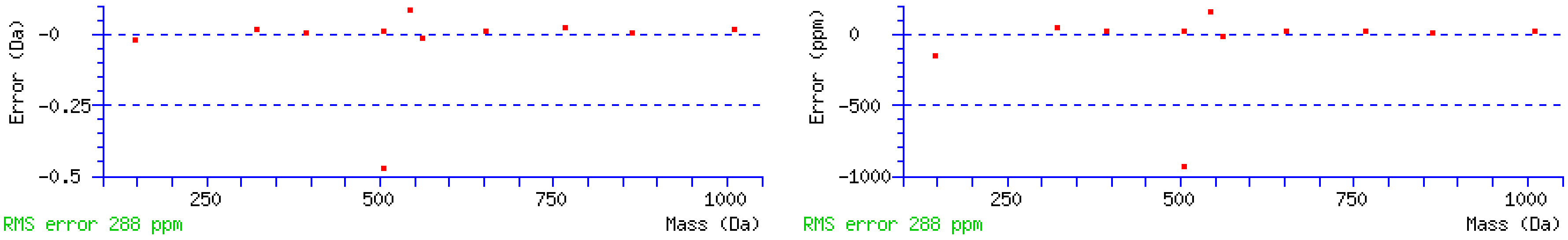
Match to Query 30168: 1211.568928 from(606.791740,2+) rtinseconds(3094) index(37805)
Title: Locus:1.1.1.2445.19
Data file 2011-11-10 - TFD - EP 3-6.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1211.564484
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 49  Expect: 9.8e-005
Matches : 11/84 fragment ions using 21 most intense peaks    (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.034219	58.520748			98.023654	49.515465	D							10
2	203.066247	102.036761			185.055682	93.031479	S	1097.544828	549.276052	1080.518279	540.762778	1079.534263	540.270770	9
3	350.134661	175.570968			332.124096	166.565686	F	**1010.512800**	505.760038	993.486251	497.246764			8
4	447.187425	224.097351			429.176860	215.092068	P	**863.444386**	432.225831	846.417837	423.712557			7
5	561.230352	281.118814	544.203803	272.605540	543.219787	272.113532	N	**766.391622**	383.699449	749.365073	375.186175			6
6	708.298766	354.653021	691.272217	346.139747	690.288201	345.647739	F	**652.348695**	326.677986	635.322146	318.164711			5
7	821.382830	411.195053	804.356281	402.681779	803.372265	402.189771	L	**505.280281**	253.143779	488.253732	244.630504			4
8	892.419944	446.713610	875.393395	438.200335	874.409379	437.708328	A	**392.196217**	196.601747	375.169668	188.088472			3
9	1066.466243	533.736760	1049.439694	525.223485	1048.455678	524.731477	C	**321.159103**	161.083190	304.132554	152.569915			2
10							K	**147.112804**	74.060040	130.086255	65.546765			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.6	1211.564484	0.004444	DSFPNFLACK
5.5	1211.567856	0.001072	MMSNQYVPVK
0.8	1211.563812	0.005116	LAMTREMNSK

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

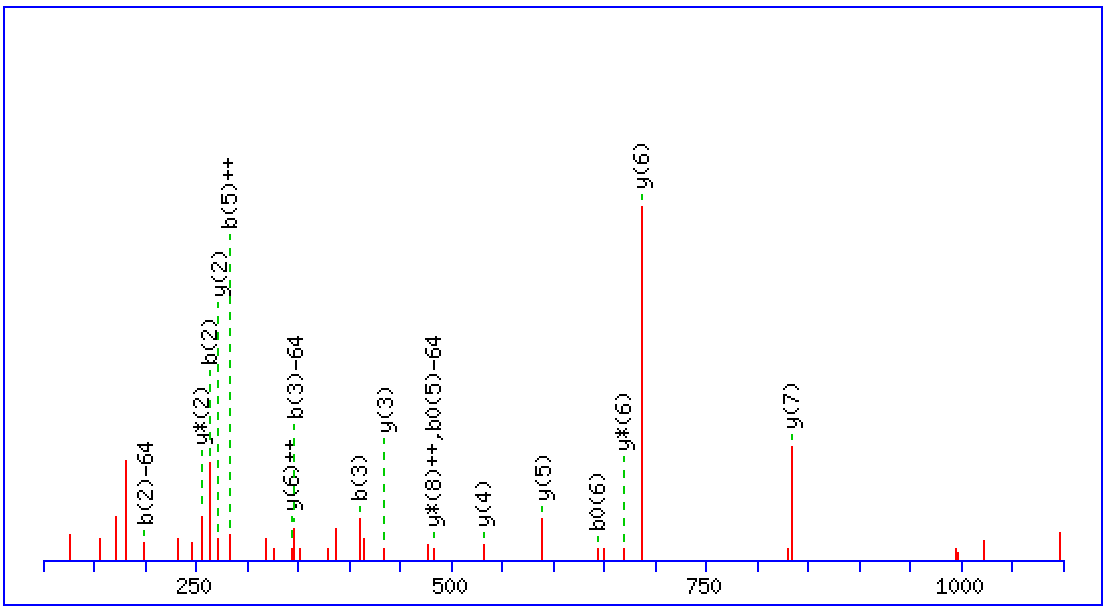
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DMFPGPYPR**
Found in **NDUB8_HUMAN**, NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial OS=Homo sapiens GN=NDUFB8 PE=1 SV=1

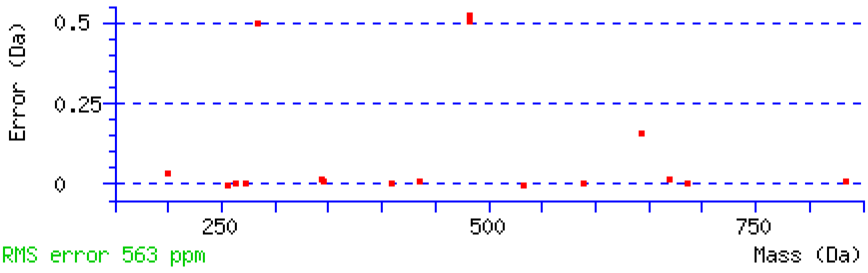
Match to Query 23177: 1094.489568 from(548.252060,2+) rtinseconds(2089) index(21314)
Title: Locus:1.1.1.2063.28
Data file 2011-11-10 - TFD - EP 3-6.mgf

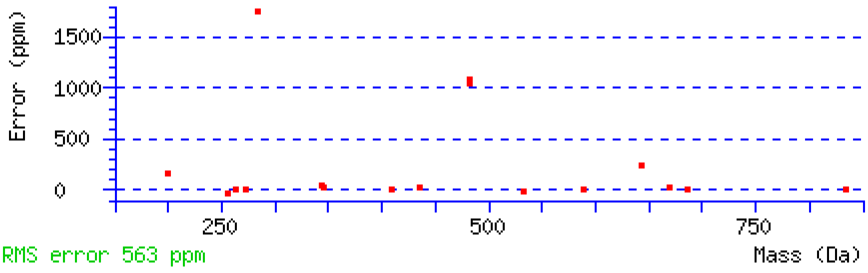
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1094.485519
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M2     : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 32  Expect: 0.0035
Matches : 17/96 fragment ions using 31 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	116.034219	58.520748	98.023654	49.515465	D					9
2	**263.069619**	132.038447	245.059054	123.033165	M	980.465851	490.736564	963.439302	482.223289	8
3	**410.138033**	205.572655	392.127468	196.567372	F	***833.430451***	417.218864	816.403902	408.705589	7
4	507.190797	254.099037	489.180232	245.093754	P	***686.362037***	343.684657	669.335488	335.171382	6
5	564.212261	282.609769	546.201696	273.604486	G	***589.309273***	295.158275	572.282724	286.645000	5
6	661.265025	331.136151	643.254460	322.130868	P	***532.287809***	266.647543	515.261260	258.134268	4
7	824.328354	412.667815	806.317789	403.662533	Y	***435.235045***	218.121161	418.208496	209.607886	3
8	921.381118	461.194197	903.370553	452.188915	P	***272.171716***	136.589496	255.145167	128.076221	2
9					R	175.118952	88.063114	158.092403	79.549839	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.8	1094.485519	0.004049	DMFPGPYPR
3.1	1094.485519	0.004049	DMFPGPYPR

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

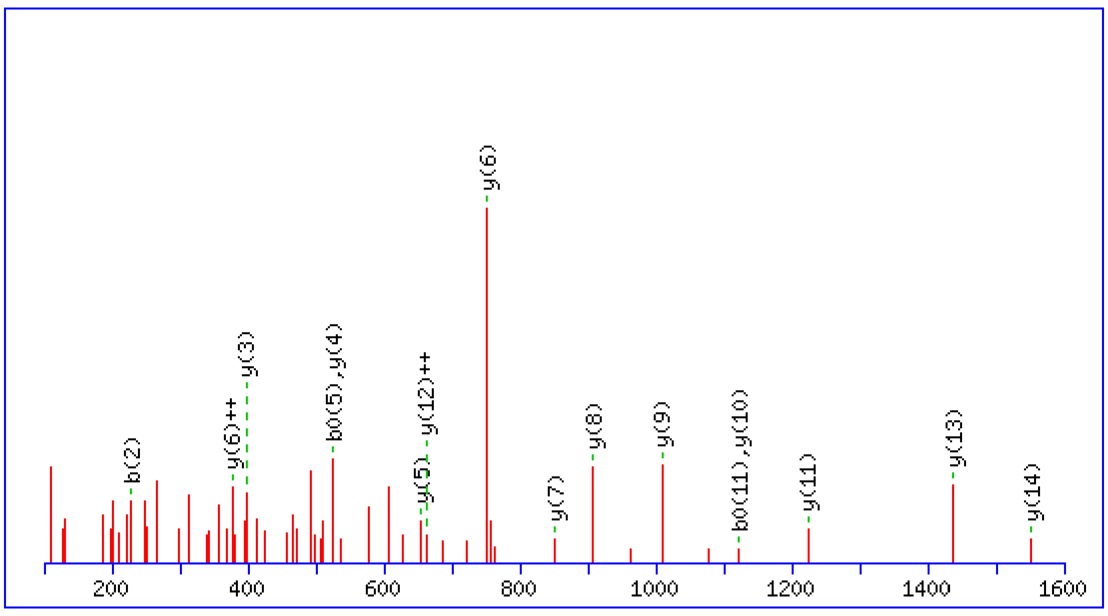
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LDITTLTGVPEEHIK**
Found in **NDUS4_HUMAN**, NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial OS=Homo sapiens GN=NDUFS4 PE=1 SV=1

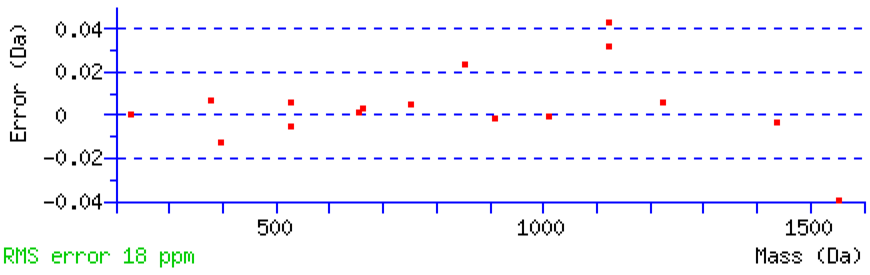
Match to Query 49342: 1664.900442 from(555.974090,3+) rtinseconds(2907) index(36221)
Title: Locus:1.1.1.2380.19
Data file 2011-11-14 - TFD - EP 8-6.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●

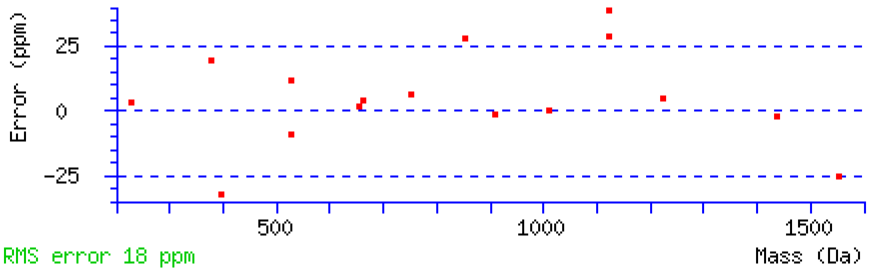


```
Monoisotopic mass of neutral peptide Mr(calc): 1664.898499
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 83  Expect: 3.7e-008
Matches : 16/132 fragment ions using 23 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							15
2	229.118283	115.062779	211.107718	106.057497	D	***1552.821716***	776.914496	1535.795167	768.401222	1534.811151	767.909214	14
3	342.202347	171.604811	324.191782	162.599529	I	***1437.794773***	719.401025	1420.768224	710.887750	1419.784208	710.395742	13
4	443.250026	222.128651	425.239461	213.123369	T	1324.710709	662.858993	1307.684160	654.345718	1306.700144	653.853710	12
5	544.297705	272.652491	526.287140	263.647208	T	***1223.663030***	612.335153	1206.636481	603.821879	1205.652465	603.329870	11
6	657.381769	329.194523	639.371204	320.189240	L	***1122.615351***	561.811314	1105.588802	553.298039	1104.604786	552.806031	10
7	758.429448	379.718362	740.418883	370.713080	T	***1009.531287***	505.269282	992.504738	496.756007	991.520722	496.263999	9
8	815.450912	408.229094	797.440347	399.223812	G	***908.483608***	454.745442	891.457059	446.232168	890.473043	445.740160	8
9	914.519326	457.763301	896.508761	448.758019	V	***851.462144***	426.234710	834.435595	417.721435	833.451579	417.229427	7
10	1011.572090	506.289683	993.561525	497.284401	P	***752.393730***	376.700503	735.367181	368.187229	734.383165	367.695221	6
11	1140.614683	570.810980	1122.604118	561.805697	E	***655.340966***	328.174121	638.314417	319.660846	637.330401	319.168838	5
12	1269.657276	635.332276	1251.646711	626.326994	E	***526.298373***	263.652825	509.271824	255.139550	508.287808	254.647542	4
13	1406.716188	703.861732	1388.705623	694.856450	H	***397.255780***	199.131528	380.229231	190.618253			3
14	1519.800252	760.403764	1501.789687	751.398482	I	260.196868	130.602072	243.170319	122.088797			2
15					K	147.112804	74.060040	130.086255	65.546765			1



RMS error 18 ppm



RMS error 18 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
82.9	1664.898499	0.001943	LDITTLTGVPEEHIK
26.1	1664.884598	0.015844	VEQGPPGGIGTAAVRPK
21.1	1664.884598	0.015844	VEQGPPGGIGTAAVRPK
6.0	1664.898499	0.001943	KPPTGPLPPSKEPLK
0.2	1664.895828	0.004614	GPRGTVAPATPTKPQR

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

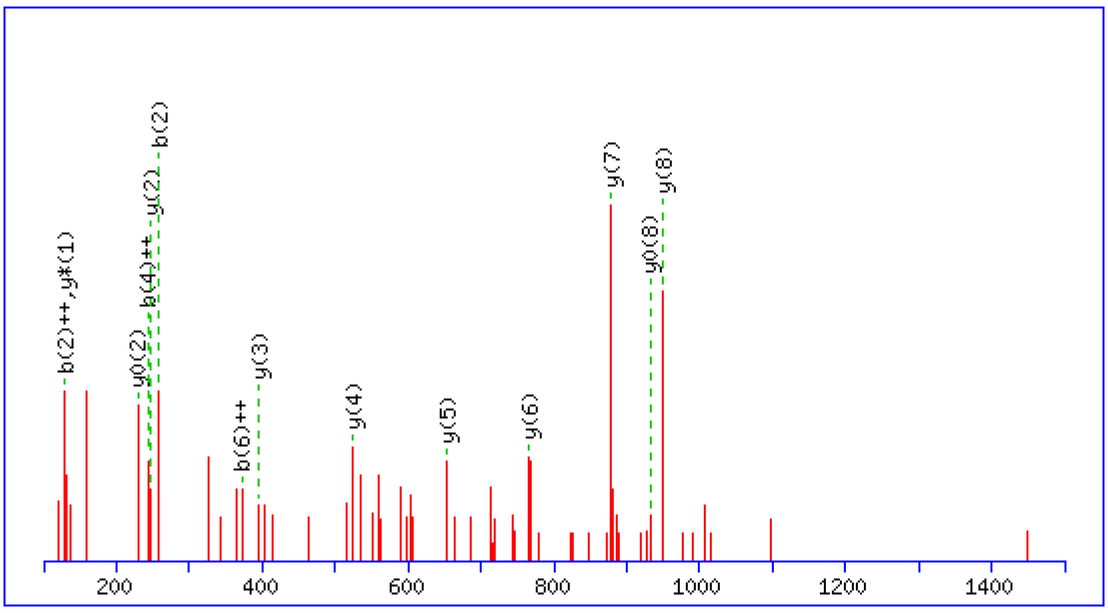
Mascot Search Results

Peptide View

MS/MS Fragmentation of **WAIIEEFTK**
Found in **NU2M_HUMAN**, NADH-ubiquinone oxidoreductase chain 2 OS=Homo sapiens GN=MT-ND2 PE=1 SV=2

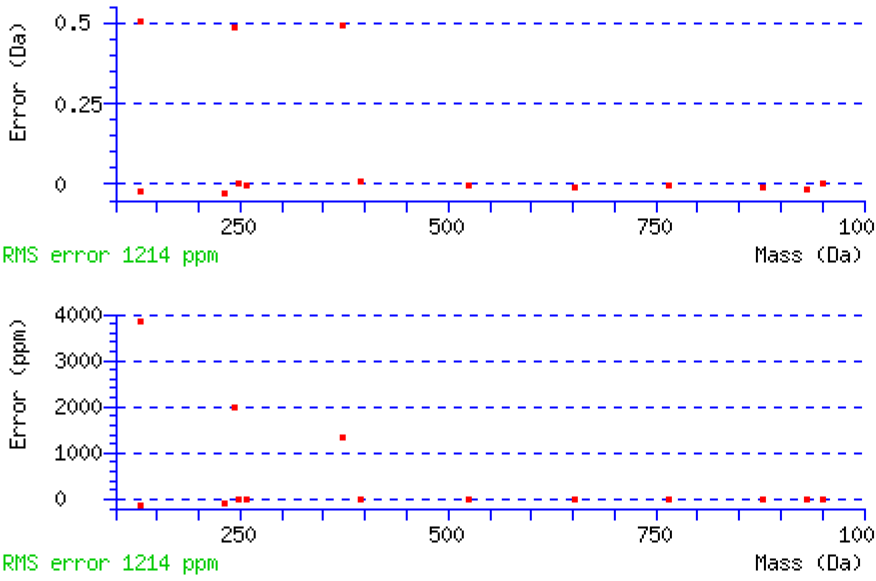
Match to Query 25400: 1135.589728 from(568.802140,2+) rtinseconds(3425) index(48305)
Title: Locus:1.1.1.2640.11
Data file 2011-11-10 - TFD - EP 4-1.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1135.591339
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.0014
Matches : 14/70 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	187.086589	94.046932			**W**							9
2	258.123703	**129.565490**			**A**	***950.519325***	475.763301	933.492776	467.250026	932.508760	466.758018	8
3	371.207767	186.107522			**I**	***879.482211***	440.244744	862.455662	431.731469	861.471646	431.239461	7
4	484.291831	**242.649554**			**I**	***766.398147***	383.702712	749.371598	375.189437	748.387582	374.697429	6
5	613.334424	307.170850	595.323859	298.165568	**E**	***653.314083***	327.160680	636.287534	318.647405	635.303518	318.155397	5
6	742.377017	**371.692147**	724.366452	362.686864	**E**	***524.271490***	262.639383	507.244941	254.126109	506.260925	253.634101	4
7	889.445431	445.226354	871.434866	436.221071	**F**	***395.228897***	198.118086	378.202348	189.604812	377.218332	189.112804	3
8	990.493110	495.750193	972.482545	486.744911	**T**	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.578597	2
9					**K**	147.112804	74.060040	130.086255	65.546765			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.8	1135.591339	-0.001611	WAIIEEFTK
2.2	1135.587311	0.002417	KQINDYVEK

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

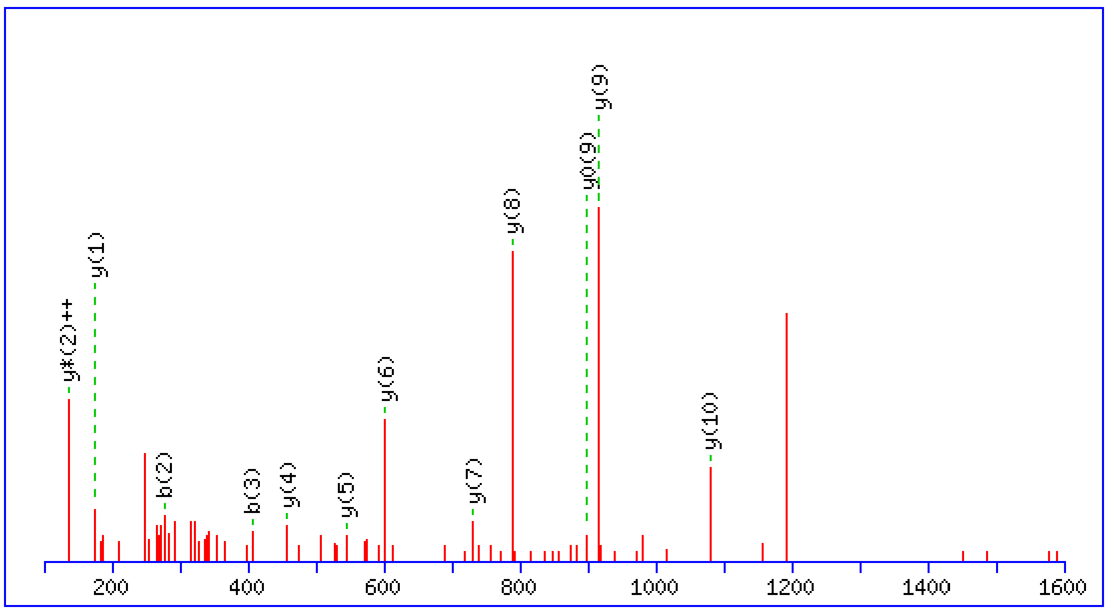
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IYEGEGSGLIR**
Found in **NU6M_HUMAN**, NADH-ubiquinone oxidoreductase chain 6 OS=Homo sapiens GN=MT-ND6 PE=1 SV=2

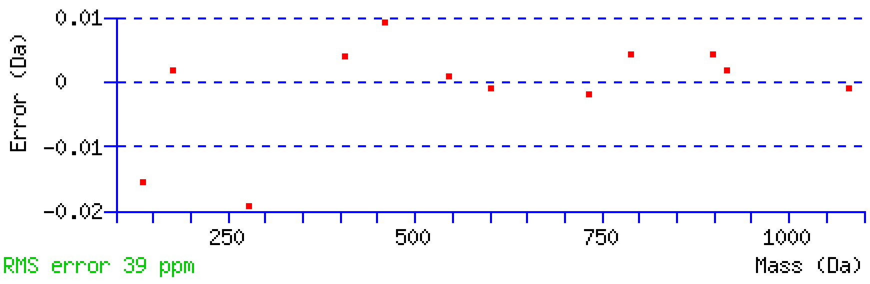
Match to Query 512406: 1192.607368 from(597.310960,2+) rtinseconds(2040) index(916616)
Title: Locus:1.1.1.1177.42
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

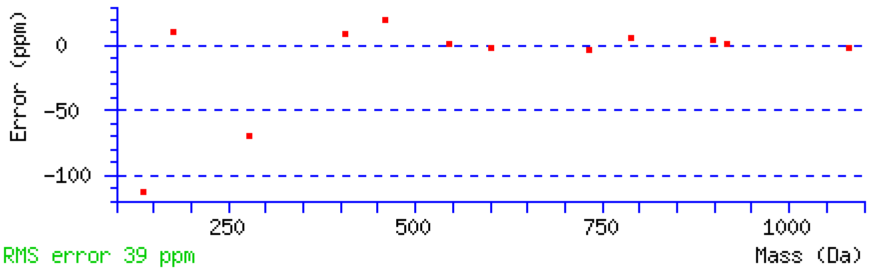
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1600] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1192.608780
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 62  Expect: 3.7e-006
Matches : 12/88 fragment ions using 21 most intense peaks    (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							11
2	**277.154669**	139.080973			Y	***1080.532015***	540.769646	1063.505466	532.256371	1062.521450	531.764363	10
3	**406.197262**	203.602269	388.186697	194.596987	E	***917.468686***	459.237981	900.442137	450.724707	899.458121	450.232699	9
4	463.218726	232.113001	445.208161	223.107719	G	***788.426093***	394.716685	771.399544	386.203410	770.415528	385.711402	8
5	592.261319	296.634298	574.250754	287.629015	E	***731.404629***	366.205953	714.378080	357.692678	713.394064	357.200670	7
6	649.282783	325.145030	631.272218	316.139747	G	***602.362036***	301.684656	585.335487	293.171382	584.351471	292.679374	6
7	736.314811	368.661044	718.304246	359.655761	S	***545.340572***	273.173924	528.314023	264.660650	527.330007	264.168642	5
8	793.336275	397.171776	775.325710	388.166493	G	***458.308544***	229.657910	441.281995	221.144635			4
9	906.420339	453.713808	888.409774	444.708525	L	401.287080	201.147178	384.260531	192.633903			3
10	1019.504403	510.255840	1001.493838	501.250557	I	288.203016	144.605146	271.176467	136.091871			2
11					R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
62.4	1192.608780	-0.001412	IYEGEGSGLIR
4.3	1192.612167	-0.004799	VLVSSEMGISR
2.8	1192.612152	-0.004784	TIAASASSVKQM
0.6	1192.608795	-0.001427	VSRTTPYEPK

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

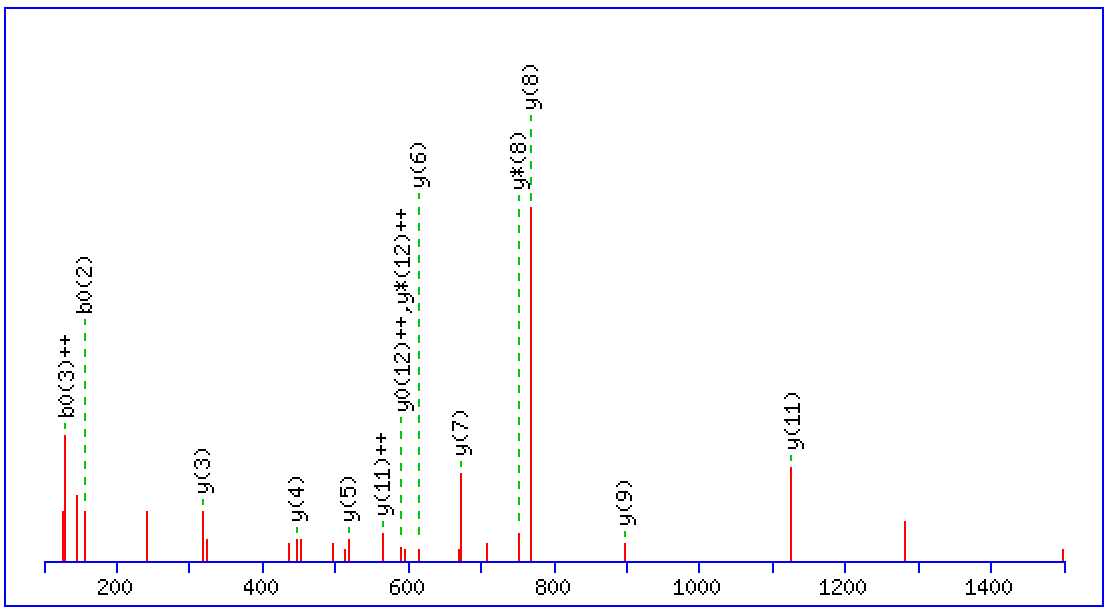
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TATEKPGPAEAAR**
Found in **ADRO_HUMAN**, NADPH:adrenodoxin oxidoreductase, mitochondrial OS=Homo sapiens GN=FDXR PE=1 SV=3

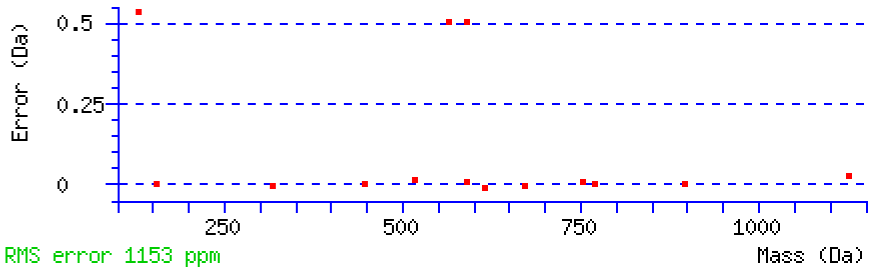
Match to Query 638448: 1297.659192 from(433.560340,3+) rtinseconds(761) index(324997)
Title: Locus:1.1.1.621.4
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

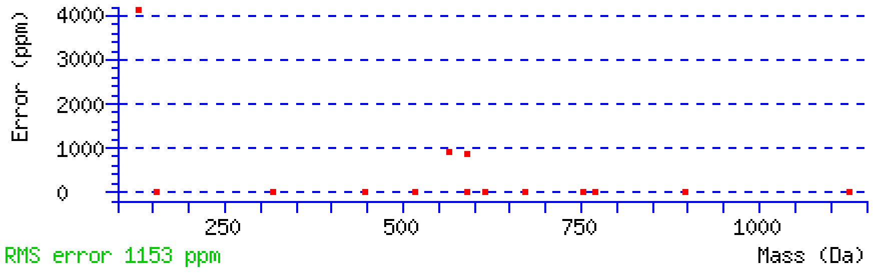
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1297.662598
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 50 **Expect:** 2.9e-005
Matches : 14/130 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							13
2	173.092069	87.049672			155.081504	78.044390	A	1197.622228	599.314752	1180.595679	590.801478	1179.611663	590.309470	12
3	274.139748	137.573512			256.129183	128.568230	T	***1126.585114***	563.796195	1109.558565	555.282921	1108.574549	554.790913	11
4	403.182341	202.094809			385.171776	193.089526	E	1025.537435	513.272356	1008.510886	504.759081	1007.526870	504.267073	10
5	531.277304	266.142290	514.250755	257.629016	513.266739	257.137008	K	***896.494842***	448.751059	879.468293	440.237785	878.484277	439.745777	9
6	628.330068	314.668672	611.303519	306.155398	610.319503	305.663390	P	***768.399879***	384.703578	751.373330	376.190303	750.389314	375.698295	8
7	685.351532	343.179404	668.324983	334.666130	667.340967	334.174122	G	***671.347115***	336.177196	654.320566	327.663921	653.336550	327.171913	7
8	782.404296	391.705786	765.377747	383.192512	764.393731	382.700504	P	***614.325651***	307.666464	597.299102	299.153189	596.315086	298.661181	6
9	853.441410	427.224343	836.414861	418.711069	835.430845	418.219061	A	***517.272887***	259.140082	500.246338	250.626807	499.262322	250.134799	5
10	982.484003	491.745640	965.457454	483.232365	964.473438	482.740357	E	***446.235773***	223.621524	429.209224	215.108250	428.225208	214.616242	4
11	1053.521117	527.264197	1036.494568	518.750922	1035.510552	518.258914	A	***317.193180***	159.100228	300.166631	150.586953			3
12	1124.558231	562.782754	1107.531682	554.269479	1106.547666	553.777471	A	246.156066	123.581671	229.129517	115.068396			2
13							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.9	1297.662598	-0.003406	TATEKPGPAEAAR
1.6	1297.662598	-0.003406	EDANKPIQEVR

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

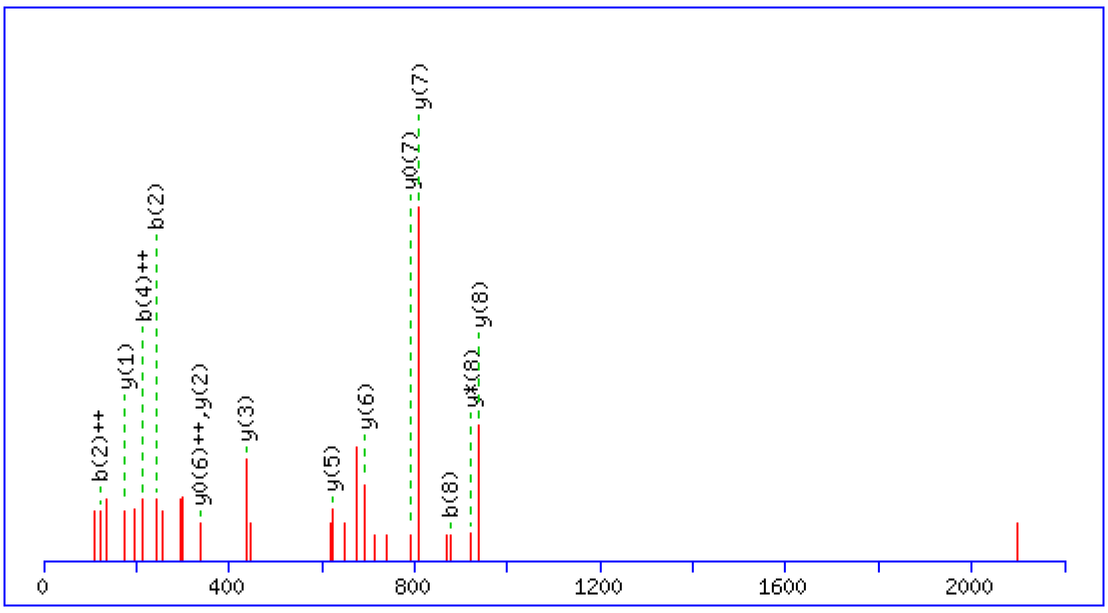
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LEDAADVYR**
Found in **NAA15_HUMAN**, N-alpha-acetyltransferase 15, NatA auxiliary subunit OS=Homo sapiens GN=NAA15 PE=1 SV=1

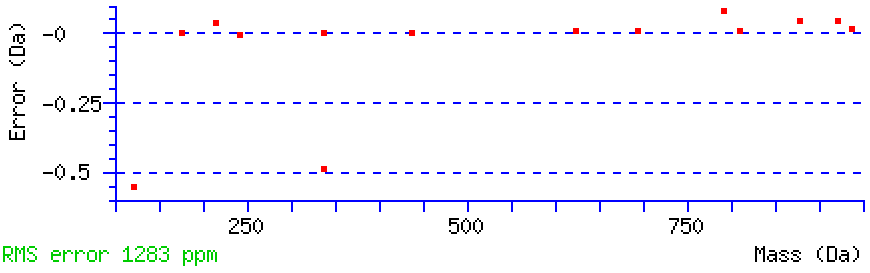
Match to Query 20258: 1050.498768 from(526.256660,2+) rtinseconds(1665) index(15438)
Title: Locus:1.1.1.2128.28
Data file 2011-11-10 - TFD - EP 4-2.mgf

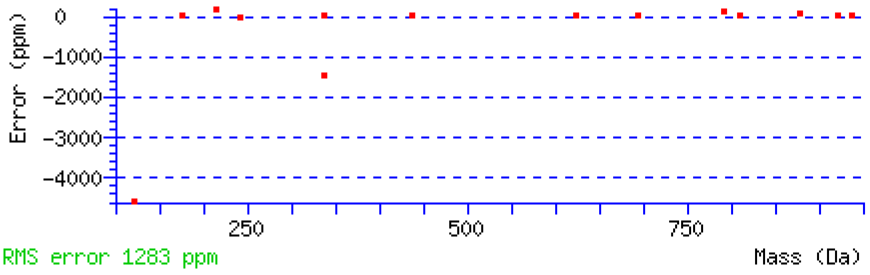
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1050.498169
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 44  Expect: 0.0003
Matches : 14/72 fragment ions using 28 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							9
2	**243.133933**	**122.070605**	225.123368	113.065322	E	***938.421402***	469.714339	921.394853	461.201065	920.410837	460.709057	8
3	358.160876	179.584076	340.150311	170.578794	D	***809.378809***	405.193043	792.352260	396.679768	791.368244	396.187760	7
4	429.197990	**215.102633**	411.187425	206.097351	A	***694.351866***	347.679571	677.325317	339.166296	676.341301	338.674288	6
5	500.235104	250.621190	482.224539	241.615908	A	***623.314752***	312.161014	606.288203	303.647740	605.304187	303.155732	5
6	615.262047	308.134662	597.251482	299.129379	D	552.277638	276.642457	535.251089	268.129183	534.267073	267.637175	4
7	714.330461	357.668869	696.319896	348.663586	V	***437.250695***	219.128985	420.224146	210.615711			3
8	**877.393790**	439.200533	859.383225	430.195251	Y	***338.182281***	169.594778	321.155732	161.081504			2
9					R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.3	1050.498169	0.000599	LEDAADVYR

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

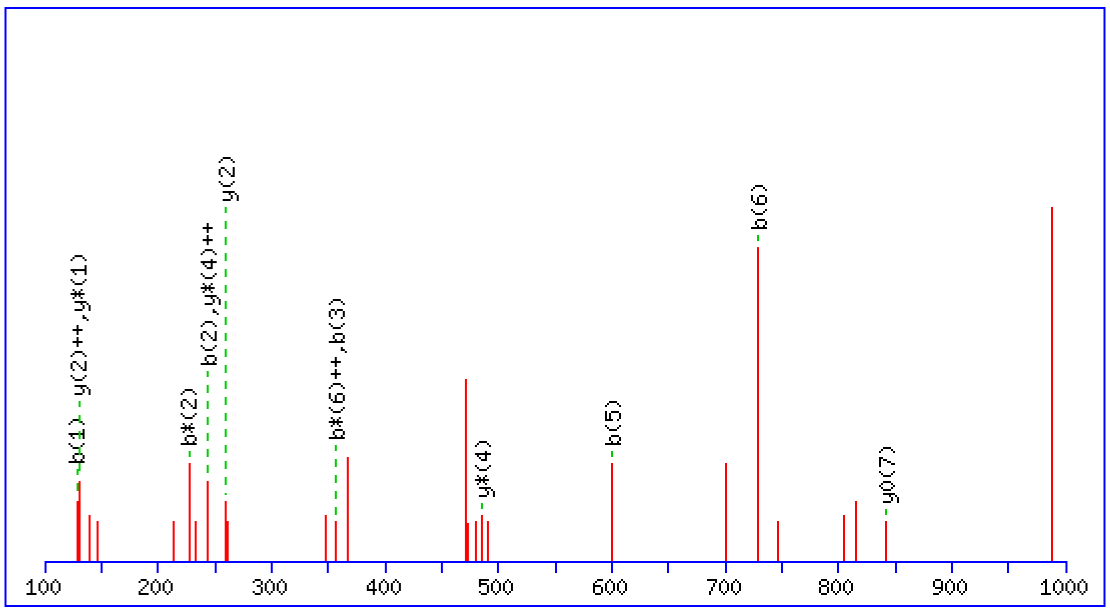
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **KDLENEIK**
Found in **NEBL_HUMAN**, Nebulette OS=Homo sapiens GN=NEBL PE=2 SV=1

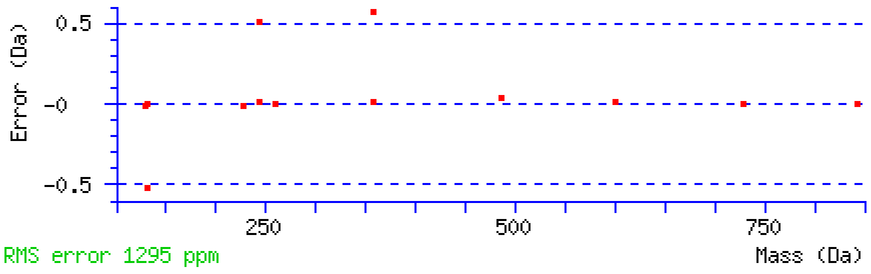
Match to Query 18770: 987.533168 from(494.773860,2+) rtinseconds(1223) index(6174)
Title: Locus:1.1.1.1720.26
Data file 2011-11-10 - TFD - EP 4-6.mgf

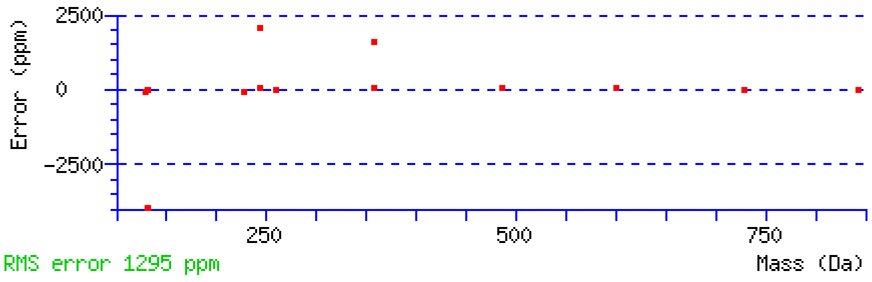
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 987.523636
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 48  Expect: 0.00037
Matches : 16/78 fragment ions using 18 most intense peaks    (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	***129.102239***	65.054757	112.075690	56.541483			K							8
2	***244.129182***	122.568229	227.102633	114.054955	226.118617	113.562947	D	860.435988	430.721632	843.409439	422.208358	842.425423	421.716350	7
3	***357.213246***	179.110261	340.186697	170.596987	339.202681	170.104979	L	745.409045	373.208161	728.382496	364.694886	727.398480	364.202878	6
4	***486.255839***	243.631558	469.229290	235.118283	468.245274	234.626275	E	632.324981	316.666129	615.298432	308.152854	614.314416	307.660846	5
5	***600.298766***	300.653021	583.272217	292.139747	582.288201	291.647739	N	503.282388	252.144832	486.255839	243.631558	485.271823	243.139550	4
6	***729.341359***	365.174318	712.314810	356.661043	711.330794	356.169035	E	389.239461	195.123369	372.212912	186.610094	371.228896	186.118086	3
7	***842.425423***	421.716350	825.398874	413.203075	824.414858	412.711067	I	260.196868	130.602072	243.170319	122.088798			2
8							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.5	987.523636	0.009532	KDLENEIK
41.7	987.534882	-0.001714	SRLDQELK
33.5	987.534866	-0.001698	ENLESRLK
26.1	987.523651	0.009517	DKLQDELK
19.9	987.534897	-0.001729	KPRTTEPK
19.8	987.538925	-0.005757	TWKTDLPK
17.8	987.523651	0.009517	DQEIKDLK
16.3	987.534882	-0.001714	EDLKNTLR
15.9	987.523666	0.009502	KDPSSVDIK
15.6	987.534882	-0.001714	DRPSKLEK

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

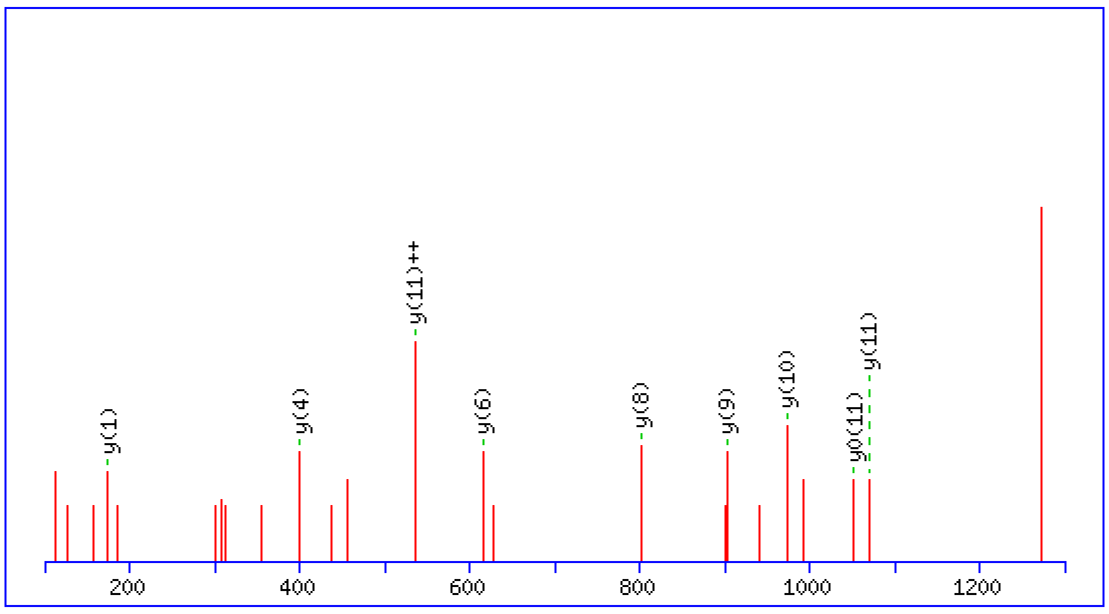
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TTPATGEQSPGAR**
Found in **WWP2_HUMAN**, NEDD4-like E3 ubiquitin-protein ligase WWP2 OS=Homo sapiens GN=WWP2 PE=1 SV=2

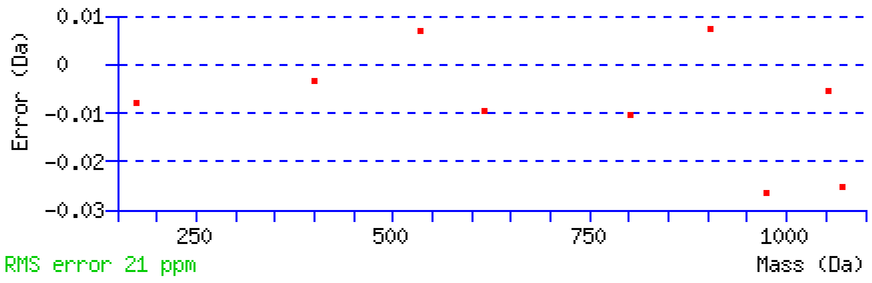
Match to Query 606718: 1271.611088 from(636.812820,2+) rtinseconds(841) index(240821)
Title: Locus:1.1.1.759.37
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

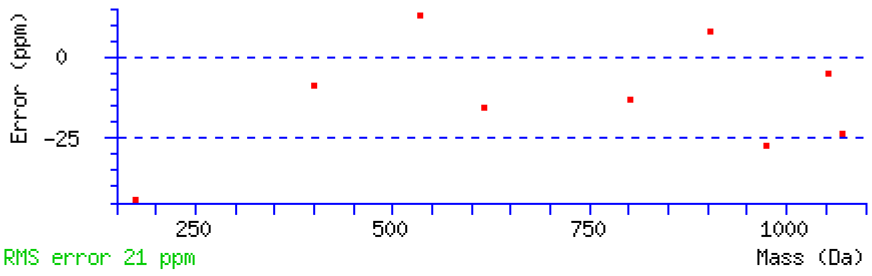
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1271.610596
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 42  Expect: 0.00082
Matches : 9/122 fragment ions using 19 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							13
2	203.102634	102.054955			185.092069	93.049672	T	1171.570193	586.288735	1154.543644	577.775460	1153.559628	577.283452	12
3	300.155398	150.581337			282.144833	141.576055	P	***1070.522514***	535.764895	1053.495965	527.251621	1052.511949	526.759613	11
4	371.192512	186.099894			353.181947	177.094612	A	***973.469750***	487.238513	956.443201	478.725238	955.459185	478.233230	10
5	472.240191	236.623734			454.229626	227.618451	T	***902.432636***	451.719956	885.406087	443.206682	884.422071	442.714674	9
6	529.261655	265.134466			511.251090	256.129183	G	***801.384957***	401.196117	784.358408	392.682842	783.374392	392.190834	8
7	658.304248	329.655762			640.293683	320.650480	E	744.363493	372.685385	727.336944	364.172110	726.352928	363.680102	7
8	786.362826	393.685051	769.336277	385.171777	768.352261	384.679769	Q	***615.320900***	308.164088	598.294351	299.650813	597.310335	299.158805	6
9	873.394854	437.201065	856.368305	428.687791	855.384289	428.195783	S	487.262322	244.134799	470.235773	235.621524	469.251757	235.129516	5
10	970.447618	485.727447	953.421069	477.214173	952.437053	476.722165	P	***400.230294***	200.618785	383.203745	192.105510			4
11	1027.469082	514.238179	1010.442533	505.724905	1009.458517	505.232897	G	303.177530	152.092403	286.150981	143.579128			3
12	1098.506196	549.756736	1081.479647	541.243462	1080.495631	540.751454	A	246.156066	123.581671	229.129517	115.068396			2
13							R	***175.118952***	88.063114	158.092403	79.549839			1



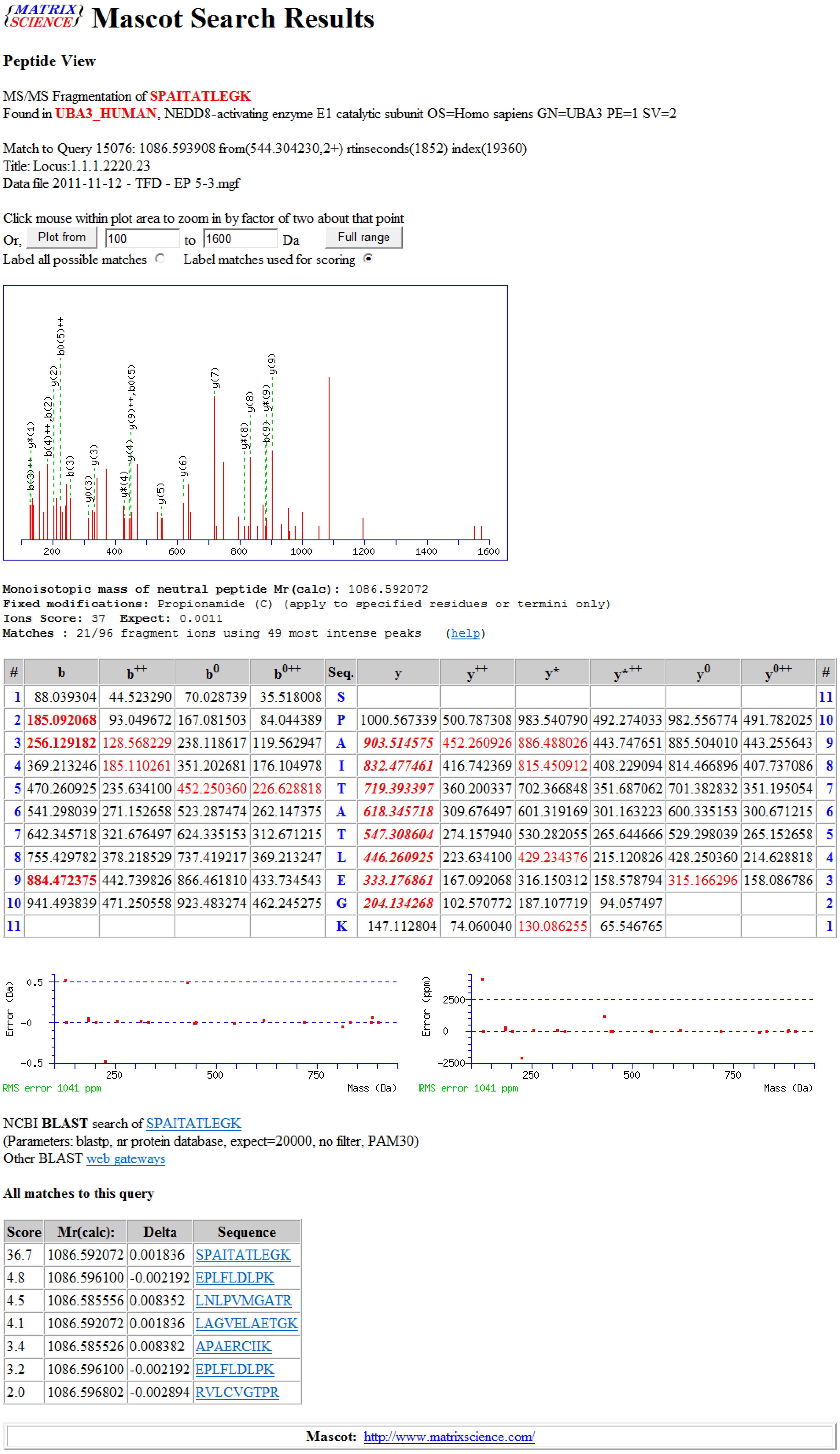


NCBI **BLAST** search of TTPATGEQSPGAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.6	1271.610596	0.000492	TTPATGEQSPGAR
8.2	1271.606750	0.004338	SDPVPAMTTPEK
3.9	1271.617966	-0.006878	MAPPLPSEINR
1.2	1271.621826	-0.010738	GGSDASQVPNGKR

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



{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SPAITATLEGK**
Found in **UBA3_HUMAN**, NEDD8-activating enzyme E1 catalytic subunit OS=Homo sapiens GN=UBA3 PE=1 SV=2

Match to Query 15076: 1086.593908 from(544.304230,2+) rtinseconds(1852) index(19360)
Title: Locus:1.1.1.2220.23
Data file 2011-11-12 - TFD - EP 5-3.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1086.592072
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 37 **Expect:** 0.0011
Matches : 21/96 fragment ions using 49 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	88.039304	44.523290	70.028739	35.518008	S							11
2	**185.092068**	93.049672	167.081503	84.044389	P	1000.567339	500.787308	983.540790	492.274033	982.556774	491.782025	10
3	**256.129182**	128.568229	238.118617	119.562947	A	***903.514575***	452.260926	886.488026	443.747651	885.504010	443.255643	9
4	369.213246	185.110261	351.202681	176.104978	I	***832.477461***	416.742369	815.450912	408.229094	814.466896	407.737086	8
5	470.260925	235.634100	452.250360	226.628818	T	***719.393397***	360.200337	702.366848	351.687062	701.382832	351.195054	7
6	541.298039	271.152658	523.287474	262.147375	A	***618.345718***	309.676497	601.319169	301.163223	600.335153	300.671215	6
7	642.345718	321.676497	624.335153	312.671215	T	***547.308604***	274.157940	530.282055	265.644666	529.298039	265.152658	5
8	755.429782	378.218529	737.419217	369.213247	L	***446.260925***	223.634100	429.234376	215.120826	428.250360	214.628818	4
9	**884.472375**	442.739826	866.461810	433.734543	E	***333.176861***	167.092068	316.150312	158.578794	315.166296	158.086786	3
10	941.493839	471.250558	923.483274	462.245275	G	***204.134268***	102.570772	187.107719	94.057497			2
11					K	147.112804	74.060040	130.086255	65.546765			1

NCBI **BLAST** search of SPAITATLEGK
(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	1086.592072	0.001836	SPAITATLEGK
4.8	1086.596100	-0.002192	EPLFLDLPK
4.5	1086.585556	0.008352	LNLPVMGATR
4.1	1086.592072	0.001836	LAGVELAETGK
3.4	1086.585526	0.008382	APAERCIIK
3.2	1086.596100	-0.002192	EPLFLDLPK
2.0	1086.596802	-0.002894	RVLCVGTPR

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

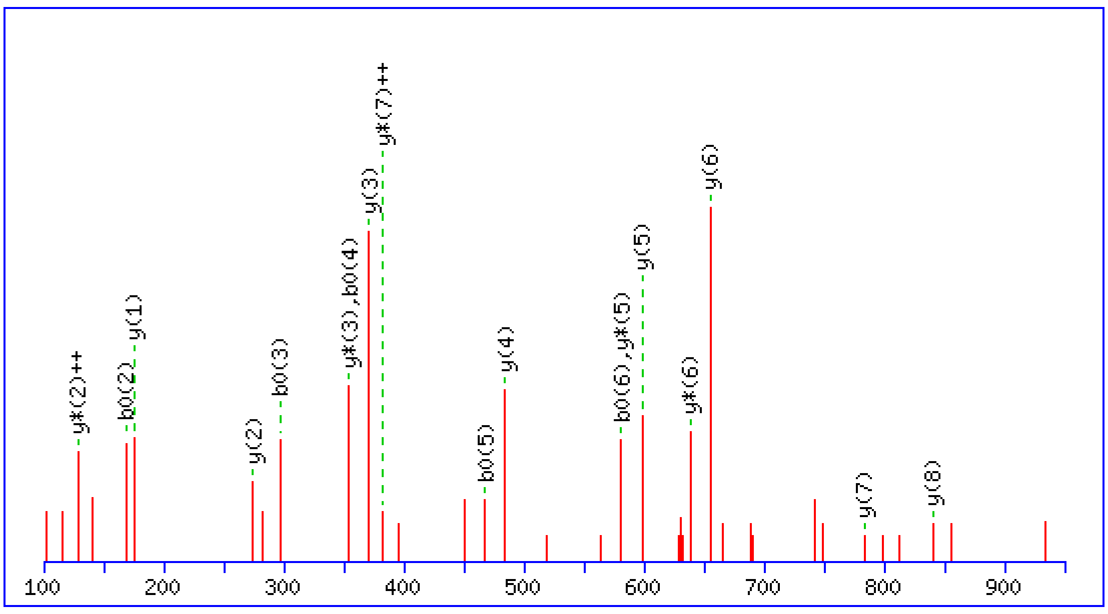
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EGQGNLPVR**
Found in **ULA1_HUMAN**, NEDD8-activating enzyme E1 regulatory subunit OS=Homo sapiens GN=NAE1 PE=1 SV=1

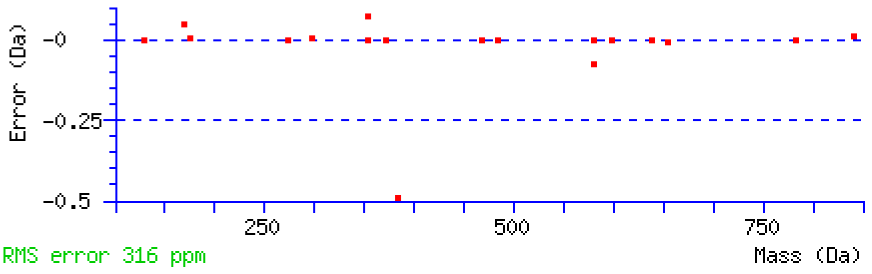
Match to Query 219818: 968.500048 from(485.257300,2+) rtinseconds(1151) index(331500)
Title: Locus:1.1.1.772.14
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

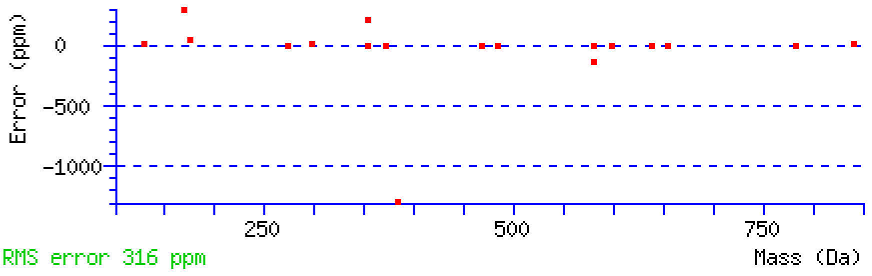
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 968.503937
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 61  Expect: 8.9e-006
Matches : 18/76 fragment ions using 25 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	130.049869	65.528572			112.039304	56.523290	E					9
2	187.071333	94.039305			169.060768	85.034022	G	***840.468627***	420.737952	823.442078	412.224677	8
3	315.129911	158.068594	298.103362	149.555319	297.119346	149.063311	Q	***783.447163***	392.227220	766.420614	383.713945	7
4	372.151375	186.579326	355.124826	178.066051	354.140810	177.574043	G	***655.388585***	328.197931	638.362036	319.684656	6
5	486.194302	243.600789	469.167753	235.087515	468.183737	234.595507	N	***598.367121***	299.687199	581.340572	291.173924	5
6	599.278366	300.142821	582.251817	291.629547	581.267801	291.137539	L	***484.324194***	242.665735	467.297645	234.152460	4
7	696.331130	348.669203	679.304581	340.155929	678.320565	339.663921	P	***371.240130***	186.123703	354.213581	177.610428	3
8	795.399544	398.203410	778.372995	389.690136	777.388979	389.198128	V	***274.187366***	137.597321	257.160817	129.084046	2
9							R	***175.118952***	88.063114	158.092403	79.549839	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
61.3	968.503937	-0.003889	EGQGNLPVR
11.9	968.492722	0.007326	GPGSGPGALPK
9.9	968.496704	0.003344	ELEFYLR
9.3	968.492722	0.007326	GPGSGPGALPK
5.6	968.503922	-0.003874	INSKGEGHK
5.4	968.503922	-0.003874	EEPGPLRR
5.1	968.503937	-0.003889	APSQQSPVR
4.2	968.503906	-0.003858	EHALSKER
3.8	968.503937	-0.003889	DSHKEVVR
1.5	968.507965	-0.007917	KGSFVPYR

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

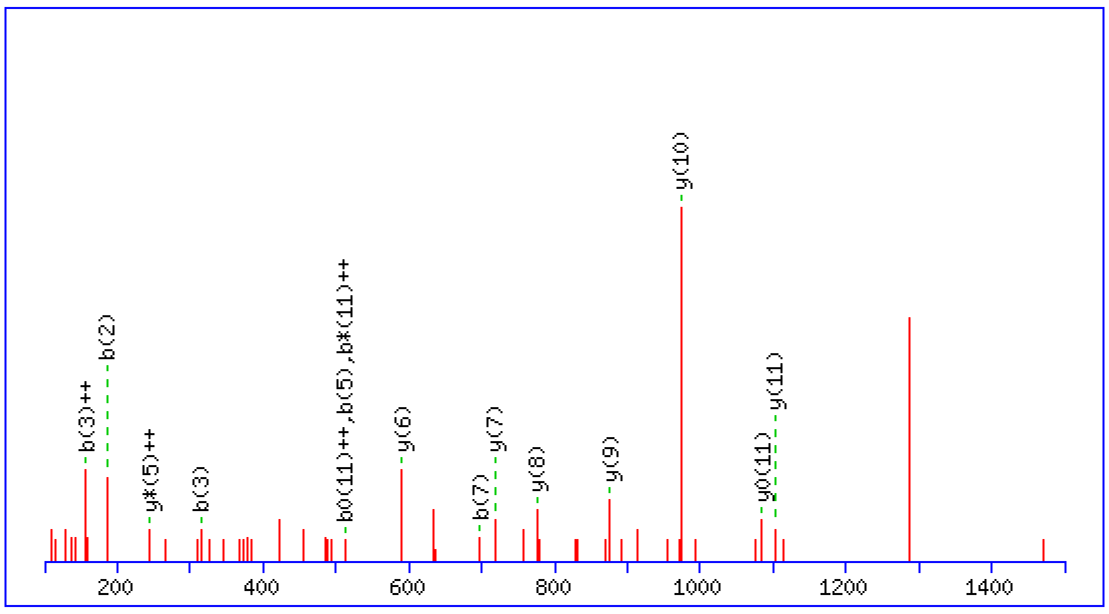
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALEPTGQSGEAVK**
Found in **NELFB_HUMAN**, Negative elongation factor B OS=Homo sapiens GN=COBRA1 PE=1 SV=1

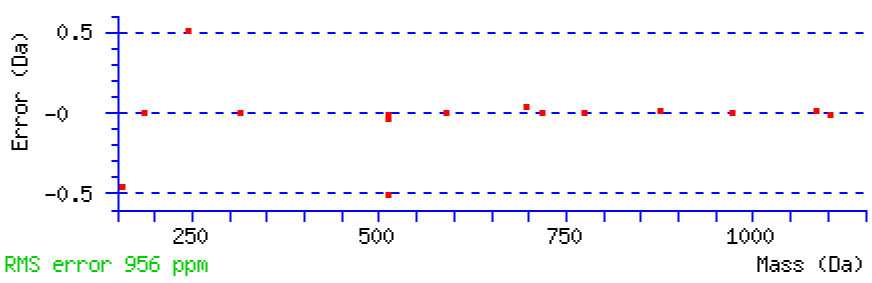
Match to Query 625033: 1285.648748 from(643.831650,2+) rtinseconds(1264) index(248802)
Title: Locus:1.1.1.924.36
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

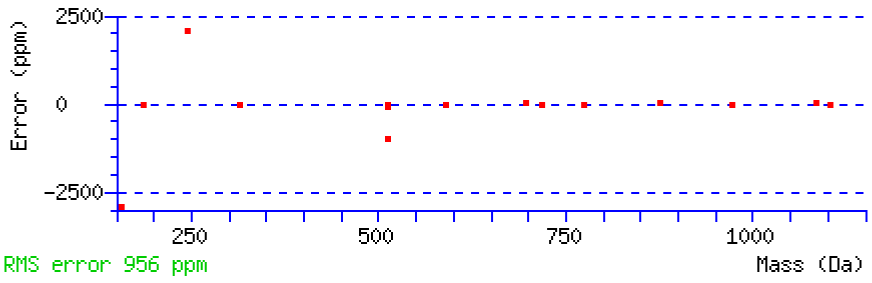
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1285.651382
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 37 **Expect:** 0.0011
Matches : 15/122 fragment ions using 21 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	72.044390	36.525833					A							13
2	**185.128454**	93.067865					L	1215.621559	608.314418	1198.595010	599.801143	1197.610994	599.309135	12
3	**314.171047**	157.589161			296.160482	148.583879	E	***1102.537495***	551.772386	1085.510946	543.259111	1084.526930	542.767103	11
4	411.223811	206.115544			393.213246	197.110261	P	***973.494902***	487.251089	956.468353	478.737815	955.484337	478.245807	10
5	**512.271490**	256.639383			494.260925	247.634101	T	***876.442138***	438.724707	859.415589	430.211433	858.431573	429.719425	9
6	569.292954	285.150115			551.282389	276.144833	G	***775.394459***	388.200868	758.367910	379.687593	757.383894	379.195585	8
7	**697.351532**	349.179404	680.324983	340.666130	679.340967	340.174122	Q	***718.372995***	359.690136	701.346446	351.176861	700.362430	350.684853	7
8	784.383560	392.695418	767.357011	384.182144	766.372995	383.690136	S	***590.314417***	295.660847	573.287868	287.147572	572.303852	286.655564	6
9	841.405024	421.206150	824.378475	412.692876	823.394459	412.200868	G	503.282389	252.144833	486.255840	243.631558	485.271824	243.139550	5
10	970.447617	485.727447	953.421068	477.214172	952.437052	476.722164	E	446.260925	223.634101	429.234376	215.120826	428.250360	214.628818	4
11	1041.484731	521.246004	1024.458182	512.732729	1023.474166	512.240721	A	317.218332	159.112804	300.191783	150.599530			3
12	1140.553145	570.780211	1123.526596	562.266936	1122.542580	561.774928	V	246.181218	123.594247	229.154669	115.080973			2
13							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.4	1285.651382	-0.002634	ALEPTGQSGEAVK
5.5	1285.652710	-0.003962	IAERQGHSNFK
1.4	1285.641464	0.007284	LAEQEAHYAVR
0.6	1285.655411	-0.006663	LVDNIFPEDPK

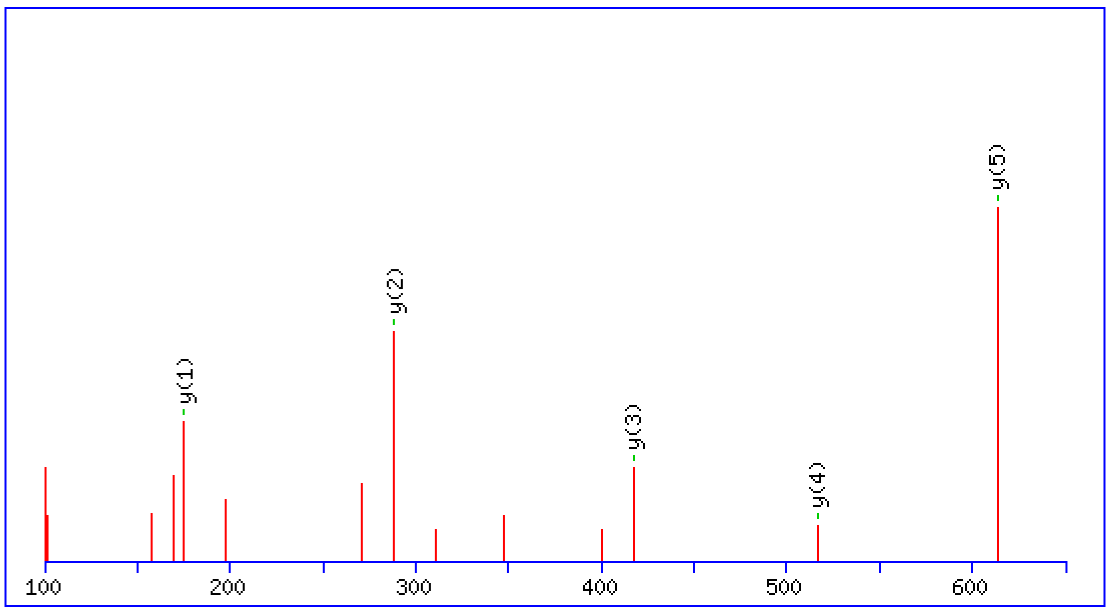
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NKPVELR**
Found in **UNC5B_HUMAN**, Netrin receptor UNC5B OS=Homo sapiens GN=UNC5B PE=1 SV=2

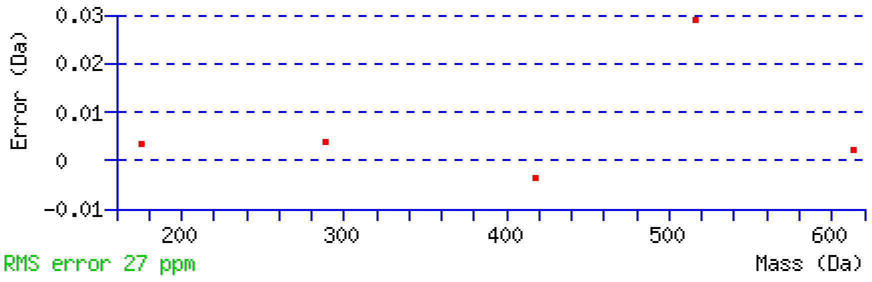
Match to Query 3750: 854.491368 from(428.252960,2+) rtinseconds(1256) index(8863)
Title: Locus:1.1.1.1892.8
Data file 2011-11-10 - TFD - EP 3-3.mgf

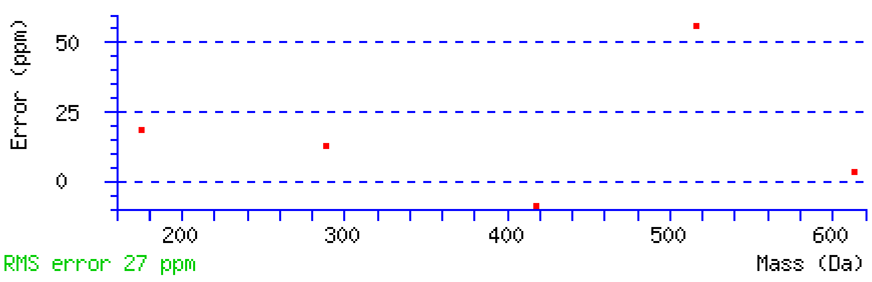
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 650 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 854.497375
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 48 **Expect:** 9.9e-005
Matches : 5/60 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			N							7
2	243.145166	122.076221	226.118617	113.562947			K	741.461750	371.234513	724.435201	362.721239	723.451185	362.229231	6
3	340.197930	170.602603	323.171381	162.089328			P	*613.366787*	307.187032	596.340238	298.673757	595.356222	298.181749	5
4	439.266344	220.136810	422.239795	211.623536			V	*516.314023*	258.660650	499.287474	250.147375	498.303458	249.655367	4
5	568.308937	284.658107	551.282388	276.144832	550.298372	275.652824	E	*417.245609*	209.126443	400.219060	200.613168	399.235044	200.121160	3
6	681.393001	341.200139	664.366452	332.686864	663.382436	332.194856	L	*288.203016*	144.605146	271.176467	136.091872			2
7							R	*175.118952*	88.063114	158.092403	79.549840			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.4	854.497375	-0.006007	NKPVELR
21.2	854.497375	-0.006007	KPVNELR
17.7	854.497391	-0.006023	QNVPIIR
9.6	854.497391	-0.006023	QPKDVLR
3.1	854.486145	0.005223	LELPLDR
2.3	854.497375	-0.006007	AGAAPALLR
2.3	854.497391	-0.006023	AQTLPGLR
2.3	854.497391	-0.006023	KAAVPTPR
2.3	854.497375	-0.006007	QAALPSLR
1.8	854.483459	0.007909	ASRPRPR

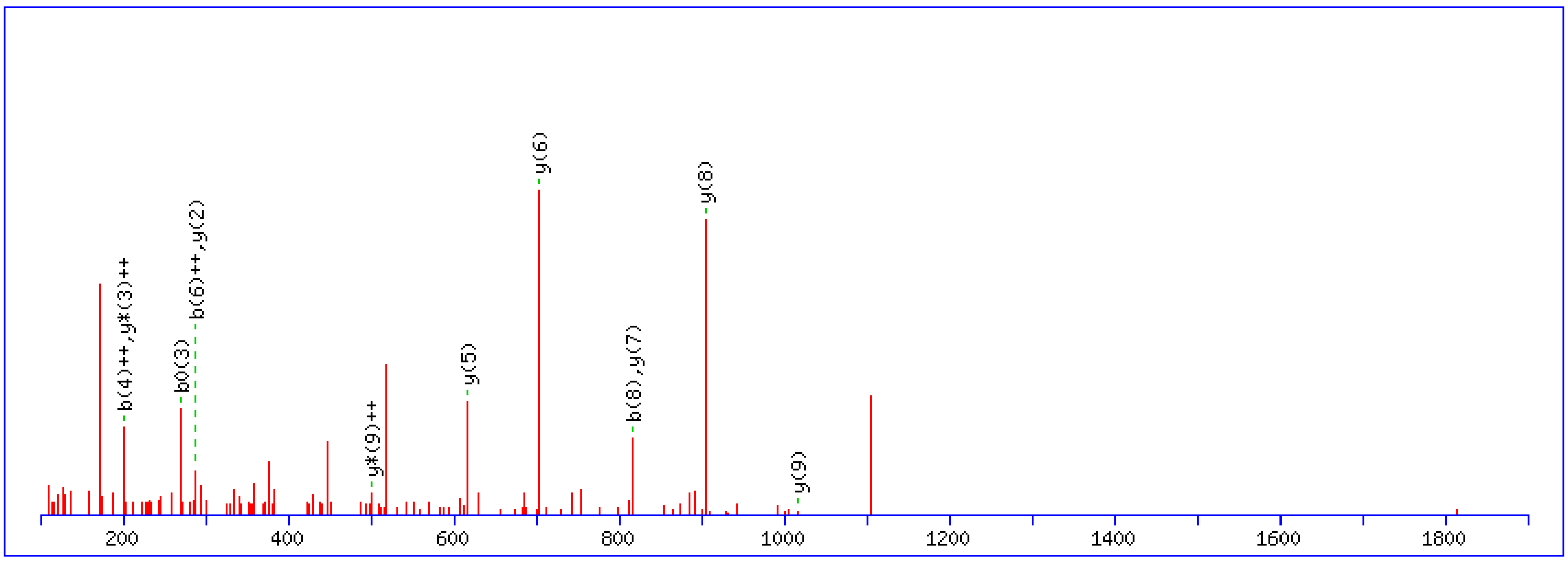
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SISLSSLEPR**
Found in **NBEL2_HUMAN**, Neurobeachin-like protein 2 OS=Homo sapiens GN=NBEAL2 PE=1 SV=2

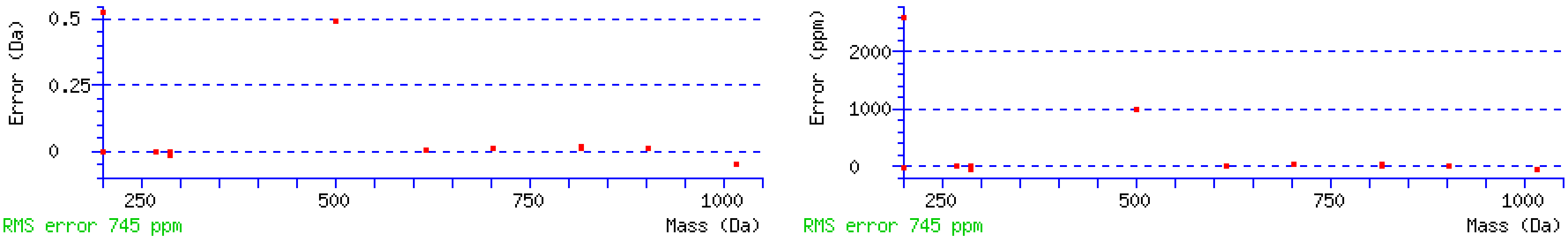
Match to Query 15295: 1103.589148 from(552.801850,2+) rtinseconds(1814) index(19179)
Title: Locus:1.1.1.1073.20
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 2.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1103.582230
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
P9      : Oxidation (P)
Ions Score: 35  Expect: 0.005
Matches : 14/86 fragment ions using 19 most intense peaks   (help)
```

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	S							10
2	**201.123368**	101.065322	183.112803	92.060039	I	***1017.557500***	509.282388	1000.530951	500.769114	999.546935	500.277106	9
3	**288.155396**	144.581336	270.144831	135.576053	S	***904.473436***	452.740356	887.446887	444.227082	886.462871	443.735074	8
4	401.239460	**201.123368**	383.228895	192.118085	L	***817.441408***	409.224342	800.414859	400.711068	799.430843	400.219060	7
5	488.271488	244.639382	470.260923	235.634099	S	***704.357344***	352.682310	687.330795	344.169036	686.346779	343.677028	6
6	575.303516	**288.155396**	557.292951	279.150113	S	***617.325316***	309.166296	600.298767	300.653022	599.314751	300.161014	5
7	688.387580	344.697428	670.377015	335.692145	L	530.293288	265.650282	513.266739	257.137008	512.282723	256.645000	4
8	**817.430173**	409.218725	799.419608	400.213442	E	417.209224	209.108250	400.182675	200.594975	399.198659	200.102967	3
9	930.477852	465.742564	912.467287	456.737281	P	***288.166631***	144.586953	271.140082	136.073679			2
10					R	175.118952	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
64.6	1103.593475	-0.004327	SISISVAAGGSR
35.0	1103.582230	0.006918	SISLSSLEPR
7.8	1103.597488	-0.008340	DPYTLNILR
5.9	1103.593460	-0.004312	LSSSLNPSKR
5.8	1103.597519	-0.008371	KFLVVDDPR
3.6	1103.593475	-0.004327	LSSTQEGVRK
2.1	1103.597504	-0.008356	EVLSFKPPR

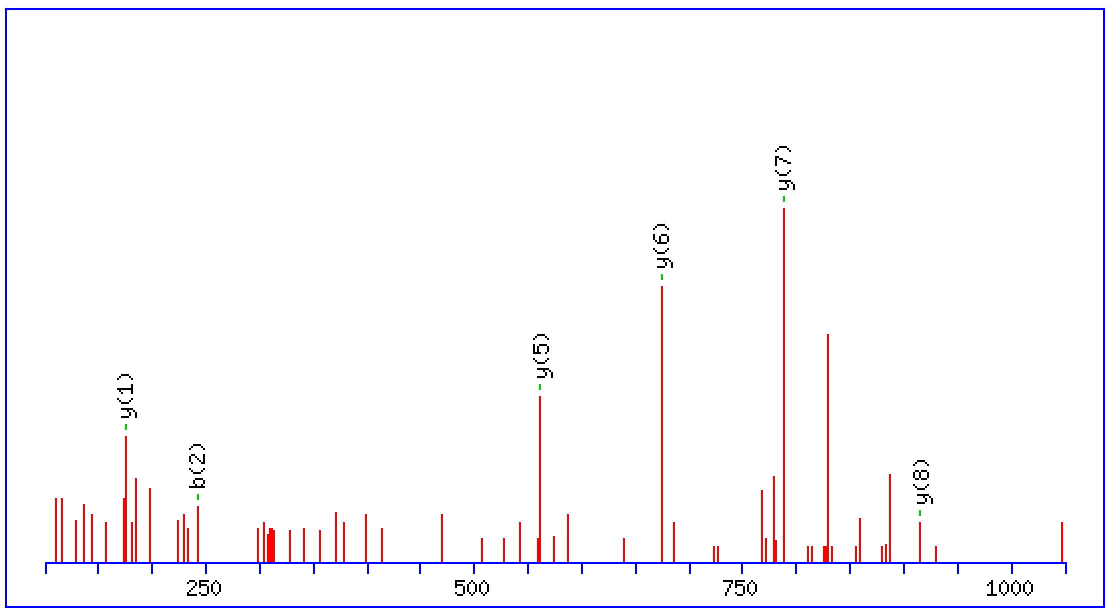
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LKPLGEAER**
Found in **NEUL_HUMAN**, Neurolysin, mitochondrial OS=Homo sapiens GN=NLN PE=1 SV=1

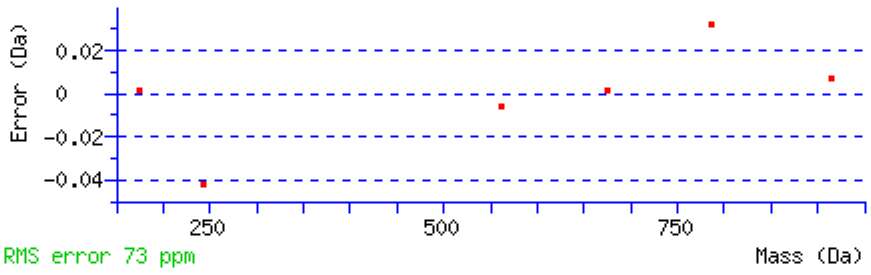
Match to Query 17672: 1027.573888 from(514.794220,2+) rtinseconds(1698) index(16750)
Title: Locus:1.1.1.2059.27
Data file 2011-11-14 - TFD - EP 8-1.mgf

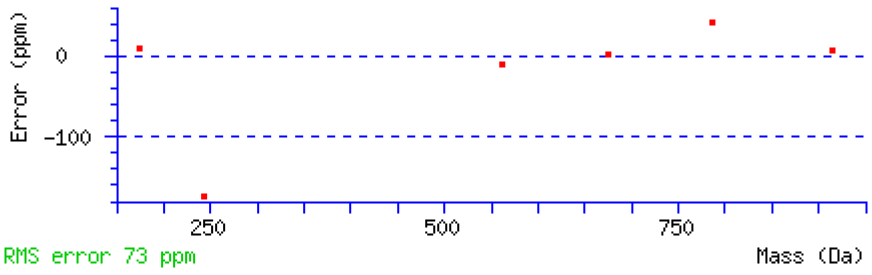
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1027.566177
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P3 : Oxidation (P)
Ions Score: 32 **Expect:** 0.0083
Matches : 6/82 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							9
2	242.186303	121.596790	225.159754	113.083515			K	*915.489422*	458.248349	898.462873	449.735075	897.478857	449.243067	8
3	355.233982	178.120629	338.207433	169.607355			P	*787.394459*	394.200868	770.367910	385.687593	769.383894	385.195585	7
4	468.318046	234.662661	451.291497	226.149387			L	*674.346780*	337.677028	657.320231	329.163754	656.336215	328.671746	6
5	525.339510	263.173393	508.312961	254.660119			G	*561.262716*	281.134996	544.236167	272.621722	543.252151	272.129714	5
6	654.382103	327.694690	637.355554	319.181415	636.371538	318.689407	E	504.241252	252.624264	487.214703	244.110990	486.230687	243.618982	4
7	725.419217	363.213247	708.392668	354.699972	707.408652	354.207964	A	375.198659	188.102968	358.172110	179.589693	357.188094	179.097685	3
8	854.461810	427.734543	837.435261	419.221269	836.451245	418.729261	E	304.161545	152.584411	287.134996	144.071136	286.150980	143.579128	2
9							R	*175.118952*	88.063114	158.092403	79.549840			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.1	1027.566177	0.007711	LKPLGEAER
19.4	1027.566177	0.007711	AAVLLEQER
19.1	1027.581451	-0.007563	IQISLWPR
7.5	1027.570221	0.003667	LQPEFVPAK
7.3	1027.566193	0.007695	IQSLPDLSR
7.3	1027.566177	0.007711	LQKLPEER
6.6	1027.566177	0.007711	LPKQIEER
6.5	1027.577438	-0.003550	SLPSVTRPR
6.1	1027.581467	-0.007579	IPQTVLWR
6.1	1027.566177	0.007711	LLQAEEVAR

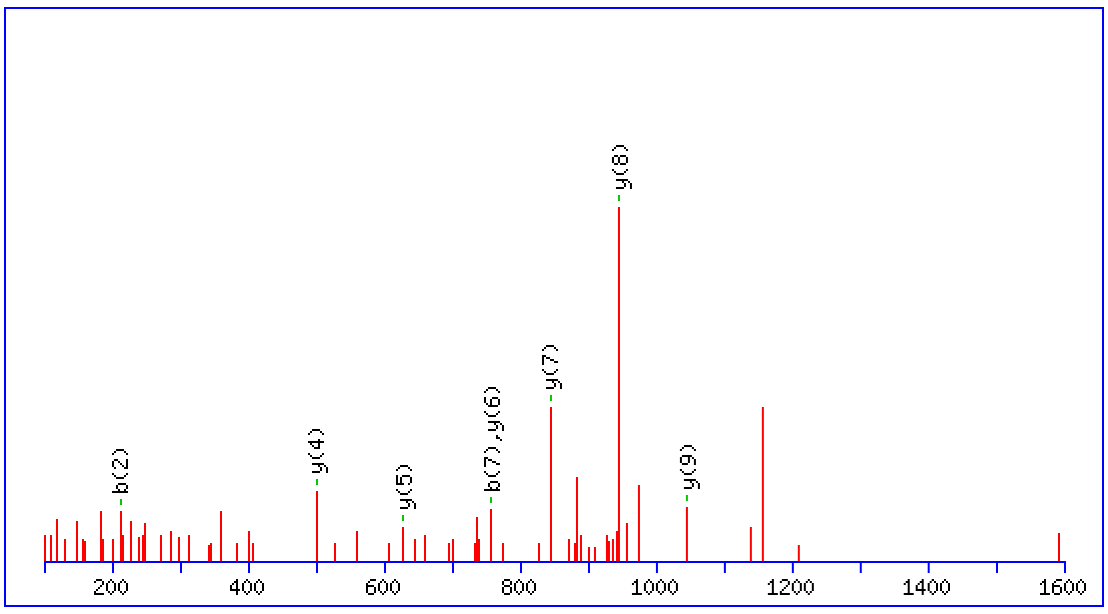
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IVTSEEVIIR**
Found in **NPTN_HUMAN**, Neuroplastin OS=Homo sapiens GN=NPTN PE=1 SV=2

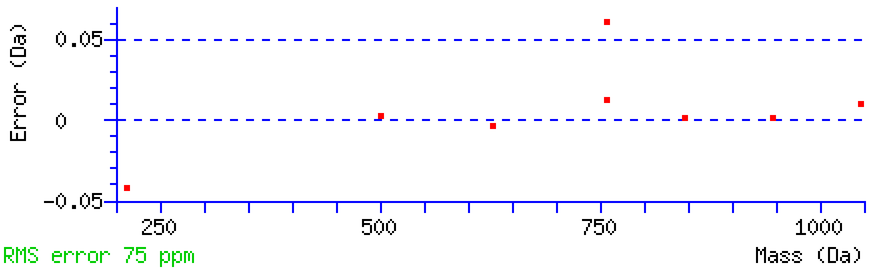
Match to Query 25517: 1157.664968 from(579.839760,2+) rtinseconds(2125) index(21434)
Title: Locus:1.1.1.2451.36
Data file 2011-11-12 - TFD - EP 5-2.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●

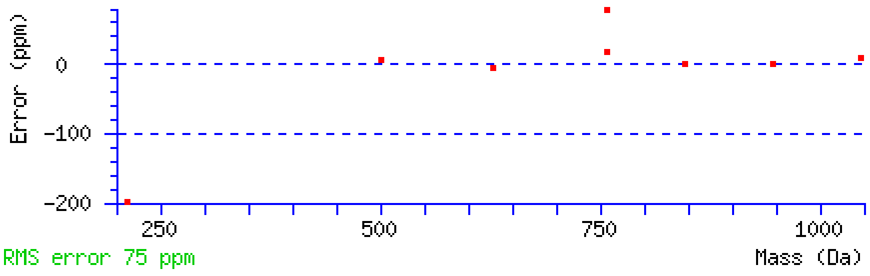


```
Monoisotopic mass of neutral peptide Mr(calc): 1157.665573
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 51  Expect: 4.7e-005
Matches : 8/78 fragment ions using 11 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							10
2	**213.159754**	107.083515			V	***1045.588801***	523.298039	1028.562252	514.784764	1027.578236	514.292756	9
3	314.207433	157.607354	296.196868	148.602072	T	***946.520387***	473.763832	929.493838	465.250557	928.509822	464.758549	8
4	401.239461	201.123368	383.228896	192.118086	S	***845.472708***	423.239992	828.446159	414.726718	827.462143	414.234710	7
5	530.282054	265.644665	512.271489	256.639383	E	***758.440680***	379.723978	741.414131	371.210704	740.430115	370.718696	6
6	659.324647	330.165962	641.314082	321.160679	E	***629.398087***	315.202682	612.371538	306.689407	611.387522	306.197399	5
7	**758.393061**	379.700169	740.382496	370.694886	V	***500.355494***	250.681385	483.328945	242.168110			4
8	871.477125	436.242201	853.466560	427.236918	I	401.287080	201.147178	384.260531	192.633903			3
9	984.561189	492.784233	966.550624	483.778950	I	288.203016	144.605146	271.176467	136.091871			2
10					R	175.118952	88.063114	158.092403	79.549839			1



RMS error 75 ppm



RMS error 75 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.0	1157.665573	-0.000605	IVTSEEVIIR
4.5	1157.665573	-0.000605	LVVGDSLKAEK
4.4	1157.655701	0.009267	NVVSGGFPIIR
3.6	1157.665573	-0.000605	ISPAKVAEVTK
2.8	1157.659027	0.005941	LCLRINEVK
1.0	1157.670273	-0.005305	LAIMVNGRLR
0.8	1157.665588	-0.000620	KPDGTVLLSTK
0.3	1157.665573	-0.000605	LPKSLSSSPVK

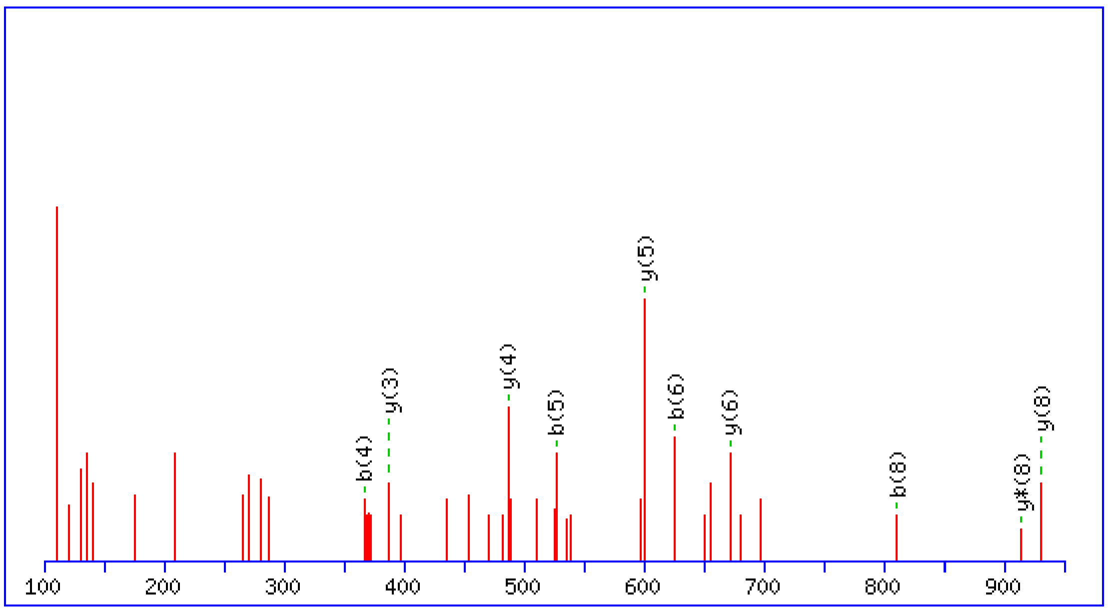
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SAAHCVANVNVR**
Found in **ELNE_HUMAN**, Neutrophil elastase OS=Homo sapiens GN=ELANE PE=1 SV=1

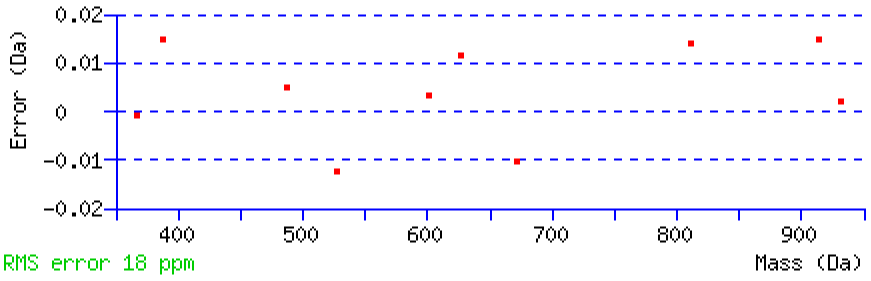
Match to Query 636981: 1296.634332 from(433.218720,3+) rtinseconds(1106) index(496016)
Title: Locus:1.1.1.746.15
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

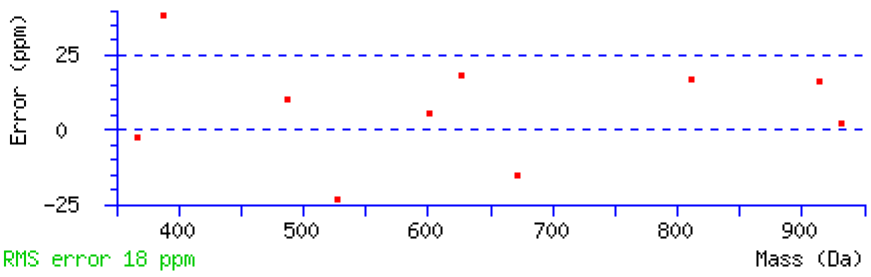
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1296.635696
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33  Expect: 0.007
Matches : 10/96 fragment ions using 15 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	88.039304	44.523290			70.028739	35.518008	S					12
2	159.076418	80.041847			141.065853	71.036564	A	1210.610951	605.809113	1193.584402	597.295839	11
3	230.113532	115.560404			212.102967	106.555121	A	1139.573837	570.290556	1122.547288	561.777282	10
4	***367.172444***	184.089860			349.161879	175.084577	H	1068.536723	534.771999	1051.510174	526.258725	9
5	***527.203093***	264.105185			509.192528	255.099902	C	***931.477811***	466.242544	914.451262	457.729269	8
6	***626.271507***	313.639392			608.260942	304.634109	V	771.447162	386.227219	754.420613	377.713944	7
7	697.308621	349.157949			679.298056	340.152666	A	***672.378748***	336.693012	655.352199	328.179737	6
8	***811.351548***	406.179412	794.324999	397.666137	793.340983	397.174129	N	***601.341634***	301.174455	584.315085	292.661181	5
9	910.419962	455.713619	893.393413	447.200344	892.409397	446.708336	V	***487.298707***	244.152991	470.272158	235.639717	4
10	1024.462889	512.735082	1007.436340	504.221808	1006.452324	503.729800	N	***388.230293***	194.618784	371.203744	186.105510	3
11	1123.531303	562.269290	1106.504754	553.756015	1105.520738	553.264007	V	274.187366	137.597321	257.160817	129.084047	2
12							R	175.118952	88.063114	158.092403	79.549839	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.8	1296.635696	-0.001364	SAAHCVANVNVR

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

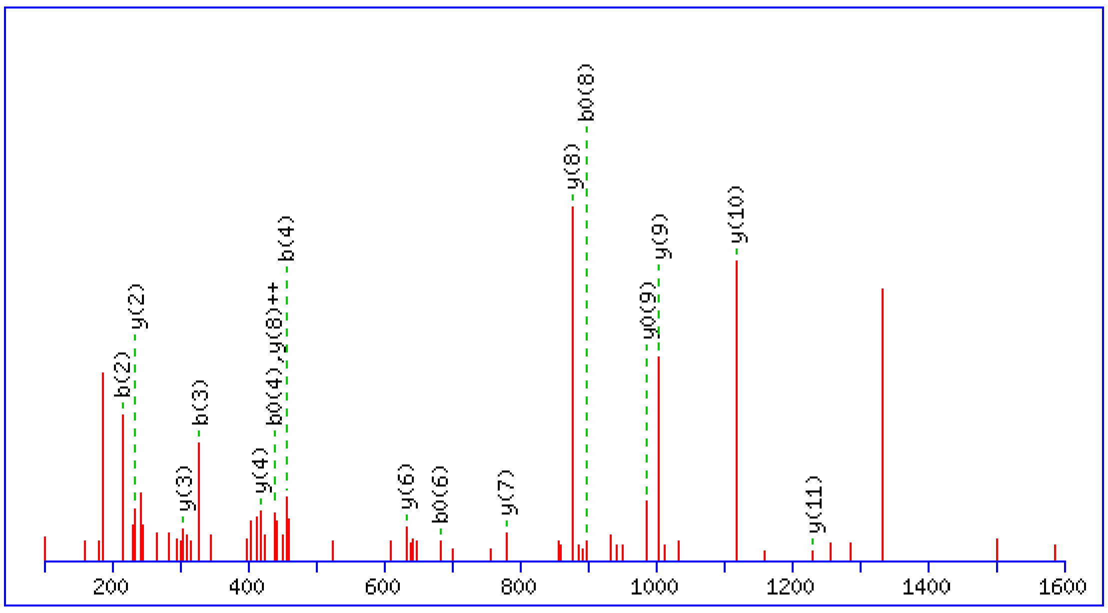
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLIEPFTLLASK**
Found in **KBRS1_HUMAN**, NF-kappa-B inhibitor-interacting Ras-like protein 1 OS=Homo sapiens GN=NKIRAS1 PE=1 SV=1

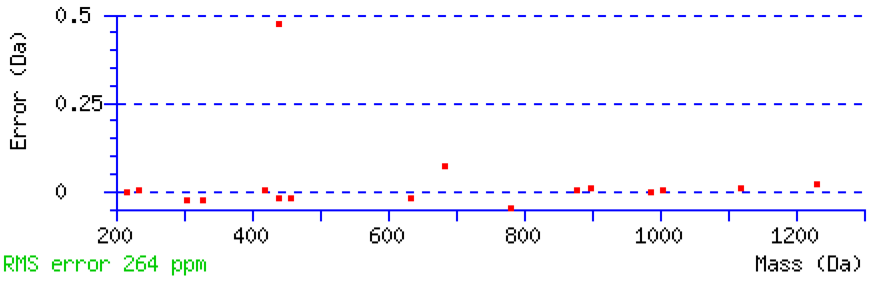
Match to Query 37658: 1331.775648 from(666.895100,2+) rtinseconds(3765) index(48324)
Title: Locus:1.1.1.2703.5
Data file 2011-11-14 - TFD - EP 8-6.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●

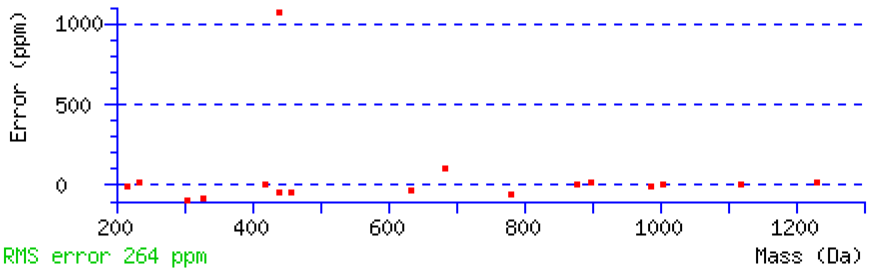


Monoisotopic mass of neutral peptide Mr(calc): 1331.770035
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 58 **Expect:** 2.8e-006
Matches : 17/108 fragment ions using 33 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116	84.044390	42.525833	T							12
2	**215.139019**	108.073147	197.128454	99.067865	L	***1231.729652***	616.368464	1214.703103	607.855190	1213.719087	607.363182	11
3	**328.223083**	164.615179	310.212518	155.609897	I	***1118.645588***	559.826432	1101.619039	551.313158	1100.635023	550.821150	10
4	**457.265676**	229.136476	439.255111	220.131193	E	***1005.561524***	503.284400	988.534975	494.771125	987.550959	494.279117	9
5	554.318440	277.662858	536.307875	268.657576	P	***876.518931***	438.763104	859.492382	430.249829	858.508366	429.757821	8
6	701.386854	351.197065	683.376289	342.191782	F	***779.466167***	390.236722	762.439618	381.723447	761.455602	381.231439	7
7	802.434533	401.720905	784.423968	392.715622	T	***632.397753***	316.702515	615.371204	308.189240	614.387188	307.697232	6
8	915.518597	458.262937	897.508032	449.257654	L	531.350074	266.178675	514.323525	257.665401	513.339509	257.173393	5
9	1028.602661	514.804968	1010.592096	505.799686	L	***418.266010***	209.636643	401.239461	201.123368	400.255445	200.631360	4
10	1099.639775	550.323525	1081.629210	541.318243	A	***305.181946***	153.094611	288.155397	144.581337	287.171381	144.089329	3
11	1186.671803	593.839540	1168.661238	584.834257	S	***234.144832***	117.576054	217.118283	109.062780	216.134267	108.570772	2
12					K	147.112804	74.060040	130.086255	65.546765			1



RMS error 264 ppm



RMS error 264 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.1	1331.770035	0.005613	TLIEPFTLLASK

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

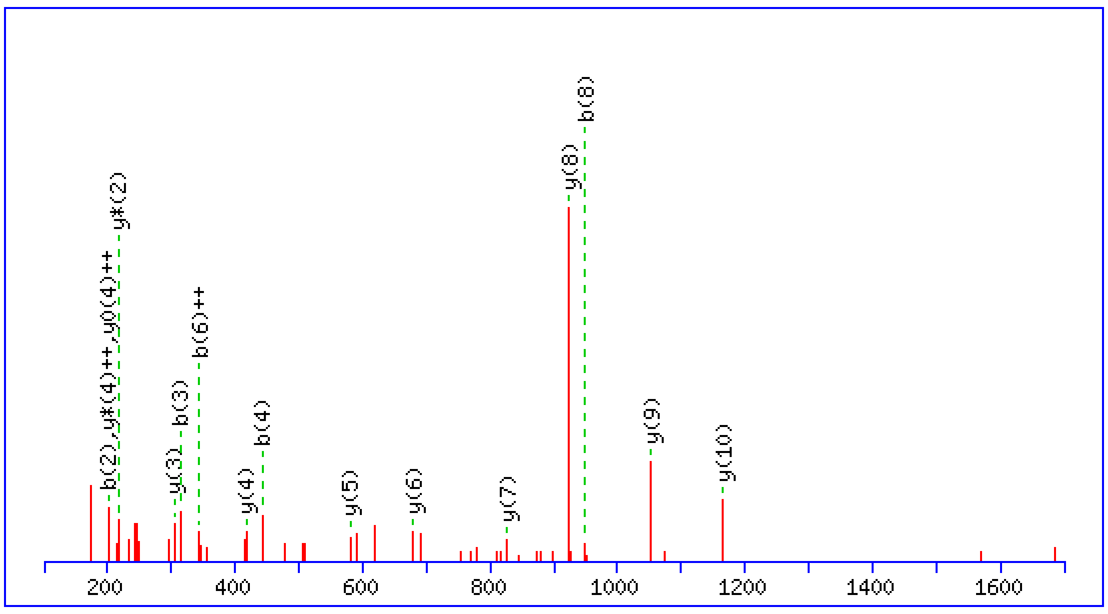
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SLLEPFVYLASK**
Found in **KBRS2_HUMAN**, NF-kappa-B inhibitor-interacting Ras-like protein 2 OS=Homo sapiens GN=NKIRAS2 PE=1 SV=1

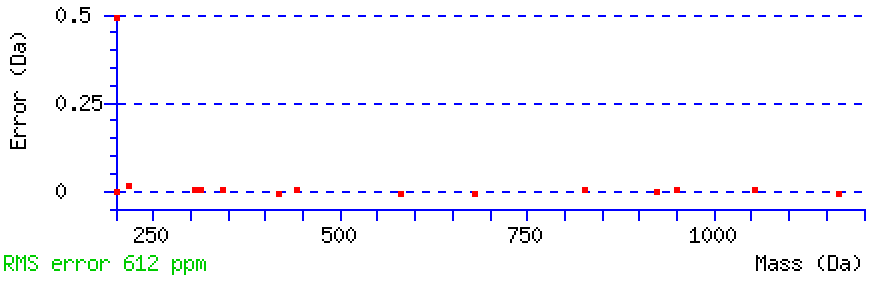
Match to Query 39974: 1365.757668 from(683.886110,2+) rtinseconds(3904) index(52058)
Title: Locus:1.1.1.2634.9
Data file 2011-11-12 - TFD - EP 6-6.mgf

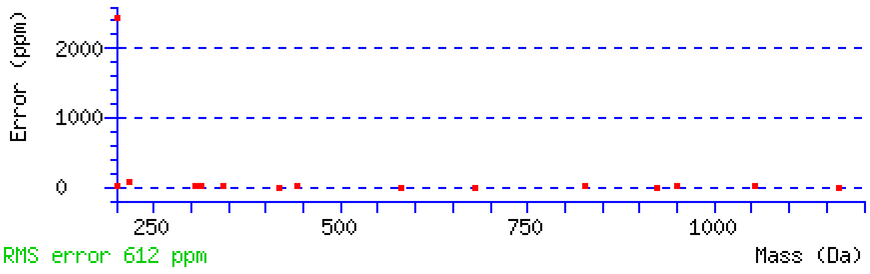
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1365.754379
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 48 **Expect:** 4.5e-005
Matches : 16/108 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	S							12
2	**201.123368**	101.065322	183.112803	92.060039	L	1279.729652	640.368464	1262.703103	631.855190	1261.719087	631.363182	11
3	**314.207432**	157.607354	296.196867	148.602071	L	***1166.645588***	583.826432	1149.619039	575.313158	1148.635023	574.821150	10
4	**443.250025**	222.128650	425.239460	213.123368	E	***1053.561524***	527.284400	1036.534975	518.771126	1035.550959	518.279117	9
5	540.302789	270.655033	522.292224	261.649750	P	***924.518931***	462.763104	907.492382	454.249829	906.508366	453.757821	8
6	687.371203	344.189240	669.360638	335.183957	F	***827.466167***	414.236722	810.439618	405.723447	809.455602	405.231439	7
7	786.439617	393.723447	768.429052	384.718164	V	***680.397753***	340.702515	663.371204	332.189240	662.387188	331.697232	6
8	**949.502946**	475.255111	931.492381	466.249829	Y	***581.329339***	291.168308	564.302790	282.655033	563.318774	282.163025	5
9	1062.587010	531.797143	1044.576445	522.791860	L	***418.266010***	209.636643	401.239461	201.123368	400.255445	200.631360	4
10	1133.624124	567.315700	1115.613559	558.310417	A	***305.181946***	153.094611	288.155397	144.581337	287.171381	144.089329	3
11	1220.656152	610.831714	1202.645587	601.826432	S	234.144832	117.576054	217.118283	109.062780	216.134267	108.570772	2
12					K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.3	1365.754379	0.003289	SLLEPFVYLASK
1.9	1365.750381	0.007287	SLPLPPLLSPPR
1.1	1365.761597	-0.003929	KDRPLPPPSSLK

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

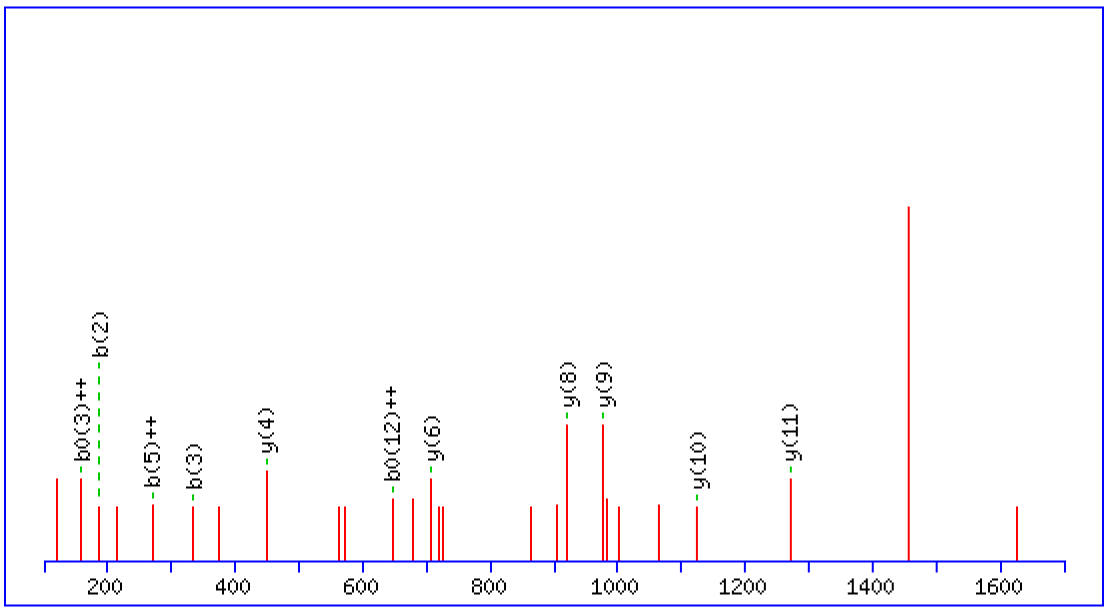
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SVFFGPDFITVTK**
Found in **NFU1_HUMAN**, NFU1 iron-sulfur cluster scaffold homolog, mitochondrial OS=Homo sapiens GN=NFU1 PE=1 SV=2

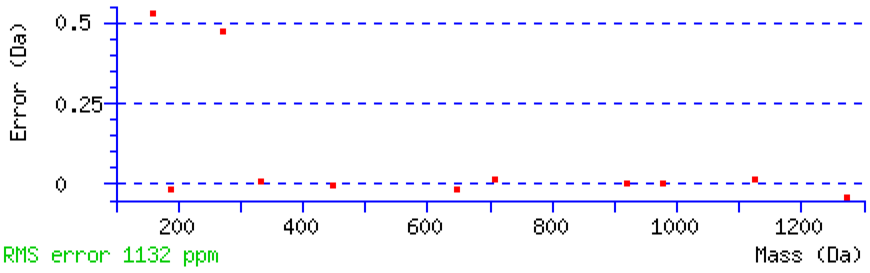
Match to Query 39009: 1456.757728 from(729.386140,2+) rtinseconds(3625) index(47988)
Title: Locus:1.1.1.2994.41
Data file 2011-11-10 - TFD - EP 3-5.mgf

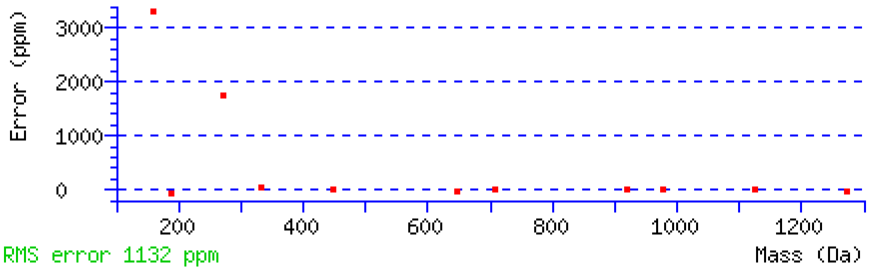
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1700] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1456.760254
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 31   Expect: 0.0032
Matches : 11/118 fragment ions using 21 most intense peaks   (help)
```

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	S							13
2	**187.107718**	94.057497	169.097153	85.052214	V	1370.735467	685.871372	1353.708918	677.358097	1352.724902	676.866089	12
3	**334.176132**	167.591704	316.165567	158.586422	F	***1271.667053***	636.337165	1254.640504	627.823890	1253.656488	627.331882	11
4	481.244546	241.125911	463.233981	232.120628	F	***1124.598639***	562.802958	1107.572090	554.289683	1106.588074	553.797675	10
5	538.266010	269.636643	520.255445	260.631361	G	***977.530225***	489.268751	960.503676	480.755476	959.519660	480.263468	9
6	635.318774	318.163025	617.308209	309.157743	P	***920.508761***	460.758019	903.482212	452.244744	902.498196	451.752736	8
7	750.345717	375.676497	732.335152	366.671214	D	823.455997	412.231637	806.429448	403.718362	805.445432	403.226354	7
8	897.414131	449.210704	879.403566	440.205421	F	***708.429054***	354.718165	691.402505	346.204891	690.418489	345.712883	6
9	1010.498195	505.752736	992.487630	496.747453	I	561.360640	281.183958	544.334091	272.670684	543.350075	272.178676	5
10	1111.545874	556.276575	1093.535309	547.271292	T	***448.276576***	224.641926	431.250027	216.128651	430.266011	215.636643	4
11	1210.614288	605.810782	1192.603723	596.805500	V	347.228897	174.118087	330.202348	165.604812	329.218332	165.112804	3
12	1311.661967	656.334622	1293.651402	647.329339	T	248.160483	124.583879	231.133934	116.070605	230.149918	115.578597	2
13					K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.5	1456.760254	-0.002526	SVFFGPDFITVTK

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

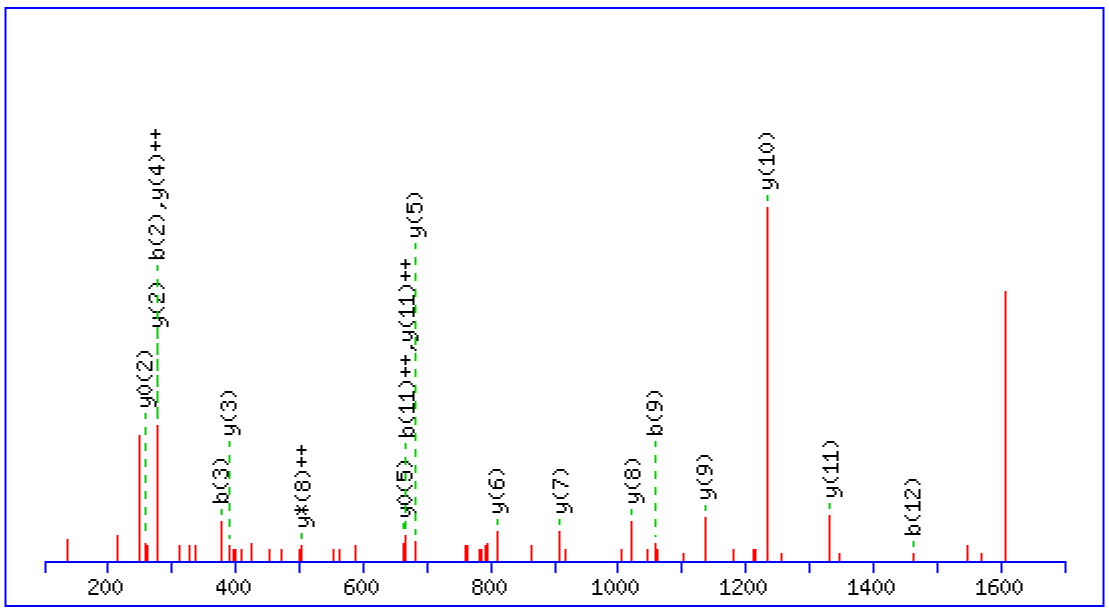
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YLVPDLVQEYIEK**
Found in **NMNA1_HUMAN**, Nicotinamide mononucleotide adenylyltransferase 1 OS=Homo sapiens GN=NMNAT1 PE=1 SV=1

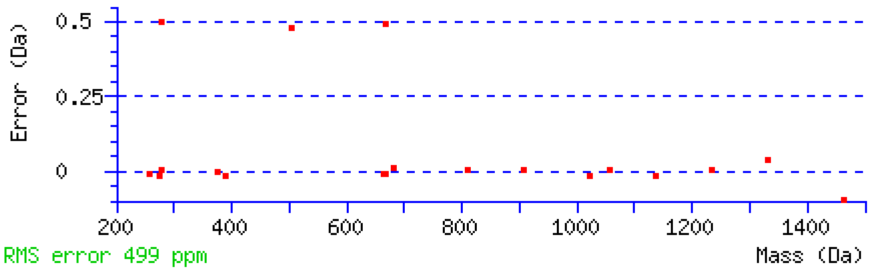
Match to Query 51937: 1607.853908 from(804.934230,2+) rtinseconds(3959) index(58909)
Title: Locus:1.1.1.2916.23
Data file 2011-11-12 - TFD - EP 5-4.mgf

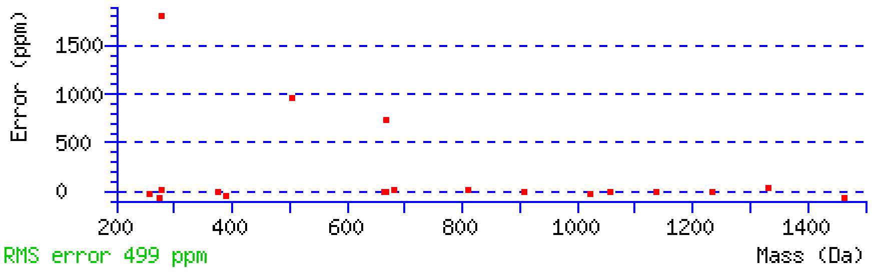
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1607.844650
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 41  Expect: 0.00084
Matches : 19/120 fragment ions using 43 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.070605	82.538940					Y							13
2	**277.154669**	139.080973					L	1445.788624	723.397950	1428.762075	714.884676	1427.778059	714.392668	12
3	**376.223083**	188.615180					V	***1332.704560***	666.855918	1315.678011	658.342644	1314.693995	657.850636	11
4	473.275847	237.141562					P	***1233.636146***	617.321711	1216.609597	608.808437	1215.625581	608.316429	10
5	588.302790	294.655033			570.292225	285.649751	D	***1136.583382***	568.795329	1119.556833	560.282055	1118.572817	559.790047	9
6	701.386854	351.197065			683.376289	342.191783	L	***1021.556439***	511.281858	1004.529890	502.768583	1003.545874	502.276575	8
7	800.455268	400.731272			782.444703	391.725990	V	***908.472375***	454.739826	891.445826	446.226551	890.461810	445.734543	7
8	928.513846	464.760561	911.487297	456.247287	910.503281	455.755279	Q	***809.403961***	405.205619	792.377412	396.692344	791.393396	396.200336	6
9	**1057.556439**	529.281858	1040.529890	520.768583	1039.545874	520.276575	E	***681.345383***	341.176330	664.318834	332.663055	663.334818	332.171047	5
10	1220.619768	610.813522	1203.593219	602.300248	1202.609203	601.808240	Y	552.302790	276.655033	535.276241	268.141758	534.292225	267.649750	4
11	1333.703832	667.355554	1316.677283	658.842280	1315.693267	658.350272	I	***389.239461***	195.123368	372.212912	186.610094	371.228896	186.118086	3
12	**1462.746425**	731.876851	1445.719876	723.363576	1444.735860	722.871568	E	***276.155397***	138.581336	259.128848	130.068062	258.144832	129.576054	2
13							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.2	1607.844650	0.009258	YLVPDLVQEYIEK
7.9	1607.841537	0.012371	MWGIMGTVLLTGGLK
5.7	1607.863113	-0.009205	GATPAPPGKAGAVASQTK
3.7	1607.840652	0.013256	TLLPNTTLTYDTQK
1.0	1607.867111	-0.013203	YIEIYVQKVNPSR

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

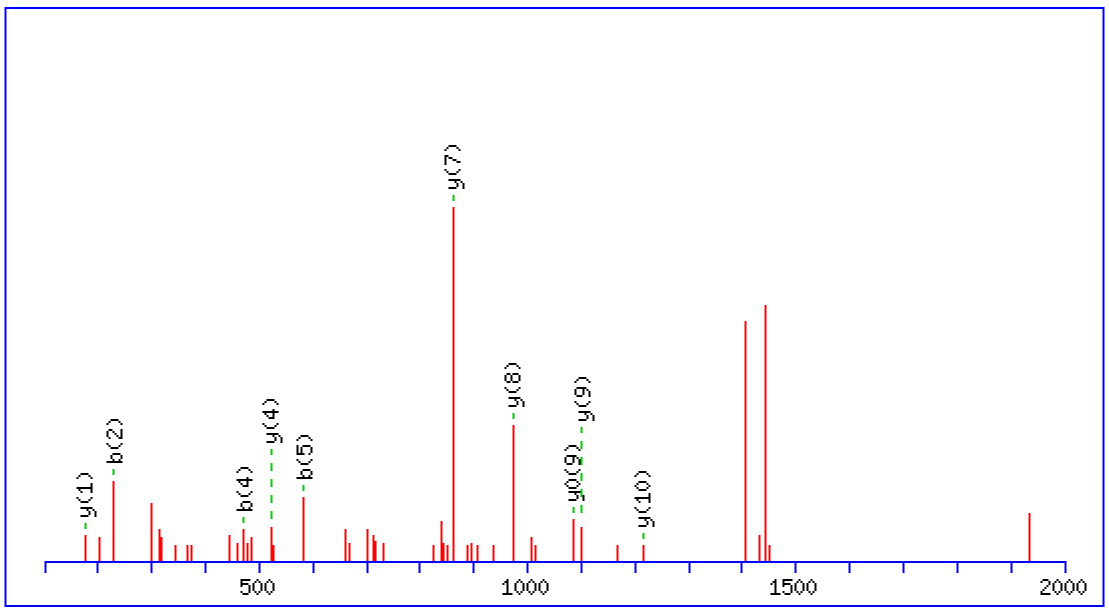
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DNLQLPLQFLSR**
Found in **NPC1_HUMAN**, Niemann-Pick C1 protein OS=Homo sapiens GN=NPC1 PE=1 SV=2

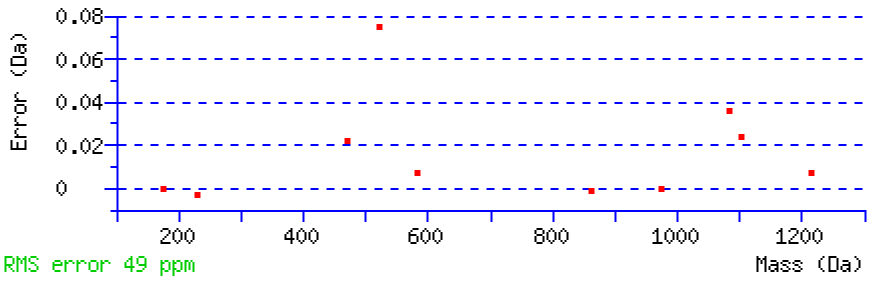
Match to Query 43578: 1442.792288 from(722.403420,2+) rtinseconds(3860) index(56382)
Title: Locus:1.1.1.2801.39
Data file 2011-11-10 - TFD - EP 4-1.mgf

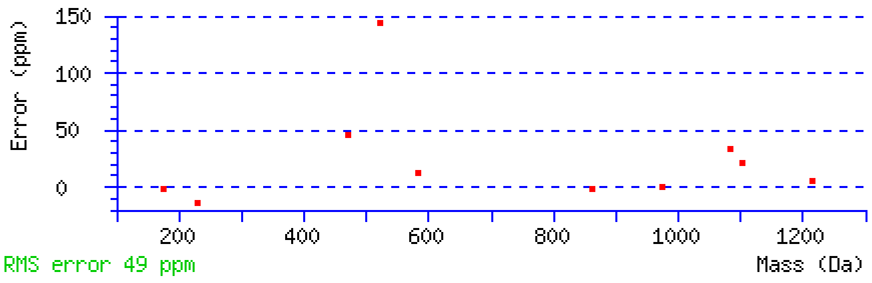
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1442.788147
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 30 **Expect:** 0.0091
Matches : 10/128 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.034219	58.520748			98.023654	49.515465	D							12
2	**230.077146**	115.542211	213.050597	107.028937	212.066581	106.536928	N	1328.768497	664.887887	1311.741948	656.374612	1310.757932	655.882604	11
3	343.161210	172.084243	326.134661	163.570968	325.150645	163.078960	L	***1214.725570***	607.866423	1197.699021	599.353149	1196.715005	598.861141	10
4	**471.219788**	236.113532	454.193239	227.600258	453.209223	227.108250	Q	***1101.641506***	551.324391	1084.614957	542.811117	1083.630941	542.319109	9
5	**584.303852**	292.655564	567.277303	284.142290	566.293287	283.650282	L	***973.582928***	487.295102	956.556379	478.781828	955.572363	478.289820	8
6	681.356616	341.181946	664.330067	332.668672	663.346051	332.176664	P	***860.498864***	430.753070	843.472315	422.239796	842.488299	421.747788	7
7	794.440680	397.723978	777.414131	389.210704	776.430115	388.718696	L	763.446100	382.226688	746.419551	373.713414	745.435535	373.221406	6
8	922.499258	461.753267	905.472709	453.239993	904.488693	452.747985	Q	650.362036	325.684656	633.335487	317.171382	632.351471	316.679374	5
9	1069.567672	535.287474	1052.541123	526.774200	1051.557107	526.282192	F	***522.303458***	261.655367	505.276909	253.142093	504.292893	252.650085	4
10	1182.651736	591.829506	1165.625187	583.316232	1164.641171	582.824224	L	375.235044	188.121160	358.208495	179.607885	357.224479	179.115877	3
11	1269.683764	635.345520	1252.657215	626.832246	1251.673199	626.340238	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
12							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.1	1442.788147	0.004141	DNLQLPLQFLSR
11.4	1442.788132	0.004156	LPEDLKNFRPAK
6.3	1442.780258	0.012030	MLPLLEVAEKER
6.3	1442.780258	0.012030	MLPLLEVAEKER
2.5	1442.788162	0.004126	DLEPPIVARFVR
1.4	1442.788147	0.004141	VSPLAAFLASAPQR

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

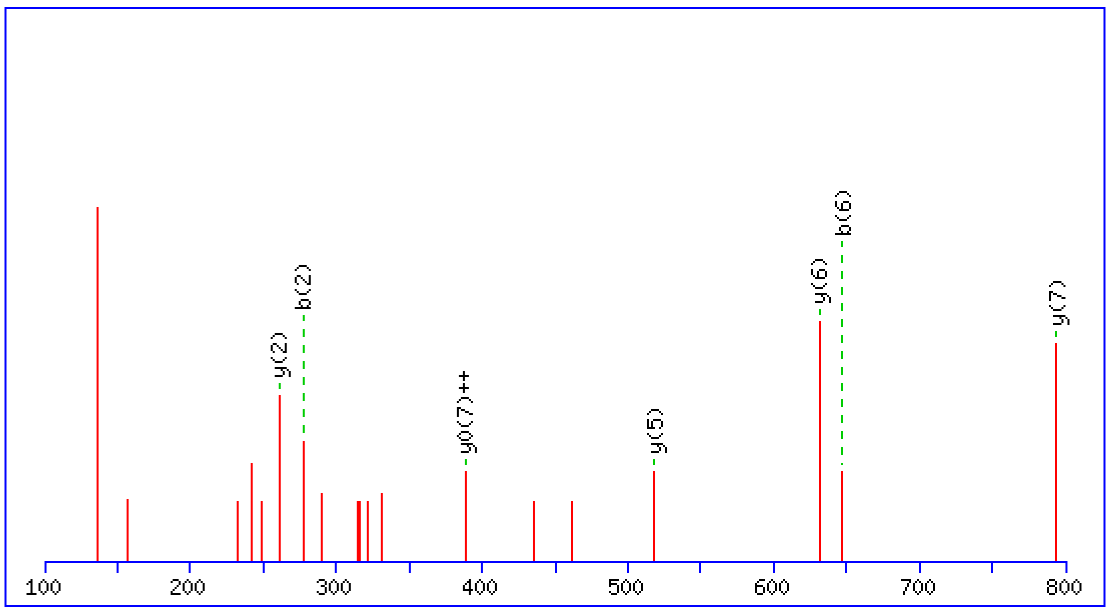
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LYISGPNK**
Found in **NPCL1_HUMAN**, Niemann-Pick C1-like protein 1 OS=Homo sapiens GN=NPC1L1 PE=1 SV=1

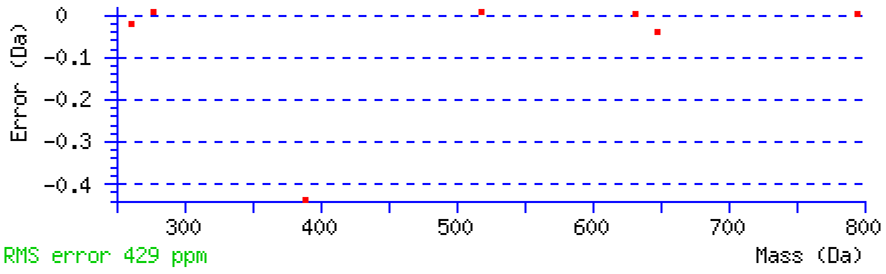
Match to Query 5786: 906.482008 from(454.248280,2+) rtinseconds(1573) index(3759)
Title: Locus:1.1.1.2247.7
Data file 2011-11-10 - TFD - EP 3-8.mgf

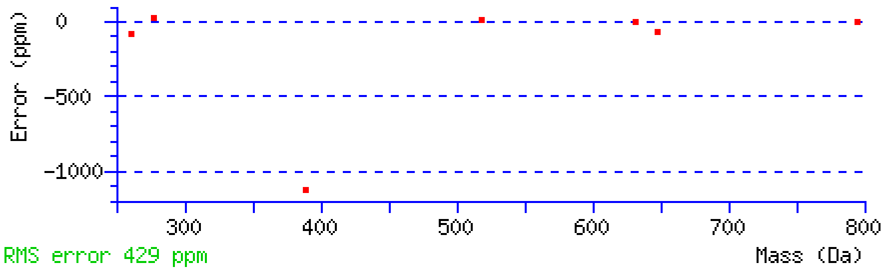
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 906.481064
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P6      : Oxidation (P)
Ions Score: 31  Expect: 0.0057
Matches : 7/58 fragment ions using 10 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							8
2	**277.154669**	139.080973					Y	***794.404295***	397.705786	777.377746	389.192511	776.393730	388.700503	7
3	390.238733	195.623005					I	***631.340966***	316.174121	614.314417	307.660847	613.330401	307.168839	6
4	477.270761	239.139019			459.260196	230.133736	S	***518.256902***	259.632089	501.230353	251.118815	500.246337	250.626807	5
5	534.292225	267.649751			516.281660	258.644468	G	431.224874	216.116075	414.198325	207.602801			4
6	**647.339904**	324.173590			629.329339	315.168308	P	374.203410	187.605343	357.176861	179.092068			3
7	761.382831	381.195054	744.356282	372.681779	743.372266	372.189771	N	***261.155731***	131.081503	244.129182	122.568229			2
8							K	147.112804	74.060040	130.086255	65.546765			1

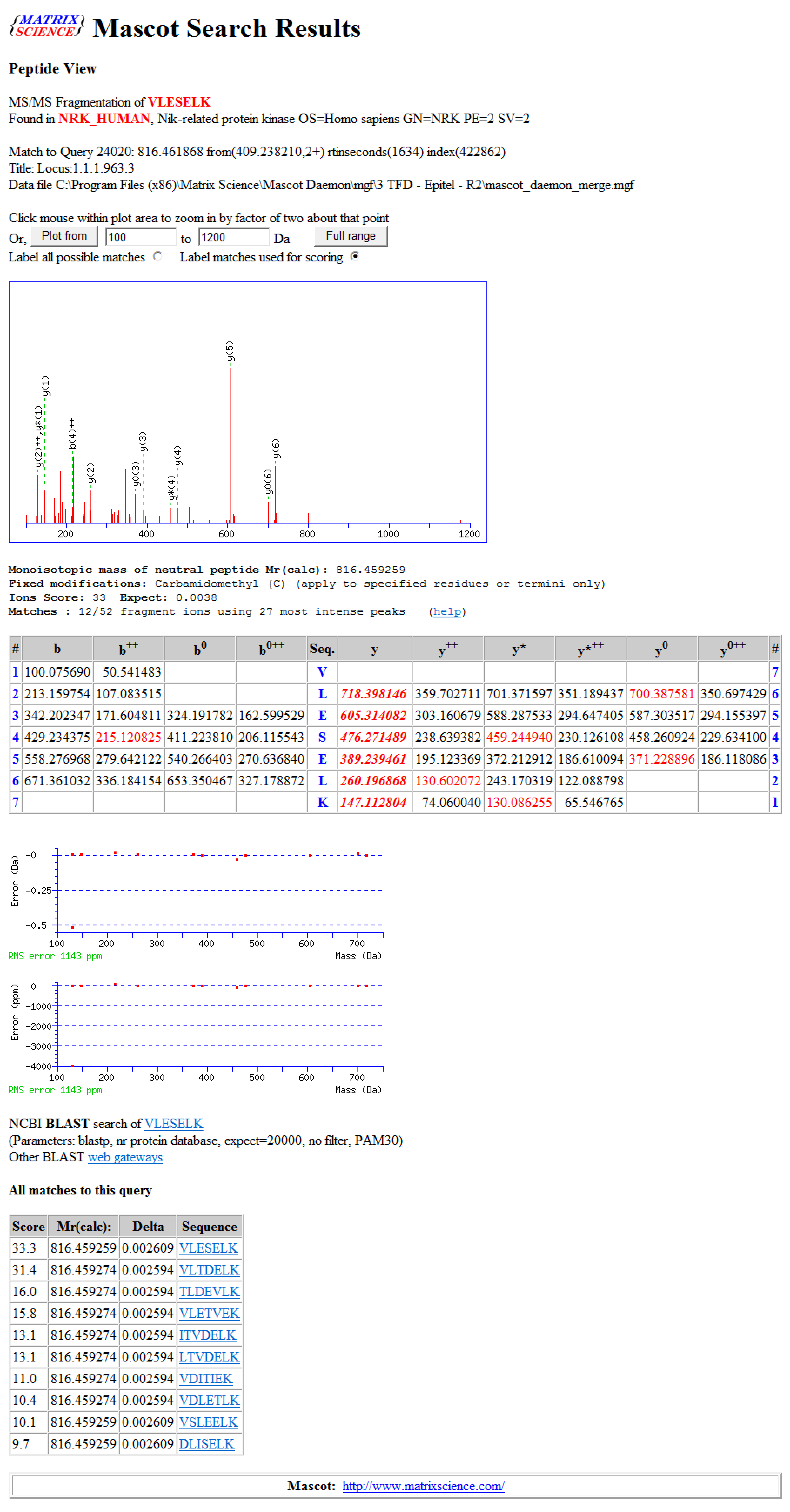




NCBI **BLAST** search of LYISGPNK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.4	906.481064	0.000944	LYISGPNK
8.1	906.481079	0.000929	LFDAVNTK
7.9	906.484436	-0.002428	LSVMSINK
7.0	906.481049	0.000959	KLFEENK
1.8	906.481079	0.000929	LFSKPDGK
1.7	906.481064	0.000944	IYDPQKK



Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLESELK**
Found in **NRK_HUMAN**, Nik-related protein kinase OS=Homo sapiens GN=NRK PE=2 SV=2

Match to Query 24020: 816.461868 from(409.238210,2+) rtinseconds(1634) index(422862)
Title: Locus:1.1.1.963.3
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.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
Label all possible matches ○ Label matches used for scoring ●

```
Monoisotopic mass of neutral peptide Mr(calc): 816.459259
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33  Expect: 0.0038
Matches : 12/52 fragment ions using 27 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483			V							7
2	213.159754	107.083515			L	***718.398146***	359.702711	701.371597	351.189437	700.387581	350.697429	6
3	342.202347	171.604811	324.191782	162.599529	E	***605.314082***	303.160679	588.287533	294.647405	587.303517	294.155397	5
4	429.234375	215.120825	411.223810	206.115543	S	***476.271489***	238.639382	459.244940	230.126108	458.260924	229.634100	4
5	558.276968	279.642122	540.266403	270.636840	E	***389.239461***	195.123369	372.212912	186.610094	371.228896	186.118086	3
6	671.361032	336.184154	653.350467	327.178872	L	***260.196868***	130.602072	243.170319	122.088798			2
7					K	***147.112804***	74.060040	130.086255	65.546765			1

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.3	816.459259	0.002609	VLESELK
31.4	816.459274	0.002594	VLTDELK
16.0	816.459274	0.002594	TLDEVLK
15.8	816.459274	0.002594	VLETVEK
13.1	816.459274	0.002594	ITVDELK
13.1	816.459274	0.002594	LTVDELK
11.0	816.459274	0.002594	VDITIEK
10.4	816.459274	0.002594	VDLETLK
10.1	816.459259	0.002609	VSLEELK
9.7	816.459259	0.002609	DLISELK

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

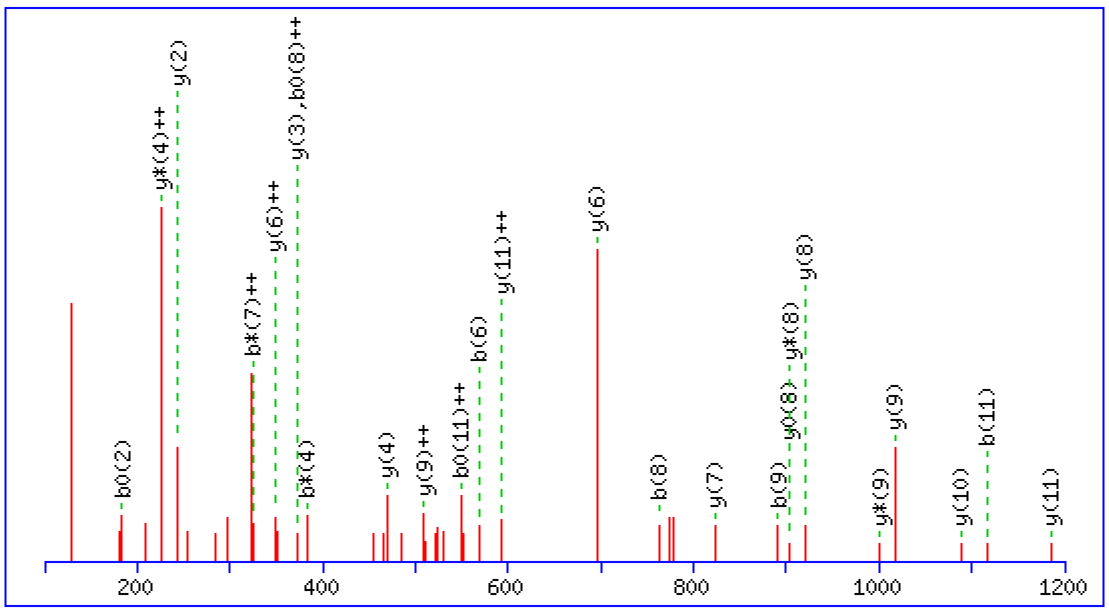
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSAKPAPPKPEPKPK**
Found in **HMGN2_HUMAN**, Non-histone chromosomal protein HMG-17 OS=Homo sapiens GN=HMGN2 PE=1 SV=3

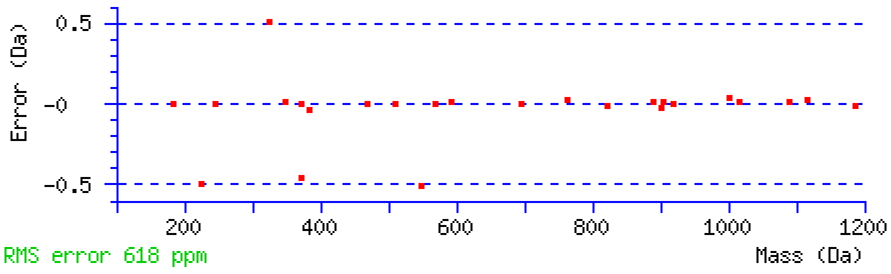
Match to Query 45402: 1583.938332 from(528.986720,3+) rtinseconds(822) index(655)
Title: Locus:1.1.1.1603.6
Data file 2011-11-13 - TFD - EP 7-6.mgf

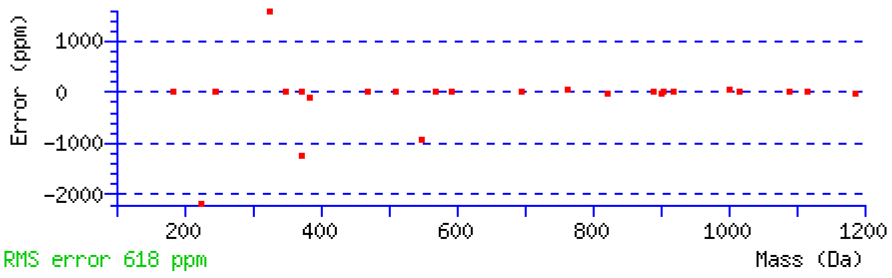
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1583.939865
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 68 **Expect:** 2.6e-007
Matches : 25/152 fragment ions using 34 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							15
2	201.123368	101.065322			183.112803	92.060039	S	1471.863126	736.435201	1454.836577	727.921927	1453.852561	727.429919	14
3	272.160482	136.583879			254.149917	127.578596	A	1384.831098	692.919187	1367.804549	684.405913	1366.820533	683.913905	13
4	400.255445	200.631360	383.228896	192.118086	382.244880	191.626078	K	1313.793984	657.400630	1296.767435	648.887356	1295.783419	648.395348	12
5	497.308209	249.157742	480.281660	240.644468	479.297644	240.152460	P	***1185.699021***	593.353149	1168.672472	584.839874	1167.688456	584.347866	11
6	**568.345323**	284.676300	551.318774	276.163025	550.334758	275.671017	A	***1088.646257***	544.826767	1071.619708	536.313492	1070.635692	535.821484	10
7	665.398087	333.202682	648.371538	324.689407	647.387522	324.197399	P	***1017.609143***	509.308210	1000.582594	500.794935	999.598578	500.302927	9
8	**762.450851**	381.729064	745.424302	373.215789	744.440286	372.723781	P	***920.556379***	460.781828	903.529830	452.268553	902.545814	451.776545	8
9	**890.545814**	445.776545	873.519265	437.263271	872.535249	436.771263	K	***823.503615***	412.255446	806.477066	403.742171	805.493050	403.250163	7
10	987.598578	494.302927	970.572029	485.789653	969.588013	485.297645	P	***695.408652***	348.207964	678.382103	339.694690	677.398087	339.202682	6
11	**1116.641171**	558.824224	1099.614622	550.310949	1098.630606	549.818941	E	598.355888	299.681582	581.329339	291.168308	580.345323	290.676300	5
12	1213.693935	607.350606	1196.667386	598.837331	1195.683370	598.345323	P	***469.313295***	235.160286	452.286746	226.647011			4
13	1341.788898	671.398087	1324.762349	662.884813	1323.778333	662.392805	K	***372.260531***	186.633904	355.233982	178.120629			3
14	1438.841662	719.924469	1421.815113	711.411195	1420.831097	710.919187	P	***244.165568***	122.586422	227.139019	114.073148			2
15							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
68.2	1583.939865	-0.001533	LSAKPAPPKPEPKPK

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

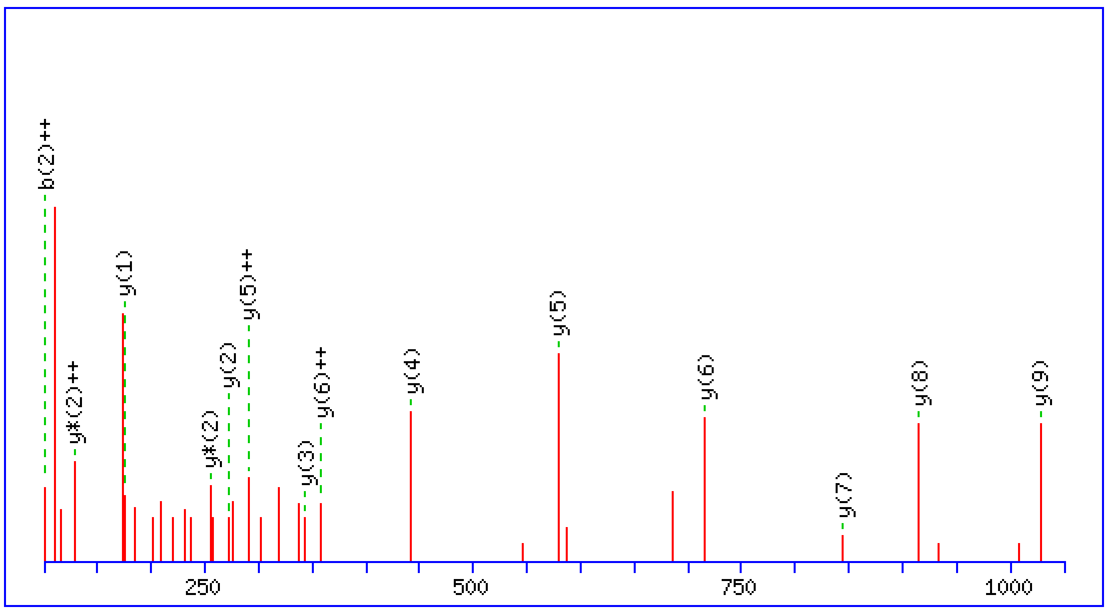
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TVIAQHHVAPR**
Found in **NCRP1_HUMAN**, Non-specific cytotoxic cell receptor protein 1 homolog OS=Homo sapiens GN=NCCRP1 PE=1 SV=1

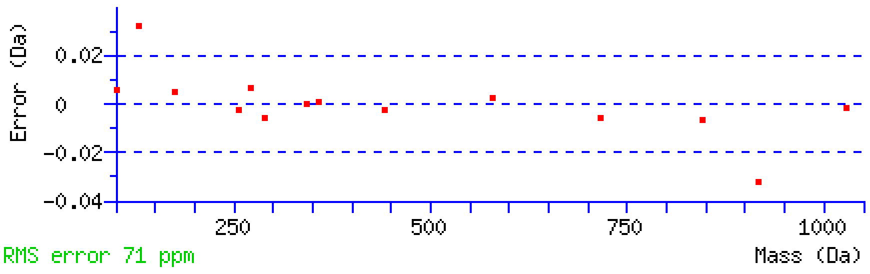
Match to Query 554367: 1227.682812 from(410.234880,3+) rtinseconds(865) index(897326)
Title: Locus:1.1.1.727.4
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

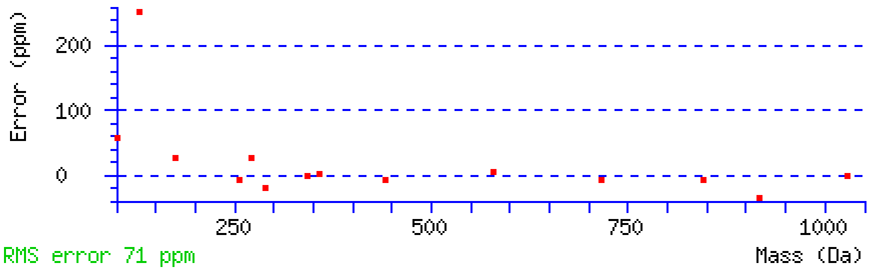
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1227.683640
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 51  Expect: 0.00017
Matches : 14/92 fragment ions using 33 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	102.054955	51.531116			84.044390	42.525833	T					11
2	201.123369	101.065322			183.112804	92.060040	V	1127.643238	564.325257	1110.616689	555.811983	10
3	314.207433	157.607354			296.196868	148.602072	I	***1028.574824***	514.791050	1011.548275	506.277776	9
4	385.244547	193.125911			367.233982	184.120629	A	***915.490760***	458.249018	898.464211	449.735743	8
5	513.303125	257.155201	496.276576	248.641926	495.292560	248.149918	Q	***844.453646***	422.730461	827.427097	414.217186	7
6	650.362037	325.684657	633.335488	317.171382	632.351472	316.679374	H	***716.395068***	358.701172	699.368519	350.187897	6
7	787.420949	394.214113	770.394400	385.700838	769.410384	385.208830	H	***579.336156***	290.171716	562.309607	281.658441	5
8	886.489363	443.748319	869.462814	435.235045	868.478798	434.743037	V	***442.277244***	221.642260	425.250695	213.128985	4
9	957.526477	479.266876	940.499928	470.753602	939.515912	470.261594	A	***343.208830***	172.108053	326.182281	163.594778	3
10	1054.579241	527.793258	1037.552692	519.279984	1036.568676	518.787976	P	***272.171716***	136.589496	255.145167	128.076221	2
11							R	***175.118952***	88.063114	158.092403	79.549839	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.4	1227.683640	-0.000828	TVIAQHHVAPR
12.9	1227.682297	0.000515	VTALVPSEAAVR
10.0	1227.671051	0.011761	ALDTLLEQTPK
9.6	1227.682281	0.000531	TVIQEALALDR
6.7	1227.682281	0.000531	LLSASPVDAAIR
4.3	1227.693527	-0.010715	ATLVQDGIAKGR
2.5	1227.693497	-0.010685	AIQLNNQTKAK

Mascot: http://www.matrixscience.com/

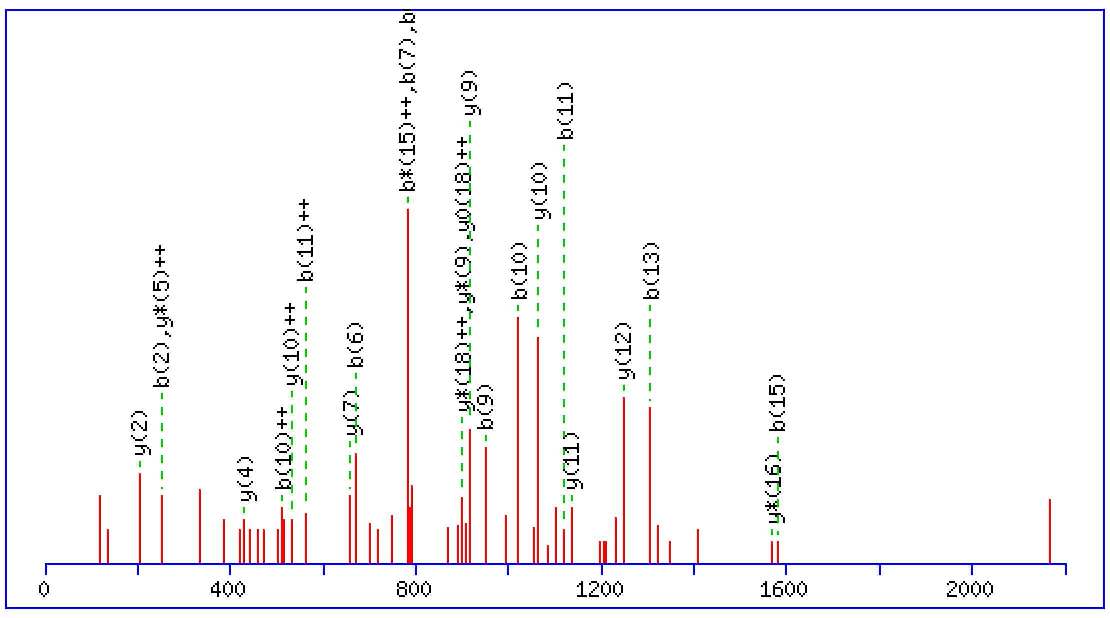
Mascot Search Results

Peptide View

MS/MS Fragmentation of **HLVMGDIPAAVNAFQEAASLLGK**
Found in **NASP_HUMAN**, Nuclear autoantigenic sperm protein OS=Homo sapiens GN=NASP PE=1 SV=2

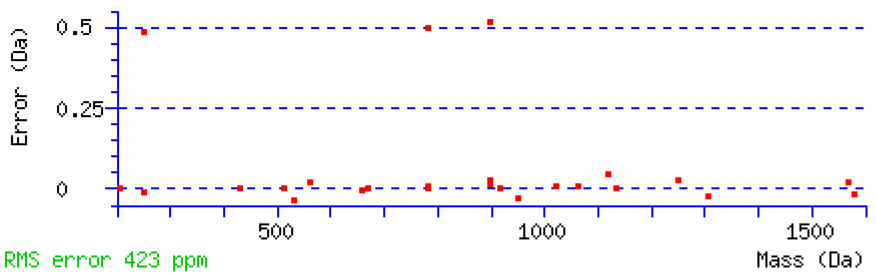
Match to Query 69874: 2367.224532 from(790.082120,3+) rtinseconds(4346) index(65484)
Title: Locus:1.1.1.3029.34
Data file 2011-11-12 - TFD - EP 6-2.mgf

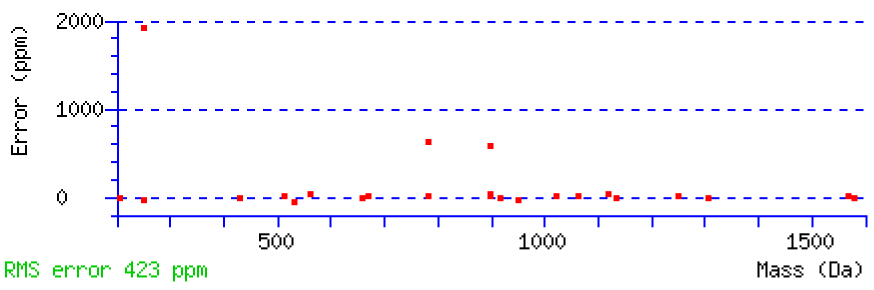
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2367.225647
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M4 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 65 **Expect:** 1.2e-006
Matches : 25/336 fragment ions using 28 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	138.066188	69.536732					H							23
2	***251.150252***	126.078764					L	2231.174033	1116.090654	2214.147484	1107.577380	2213.163468	1107.085372	22
3	350.218666	175.612971					V	2118.089969	1059.548622	2101.063420	1051.035348	2100.079404	1050.543340	21
4	497.254066	249.130671					M	2019.021555	1010.014416	2001.995006	1001.501141	2001.010990	1001.009133	20
5	554.275530	277.641403					G	1871.986155	936.496716	1854.959606	927.983441	1853.975590	927.491433	19
6	***669.302473***	335.154875			651.291908	326.149592	D	1814.964691	907.985984	1797.938142	899.472709	1796.954126	898.980701	18
7	***782.386537***	391.696907			764.375972	382.691624	I	1699.937748	850.472512	1682.911199	841.959238	1681.927183	841.467230	17
8	879.439301	440.223289			861.428736	431.218006	P	1586.853684	793.930480	1569.827135	785.417206	1568.843119	784.925198	16
9	***950.476415***	475.741846			932.465850	466.736563	A	1489.800920	745.404098	1472.774371	736.890824	1471.790355	736.398816	15
10	***1021.513529***	**511.260403**			1003.502964	502.255120	A	1418.763806	709.885541	1401.737257	701.372267	1400.753241	700.880259	14
11	***1120.581943***	**560.794609**			1102.571378	551.789327	V	1347.726692	674.366984	1330.700143	665.853710	1329.716127	665.361702	13
12	1234.624870	617.816073	1217.598321	609.302798	1216.614305	608.810790	N	***1248.658278***	624.832777	1231.631729	616.319503	1230.647713	615.827495	12
13	***1305.661984***	653.334630	1288.635435	644.821355	1287.651419	644.329347	A	***1134.615351***	567.811314	1117.588802	559.298039	1116.604786	558.806031	11
14	1452.730398	726.868837	1435.703849	718.355563	1434.719833	717.863554	F	***1063.578237***	532.292757	1046.551688	523.779482	1045.567672	523.287474	10
15	***1580.788976***	790.898126	1563.762427	782.384852	1562.778411	781.892844	Q	***916.509823***	458.758550	899.483274	450.245275	898.499258	449.753267	9
16	1709.831569	855.419423	1692.805020	846.906148	1691.821004	846.414140	E	788.451245	394.729261	771.424696	386.215986	770.440680	385.723978	8
17	1780.868683	890.937980	1763.842134	882.424705	1762.858118	881.932697	A	***659.408652***	330.207964	642.382103	321.694690	641.398087	321.202682	7
18	1851.905797	926.456537	1834.879248	917.943262	1833.895232	917.451254	A	588.371538	294.689407	571.344989	286.176133	570.360973	285.684125	6
19	1938.937825	969.972551	1921.911276	961.459276	1920.927260	960.967268	S	517.334424	259.170850	500.307875	250.657576	499.323859	250.165568	5
20	2052.021889	1026.514583	2034.995340	1018.001308	2034.011324	1017.509300	L	***430.302396***	215.654836	413.275847	207.141562			4
21	2165.105953	1083.056615	2148.079404	1074.543340	2147.095388	1074.051332	L	317.218332	159.112804	300.191783	150.599530			3
22	2222.127417	1111.567347	2205.100868	1103.054072	2204.116852	1102.562064	G	***204.134268***	102.570772	187.107719	94.057497			2
23							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of HLVMGDIPAAVNAFQEAASLLGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
65.3	2367.225647	-0.001115	HLVMGDIPAAVNAFQEAASLLGK
45.8	2367.225647	-0.001115	HLVMGDIPAAVNAFQEAASLLGK
2.0	2367.210403	0.014129	SPGVEKPIVKPTAGAGPQETNMK
1.4	2367.228165	-0.003633	TAPAVPTPGSAPTGSKKPIGSEASK
1.3	2367.214371	0.010161	EYQDLLNVKMALDIEIAAYR
0.3	2367.239578	-0.015046	FLLSGCAATVAELATFPLDLTK

Mascot: http://www.matrixscience.com/

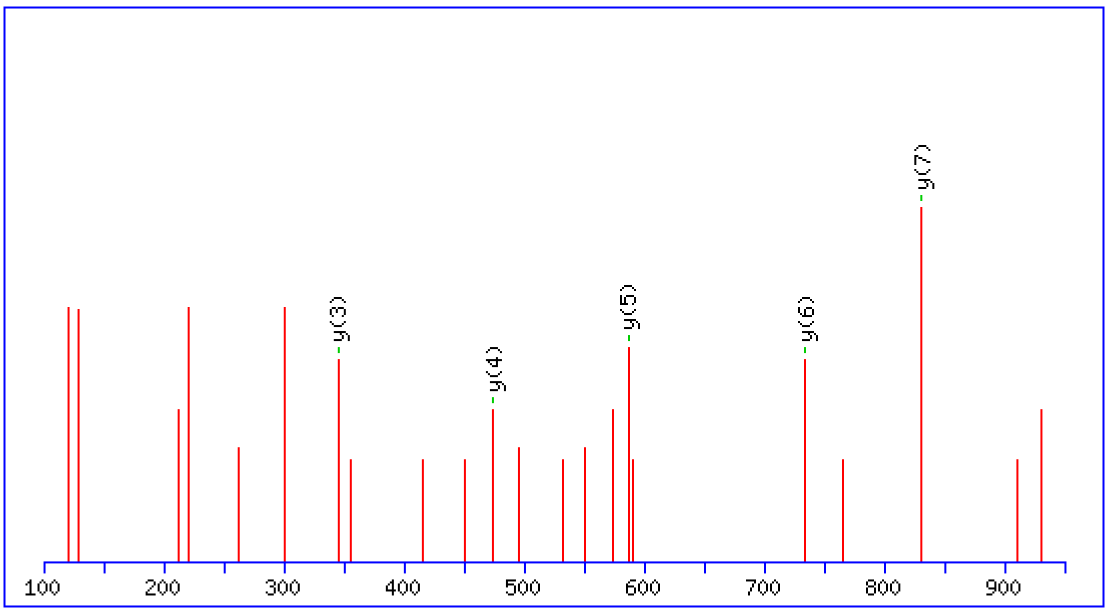
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TFPFLEGLR**
Found in **LY10L_HUMAN**, Nuclear body protein SP140-like protein OS=Homo sapiens GN=SP140L PE=2 SV=2

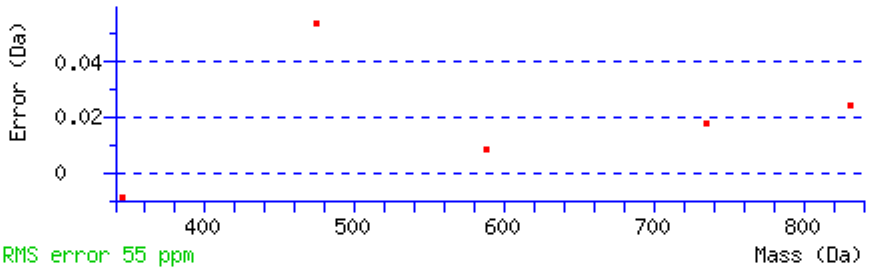
Match to Query 22492: 1078.575428 from(540.294990,2+) rtinseconds(3628) index(52788)
Title: Locus:1.1.1.2812.2
Data file 2011-11-10 - TFD - EP 3-2.mgf

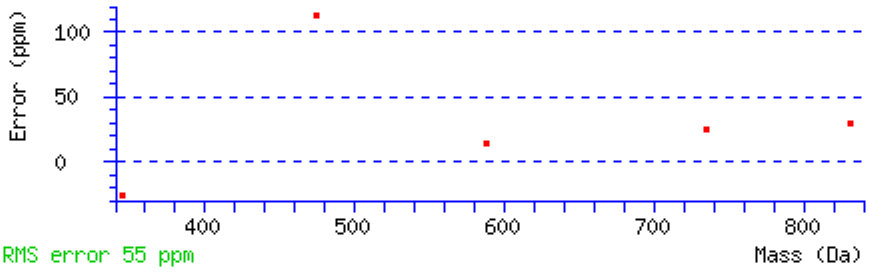
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1078.581131
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 35 **Expect:** 0.0013
Matches : 5/74 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	102.054955	51.531116	84.044390	42.525833	T							9
2	249.123369	125.065322	231.112804	116.060040	F	978.540729	489.774003	961.514180	481.260728	960.530164	480.768720	8
3	346.176133	173.591704	328.165568	164.586422	P	*831.472315*	416.239796	814.445766	407.726521	813.461750	407.234513	7
4	493.244547	247.125911	475.233982	238.120629	F	*734.419551*	367.713414	717.393002	359.200139	716.408986	358.708131	6
5	606.328611	303.667944	588.318046	294.662661	L	*587.351137*	294.179207	570.324588	285.665932	569.340572	285.173924	5
6	735.371204	368.189240	717.360639	359.183958	E	*474.267073*	237.637174	457.240524	229.123900	456.256508	228.631892	4
7	792.392668	396.699972	774.382103	387.694690	G	*345.224480*	173.115878	328.197931	164.602603			3
8	905.476732	453.242004	887.466167	444.236722	L	288.203016	144.605146	271.176467	136.091871			2
9					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of TFPFLEGLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.6	1078.581131	-0.005703	TFPFLEGLR

Mascot: http://www.matrixscience.com/

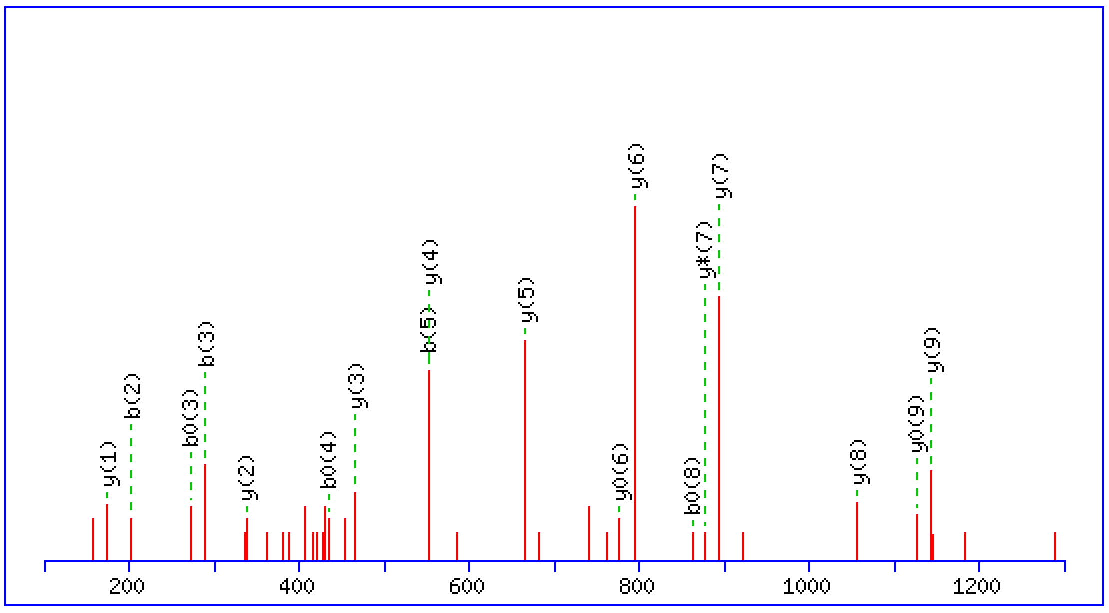
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SDSYVELSQYR**
Found in **NCBP2_HUMAN**, Nuclear cap-binding protein subunit 2 OS=Homo sapiens GN=NCBP2 PE=1 SV=1

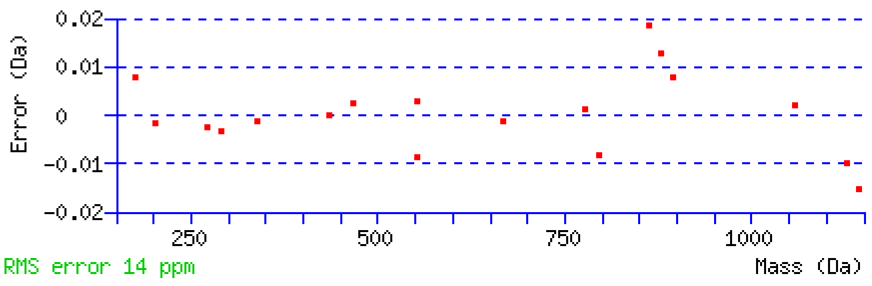
Match to Query 33273: 1345.619208 from(673.816880,2+) rtinseconds(2327) index(22830)
Title: Locus:1.1.1.2294.43
Data file 2011-11-10 - TFD - EP 3-7.mgf

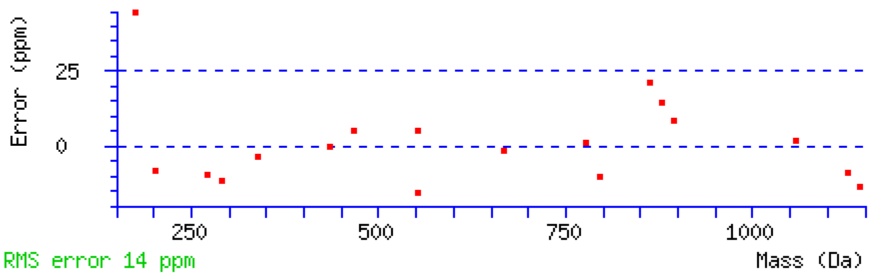
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1345.614990
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 73  Expect: 2.4e-007
Matches : 18/98 fragment ions using 27 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							11
2	**203.066247**	102.036761			185.055682	93.031479	D	1259.590258	630.298767	1242.563709	621.785493	1241.579693	621.293484	10
3	**290.098275**	145.552776			272.087710	136.547493	S	***1144.563315***	572.785296	1127.536766	564.272021	1126.552750	563.780013	9
4	453.161604	227.084440			435.151039	218.079158	Y	***1057.531287***	529.269282	1040.504738	520.756007	1039.520722	520.263999	8
5	**552.230018**	276.618647			534.219453	267.613365	V	***894.467958***	447.737617	877.441409	439.224342	876.457393	438.732334	7
6	681.272611	341.139944			663.262046	332.134661	E	***795.399544***	398.203410	778.372995	389.690136	777.388979	389.198128	6
7	794.356675	397.681976			776.346110	388.676693	L	***666.356951***	333.682114	649.330402	325.168839	648.346386	324.676831	5
8	881.388703	441.197990			863.378138	432.192707	S	***553.272887***	277.140082	536.246338	268.626807	535.262322	268.134799	4
9	1009.447281	505.227279	992.420732	496.714004	991.436716	496.221996	Q	***466.240859***	233.624067	449.214310	225.110793			3
10	1172.510610	586.758943	1155.484061	578.245669	1154.500045	577.753661	Y	***338.182281***	169.594778	321.155732	161.081504			2
11							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of SDSYVELSQYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
73.3	1345.614990	0.004218	SDSYVELSQYR
2.6	1345.629608	-0.010400	DSSPCVGLPAASR
2.6	1345.615860	0.003348	IMGSYLCFGER

Mascot: http://www.matrixscience.com/

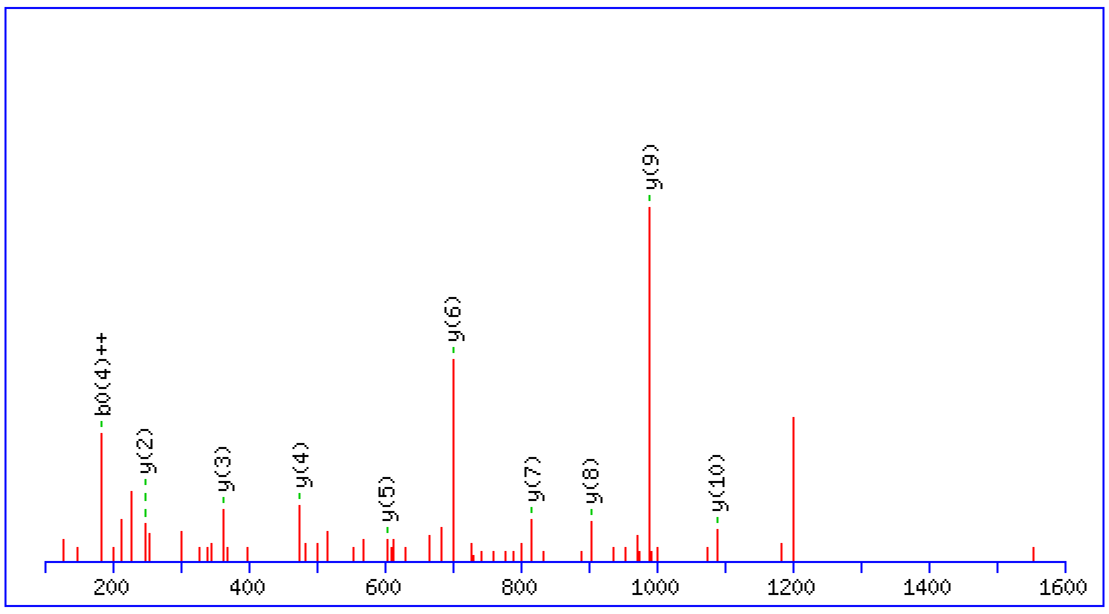
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LVSSDPEINTK**
Found in **NUDC_HUMAN**, Nuclear migration protein nudC OS=Homo sapiens GN=NUDC PE=1 SV=1

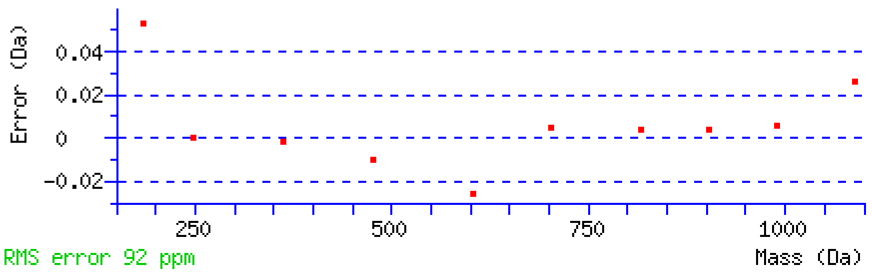
Match to Query 29716: 1201.619528 from(601.817040,2+) rtinseconds(1391) index(11481)
Title: Locus:1.1.1.1829.41
Data file 2011-11-12 - TFD - EP 6-4.mgf

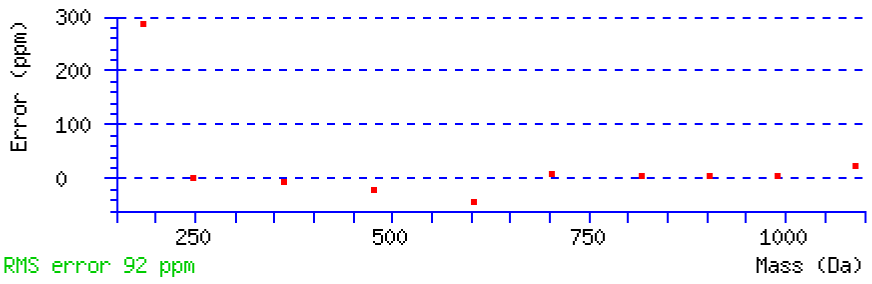
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1201.619019
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 99 **Expect:** 2.4e-009
Matches : 10/98 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					L							11
2	213.159754	107.083515					V	***1089.542244***	545.274760	1072.515695	536.761486	1071.531679	536.269478	10
3	300.191782	150.599529			282.181217	141.594247	S	***990.473830***	495.740553	973.447281	487.227279	972.463265	486.735271	9
4	387.223810	194.115543			369.213245	185.110261	S	***903.441802***	452.224539	886.415253	443.711265	885.431237	443.219257	8
5	502.250753	251.629015			484.240188	242.623732	D	***816.409774***	408.708525	799.383225	400.195251	798.399209	399.703243	7
6	599.303517	300.155397			581.292952	291.150114	P	***701.382831***	351.195054	684.356282	342.681779	683.372266	342.189771	6
7	728.346110	364.676693			710.335545	355.671411	E	***604.330067***	302.668672	587.303518	294.155397	586.319502	293.663389	5
8	841.430174	421.218725			823.419609	412.213443	I	***475.287474***	238.147375	458.260925	229.634100	457.276909	229.142092	4
9	955.473101	478.240189	938.446552	469.726914	937.462536	469.234906	N	***362.203410***	181.605343	345.176861	173.092068	344.192845	172.600060	3
10	1056.520780	528.764028	1039.494231	520.250754	1038.510215	519.758746	T	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.578597	2
11							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of LVSSDPEINTK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
98.6	1201.619019	0.000509	LVSSDPEINTK
9.1	1201.612503	0.007025	LSVSNMVHTAK
8.4	1201.619003	0.000525	LPSAEETLSQK
3.8	1201.630249	-0.010721	LADIEQSTGIR

Mascot: http://www.matrixscience.com/

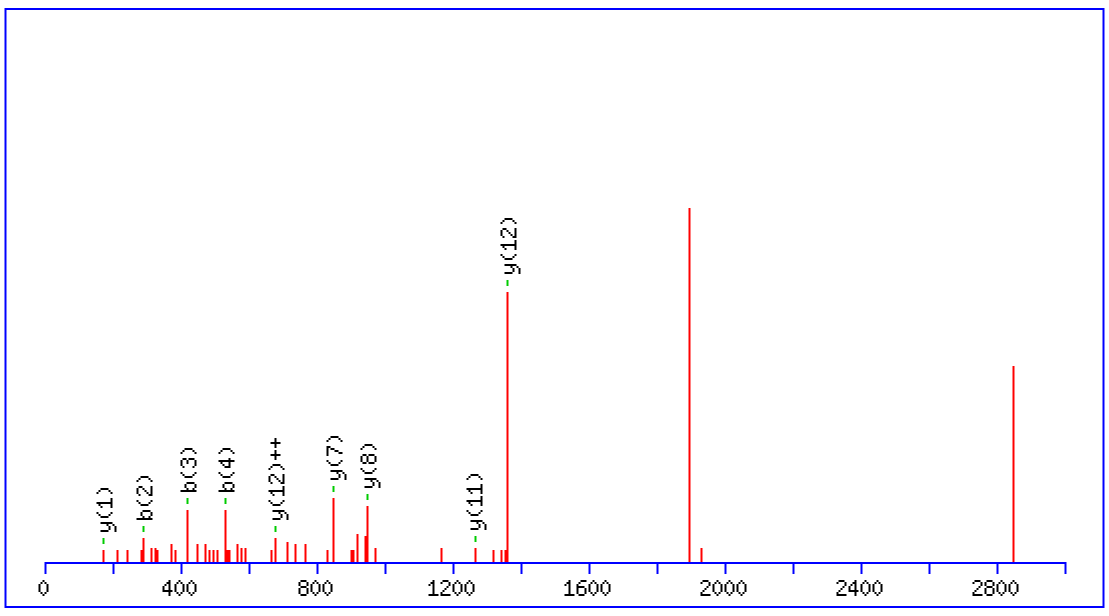
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **EYEIPSNLTPADVFFR**
Found in **NU133_HUMAN**, Nuclear pore complex protein Nup133 OS=Homo sapiens GN=NUP133 PE=1 SV=2

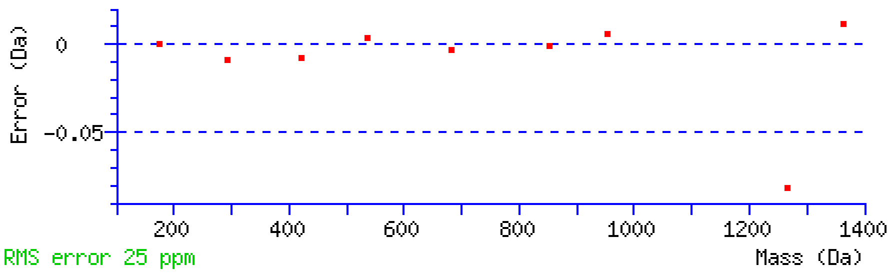
Match to Query 60359: 1896.930388 from(949.472470,2+) rtinseconds(3913) index(58486)
Title: Locus:1.1.1.2789.47
Data file 2011-11-12 - TFD - EP 6-1.mgf

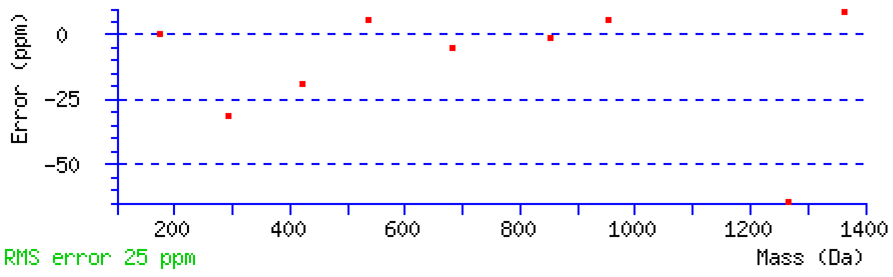
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1896.925766
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 35 **Expect:** 0.0032
Matches : 9/160 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	E							16
2	***293.113198***	147.060237			275.102633	138.054955	Y	1768.890463	884.948870	1751.863914	876.435595	1750.879898	875.943587	15
3	***422.155791***	211.581534			404.145226	202.576251	E	1605.827134	803.417205	1588.800585	794.903931	1587.816569	794.411923	14
4	***535.239855***	268.123566			517.229290	259.118283	I	1476.784541	738.895909	1459.757992	730.382634	1458.773976	729.890626	13
5	632.292619	316.649948			614.282054	307.644665	P	***1363.700477***	682.353877	1346.673928	673.840602	1345.689912	673.348594	12
6	719.324647	360.165962			701.314082	351.160679	S	***1266.647713***	633.827495	1249.621164	625.314220	1248.637148	624.822212	11
7	833.367574	417.187425	816.341025	408.674151	815.357009	408.182143	N	1179.615685	590.311481	1162.589136	581.798206	1161.605120	581.306198	10
8	946.451638	473.729457	929.425089	465.216183	928.441073	464.724175	L	1065.572758	533.290017	1048.546209	524.776743	1047.562193	524.284735	9
9	1047.499317	524.253297	1030.472768	515.740022	1029.488752	515.248014	T	***952.488694***	476.747985	935.462145	468.234711	934.478129	467.742703	8
10	1144.552081	572.779679	1127.525532	564.266404	1126.541516	563.774396	P	***851.441015***	426.224146	834.414466	417.710871	833.430450	417.218863	7
11	1215.589195	608.298236	1198.562646	599.784961	1197.578630	599.292953	A	754.388251	377.697764	737.361702	369.184489	736.377686	368.692481	6
12	1330.616138	665.811707	1313.589589	657.298433	1312.605573	656.806425	D	683.351137	342.179207	666.324588	333.665932	665.340572	333.173924	5
13	1429.684552	715.345914	1412.658003	706.832640	1411.673987	706.340632	V	568.324194	284.665735	551.297645	276.152461			4
14	1576.752966	788.880121	1559.726417	780.366847	1558.742401	779.874839	F	469.255780	235.131528	452.229231	226.618254			3
15	1723.821380	862.414328	1706.794831	853.901054	1705.810815	853.409046	F	322.187366	161.597321	305.160817	153.084047			2
16							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of EYEIPSNLTPADVFFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.0	1896.925766	0.004622	EYEIPSNLTPADVFFR
7.8	1896.933014	-0.002626	GPPGPPGPPGEQGLPGLEGR
6.4	1896.933014	-0.002626	GPPGPPGPPGEQGLPGLEGR
6.4	1896.933014	-0.002626	GPPGPPGPPGEQGLPGLEGR
6.3	1896.947571	-0.017183	NVKEIEHVMNLGNQTR
4.3	1896.926010	0.004378	LPMLHDPPKMGMPVVR
3.1	1896.933868	-0.003480	SCCVFTFQPNGKLVGR
1.3	1896.926010	0.004378	LPMLHDPPKMGMPVVR
1.3	1896.940201	-0.009813	RSSGSIVSGSLGHPGDAAAR
0.7	1896.933838	-0.003450	MSLWVDKYRPCSLGR

Mascot: http://www.matrixscience.com/

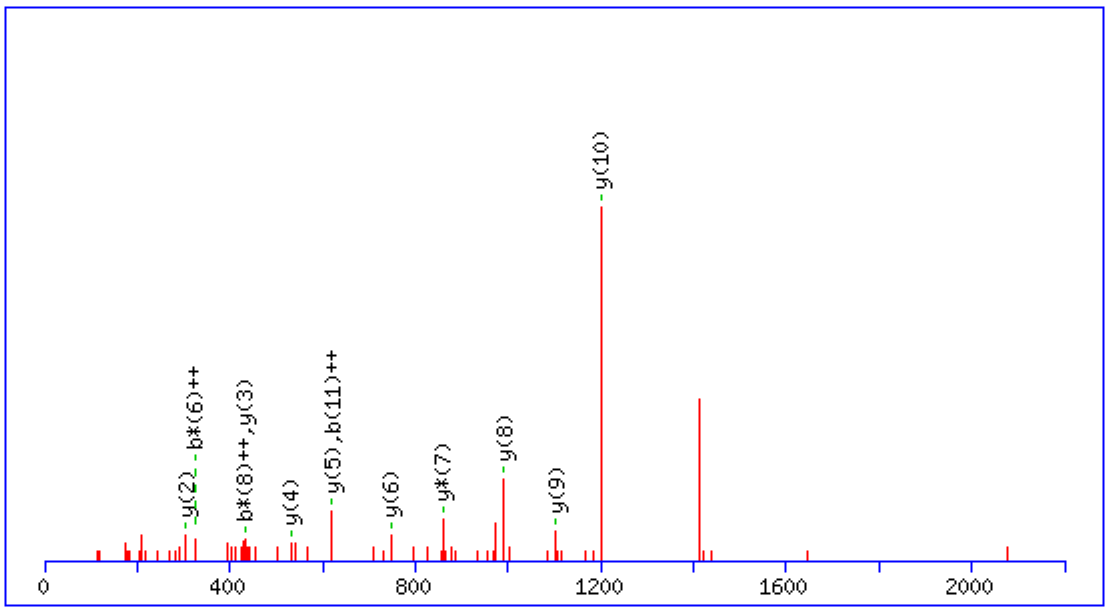
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LVPLNQESVEER**
Found in **NUP93_HUMAN**, Nuclear pore complex protein Nup93 OS=Homo sapiens GN=NUP93 PE=1 SV=2

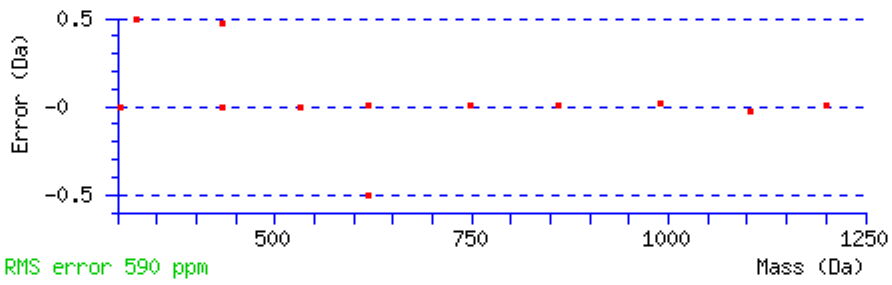
Match to Query 40375: 1411.731308 from(706.872930,2+) rtinseconds(1956) index(18295)
Title: Locus:1.1.1.2388.47
Data file 2011-11-12 - TFD - EP 5-2.mgf

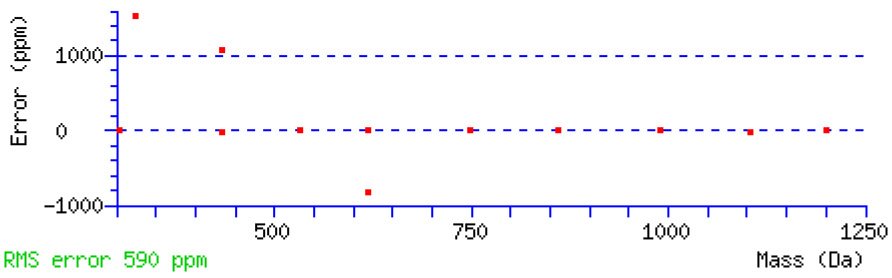
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1411.730682
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 74  Expect: 3.9e-007
Matches : 12/110 fragment ions using 11 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							12
2	213.159754	107.083515					V	1299.653920	650.330598	1282.627371	641.817324	1281.643355	641.325316	11
3	310.212518	155.609897					P	***1200.585506***	600.796391	1183.558957	592.283117	1182.574941	591.791109	10
4	423.296582	212.151929					L	***1103.532742***	552.270009	1086.506193	543.756735	1085.522177	543.264727	9
5	537.339509	269.173393	520.312960	260.660118			N	***990.448678***	495.727977	973.422129	487.214703	972.438113	486.722695	8
6	665.398087	333.202682	648.371538	324.689407			Q	876.405751	438.706514	859.379202	430.193239	858.395186	429.701231	7
7	794.440680	397.723978	777.414131	389.210704	776.430115	388.718696	E	***748.347173***	374.677225	731.320624	366.163950	730.336608	365.671942	6
8	881.472708	441.239992	864.446159	432.726718	863.462143	432.234710	S	***619.304580***	310.155928	602.278031	301.642654	601.294015	301.150646	5
9	980.541122	490.774199	963.514573	482.260924	962.530557	481.768916	V	***532.272552***	266.639914	515.246003	258.126640	514.261987	257.634632	4
10	1109.583715	555.295496	1092.557166	546.782221	1091.573150	546.290213	E	***433.204138***	217.105707	416.177589	208.592433	415.193573	208.100425	3
11	1238.626308	619.816792	1221.599759	611.303518	1220.615743	610.811510	E	***304.161545***	152.584411	287.134996	144.071136	286.150980	143.579128	2
12							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LVPLNQESVEER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
74.3	1411.730682	0.000626	LVPLNQESVEER
15.7	1411.730682	0.000626	VPALLENQVEER

Mascot: http://www.matrixscience.com/

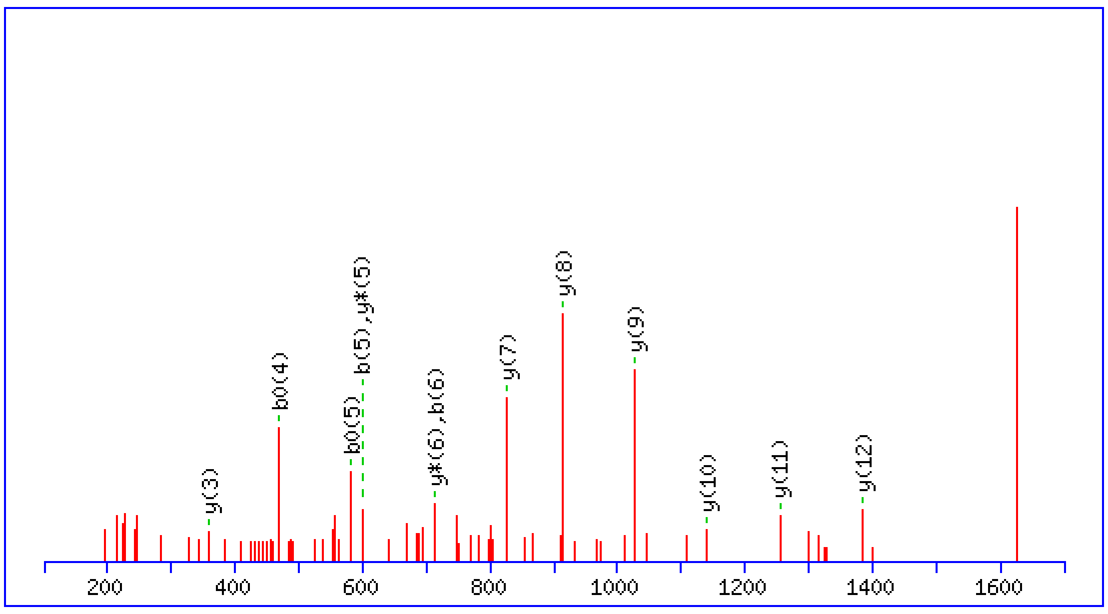
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELEDLLSPLEELVK**
Found in **NUP62_HUMAN**, Nuclear pore glycoprotein p62 OS=Homo sapiens GN=NUP62 PE=1 SV=3

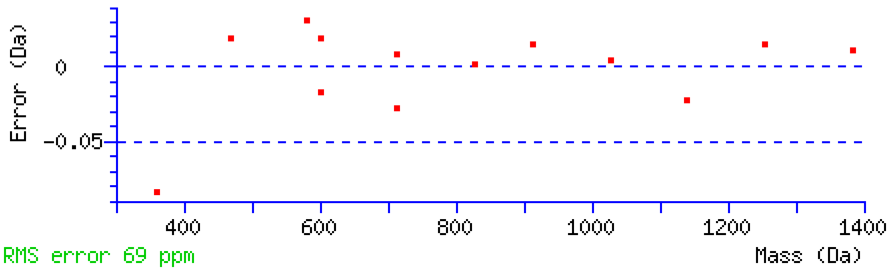
Match to Query 46218: 1625.888828 from(813.951690,2+) rtinseconds(4516) index(69856)
Title: Locus:1.1.1.3230.23
Data file 2011-11-12 - TFD - EP 5-3.mgf

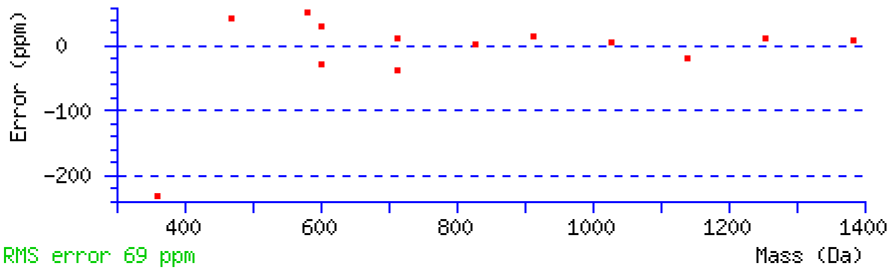
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1625.876328
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 59  Expect: 1.1e-005
Matches : 13/124 fragment ions using 13 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572	112.039304	56.523290	E							14
2	243.133933	122.070605	225.123368	113.065322	L	1497.841052	749.424164	1480.814503	740.910890	1479.830487	740.418882	13
3	372.176526	186.591901	354.165961	177.586619	E	***1384.756988***	692.882132	1367.730439	684.368858	1366.746423	683.876850	12
4	487.203469	244.105373	469.192904	235.100090	D	***1255.714395***	628.360836	1238.687846	619.847561	1237.703830	619.355553	11
5	**600.287533**	300.647405	582.276968	291.642122	L	***1140.687452***	570.847364	1123.660903	562.334090	1122.676887	561.842082	10
6	**713.371597**	357.189437	695.361032	348.184154	L	***1027.603388***	514.305332	1010.576839	505.792058	1009.592823	505.300050	9
7	800.403625	400.705451	782.393060	391.700168	S	***914.519324***	457.763300	897.492775	449.250026	896.508759	448.758018	8
8	897.456389	449.231833	879.445824	440.226550	P	***827.487296***	414.247286	810.460747	405.734012	809.476731	405.242004	7
9	1010.540453	505.773865	992.529888	496.768582	L	730.434532	365.720904	713.407983	357.207630	712.423967	356.715622	6
10	1139.583046	570.295161	1121.572481	561.289878	E	617.350468	309.178872	600.323919	300.665598	599.339903	300.173590	5
11	1268.625639	634.816458	1250.615074	625.811175	E	488.307875	244.657576	471.281326	236.144301	470.297310	235.652293	4
12	1381.709703	691.358490	1363.699138	682.353207	L	***359.265282***	180.136279	342.238733	171.623004			3
13	1480.778117	740.892697	1462.767552	731.887414	V	246.181218	123.594247	229.154669	115.080973			2
14					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of ELEDLLSPLEELVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.8	1625.876328	0.012500	ELEDLLSPLEELVK
9.7	1625.877701	0.011127	QETPKLWPVQLQK
4.4	1625.877686	0.011142	GYHLLLASATLQPDK
2.0	1625.900162	-0.011334	LLARQAGWQDVLTR

Mascot: http://www.matrixscience.com/

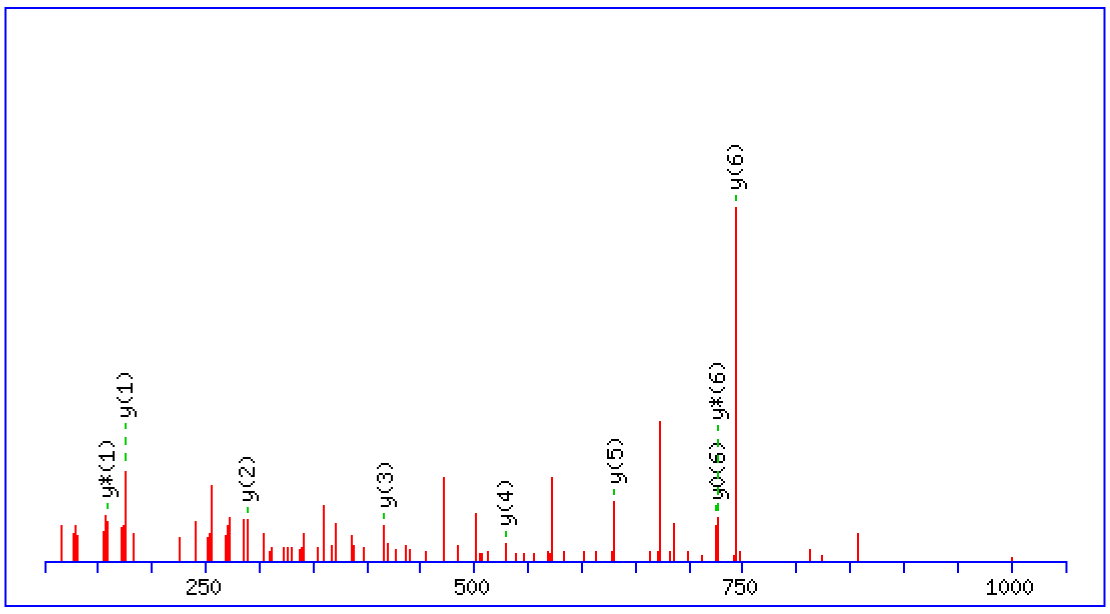
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LPTPKLR**
Found in **MDM1_HUMAN**, Nuclear protein MDM1 OS=Homo sapiens GN=MDM1 PE=1 SV=2

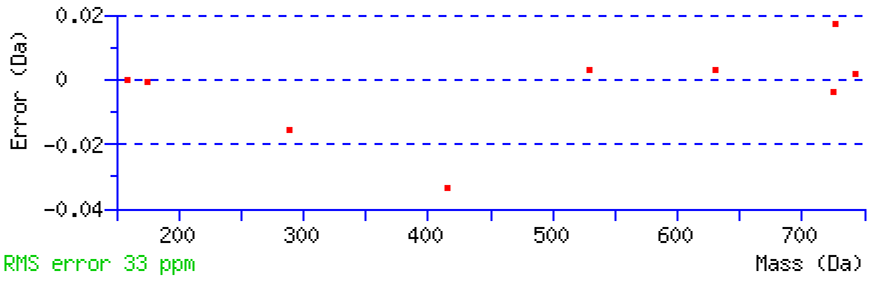
Match to Query 3632: 855.509668 from(428.762110,2+) rtinseconds(1733) index(14581)
Title: Locus:1.1.1.2221.8
Data file 2011-11-12 - TFD - EP 5-1.mgf

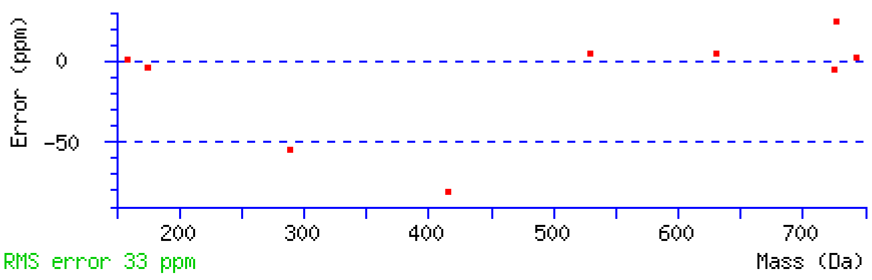
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 855.517792
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P2      : Oxidation (P)
P4      : Oxidation (P)
Ions Score: 34  Expect: 0.004
Matches : 9/52 fragment ions using 22 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					L							7
2	227.139019	114.073147					P	*743.441016*	372.224146	726.414467	363.710872	725.430451	363.218864	6
3	328.186698	164.596987			310.176133	155.591704	T	*630.393337*	315.700307	613.366788	307.187032	612.382772	306.695024	5
4	441.234377	221.120826			423.223812	212.115544	P	*529.345658*	265.176467	512.319109	256.663193			4
5	569.329340	285.168308	552.302791	276.655034	551.318775	276.163026	K	*416.297979*	208.652628	399.271430	200.139353			3
6	682.413404	341.710340	665.386855	333.197066	664.402839	332.705058	L	*288.203016*	144.605146	271.176467	136.091872			2
7							R	*175.118952*	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of LPTPKLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.6	855.517792	-0.008124	LPTPKLR
21.9	855.517792	-0.008124	LPTLPKR
20.8	855.517776	-0.008108	SPLSLIAR
19.3	855.517792	-0.008124	LLSTLGPR
12.5	855.517792	-0.008124	LLGDLGLR
12.4	855.517792	-0.008124	LEVVAGLR
12.4	855.517792	-0.008124	LVLDQLR
11.3	855.503860	0.005808	LAGAVRNR
9.3	855.517792	-0.008124	ALLSTPVR
8.9	855.517761	-0.008093	EAALIALR

Mascot: http://www.matrixscience.com/

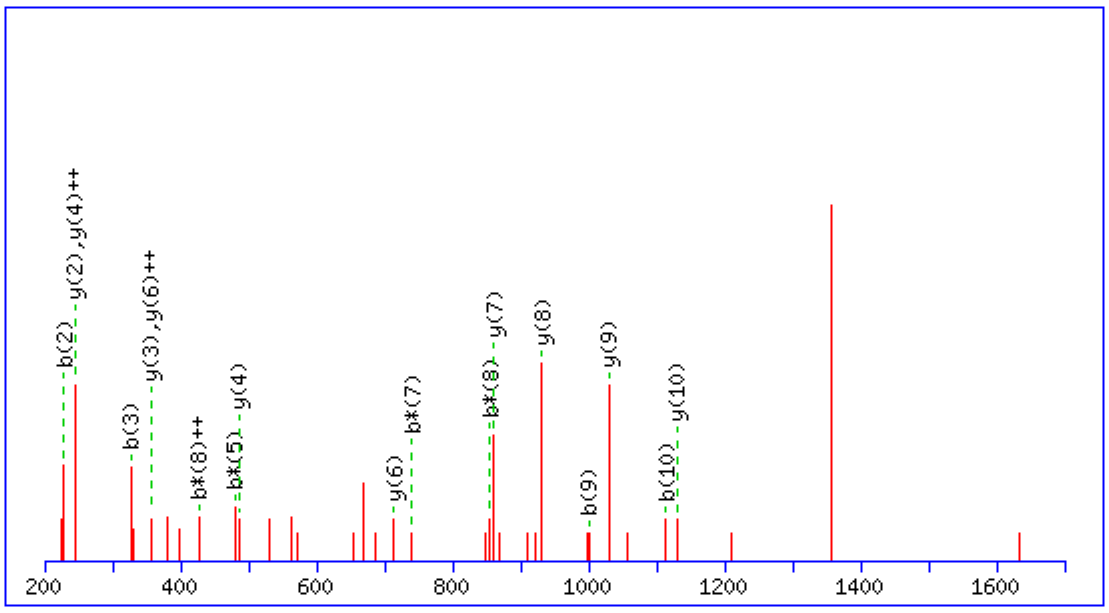
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LNVVAFLNELPK**
Found in **NXF1_HUMAN**, Nuclear RNA export factor 1 OS=Homo sapiens GN=NXF1 PE=1 SV=1

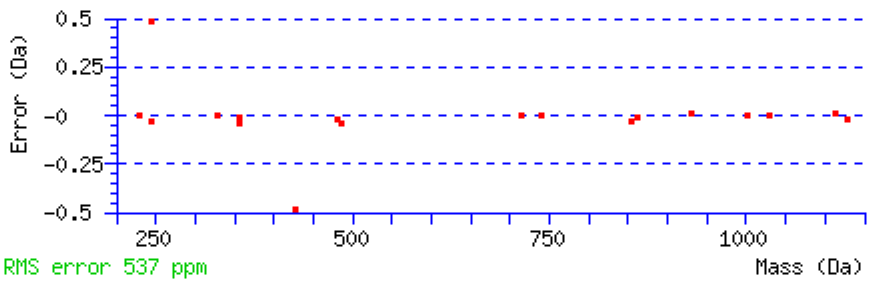
Match to Query 40715: 1355.783708 from(678.899130,2+) rtinseconds(4293) index(63905)
Title: Locus:1.1.1.3044.17
Data file 2011-11-14 - TFD - EP 8-2.mgf

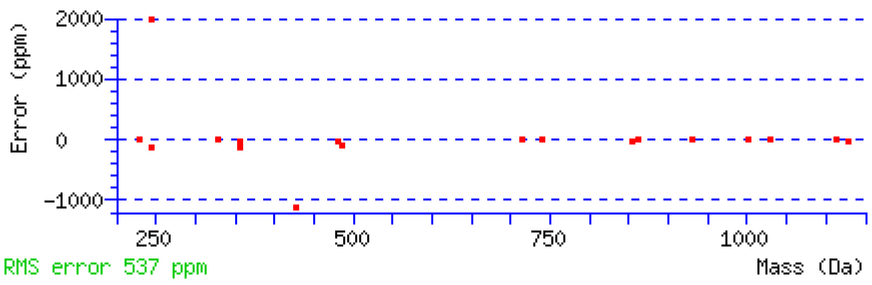
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1355.781265
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 52 **Expect:** 2.9e-005
Matches : 18/108 fragment ions using 30 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							12
2	**228.134267**	114.570771	211.107718	106.057497			N	1243.704499	622.355888	1226.677950	613.842613	1225.693934	613.350605	11
3	**327.202681**	164.104978	310.176132	155.591704			V	***1129.661572***	565.334424	1112.635023	556.821150	1111.651007	556.329141	10
4	426.271095	213.639186	409.244546	205.125911			V	***1030.593158***	515.800217	1013.566609	507.286943	1012.582593	506.794935	9
5	497.308209	249.157742	480.281660	240.644468			A	***931.524744***	466.266010	914.498195	457.752736	913.514179	457.260728	8
6	644.376623	322.691950	627.350074	314.178675			F	***860.487630***	430.747453	843.461081	422.234179	842.477065	421.742171	7
7	757.460687	379.233982	740.434138	370.720707			L	***713.419216***	357.213246	696.392667	348.699972	695.408651	348.207964	6
8	871.503614	436.255445	854.477065	427.742170			N	600.335152	300.671214	583.308603	292.157940	582.324587	291.665932	5
9	**1000.546207**	500.776742	983.519658	492.263467	982.535642	491.771459	E	***486.292225***	243.649751	469.265676	235.136476	468.281660	234.644468	4
10	**1113.630271**	557.318774	1096.603722	548.805499	1095.619706	548.313491	L	***357.249632***	179.128454	340.223083	170.615180			3
11	1210.683035	605.845156	1193.656486	597.331881	1192.672470	596.839873	P	***244.165568***	122.586422	227.139019	114.073148			2
12							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of LNVVAFLNELPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.2	1355.781265	0.002443	LNVVAFLNELPK
2.7	1355.777252	0.006456	VNLEVTGEIRVK

Mascot: http://www.matrixscience.com/

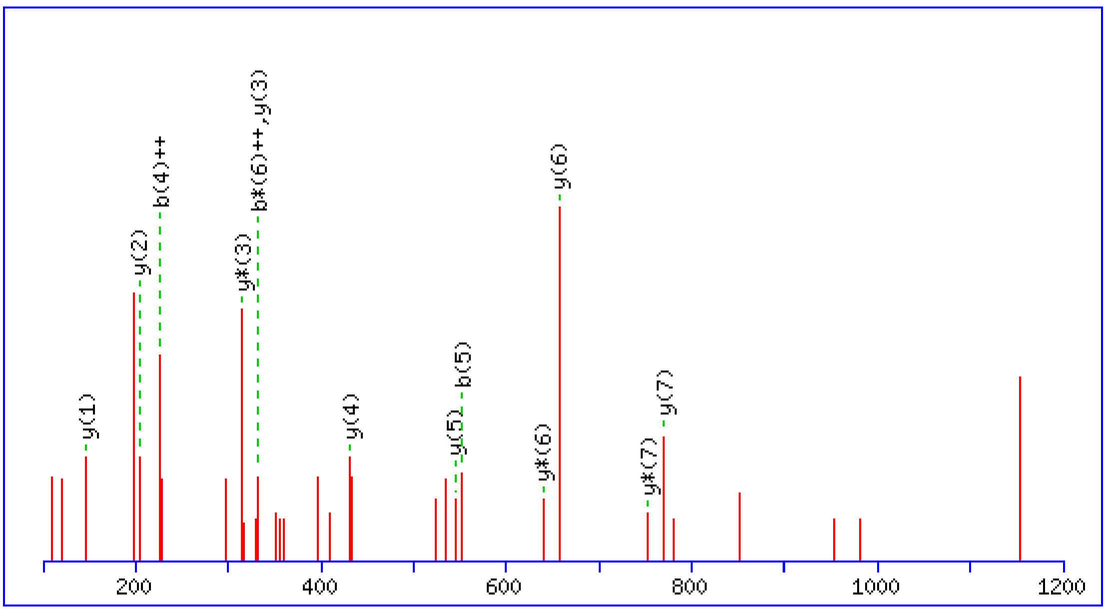
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLLLVQGK**
Found in **NOL3_HUMAN**, Nucleolar protein 3 OS=Homo sapiens GN=NOL3 PE=1 SV=1

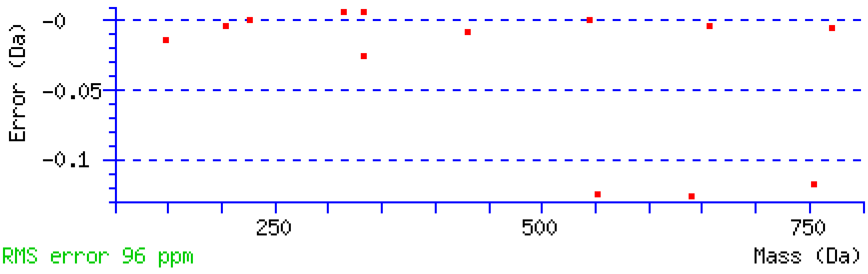
Match to Query 6399: 882.593608 from(442.304080,2+) rtinseconds(2545) index(30784)
Title: Locus:1.1.1.2387.5
Data file 2011-11-13 - TFD - EP 7-5.mgf

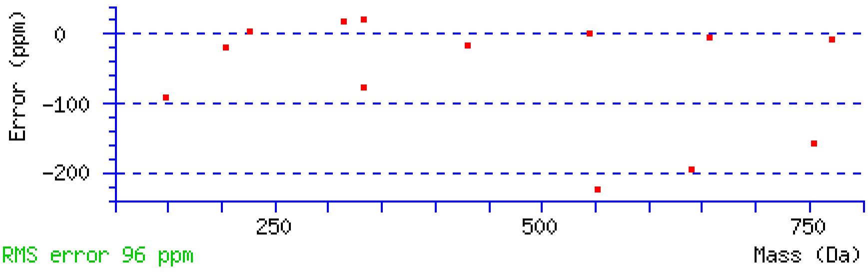
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 882.590225
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 51 **Expect:** 1.4e-005
Matches : 14/46 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	114.091340	57.549308			L					8
2	**227.175404**	114.091340			L	***770.513452***	385.760364	753.486903	377.247090	7
3	340.259468	170.633372			L	***657.429388***	329.218332	640.402839	320.705058	6
4	453.343532	227.175404			L	***544.345324***	272.676300	527.318775	264.163026	5
5	**552.411946**	276.709611			V	***431.261260***	216.134268	414.234711	207.620994	4
6	680.470524	340.738900	663.443975	332.225626	Q	***332.192846***	166.600061	315.166297	158.086787	3
7	737.491988	369.249632	720.465439	360.736358	G	***204.134268***	102.570772	187.107719	94.057498	2
8					K	***147.112804***	74.060040	130.086255	65.546765	1





NCBI **BLAST** search of LLLLVQGK
(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	882.590225	0.003383	LLLLVQGK
8.3	882.590210	0.003398	ILTPALKK
8.3	882.601440	-0.007832	LLQRLLK
8.3	882.601440	-0.007832	LLRLLQK
3.6	882.601440	-0.007832	LLLKLQR

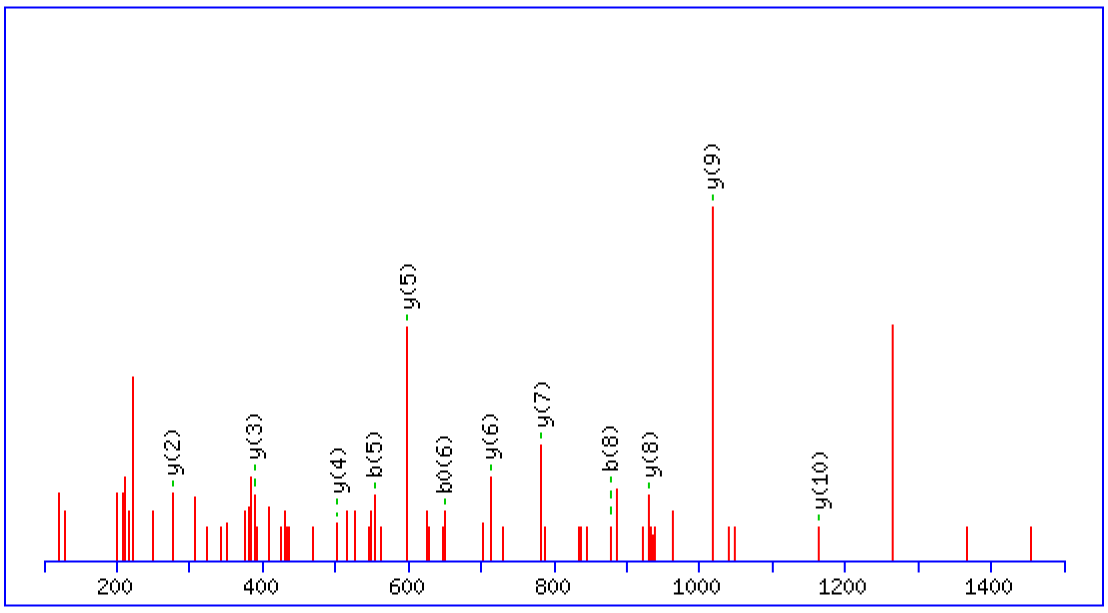
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TFSFAIPLIEK**
Found in **DDX21_HUMAN**, Nucleolar RNA helicase 2 OS=Homo sapiens GN=DDX21 PE=1 SV=5

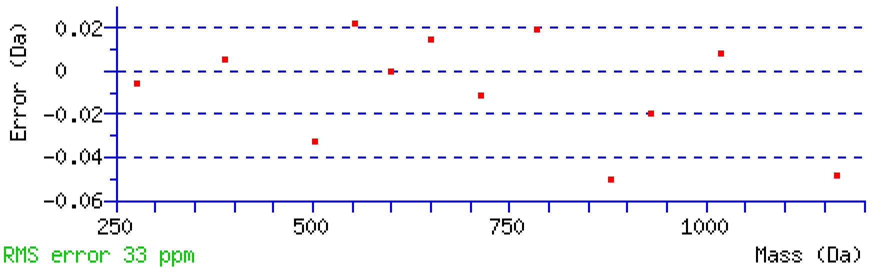
Match to Query 34581: 1264.709968 from(633.362260,2+) rtinseconds(3798) index(55951)
Title: Locus:1.1.1.2875.15
Data file 2011-11-10 - TFD - EP 3-2.mgf

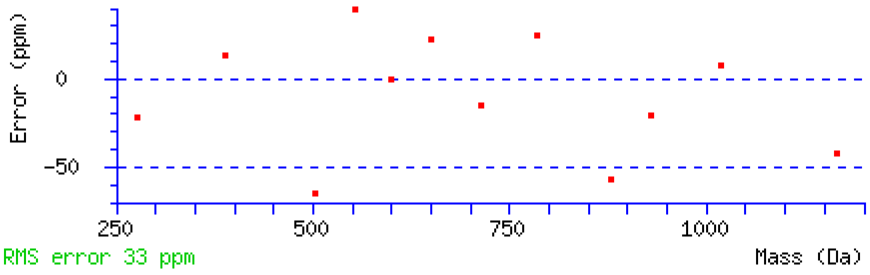
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1264.706711
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 54 **Expect:** 2e-005
Matches : 12/98 fragment ions using 30 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	102.054955	51.531116	84.044390	42.525833	T							11
2	249.123369	125.065322	231.112804	116.060040	F	***1164.666323***	582.836799	1147.639774	574.323525	1146.655758	573.831517	10
3	336.155397	168.581336	318.144832	159.576054	S	***1017.597909***	509.302593	1000.571360	500.789318	999.587344	500.297310	9
4	483.223811	242.115543	465.213246	233.110261	F	***930.565881***	465.786579	913.539332	457.273304	912.555316	456.781296	8
5	**554.260925**	277.634100	536.250360	268.628818	A	***783.497467***	392.252372	766.470918	383.739097	765.486902	383.247089	7
6	667.344989	334.176132	649.334424	325.170850	I	***712.460353***	356.733815	695.433804	348.220540	694.449788	347.728532	6
7	764.397753	382.702515	746.387188	373.697232	P	***599.376289***	300.191783	582.349740	291.678508	581.365724	291.186500	5
8	**877.481817**	439.244547	859.471252	430.239264	L	***502.323525***	251.665400	485.296976	243.152126	484.312960	242.660118	4
9	990.565881	495.786579	972.555316	486.781296	I	***389.239461***	195.123368	372.212912	186.610094	371.228896	186.118086	3
10	1119.608474	560.307875	1101.597909	551.302592	E	***276.155397***	138.581336	259.128848	130.068062	258.144832	129.576054	2
11					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of TFSFAIPLIEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.1	1264.706711	0.003257	TFSFAIPLIEK

Mascot: http://www.matrixscience.com/

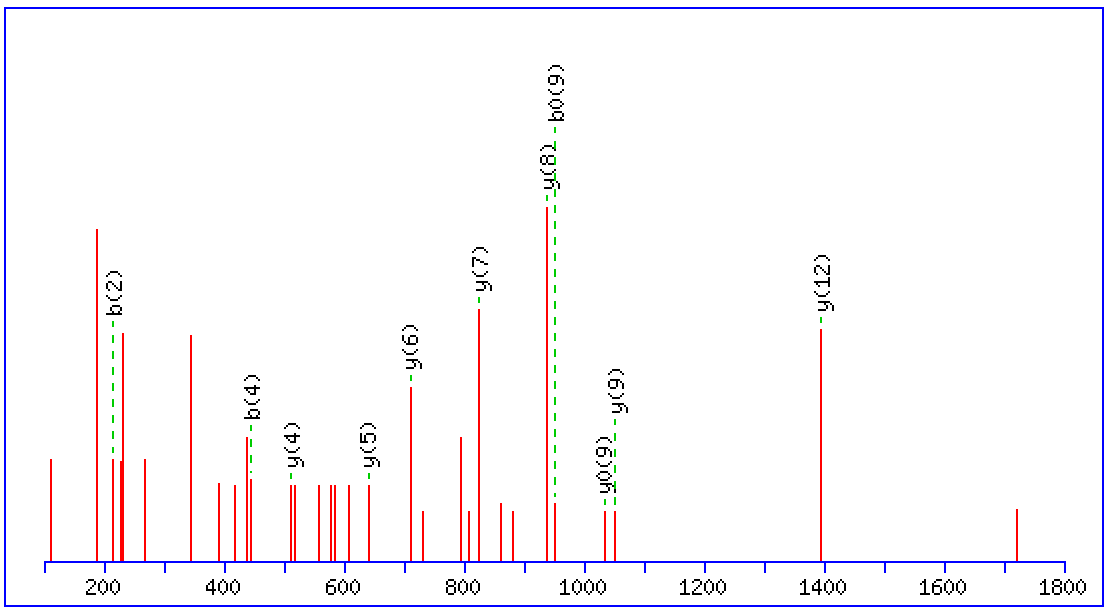
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLTELILDAQEHVK**
Found in **UBF1_HUMAN**, Nucleolar transcription factor 1 OS=Homo sapiens GN=UBTF PE=1 SV=1

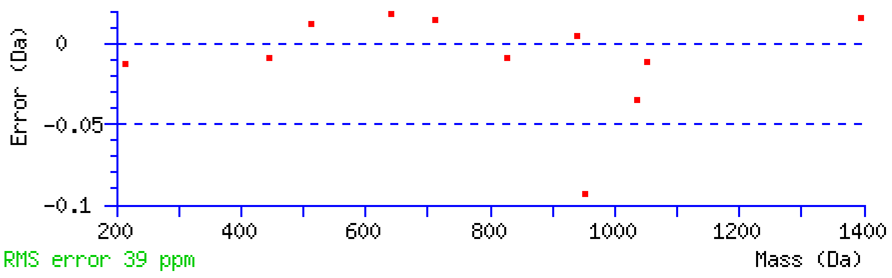
Match to Query 52015: 1608.879822 from(537.300550,3+) rtinseconds(3392) index(48425)
Title: Locus:1.1.1.2724.8
Data file 2011-11-10 - TFD - EP 3-2.mgf

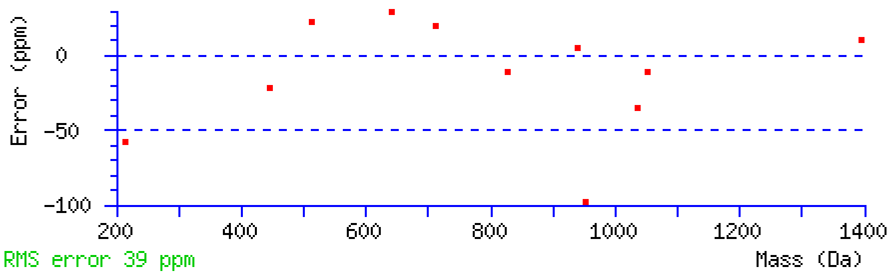
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 1800 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1608.872269
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 41  Expect: 0.00023
Matches : 11/132 fragment ions using 20 most intense peaks    (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							14
2	**215.139019**	108.073147			197.128454	99.067865	L	1508.831886	754.919581	1491.805337	746.406307	1490.821321	745.914299	13
3	316.186698	158.596987			298.176133	149.591704	T	***1395.747822***	698.377549	1378.721273	689.864275	1377.737257	689.372267	12
4	**445.229291**	223.118283			427.218726	214.113001	E	1294.700143	647.853710	1277.673594	639.340435	1276.689578	638.848427	11
5	558.313355	279.660316			540.302790	270.655033	L	1165.657550	583.332413	1148.631001	574.819139	1147.646985	574.327131	10
6	671.397419	336.202348			653.386854	327.197065	I	***1052.573486***	526.790381	1035.546937	518.277107	1034.562921	517.785099	9
7	784.481483	392.744380			766.470918	383.739097	L	***939.489422***	470.248349	922.462873	461.735075	921.478857	461.243067	8
8	899.508426	450.257851			881.497861	441.252569	D	***826.405358***	413.706317	809.378809	405.193043	808.394793	404.701035	7
9	970.545540	485.776408			952.534975	476.771125	A	***711.378415***	356.192846	694.351866	347.679571	693.367850	347.187563	6
10	1098.604118	549.805697	1081.577569	541.292423	1080.593553	540.800414	Q	***640.341301***	320.674289	623.314752	312.161014	622.330736	311.669006	5
11	1227.646711	614.326994	1210.620162	605.813719	1209.636146	605.321711	E	***512.282723***	256.645000	495.256174	248.131725	494.272158	247.639717	4
12	1364.705623	682.856450	1347.679074	674.343175	1346.695058	673.851167	H	383.240130	192.123703	366.213581	183.610429			3
13	1463.774037	732.390657	1446.747488	723.877382	1445.763472	723.385374	V	246.181218	123.594247	229.154669	115.080973			2
14							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of TLTELILDAQEHVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.7	1608.872269	0.007553	TLTELILDAQEHVK
2.0	1608.879654	0.000168	LTDKDYMKPLLLK

Mascot: http://www.matrixscience.com/

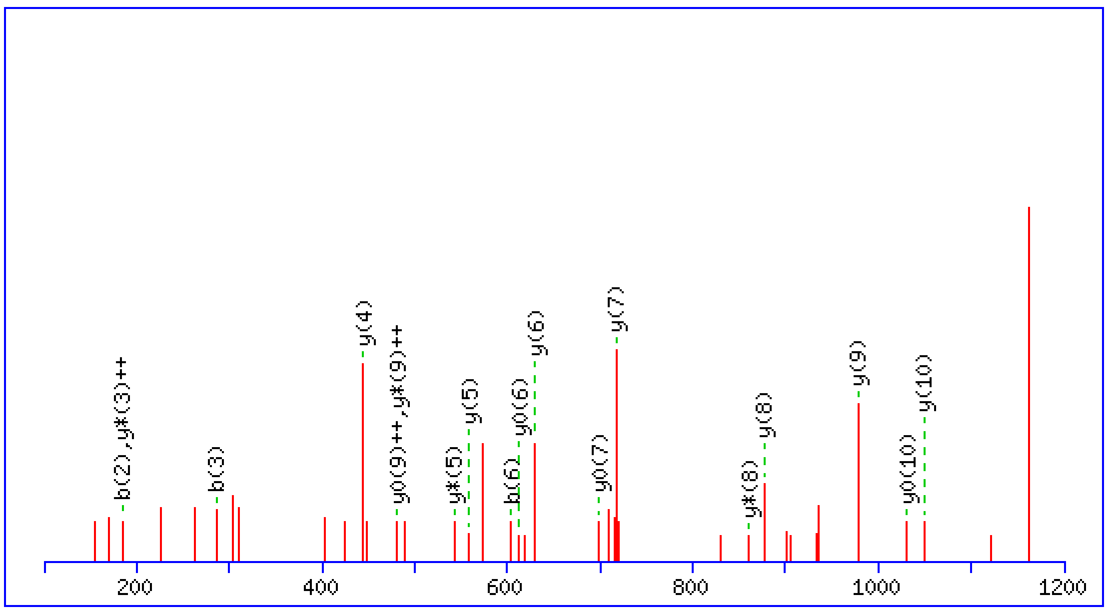
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LATCSADGIVR**
Found in **SEH1_HUMAN**, Nucleoporin SEH1 OS=Homo sapiens GN=SEH1L PE=1 SV=3

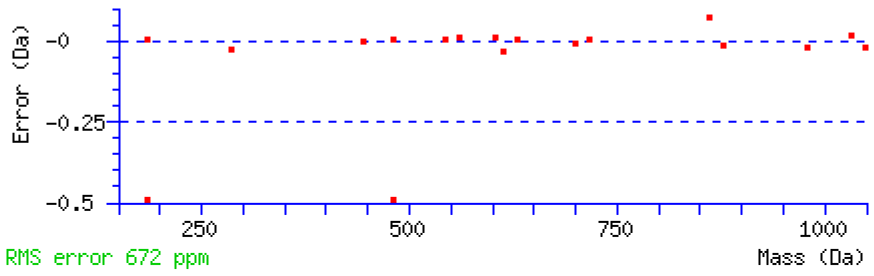
Match to Query 473471: 1161.580208 from(581.797380,2+) rtinseconds(1622) index(422638)
Title: Locus:1.1.1.958.29
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

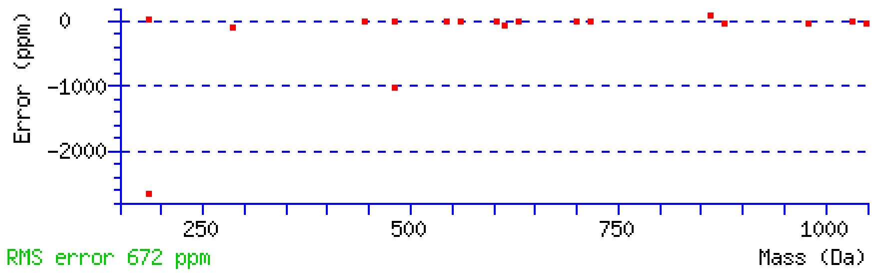
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1161.581207
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.00054
Matches : 18/88 fragment ions using 35 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							11
2	185.128454	93.067865			A	1049.504421	525.255849	1032.477872	516.742574	1031.493856	516.250566	10
3	286.176133	143.591704	268.165568	134.586422	T	978.467307	489.737292	961.440758	481.224017	960.456742	480.732009	9
4	446.206782	223.607029	428.196217	214.601747	C	877.419628	439.213452	860.393079	430.700178	859.409063	430.208170	8
5	533.238810	267.123043	515.228245	258.117761	S	717.388979	359.198128	700.362430	350.684853	699.378414	350.192845	7
6	604.275924	302.641600	586.265359	293.636318	A	630.356951	315.682114	613.330402	307.168839	612.346386	306.676831	6
7	719.302867	360.155072	701.292302	351.149789	D	559.319837	280.163557	542.293288	271.650282	541.309272	271.158274	5
8	776.324331	388.665804	758.313766	379.660521	G	444.292894	222.650085	427.266345	214.136810			4
9	889.408395	445.207836	871.397830	436.202553	I	387.271430	194.139353	370.244881	185.626078			3
10	988.476809	494.742043	970.466244	485.736760	V	274.187366	137.597321	257.160817	129.084046			2
11					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LATCSADGIVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.3	1161.581207	-0.000999	LATCSADGIVR
4.3	1161.585861	-0.005653	LATFWYYAK
4.0	1161.589066	-0.008858	APLRFQGDSR
3.6	1161.581207	-0.000999	MSGRVGDLSPK
1.0	1161.577362	0.002846	VQLIAMDLPM
1.0	1161.577362	0.002846	VQLIAMDLPM
1.0	1161.577362	0.002846	VQLIAMDLPM

Mascot: http://www.matrixscience.com/

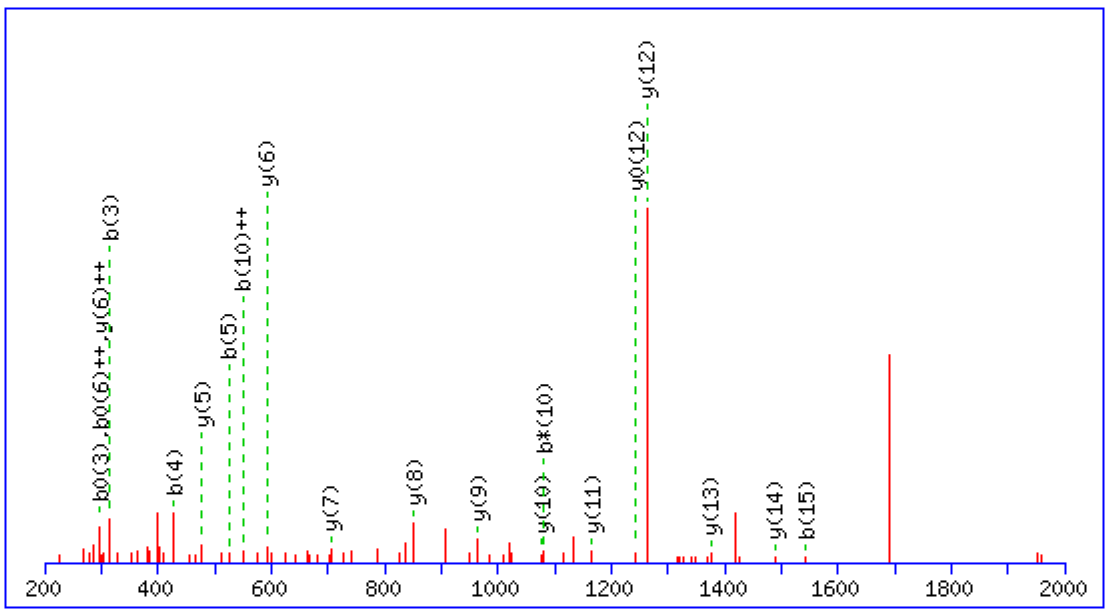
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ISNIPSLIFLDATTGK**
Found in **NXN_HUMAN**, Nucleoredoxin OS=Homo sapiens GN=NXN PE=1 SV=2

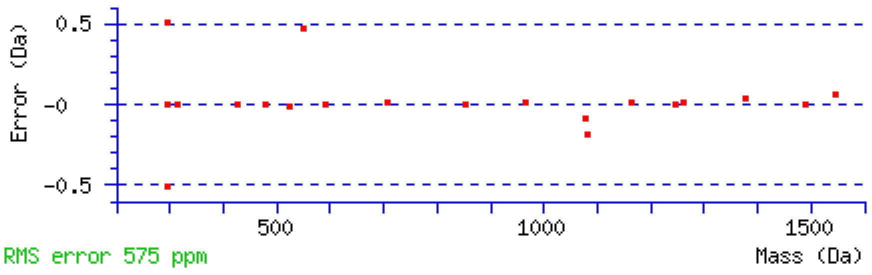
Match to Query 50028: 1688.942508 from(845.478530,2+) rtinseconds(3911) index(59141)
Title: Locus:1.1.1.2977.25
Data file 2011-11-10 - TFD - EP 4-3.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●

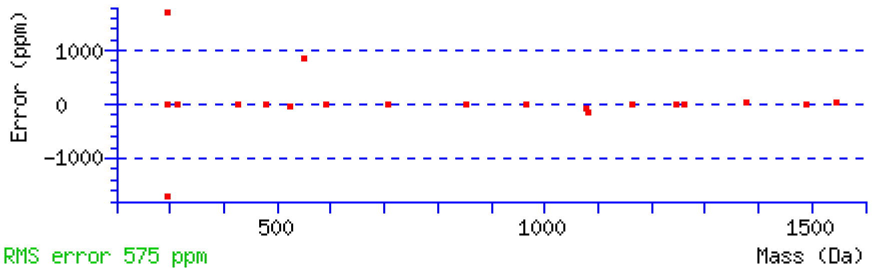


```
Monoisotopic mass of neutral peptide Mr(calc): 1688.934875
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 58  Expect: 5.3e-006
Matches : 20/170 fragment ions using 37 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					I							16
2	201.123368	101.065322			183.112803	92.060039	S	1576.858100	788.932688	1559.831551	780.419414	1558.847535	779.927406	15
3	**315.166295**	158.086785	298.139746	149.573511	297.155730	149.081503	N	***1489.826072***	745.416674	1472.799523	736.903400	1471.815507	736.411392	14
4	**428.250359**	214.628818	411.223810	206.115543	410.239794	205.623535	I	***1375.783145***	688.395211	1358.756596	679.881936	1357.772580	679.389928	13
5	**525.303123**	263.155200	508.276574	254.641925	507.292558	254.149917	P	***1262.699081***	631.853179	1245.672532	623.339904	1244.688516	622.847896	12
6	612.335151	306.671214	595.308602	298.157939	594.324586	297.665931	S	***1165.646317***	583.326797	1148.619768	574.813522	1147.635752	574.321514	11
7	725.419215	363.213246	708.392666	354.699971	707.408650	354.207963	L	***1078.614289***	539.810783	1061.587740	531.297508	1060.603724	530.805500	10
8	838.503279	419.755278	821.476730	411.242003	820.492714	410.749995	I	***965.530225***	483.268751	948.503676	474.755476	947.519660	474.263468	9
9	985.571693	493.289485	968.545144	484.776210	967.561128	484.284202	F	***852.446161***	426.726719	835.419612	418.213444	834.435596	417.721436	8
10	1098.655757	549.831517	1081.629208	541.318242	1080.645192	540.826234	L	***705.377747***	353.192512	688.351198	344.679237	687.367182	344.187229	7
11	1213.682700	607.344988	1196.656151	598.831714	1195.672135	598.339706	D	***592.293683***	296.650480	575.267134	288.137205	574.283118	287.645197	6
12	1284.719814	642.863545	1267.693265	634.350271	1266.709249	633.858263	A	***477.266740***	239.137008	460.240191	230.623733	459.256175	230.131725	5
13	1385.767493	693.387385	1368.740944	684.874110	1367.756928	684.382102	T	406.229626	203.618451	389.203077	195.105176	388.219061	194.613168	4
14	1486.815172	743.911224	1469.788623	735.397950	1468.804607	734.905942	T	305.181947	153.094611	288.155398	144.581337	287.171382	144.089329	3
15	**1543.836636**	772.421956	1526.810087	763.908682	1525.826071	763.416674	G	204.134268	102.570772	187.107719	94.057497			2
16							K	147.112804	74.060040	130.086255	65.546765			1



RMS error 575 ppm



RMS error 575 ppm

NCBI **BLAST** search of ISNIPSLIFLDATTGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.4	1688.934875	0.007633	ISNIPSLIFLDATTGK
5.3	1688.934845	0.007663	SLAPEPKEPLIPASPK
3.1	1688.934845	0.007663	SLAPEPKEPLIPASPK
2.7	1688.950806	-0.008298	LLHGVMEQLGIARPR
0.9	1688.934845	0.007663	SLAPEPKEPLIPASPK

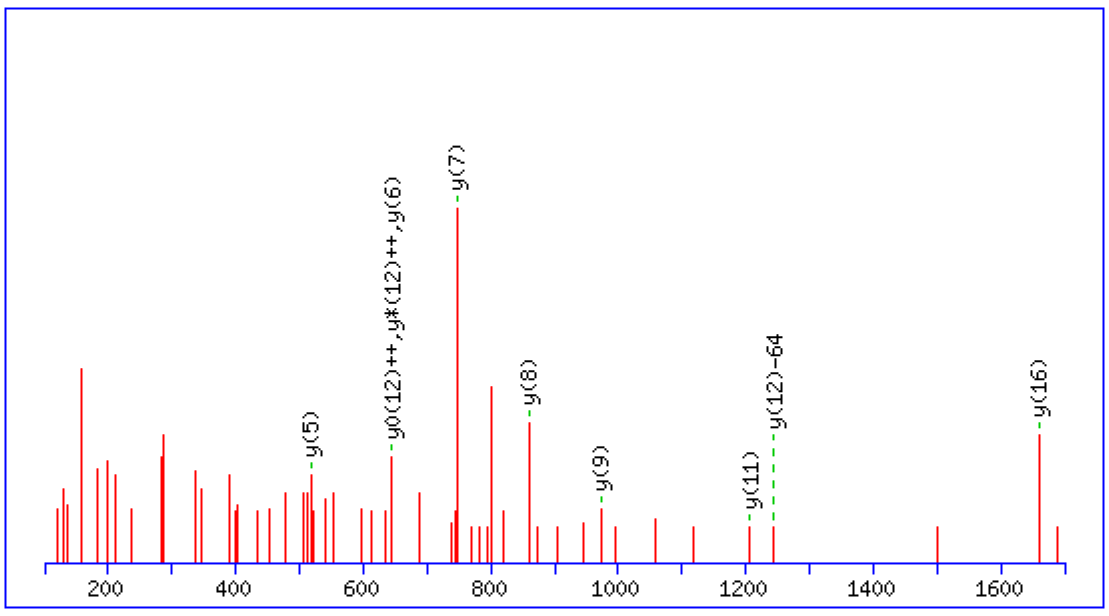
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SVPLAATSMLITQGLISK**
Found in **OCAD1_HUMAN**, OCIA domain-containing protein 1 OS=Homo sapiens GN=OCIAD1 PE=1 SV=1

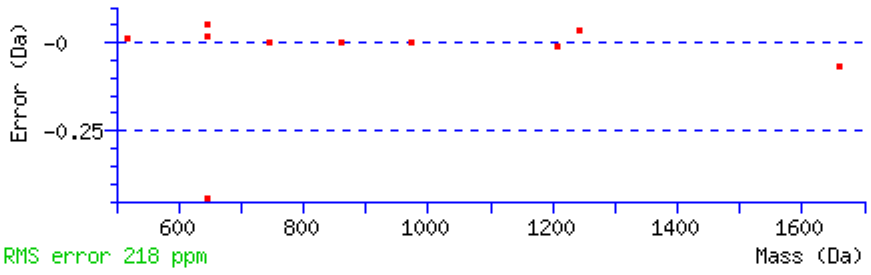
Match to Query 59319: 1845.034362 from(616.018730,3+) rtinseconds(3576) index(52330)
Title: Locus:1.1.1.2700.12
Data file 2011-11-10 - TFD - EP 3-4.mgf

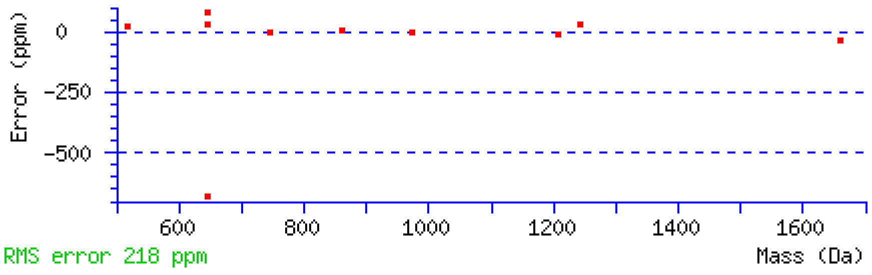
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1700] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1845.028122
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M9     : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 40  Expect: 0.0003
Matches : 10/272 fragment ions using 14 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							18
2	187.107718	94.057497			169.097153	85.052214	V	1759.003386	880.005331	1741.976837	871.492056	1740.992821	871.000048	17
3	284.160482	142.583879			266.149917	133.578596	P	***1659.934972***	830.471124	1642.908423	821.957849	1641.924407	821.465841	16
4	397.244546	199.125911			379.233981	190.120628	L	1562.882208	781.944742	1545.855659	773.431467	1544.871643	772.939459	15
5	468.281660	234.644468			450.271095	225.639185	A	1449.798144	725.402710	1432.771595	716.889435	1431.787579	716.397427	14
6	539.318774	270.163025			521.308209	261.157742	A	1378.761030	689.884153	1361.734481	681.370879	1360.750465	680.878870	13
7	640.366453	320.686865			622.355888	311.681582	T	1307.723916	654.365596	1290.697367	645.852321	1289.713351	645.360313	12
8	727.398481	364.202879			709.387916	355.197596	S	***1206.676237***	603.841756	1189.649688	595.328482	1188.665672	594.836474	11
9	874.433881	437.720578			856.423316	428.715296	M	1119.644209	560.325742	1102.617660	551.812468	1101.633644	551.320460	10
10	987.517945	494.262610			969.507380	485.257328	L	***972.608809***	486.808042	955.582260	478.294768	954.598244	477.802760	9
11	1100.602009	550.804643			1082.591444	541.799360	I	***859.524745***	430.266010	842.498196	421.752736	841.514180	421.260728	8
12	1201.649688	601.328482			1183.639123	592.323199	T	***746.440681***	373.723978	729.414132	365.210704	728.430116	364.718696	7
13	1329.708266	665.357771	1312.681717	656.844496	1311.697701	656.352488	Q	***645.393002***	323.200139	628.366453	314.686864	627.382437	314.194856	6
14	1386.729730	693.868503	1369.703181	685.355228	1368.719165	684.863220	G	***517.334424***	259.170850	500.307875	250.657575	499.323859	250.165567	5
15	1499.813794	750.410535	1482.787245	741.897260	1481.803229	741.405252	L	460.312960	230.660118	443.286411	222.146843	442.302395	221.654835	4
16	1612.897858	806.952567	1595.871309	798.439292	1594.887293	797.947284	I	347.228896	174.118086	330.202347	165.604811	329.218331	165.112803	3
17	1699.929886	850.468581	1682.903337	841.955306	1681.919321	841.463298	S	234.144832	117.576054	217.118283	109.062780	216.134267	108.570772	2
18							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of SVPLAATSMLITQGLISK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.1	1845.028122	0.006240	SVPLAATSMLITQGLISK
25.6	1845.028122	0.006240	SVPLAATSMLITQGLISK
0.4	1845.022049	0.012313	EPLPSRPLNARPGPGKK
0.4	1845.035965	-0.001603	KLPELAAGVAPEPPLATR

Mascot: http://www.matrixscience.com/

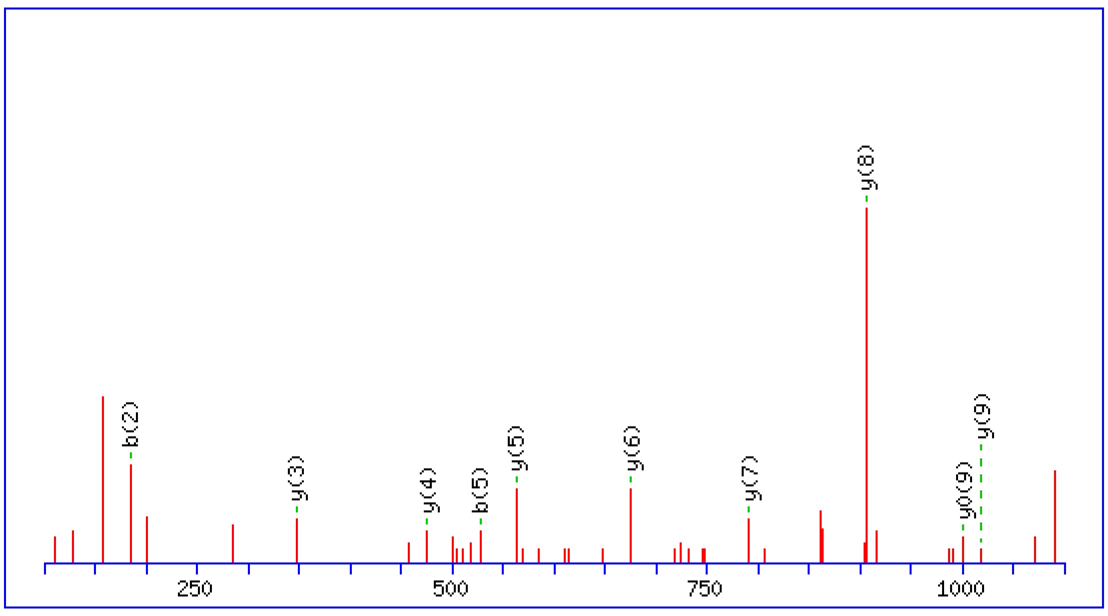
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALDDISESIK**
Found in **ORN_HUMAN**, Oligoribonuclease, mitochondrial OS=Homo sapiens GN=REXO2 PE=1 SV=3

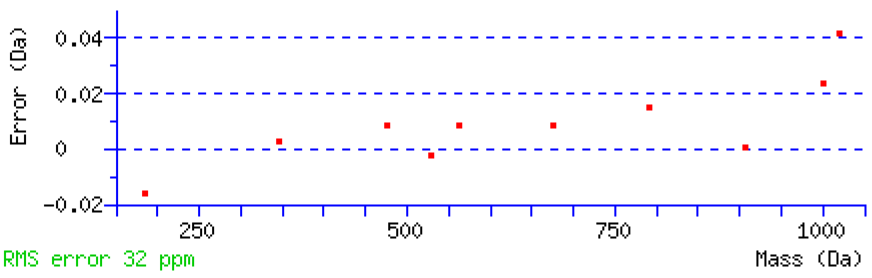
Match to Query 21649: 1089.554528 from(545.784540,2+) rtinseconds(2171) index(21690)
Title: Locus:1.1.1.2412.25
Data file 2011-11-12 - TFD - EP 5-5.mgf

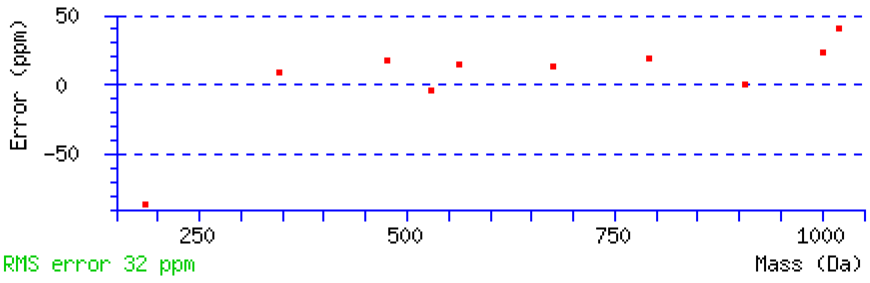
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1089.555344
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 51 **Expect:** 0.00012
Matches : 10/82 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	72.044390	36.525833			A							10
2	**185.128454**	93.067865			L	*1019.525531*	510.266404	1002.498982	501.753129	1001.514966	501.261121	9
3	300.155397	150.581336	282.144832	141.576054	D	*906.441467*	453.724372	889.414918	445.211097	888.430902	444.719089	8
4	415.182340	208.094808	397.171775	199.089526	D	*791.414524*	396.210900	774.387975	387.697626	773.403959	387.205618	7
5	**528.266404**	264.636840	510.255839	255.631558	I	*676.387581*	338.697429	659.361032	330.184154	658.377016	329.692146	6
6	615.298432	308.152854	597.287867	299.147572	S	*563.303517*	282.155397	546.276968	273.642122	545.292952	273.150114	5
7	744.341025	372.674151	726.330460	363.668868	E	*476.271489*	238.639383	459.244940	230.126108	458.260924	229.634100	4
8	831.373053	416.190165	813.362488	407.184882	S	*347.228896*	174.118086	330.202347	165.604812	329.218331	165.112804	3
9	944.457117	472.732197	926.446552	463.726914	I	260.196868	130.602072	243.170319	122.088798			2
10					K	147.112804	74.060040	130.086255	65.546766			1





NCBI **BLAST** search of ALDDISESIK
(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	1089.555344	-0.000816	ALDDISESIK
9.5	1089.548828	0.005700	AIDATLMSPR
9.5	1089.548828	0.005700	AIDATLMSPR
9.5	1089.548813	0.005715	ALDLENIMR
6.9	1089.548828	0.005700	ALEMPQITR
6.8	1089.556671	-0.002143	REEEKPFR
4.4	1089.545441	0.009087	AINNSFAPEK
3.5	1089.549484	0.005044	PWPFSESIK
2.8	1089.560059	-0.005531	RVAMIDETR
0.4	1089.548828	0.005700	SPEVKLMDR

Mascot: http://www.matrixscience.com/

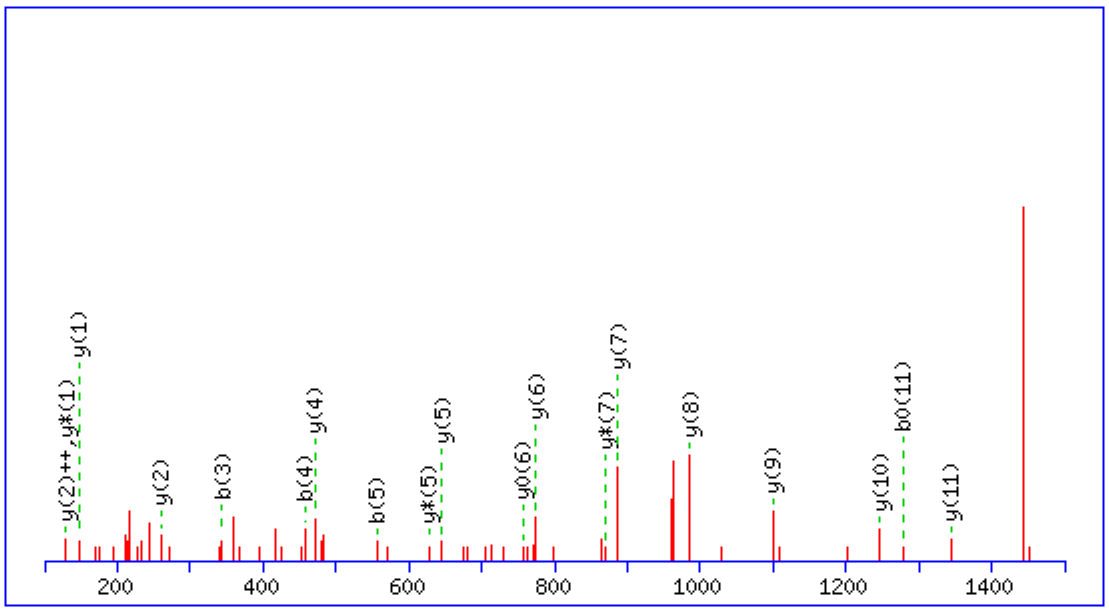
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VPFLVLECPNLK**
Found in **OSTC_HUMAN**, Oligosaccharyltransferase complex subunit OSTC OS=Homo sapiens GN=OSTC PE=1 SV=1

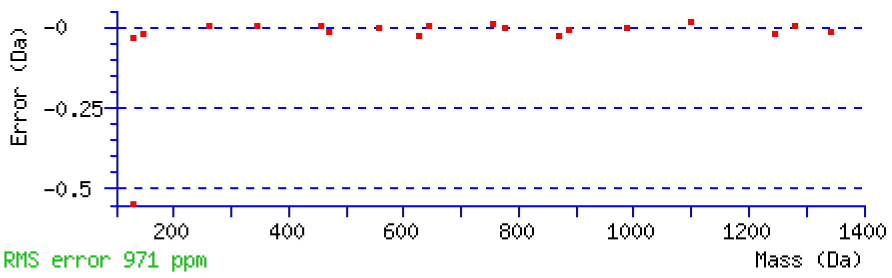
Match to Query 38687: 1441.801388 from(721.907970,2+) rtinseconds(3462) index(39892)
Title: Locus:1.1.1.2651.27
Data file 2011-11-12 - TFD - EP 6-7.mgf

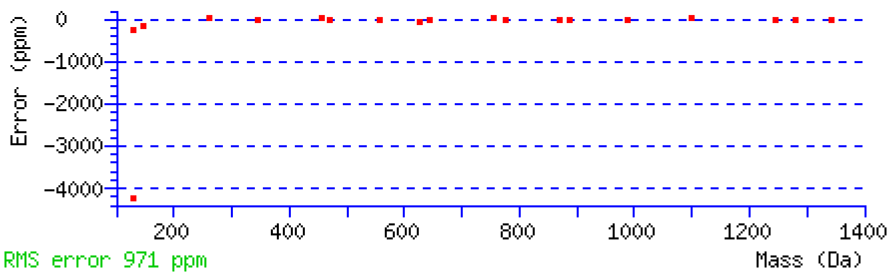
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1441.800293
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 62  Expect: 3.6e-006
Matches : 19/92 fragment ions using 40 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							12
2	197.128454	99.067865					P	*1343.739171*	672.373223	1326.712622	663.859949	1325.728606	663.367941	11
3	**344.196868**	172.602072					F	*1246.686407*	623.846841	1229.659858	615.333567	1228.675842	614.841559	10
4	**457.280932**	229.144104					L	*1099.617993*	550.312634	1082.591444	541.799360	1081.607428	541.307352	9
5	**556.349346**	278.678311					V	*986.533929*	493.770602	969.507380	485.257328	968.523364	484.765320	8
6	669.433410	335.220343					L	*887.465515*	444.236395	870.438966	435.723121	869.454950	435.231113	7
7	798.476003	399.741640			780.465438	390.736357	E	*774.381451*	387.694363	757.354902	379.181089	756.370886	378.689081	6
8	972.522302	486.764789			954.511737	477.759506	C	*645.338858*	323.173067	628.312309	314.659792			5
9	1069.575066	535.291171			1051.564501	526.285888	P	*471.292559*	236.149917	454.266010	227.636643			4
10	1183.617993	592.312634	1166.591444	583.799360	1165.607428	583.307352	N	374.239795	187.623535	357.213246	179.110261			3
11	1296.702057	648.854666	1279.675508	640.341392	1278.691492	639.849384	L	*260.196868*	130.602072	243.170319	122.088797			2
12							K	*147.112804*	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of VPFLVLECPNLK
(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	1441.800293	0.001095	VPFLVLECPNLK
4.1	1441.814011	-0.012623	ITELLNDVERLK

Mascot: http://www.matrixscience.com/

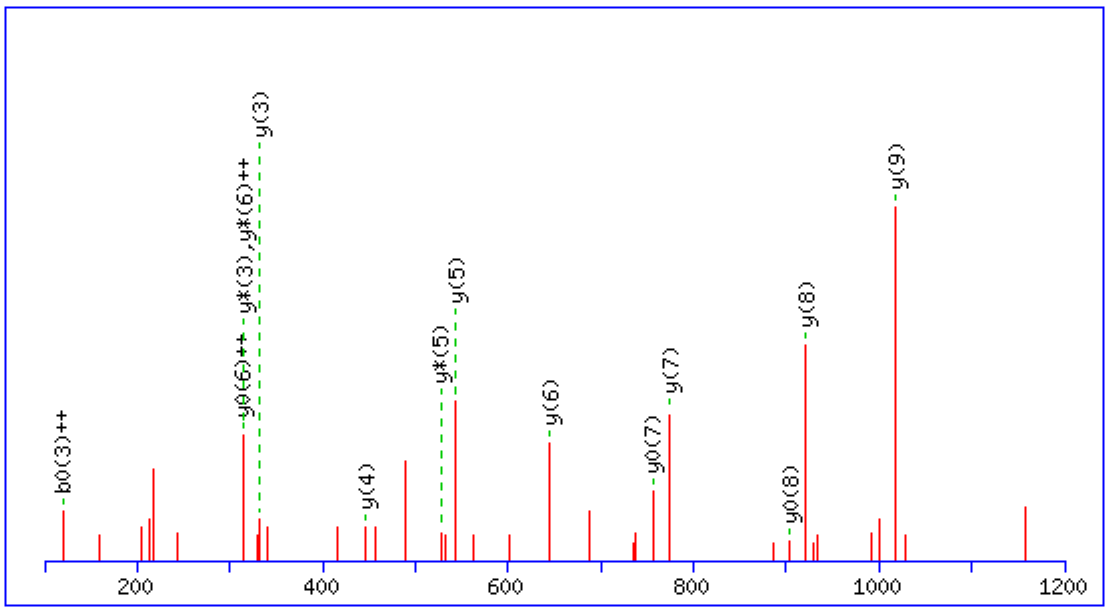
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GTPFETPDQGK**
Found in **ORML1_HUMAN**, ORM1-like protein 1 OS=Homo sapiens GN=ORMDL1 PE=2 SV=1

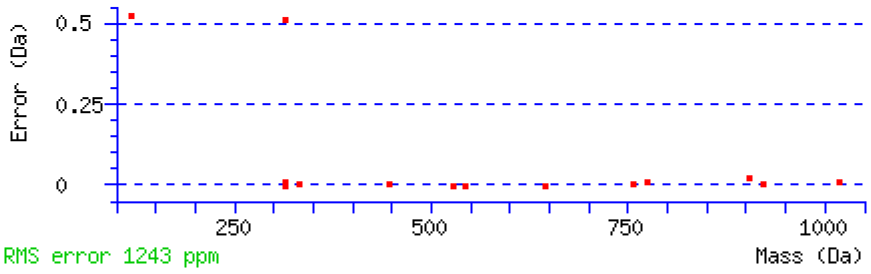
Match to Query 26581: 1175.546228 from(588.780390,2+) rtinseconds(1601) index(7923)
Title: Locus:1.1.1.2066.25
Data file 2011-11-10 - TFD - EP 4-7.mgf

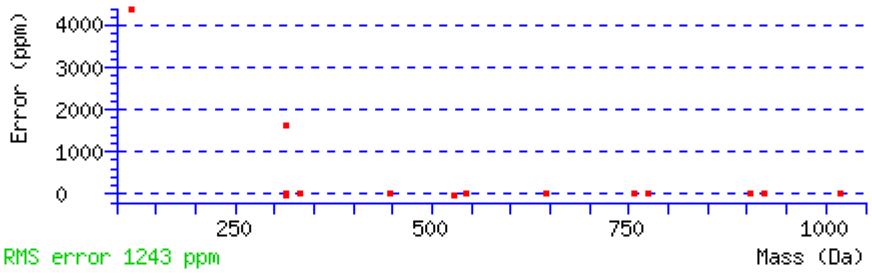
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1175.545883
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 53 **Expect:** 4.3e-005
Matches : 14/96 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	58.028740	29.518008					G							11
2	159.076419	80.041847			141.065854	71.036565	T	1119.531682	560.269479	1102.505133	551.756205	1101.521117	551.264197	10
3	256.129183	128.568230			238.118618	119.562947	P	***1018.484003***	509.745640	1001.457454	501.232365	1000.473438	500.740357	9
4	403.197597	202.102436			385.187032	193.097154	F	***921.431239***	461.219258	904.404690	452.705983	903.420674	452.213975	8
5	532.240190	266.623733			514.229625	257.618450	E	***774.362825***	387.685050	757.336276	379.171776	756.352260	378.679768	7
6	633.287869	317.147573			615.277304	308.142290	T	***645.320232***	323.163754	628.293683	314.650480	627.309667	314.158472	6
7	730.340633	365.673955			712.330068	356.668672	P	***544.272553***	272.639915	527.246004	264.126640	526.261988	263.634632	5
8	845.367576	423.187426			827.357011	414.182144	D	***447.219789***	224.113532	430.193240	215.600258	429.209224	215.108250	4
9	973.426154	487.216715	956.399605	478.703441	955.415589	478.211433	Q	***332.192846***	166.600061	315.166297	158.086786			3
10	1030.447618	515.727447	1013.421069	507.214172	1012.437053	506.722164	G	204.134268	102.570772	187.107719	94.057497			2
11							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of GTPFETPDQGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
53.2	1175.545883	0.000345	GTPFETPDQGK
6.4	1175.543365	0.002863	AAPFSMFSFR
2.4	1175.549225	-0.002997	TMEGPLPSNAK

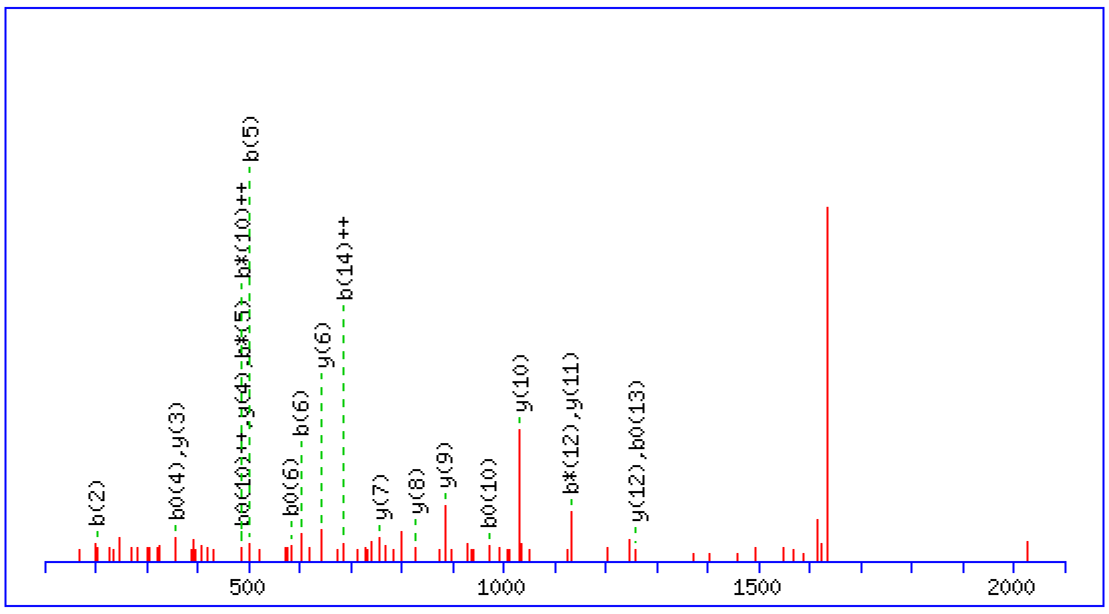
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DSDGQVFGALASEPLK**
Found in **OXR1_HUMAN**, Oxidation resistance protein 1 OS=Homo sapiens GN=OXR1 PE=1 SV=2

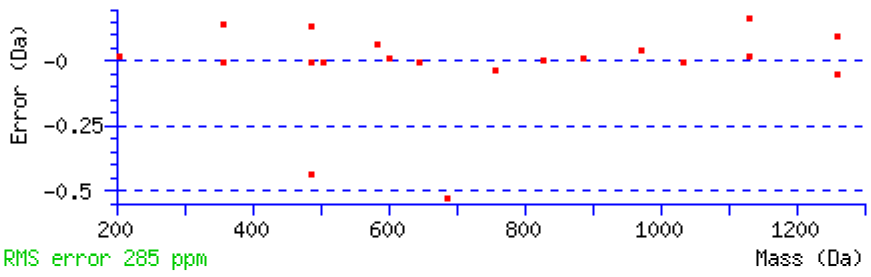
Match to Query 51525: 1632.798048 from(817.406300,2+) rtinseconds(3050) index(41386)
Title: Locus:1.1.1.2501.41
Data file 2011-11-10 - TFD - EP 4-1.mgf

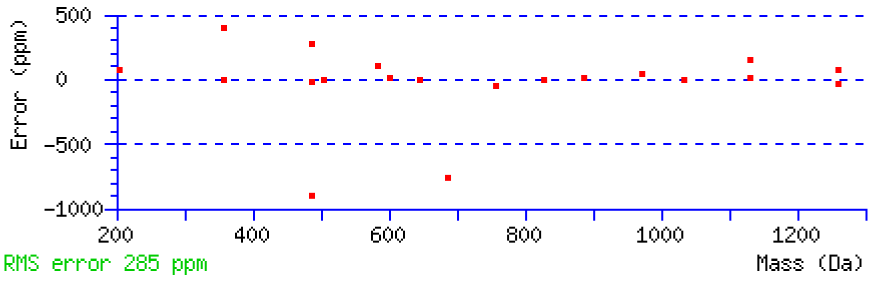
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1632.799515
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 41  Expect: 0.0013
Matches : 21/166 fragment ions using 42 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.034219	58.520748			98.023654	49.515465	D							16
2	**203.066247**	102.036761			185.055682	93.031479	S	1518.779850	759.893563	1501.753301	751.380289	1500.769285	750.888281	15
3	318.093190	159.550233			300.082625	150.544951	D	1431.747822	716.377549	1414.721273	707.864275	1413.737257	707.372267	14
4	375.114654	188.060965			357.104089	179.055682	G	1316.720879	658.864078	1299.694330	650.350803	1298.710314	649.858795	13
5	**503.173232**	252.090254	486.146683	243.576979	485.162667	243.084971	Q	***1259.699415***	630.353346	1242.672866	621.840071	1241.688850	621.348063	12
6	**602.241646**	301.624461	585.215097	293.111187	584.231081	292.619179	V	***1131.640837***	566.324057	1114.614288	557.810782	1113.630272	557.318774	11
7	749.310060	375.158668	732.283511	366.645394	731.299495	366.153386	F	***1032.572423***	516.789850	1015.545874	508.276575	1014.561858	507.784567	10
8	806.331524	403.669400	789.304975	395.156126	788.320959	394.664118	G	***885.504009***	443.255643	868.477460	434.742368	867.493444	434.250360	9
9	877.368638	439.187957	860.342089	430.674683	859.358073	430.182675	A	***828.482545***	414.744911	811.455996	406.231636	810.471980	405.739628	8
10	990.452702	495.729989	973.426153	487.216715	972.442137	486.724707	L	***757.445431***	379.226354	740.418882	370.713079	739.434866	370.221071	7
11	1061.489816	531.248546	1044.463267	522.735272	1043.479251	522.243264	A	***644.361367***	322.684322	627.334818	314.171047	626.350802	313.679039	6
12	1148.521844	574.764560	1131.495295	566.251286	1130.511279	565.759278	S	573.324253	287.165765	556.297704	278.652490	555.313688	278.160482	5
13	1277.564437	639.285857	1260.537888	630.772582	1259.553872	630.280574	E	***486.292225***	243.649751	469.265676	235.136476	468.281660	234.644468	4
14	1374.617201	687.812239	1357.590652	679.298964	1356.606636	678.806956	P	***357.249632***	179.128454	340.223083	170.615179			3
15	1487.701265	744.354271	1470.674716	735.840996	1469.690700	735.348988	L	260.196868	130.602072	243.170319	122.088797			2
16							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of DSDGQVFGALASEPLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.8	1632.799515	-0.001467	DSDGQVFGALASEPLK
4.0	1632.814148	-0.016100	VTADVTSAVMGNPVTR

Mascot: http://www.matrixscience.com/

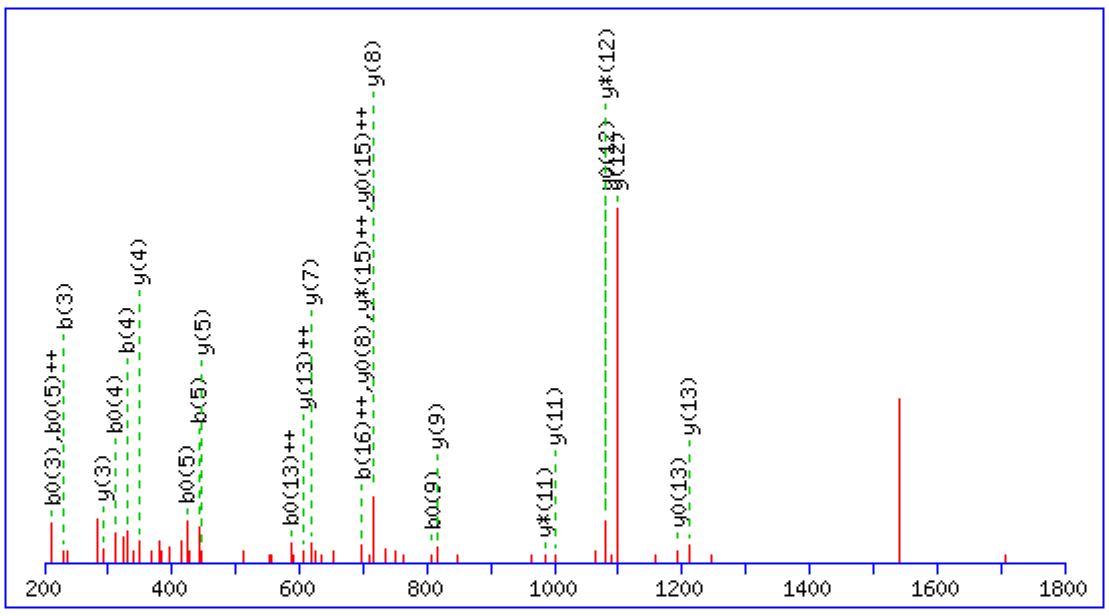
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of GATVLPANTPGNVGSGK
Found in OSBP1_HUMAN, Oxysterol-binding protein 1 OS=Homo sapiens GN=OSBP PE=1 SV=1

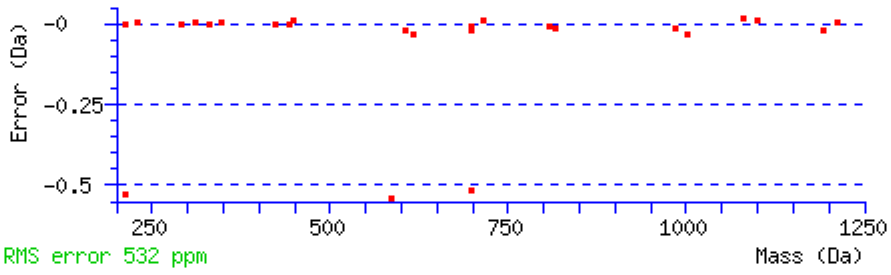
Match to Query 46458: 1538.808128 from(770.411340,2+) rtinseconds(1770) index(14798)
Title: Locus:1.1.1.2318.50
Data file 2011-11-12 - TFD - EP 5-2.mgf

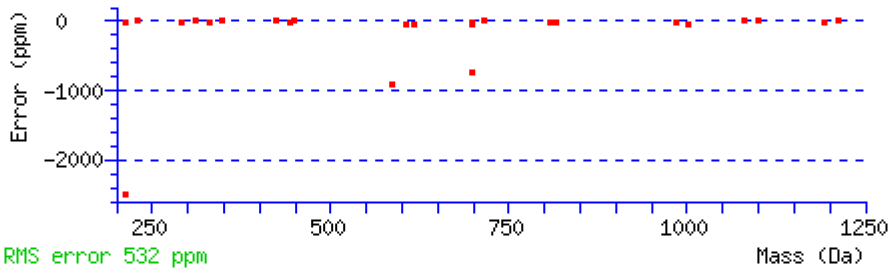
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1538.805283
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 48 **Expect:** 0.00015
Matches : 27/170 fragment ions using 44 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							17
2	129.065854	65.036565					A	1482.791084	741.899180	1465.764535	733.385906	1464.780519	732.893898	16
3	**230.113533**	115.560405			212.102968	106.555122	T	1411.753970	706.380623	1394.727421	697.867349	1393.743405	697.375340	15
4	**329.181947**	165.094612			311.171382	156.089329	V	1310.706291	655.856784	1293.679742	647.343509	1292.695726	646.851501	14
5	**442.266011**	221.636644			424.255446	212.631361	L	***1211.637877***	606.322577	1194.611328	597.809302	1193.627312	597.317294	13
6	539.318775	270.163026			521.308210	261.157743	P	***1098.553813***	549.780545	1081.527264	541.267270	1080.543248	540.775262	12
7	610.355889	305.681583			592.345324	296.676300	A	***1001.501049***	501.254163	984.474500	492.740888	983.490484	492.248880	11
8	724.398816	362.703046	707.372267	354.189772	706.388251	353.697764	N	930.463935	465.735606	913.437386	457.222331	912.453370	456.730323	10
9	825.446495	413.226886	808.419946	404.713611	807.435930	404.221603	T	***816.421008***	408.714142	799.394459	400.200868	798.410443	399.708860	9
10	922.499259	461.753268	905.472710	453.239993	904.488694	452.747985	P	***715.373329***	358.190303	698.346780	349.677028	697.362764	349.185020	8
11	979.520723	490.264000	962.494174	481.750725	961.510158	481.258717	G	***618.320565***	309.663921	601.294016	301.150646	600.310000	300.658638	7
12	1093.563650	547.285463	1076.537101	538.772189	1075.553085	538.280181	N	561.299101	281.153189	544.272552	272.639914	543.288536	272.147906	6
13	1192.632064	596.819670	1175.605515	588.306396	1174.621499	587.814388	V	***447.256174***	224.131725	430.229625	215.618450	429.245609	215.126443	5
14	1249.653528	625.330402	1232.626979	616.817128	1231.642963	616.325120	G	***348.187760***	174.597518	331.161211	166.084243	330.177195	165.592235	4
15	1336.685556	668.846416	1319.659007	660.333142	1318.674991	659.841134	S	***291.166296***	146.086786	274.139747	137.573512	273.155731	137.081504	3
16	1393.707020	697.357148	1376.680471	688.843874	1375.696455	688.351866	G	204.134268	102.570772	187.107719	94.057497			2
17							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of GATVLPANTPGNVGSGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.5	1538.805283	0.002845	GATVLPANTPGNVGSGK
11.1	1538.795349	0.012779	EQALRHPQLFER
3.4	1538.805237	0.002891	EAQPEAGAKKPPLR

Mascot: http://www.matrixscience.com/

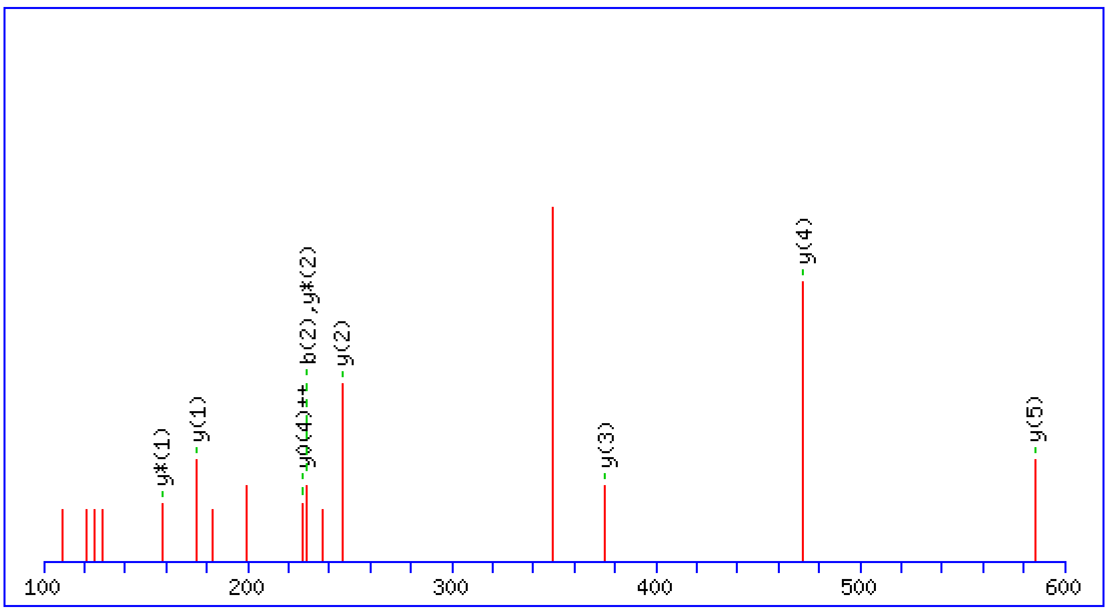
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IDLPEAR**
Found in **PAX6_HUMAN**, Paired box protein Pax-6 OS=Homo sapiens GN=PAX6 PE=1 SV=2

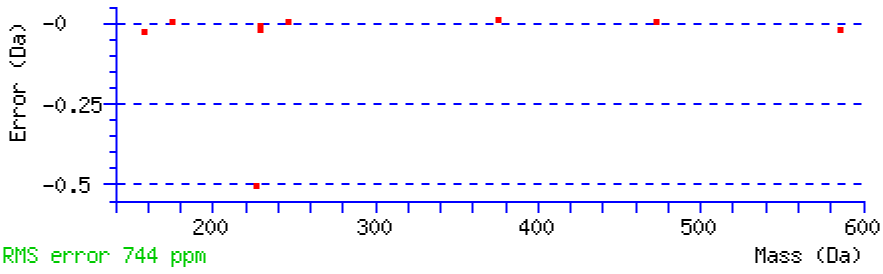
Match to Query 18556: 812.442608 from(407.228580,2+) rtinseconds(1773) index(507591)
Title: Locus:1.1.1.1006.4
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

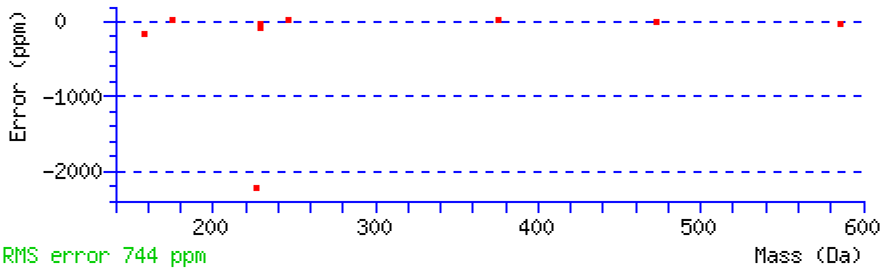
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 812.439194
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 45  Expect: 0.00084
Matches : 9/54 fragment ions using 10 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							7
2	229.118283	115.062779	211.107718	106.057497	D	700.362430	350.684853	683.335881	342.171579	682.351865	341.679571	6
3	342.202347	171.604811	324.191782	162.599529	L	***585.335487***	293.171382	568.308938	284.658107	567.324922	284.166099	5
4	439.255111	220.131193	421.244546	211.125911	P	***472.251423***	236.629349	455.224874	228.116075	454.240858	227.624067	4
5	568.297704	284.652490	550.287139	275.647208	E	***375.198659***	188.102967	358.172110	179.589693	357.188094	179.097685	3
6	639.334818	320.171047	621.324253	311.165765	A	***246.156066***	123.581671	229.129517	115.068396			2
7					R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of IDLPEAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.9	812.439194	0.003414	IDLPEAR
18.1	812.450424	-0.007816	NLNLPAR
17.5	812.439209	0.003399	LDPSPLR
9.1	812.440536	0.002072	ARPGWAR
5.5	812.450439	-0.007831	TLQQPAR
3.5	812.439194	0.003414	DLALEPR
3.5	812.439209	0.003399	DLAPLPR
1.8	812.439178	0.003430	ENLAAPAK
1.0	812.450455	-0.007847	GGSPVLGAR
0.9	812.439194	0.003414	EPVELAR

Mascot: http://www.matrixscience.com/

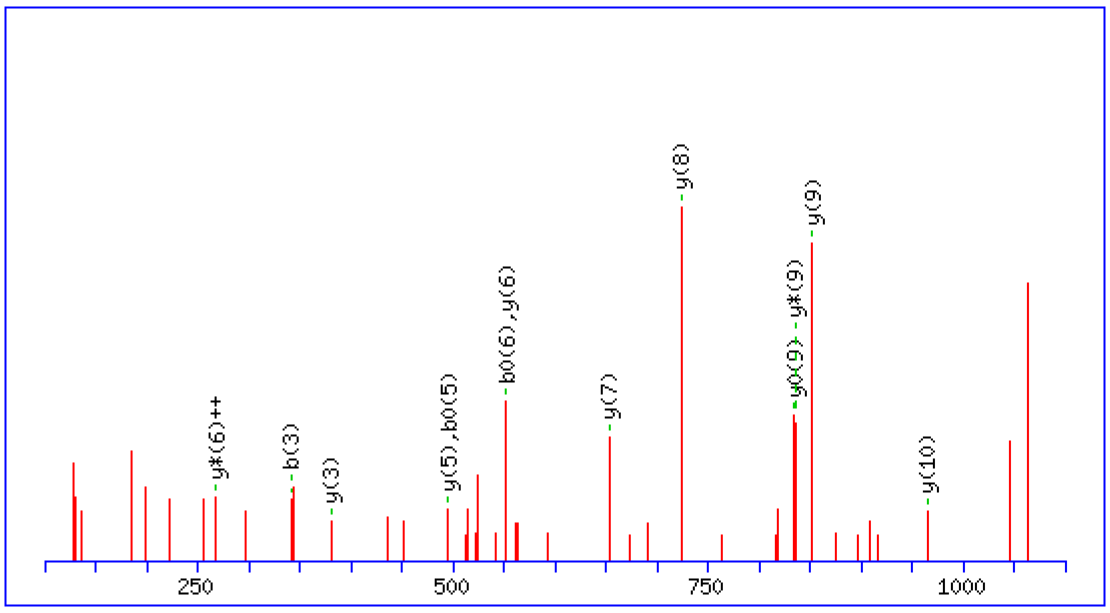
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VIQATGGGAYK**
Found in **PANK4_HUMAN**, Pantothenate kinase 4 OS=Homo sapiens GN=PANK4 PE=1 SV=1

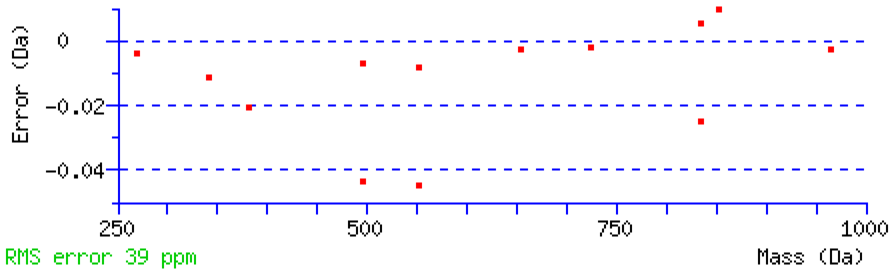
Match to Query 347064: 1063.564088 from(532.789320,2+) rtinseconds(1105) index(330616)
Title: Locus:1.1.1.754.25
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

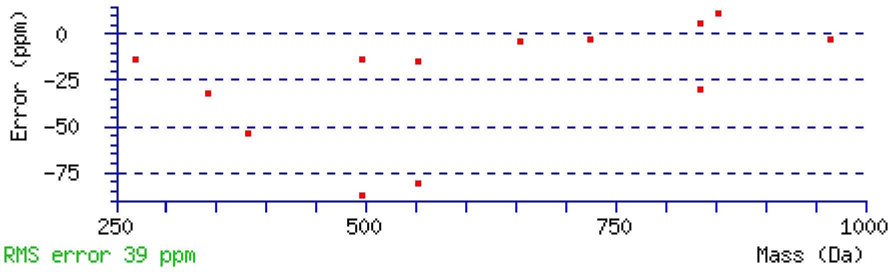
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1063.566208
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 38 **Expect:** 0.0023
Matches : 13/96 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							11
2	213.159754	107.083515					I	***965.505074***	483.256175	948.478525	474.742901	947.494509	474.250893	10
3	341.218332	171.112804	324.191783	162.599529			Q	***852.421010***	426.714143	835.394461	418.200869	834.410445	417.708861	9
4	412.255446	206.631361	395.228897	198.118086			A	***724.362432***	362.684854	707.335883	354.171580	706.351867	353.679572	8
5	513.303125	257.155201	496.276576	248.641926	495.292560	248.149918	T	***653.325318***	327.166297	636.298769	318.653023	635.314753	318.161015	7
6	570.324589	285.665933	553.298040	277.152658	552.314024	276.660650	G	***552.277639***	276.642458	535.251090	268.129183			6
7	627.346053	314.176665	610.319504	305.663390	609.335488	305.171382	G	***495.256175***	248.131726	478.229626	239.618451			5
8	684.367517	342.687397	667.340968	334.174122	666.356952	333.682114	G	438.234711	219.620994	421.208162	211.107719			4
9	755.404631	378.205954	738.378082	369.692679	737.394066	369.200671	A	***381.213247***	191.110262	364.186698	182.596987			3
10	918.467960	459.737618	901.441411	451.224344	900.457395	450.732336	Y	310.176133	155.591705	293.149584	147.078430			2
11							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of VIQATGGGAYK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.5	1063.566208	-0.002120	VIQATGGGAYK
10.0	1063.566177	-0.002089	VLQEEYRK

Mascot: http://www.matrixscience.com/

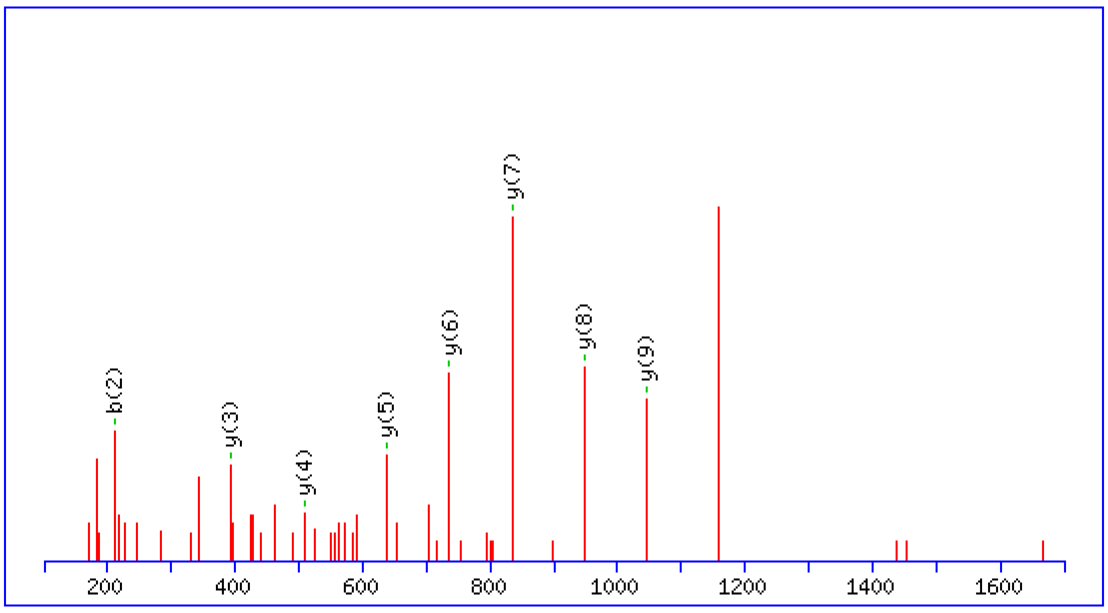
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LPLVVEDFVK**
Found in **PDDC1_HUMAN**, Parkinson disease 7 domain-containing protein 1 OS=Homo sapiens GN=PDDC1 PE=1 SV=1

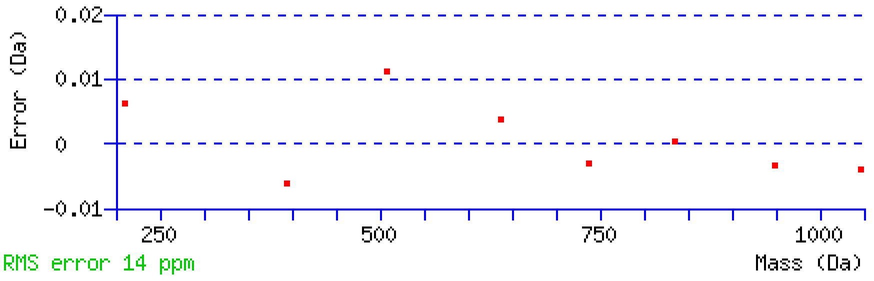
Match to Query 25780: 1157.670008 from(579.842280,2+) rtinseconds(3490) index(48234)
Title: Locus:1.1.1.2745.14
Data file 2011-11-13 - TFD - EP 7-5.mgf

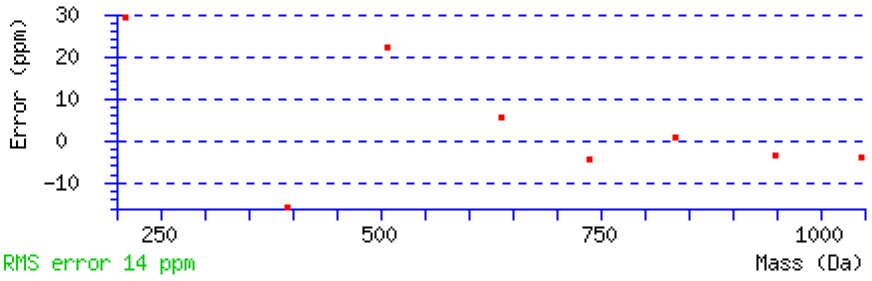
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1157.669617
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 64 **Expect:** 2.8e-006
Matches : 8/74 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							10
2	211.144104	106.075690			P	***1045.592824***	523.300050	1028.566275	514.786776	1027.582259	514.294768	9
3	324.228168	162.617722			L	***948.540060***	474.773668	931.513511	466.260394	930.529495	465.768386	8
4	423.296582	212.151929			V	***835.455996***	418.231636	818.429447	409.718361	817.445431	409.226353	7
5	522.364996	261.686136			V	***736.387582***	368.697429	719.361033	360.184154	718.377017	359.692146	6
6	651.407589	326.207433	633.397024	317.202150	E	***637.319168***	319.163222	620.292619	310.649948	619.308603	310.157940	5
7	766.434532	383.720904	748.423967	374.715622	D	***508.276575***	254.641925	491.250026	246.128651	490.266010	245.636643	4
8	913.502946	457.255111	895.492381	448.249828	F	***393.249632***	197.128454	376.223083	188.615179			3
9	1012.571360	506.789318	994.560795	497.784035	V	246.181218	123.594247	229.154669	115.080972			2
10					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of LPLVVEDFVK
(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	1157.669617	0.000391	LPLVVEDFVK

Mascot: http://www.matrixscience.com/

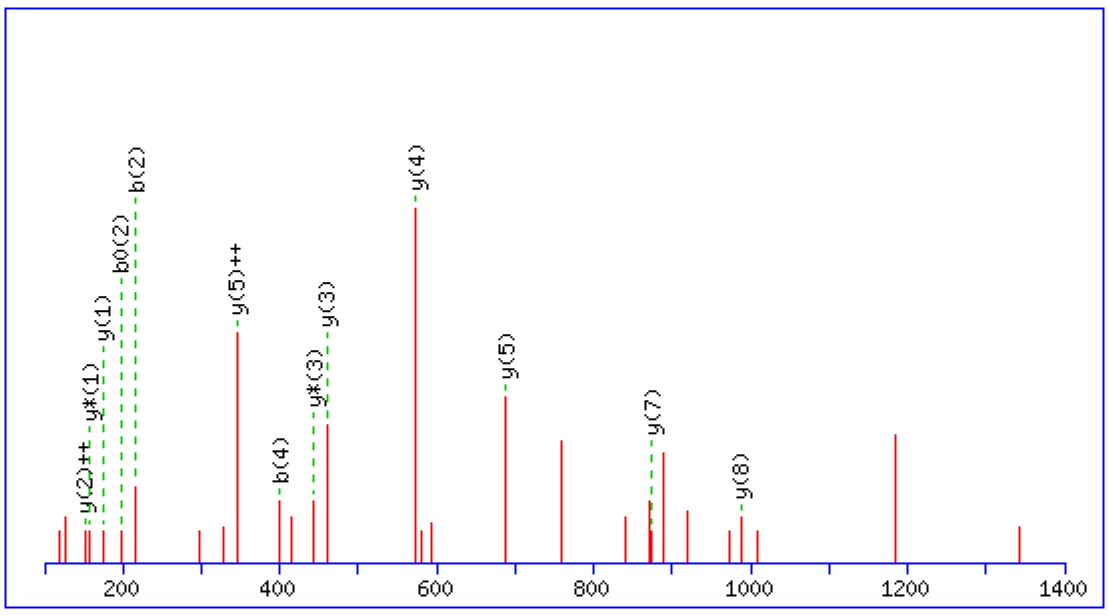
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TNLADDIRER**
Found in **PTHD3_HUMAN**, Patched domain-containing protein 3 OS=Homo sapiens GN=PTCHD3 PE=1 SV=2

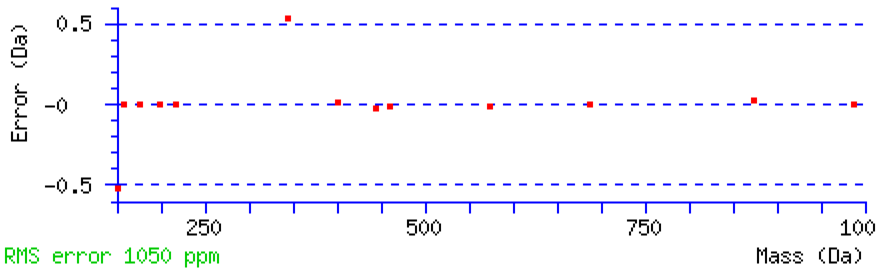
Match to Query 18114: 1201.601388 from(601.807970,2+) rtinseconds(1930) index(8958)
Title: Locus:1.1.1.2458.22
Data file 2011-11-14 - TFD - EP 8-8.mgf

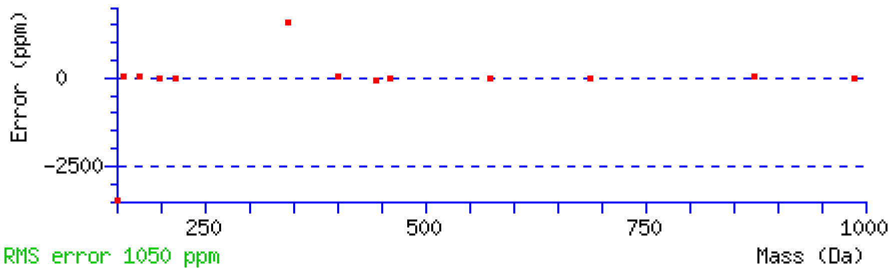
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1201.605087
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 34 **Expect:** 0.006
Matches : 13/104 fragment ions using 29 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							10
2	**216.097882**	108.552579	199.071333	100.039305	198.087317	99.547296	N	1101.564711	551.285994	1084.538162	542.772719	1083.554146	542.280711	9
3	329.181946	165.094611	312.155397	156.581336	311.171381	156.089328	L	***987.521784***	494.264530	970.495235	485.751256	969.511219	485.259248	8
4	**400.219060**	200.613168	383.192511	192.099893	382.208495	191.607885	A	***874.437720***	437.722498	857.411171	429.209224	856.427155	428.717216	7
5	515.246003	258.126640	498.219454	249.613365	497.235438	249.121357	D	803.400606	402.203941	786.374057	393.690667	785.390041	393.198659	6
6	630.272946	315.640111	613.246397	307.126836	612.262381	306.634828	D	***688.373663***	344.690470	671.347114	336.177195	670.363098	335.685187	5
7	743.357010	372.182143	726.330461	363.668868	725.346445	363.176860	I	***573.346720***	287.176998	556.320171	278.663724	555.336155	278.171716	4
8	899.458121	450.232698	882.431572	441.719424	881.447556	441.227416	R	***460.262656***	230.634966	443.236107	222.121692	442.252091	221.629684	3
9	1028.500714	514.753995	1011.474165	506.240721	1010.490149	505.748713	E	304.161545	152.584411	287.134996	144.071136	286.150980	143.579128	2
10							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of TNLADDIRER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.6	1201.605087	-0.003699	TNLADDIRER
11.0	1201.605087	-0.003699	SQELDNKNVR
8.6	1201.601273	0.000115	GKPEDVMPSVK
8.6	1201.593887	0.007501	GPPVTPSSEKR
4.5	1201.605103	-0.003715	SLQDEVSPRR
1.8	1201.593872	0.007516	QDTVELQNQK
1.3	1201.593857	0.007531	GKEEELQDVR
0.8	1201.597916	0.003472	GFDGLPGLPGEK
0.5	1201.601242	0.000146	EMAQGLLPEAK
0.3	1201.595215	0.006173	GKGAAGGSWQQR

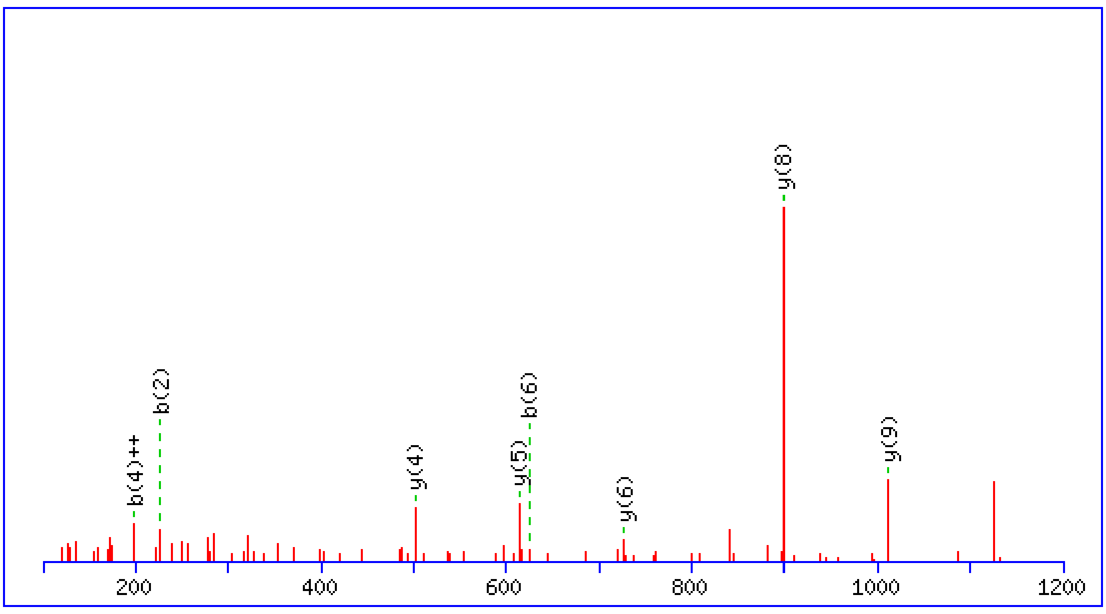
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLNGPPRGIR**
Found in **PDZD7_HUMAN**, PDZ domain-containing protein 7 OS=Homo sapiens GN=PDZD7 PE=1 SV=1

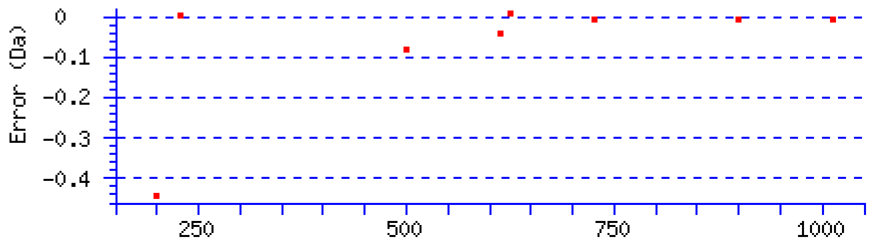
Match to Query 23951: 1123.641708 from(562.828130,2+) rtinseconds(2948) index(39571)
Title: Locus:1.1.1.2543.12
Data file 2011-11-10 - TFD - EP 3-1.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●

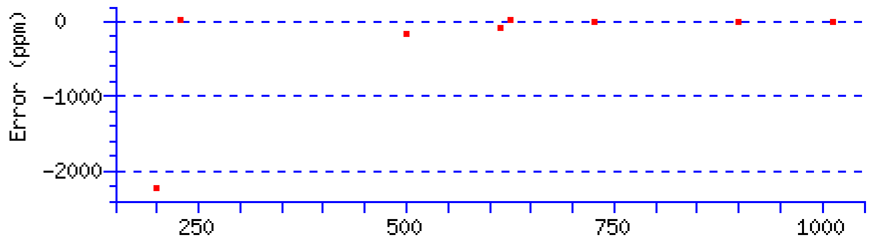


```
Monoisotopic mass of neutral peptide Mr(calc): 1123.646179
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P5      : Oxidation (P)
P6      : Oxidation (P)
Ions Score: 37  Expect: 0.0012
Matches : 8/68 fragment ions using 10 most intense peaks   (help)
```

#	b	b^{++}	b*	b*$^{++}$	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	114.091340	57.549308			L					10
2	227.175404	114.091340			L	*1011.569404*	506.288340	994.542855	497.775065	9
3	341.218331	171.112803	324.191782	162.599529	N	*898.485340*	449.746308	881.458791	441.233033	8
4	398.239795	199.623535	381.213246	191.110261	G	784.442413	392.724845	767.415864	384.211570	7
5	511.287474	256.147375	494.260925	247.634100	P	*727.420949*	364.214113	710.394400	355.700838	6
6	624.335153	312.671215	607.308604	304.157940	P	*614.373270*	307.690273	597.346721	299.176999	5
7	780.436264	390.721770	763.409715	382.208495	R	*501.325591*	251.166433	484.299042	242.653159	4
8	837.457728	419.232502	820.431179	410.719227	G	345.224480	173.115878	328.197931	164.602603	3
9	950.541792	475.774534	933.515243	467.261259	I	288.203016	144.605146	271.176467	136.091871	2
10					R	175.118952	88.063114	158.092403	79.549839	1



RMS error 786 ppm



RMS error 786 ppm

NCBI **BLAST** search of LLNGPPRGIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.4	1123.638947	0.002761	IIGNLLYYR
36.8	1123.646179	-0.004471	LLNGPPRGIR
5.3	1123.634949	0.006759	INIGPEVVQR
4.6	1123.646179	-0.004471	LLTHRTLDR
1.4	1123.638962	0.002746	LILDLSHWK
1.3	1123.634918	0.006790	LLEEHSRIK
1.0	1123.631088	0.010620	LLSKFEMIK

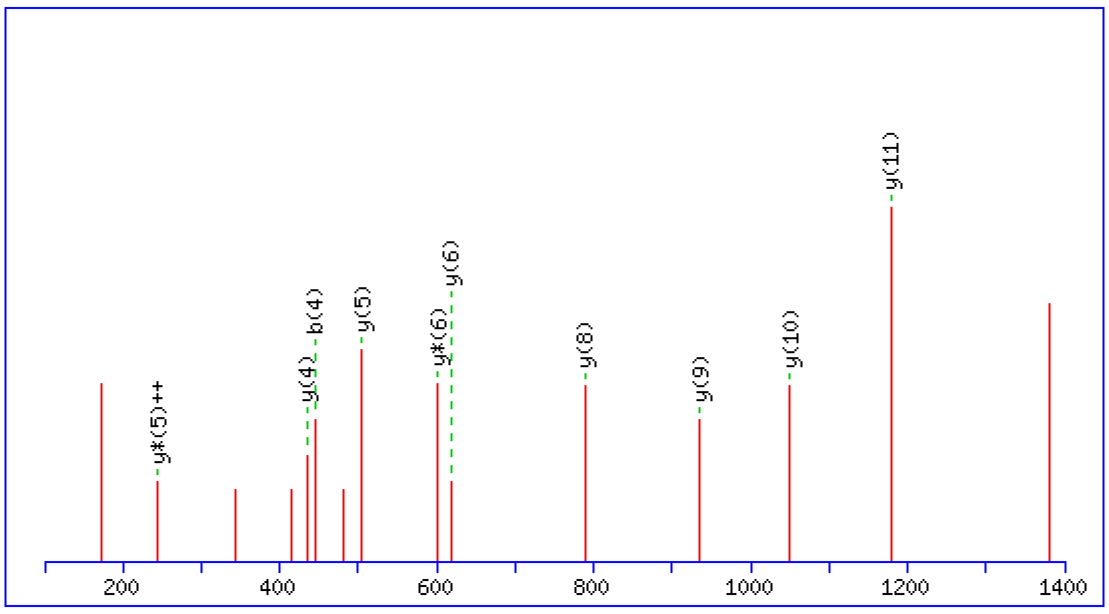
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TVENFVALATGEK**
Found in **PPIC_HUMAN**, Peptidyl-prolyl cis-trans isomerase C OS=Homo sapiens GN=PPIC PE=1 SV=1

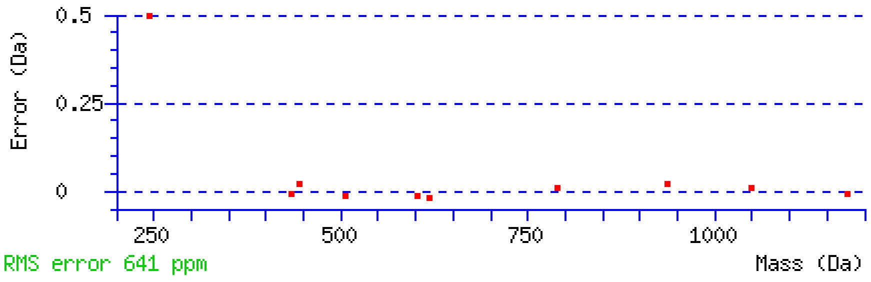
Match to Query 45659: 1377.712728 from(689.863640,2+) rtinseconds(3181) index(42857)
Title: Locus:1.1.1.2467.37
Data file 2011-11-10 - TFD - EP 4-6.mgf

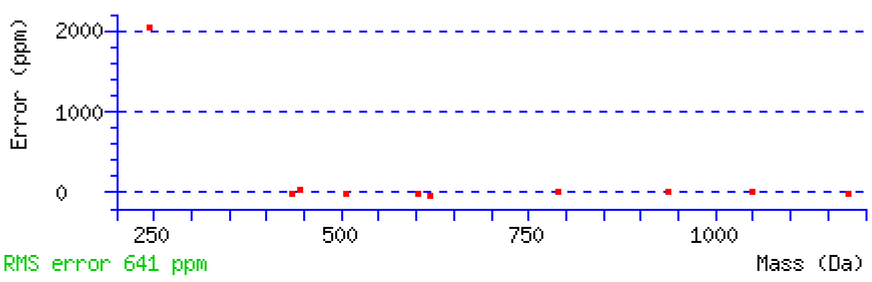
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1377.713989
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 53 **Expect:** 5.2e-005
Matches : 10/136 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							13
2	201.123369	101.065322			183.112804	92.060040	V	1277.673594	639.340435	1260.647045	630.827160	1259.663029	630.335152	12
3	330.165962	165.586619			312.155397	156.581336	E	***1178.605180***	589.806228	1161.578631	581.292953	1160.594615	580.800945	11
4	444.208889	222.608082	427.182340	214.094808	426.198324	213.602800	N	***1049.562587***	525.284931	1032.536038	516.771657	1031.552022	516.279649	10
5	591.277303	296.142290	574.250754	287.629015	573.266738	287.137007	F	***935.519660***	468.263468	918.493111	459.750193	917.509095	459.258185	9
6	690.345717	345.676497	673.319168	337.163222	672.335152	336.671214	V	***788.451246***	394.729261	771.424697	386.215986	770.440681	385.723978	8
7	761.382831	381.195054	744.356282	372.681779	743.372266	372.189771	A	689.382832	345.195054	672.356283	336.681779	671.372267	336.189771	7
8	874.466895	437.737086	857.440346	429.223811	856.456330	428.731803	L	***618.345718***	309.676497	601.319169	301.163222	600.335153	300.671214	6
9	945.504009	473.255643	928.477460	464.742368	927.493444	464.250360	A	***505.261654***	253.134465	488.235105	244.621190	487.251089	244.129182	5
10	1046.551688	523.779482	1029.525139	515.266208	1028.541123	514.774200	T	***434.224540***	217.615908	417.197991	209.102633	416.213975	208.610625	4
11	1103.573152	552.290214	1086.546603	543.776940	1085.562587	543.284931	G	333.176861	167.092068	316.150312	158.578794	315.166296	158.086786	3
12	1232.615745	616.811510	1215.589196	608.298236	1214.605180	607.806228	E	276.155397	138.581336	259.128848	130.068062	258.144832	129.576054	2
13							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of TVENFVALATGEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
53.4	1377.713989	-0.001261	TVENFVALATGEK
7.3	1377.707458	0.005270	QLYVLGSPAMQR
2.6	1377.700027	0.012701	LSERENQYALR
0.7	1377.707443	0.005285	LLQEKFPNMSR
0.6	1377.718689	-0.005961	SPAMSGGIFAIRR

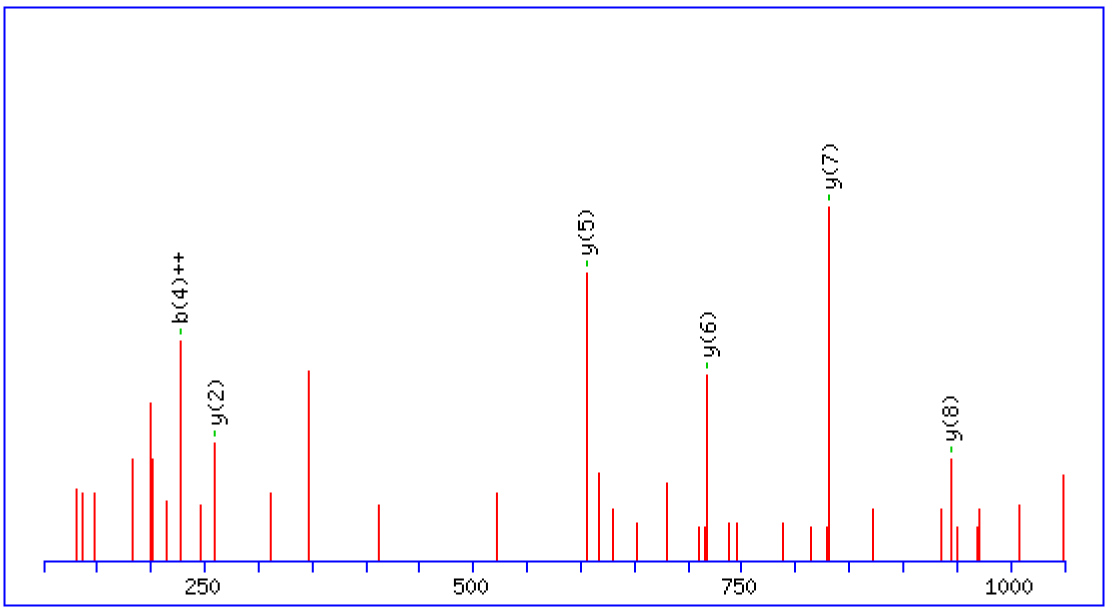
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILLITEDLK**
Found in **PPID_HUMAN**, Peptidyl-prolyl cis-trans isomerase D OS=Homo sapiens GN=PPID PE=1 SV=3

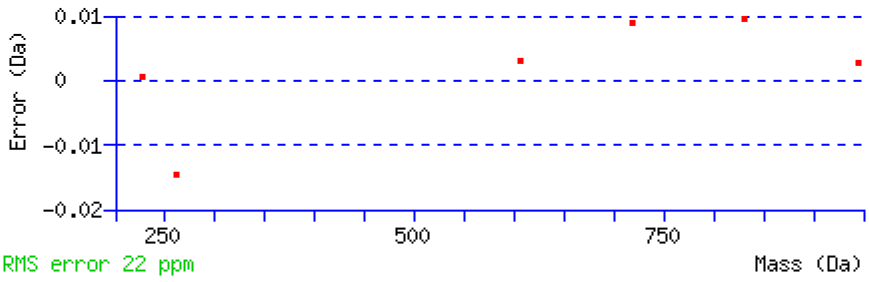
Match to Query 19271: 1056.640968 from(529.327760,2+) rtinseconds(2960) index(40503)
Title: Locus:1.1.1.2555.7
Data file 2011-11-13 - TFD - EP 7-4.mgf

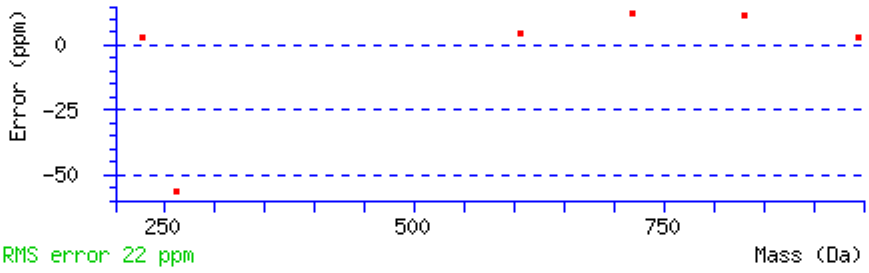
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1056.643036
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 31  Expect: 0.0011
Matches : 7/68 fragment ions using 10 most intense peaks   (help)
```

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308			I							9
2	227.175404	114.091340			L	*944.566275*	472.786776	927.539726	464.273501	926.555710	463.781493	8
3	340.259468	170.633372			L	*831.482211*	416.244744	814.455662	407.731469	813.471646	407.239461	7
4	453.343532	227.175404			I	*718.398147*	359.702712	701.371598	351.189437	700.387582	350.697429	6
5	554.391211	277.699244	536.380646	268.693961	T	*605.314083*	303.160680	588.287534	294.647405	587.303518	294.155397	5
6	683.433804	342.220540	665.423239	333.215258	E	504.266404	252.636840	487.239855	244.123565	486.255839	243.631557	4
7	798.460747	399.734012	780.450182	390.728729	D	375.223811	188.115543	358.197262	179.602269	357.213246	179.110261	3
8	911.544811	456.276044	893.534246	447.270761	L	*260.196868*	130.602072	243.170319	122.088798			2
9					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of ILLITEDLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.7	1056.643036	-0.002068	ILLITEDLK
17.8	1056.647736	-0.006768	LLLRCQLK
17.5	1056.633179	0.007789	LPLPVFTVR
4.5	1056.636505	0.004463	LMALLGQALK

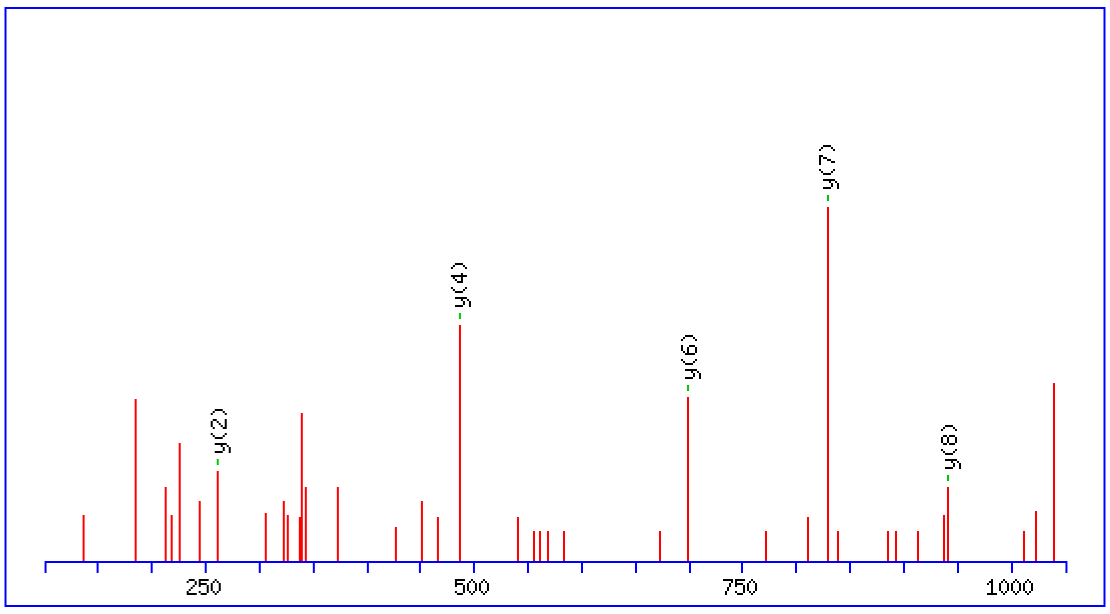
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLEVNPQNK**
Found in **FKBP5_HUMAN**, Peptidyl-prolyl cis-trans isomerase FKBP5 OS=Homo sapiens GN=FKBP5 PE=1 SV=2

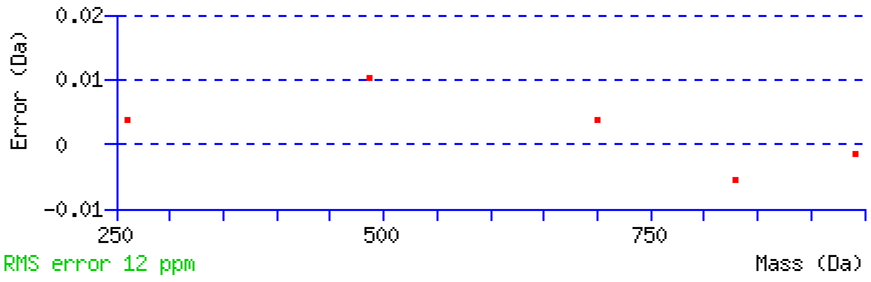
Match to Query 12439: 1039.563648 from(520.789100,2+) rtinseconds(1152) index(5868)
Title: Locus:1.1.1.1950.30
Data file 2011-11-12 - TFD - EP 5-3.mgf

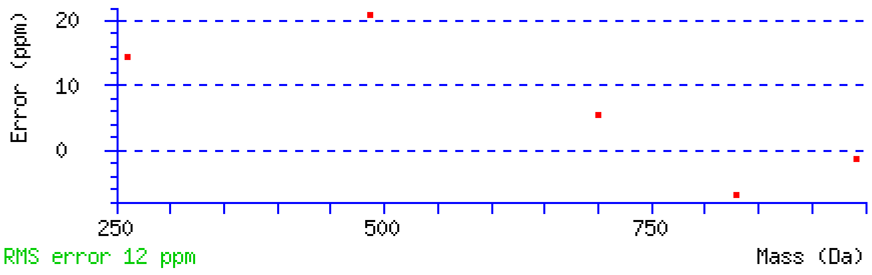
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1039.566193
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 33  Expect: 0.0044
Matches : 5/72 fragment ions using 9 most intense peaks   (help)
```

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	100.075690	50.541483					**V**							9
2	213.159754	107.083515					**L**	*941.505071*	471.256174	924.478522	462.742899	923.494506	462.250891	8
3	342.202347	171.604811			324.191782	162.599529	**E**	*828.421007*	414.714142	811.394458	406.200867	810.410442	405.708859	7
4	441.270761	221.139018			423.260196	212.133736	**V**	*699.378414*	350.192845	682.351865	341.679571			6
5	555.313688	278.160482	538.287139	269.647208	537.303123	269.155200	**N**	600.310000	300.658638	583.283451	292.145364			5
6	652.366452	326.686864	635.339903	318.173590	634.355887	317.681582	**P**	*486.267073*	243.637174	469.240524	235.123900			4
7	780.425030	390.716153	763.398481	382.202879	762.414465	381.710871	**Q**	389.214309	195.110792	372.187760	186.597518			3
8	894.467957	447.737617	877.441408	439.224342	876.457392	438.732334	**N**	*261.155731*	131.081503	244.129182	122.568229			2
9							**K**	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of VLEVNPQNK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.6	1039.566193	-0.002545	VLEVNPQNK
15.4	1039.554977	0.008671	VPEKPPTPK
9.3	1039.554977	0.008671	VPEKPPTPK
9.3	1039.554977	0.008671	VPEKPPTPK
9.0	1039.559677	0.003971	VLMQVHASR
7.0	1039.566208	-0.002560	VPGIPGEISR
6.6	1039.566208	-0.002560	DPVGLQLGNK

{MATRIX SCIENCE}

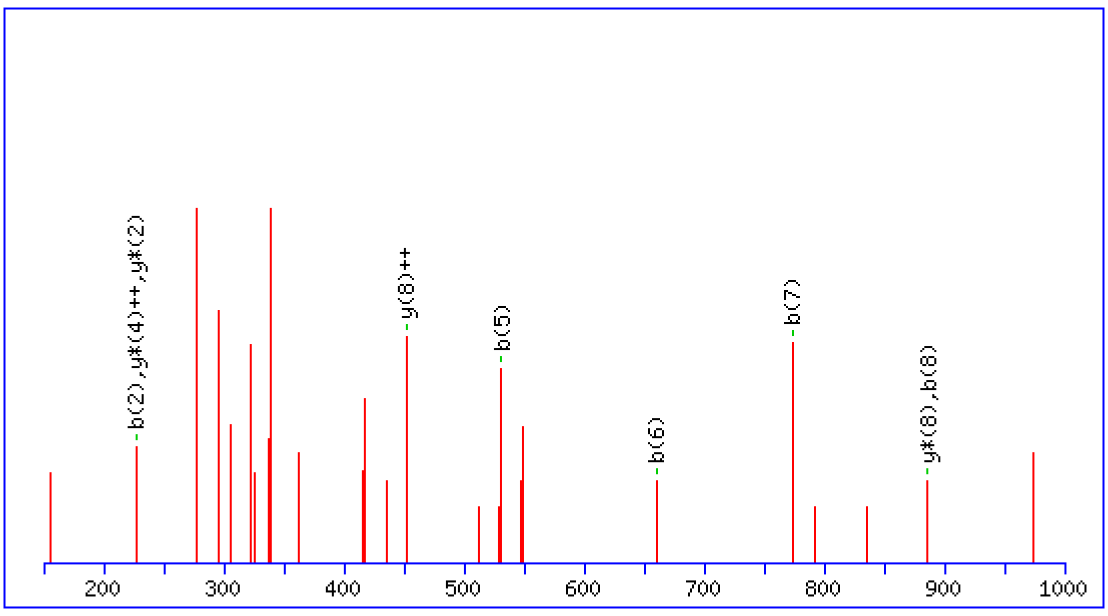
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILSCGELIPK**
Found in **PPIG_HUMAN**, Peptidyl-prolyl cis-trans isomerase G OS=Homo sapiens GN=PPIG PE=1 SV=2

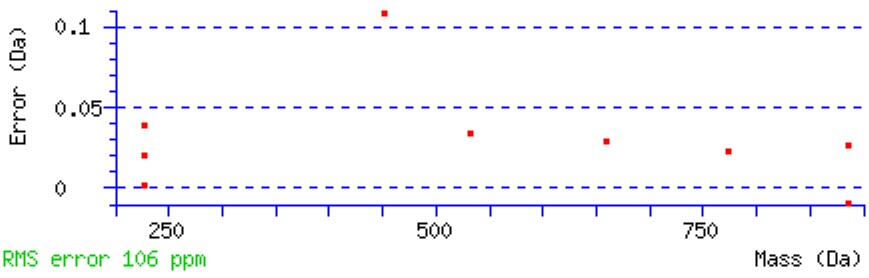
Match to Query 431555: 1128.612388 from(565.313470,2+) rtinseconds(3149) index(450743)
Title: Locus:1.1.1.1544.9
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

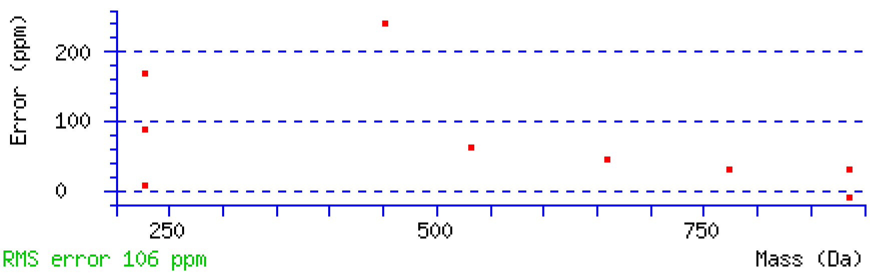
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1128.621262
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.005
Matches : 9/78 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							10
2	***227.175404***	114.091340			L	1016.544494	508.775885	999.517945	500.262611	998.533929	499.770603	9
3	314.207432	157.607354	296.196867	148.602071	S	903.460430	452.233853	886.433881	443.720579	885.449865	443.228571	8
4	474.238081	237.622679	456.227516	228.617396	C	816.428402	408.717839	799.401853	400.204565	798.417837	399.712557	7
5	***531.259545***	266.133411	513.248980	257.128128	G	656.397753	328.702515	639.371204	320.189240	638.387188	319.697232	6
6	***660.302138***	330.654707	642.291573	321.649425	E	599.376289	300.191783	582.349740	291.678508	581.365724	291.186500	5
7	***773.386202***	387.196739	755.375637	378.191457	L	470.333696	235.670486	453.307147	227.157211			4
8	***886.470266***	443.738771	868.459701	434.733489	I	357.249632	179.128454	340.223083	170.615179			3
9	983.523030	492.265153	965.512465	483.259871	P	244.165568	122.586422	227.139019	114.073147			2
10					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of ILSCGELIPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.0	1128.621262	-0.008874	ILSCGELIPK
8.0	1128.613861	-0.001473	DQLELDRLK
7.1	1128.613861	-0.001473	LQDLEVREK
7.1	1128.617905	-0.005517	FVNLGIEPPK
6.0	1128.602646	0.009742	TDVEKSLPPK
5.8	1128.621262	-0.008874	LPQITEIGMK
5.8	1128.621277	-0.008889	QLPPTVISMK
4.2	1128.621277	-0.008889	PNILVLGAAVM
1.4	1128.621262	-0.008874	PAGLIAGASLLM
0.7	1128.617889	-0.005501	WIGELQLSIA

Mascot: http://www.matrixscience.com/

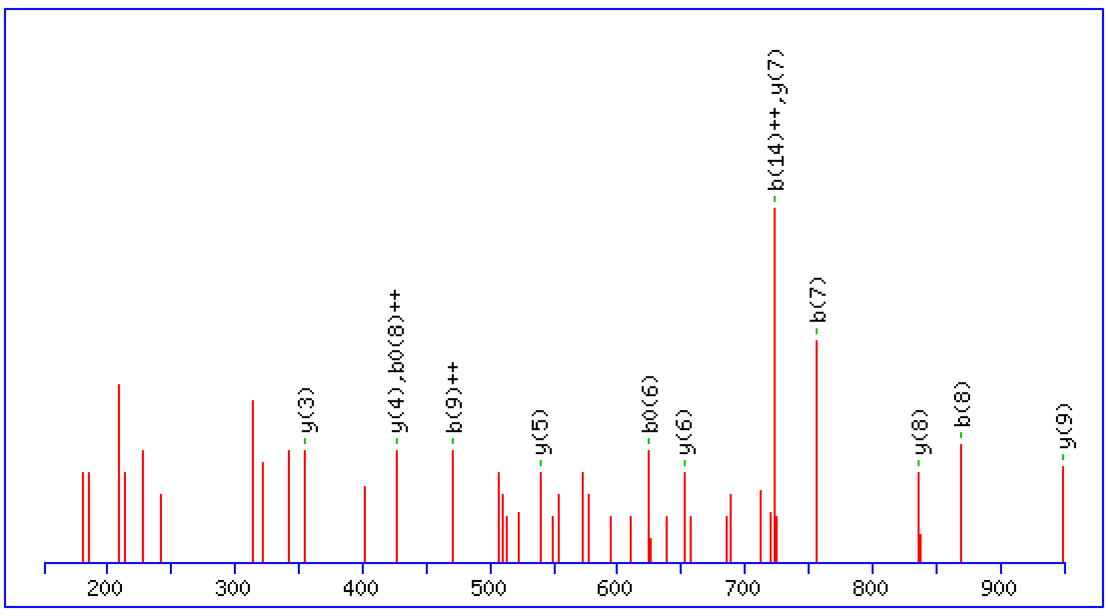
Mascot Search Results

Peptide View

MS/MS Fragmentation of **APDEETLIALLAHAK**
Found in **PTH2_HUMAN**, Peptidyl-tRNA hydrolase 2, mitochondrial OS=Homo sapiens GN=PTRH2 PE=1 SV=1

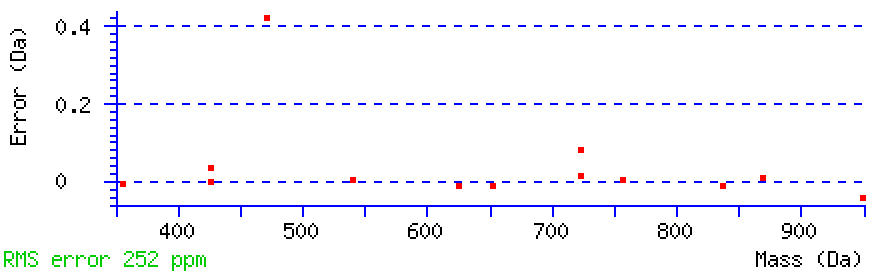
Match to Query 48247: 1590.858942 from(531.293590,3+) rtinseconds(3685) index(51070)
Title: Locus:1.1.1.2553.6
Data file 2011-11-12 - TFD - EP 6-6.mgf

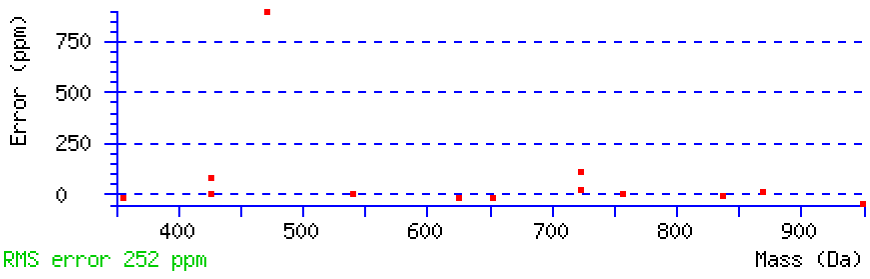
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1590.861679
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 52 **Expect:** 5.2e-005
Matches : 13/118 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			A							15
2	169.097154	85.052215			P	1520.831886	760.919581	1503.805337	752.406307	1502.821321	751.914298	14
3	284.124097	142.565687	266.113532	133.560404	D	1423.779122	712.393199	1406.752573	703.879925	1405.768557	703.387916	13
4	413.166690	207.086983	395.156125	198.081701	E	1308.752179	654.879727	1291.725630	646.366453	1290.741614	645.874445	12
5	542.209283	271.608280	524.198718	262.602997	E	1179.709586	590.358431	1162.683037	581.845157	1161.699021	581.353148	11
6	643.256962	322.132119	625.246397	313.126837	T	1050.666993	525.837134	1033.640444	517.323860	1032.656428	516.831852	10
7	**756.341026**	378.674151	738.330461	369.668869	L	***949.619314***	475.313295	932.592765	466.800020			9
8	**869.425090**	435.216183	851.414525	426.210901	I	***836.535250***	418.771263	819.508701	410.257988			8
9	940.462204	**470.734740**	922.451639	461.729458	A	***723.451186***	362.229231	706.424637	353.715956			7
10	1053.546268	527.276772	1035.535703	518.271490	L	***652.414072***	326.710674	635.387523	318.197399			6
11	1166.630332	583.818804	1148.619767	574.813521	L	***539.330008***	270.168642	522.303459	261.655367			5
12	1237.667446	619.337361	1219.656881	610.332078	A	***426.245944***	213.626610	409.219395	205.113335			4
13	1374.726358	687.866817	1356.715793	678.861534	H	***355.208830***	178.108053	338.182281	169.594778			3
14	1445.763472	**723.385374**	1427.752907	714.380091	A	218.149918	109.578597	201.123369	101.065322			2
15					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of APDEETLIALLAHAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.8	1590.861679	-0.002737	APDEETLIALLAHAK
8.0	1590.850449	0.008493	ILSESLLTPAEYQK
5.6	1590.859009	-0.000067	QTLNRPPAAPNQLR
4.5	1590.861725	-0.002783	DVPKPISNGLPPTPK
3.2	1590.859009	-0.000067	SLQRDPRPAGPAQAK
2.1	1590.859009	-0.000067	QTLNRPPAAPNQLR
1.4	1590.843979	0.014963	ALMTGSLPGFVDVIR
1.4	1590.855179	0.003763	SVAHGQAPEMPLVKK
0.8	1590.859009	-0.000067	QTLNRPPAAPNQLR
0.4	1590.861710	-0.002768	KTTSNTPPITGAIYK

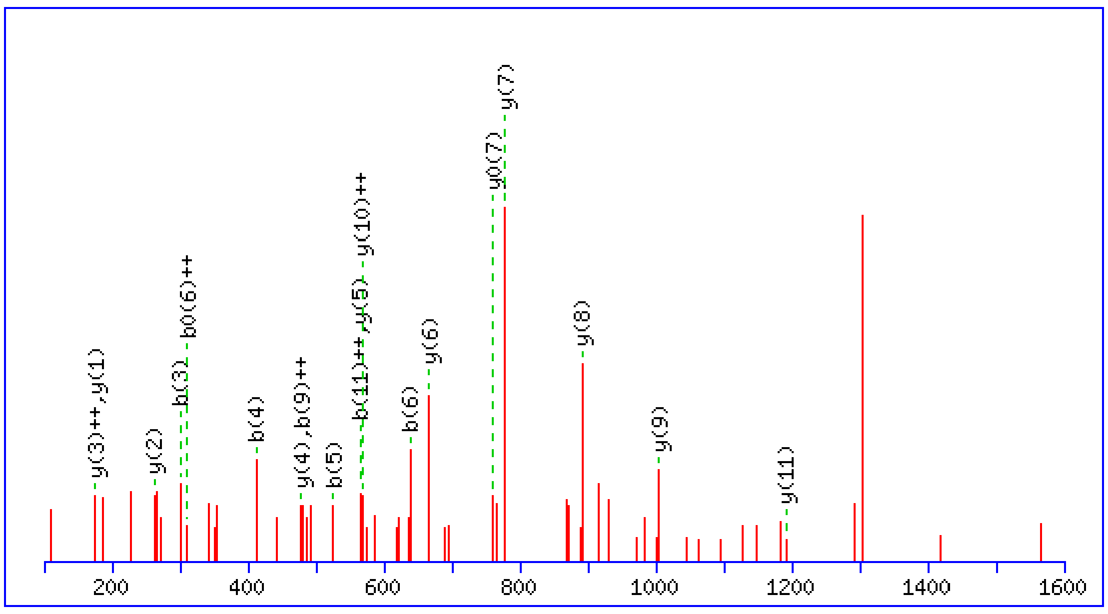
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGELILTSESSR**
Found in **ICT1_HUMAN**, Peptidyl-tRNA hydrolase ICT1, mitochondrial OS=Homo sapiens GN=ICT1 PE=1 SV=1

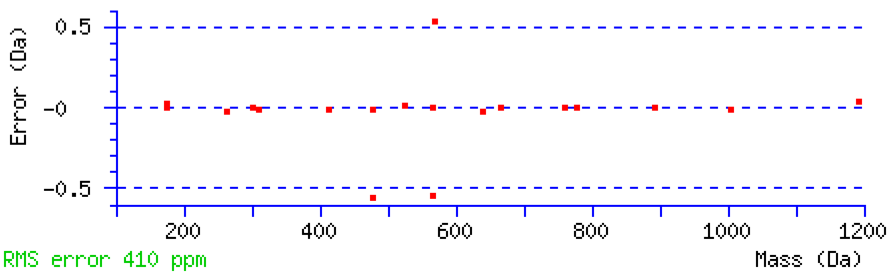
Match to Query 34875: 1303.696528 from(652.855540,2+) rtinseconds(2459) index(28260)
Title: Locus:1.1.1.2227.42
Data file 2011-11-13 - TFD - EP 7-6.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●

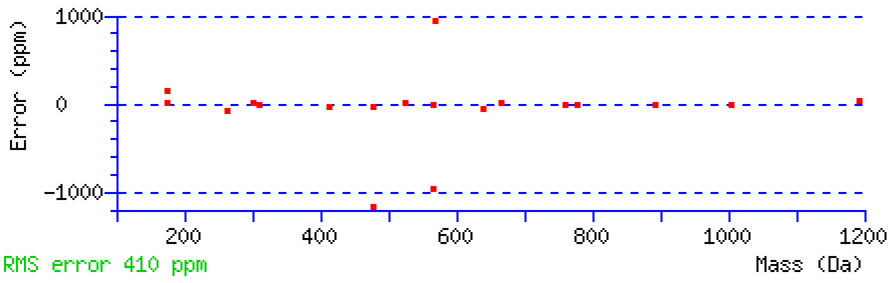


```
Monoisotopic mass of neutral peptide Mr(calc): 1303.698318
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 48  Expect: 0.00014
Matches : 19/104 fragment ions using 42 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							12
2	171.112804	86.060040			G	***1191.621557***	596.314417	1174.595008	587.801142	1173.610992	587.309134	11
3	**300.155397**	150.581336	282.144832	141.576054	E	1134.600093	567.803685	1117.573544	559.290410	1116.589528	558.798402	10
4	**413.239461**	207.123369	395.228896	198.118086	L	***1005.557500***	503.282388	988.530951	494.769114	987.546935	494.277106	9
5	**526.323525**	263.665401	508.312960	254.660118	I	***892.473436***	446.740356	875.446887	438.227082	874.462871	437.735074	8
6	**639.407589**	320.207433	621.397024	311.202150	L	***779.389372***	390.198324	762.362823	381.685050	761.378807	381.193042	7
7	740.455268	370.731272	722.444703	361.725990	T	***666.305308***	333.656292	649.278759	325.143018	648.294743	324.651010	6
8	827.487296	414.247286	809.476731	405.242004	S	***565.257629***	283.132453	548.231080	274.619178	547.247064	274.127170	5
9	956.529889	478.768583	938.519324	469.763300	E	***478.225601***	239.616438	461.199052	231.103164	460.215036	230.611156	4
10	1043.561917	522.284597	1025.551352	513.279314	S	349.183008	175.095142	332.156459	166.581867	331.172443	166.089859	3
11	1130.593945	565.800611	1112.583380	556.795328	S	***262.150980***	131.579128	245.124431	123.065854	244.140415	122.573846	2
12					R	***175.118952***	88.063114	158.092403	79.549839			1



RMS error 410 ppm



RMS error 410 ppm

NCBI **BLAST** search of LGELILTSESSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.5	1303.698318	-0.001790	LGELILTSESSR
22.7	1303.688431	0.008097	ISVLEPPQEHR
14.9	1303.703049	-0.006521	GRVVNISSMLGR
0.4	1303.703033	-0.006505	LVSLSACGRTAR
0.4	1303.699722	-0.003194	VTVPSHTVHGVR
0.0	1303.702347	-0.005819	IISEPVKYPDK

Mascot: http://www.matrixscience.com/

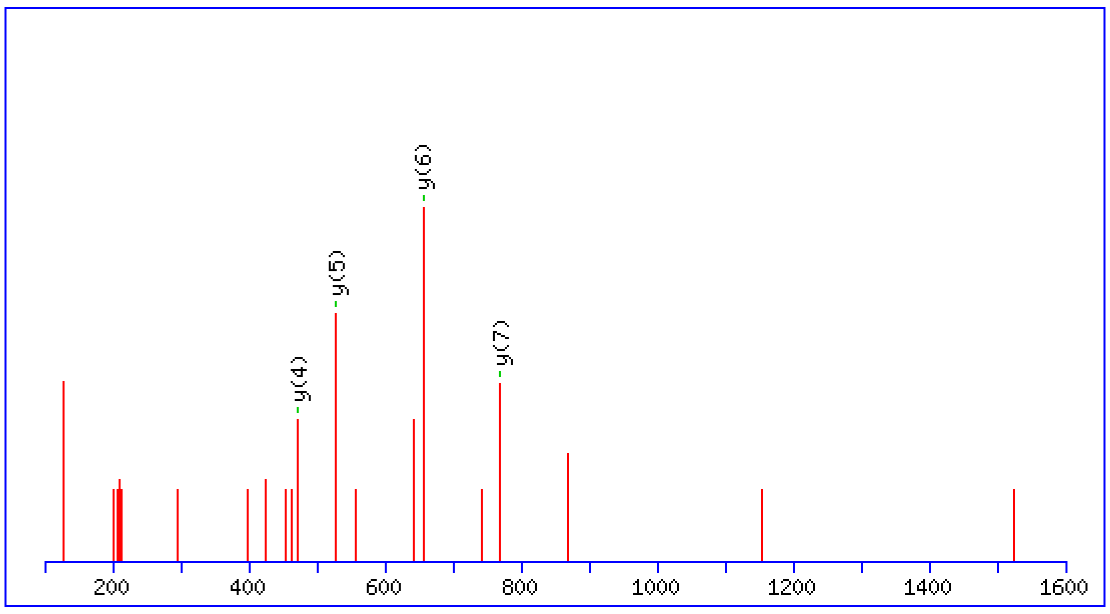
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VPKGPEVK**
Found in **PRAX_HUMAN**, Periaxin OS=Homo sapiens GN=PRX PE=1 SV=2

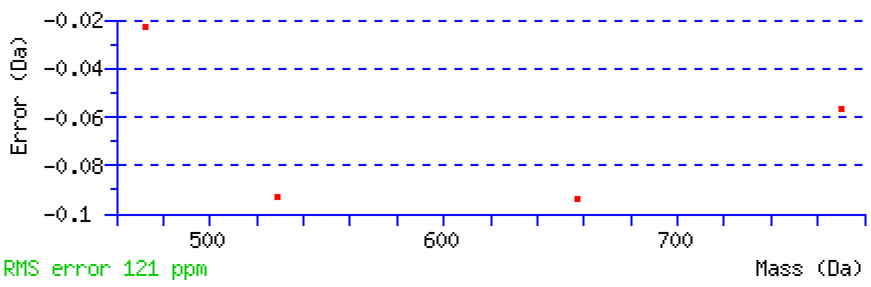
Match to Query 5855: 868.504568 from(435.259560,2+) rtinseconds(847) index(639)
Title: Locus:1.1.1.1642.8
Data file 2011-11-14 - TFD - EP 8-5.mgf

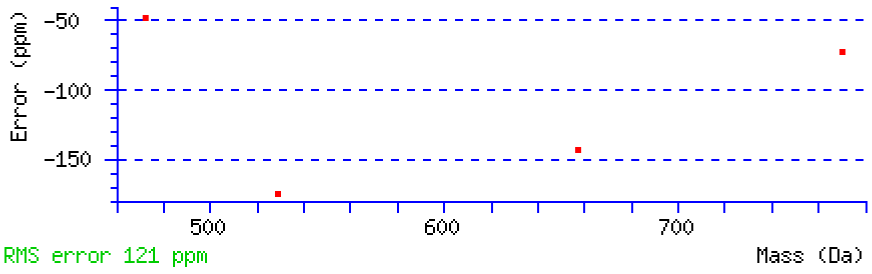
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 868.501816
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P2      : Oxidation (P)
Ions Score: 31  Expect: 0.0047
Matches : 4/66 fragment ions using 7 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							8
2	213.123369	107.065322					P	*770.440681*	385.723979	753.414132	377.210704	752.430116	376.718696	7
3	341.218332	171.112804	324.191783	162.599529			K	*657.393002*	329.200139	640.366453	320.686865	639.382437	320.194857	6
4	398.239796	199.623536	381.213247	191.110261			G	*529.298039*	265.152658	512.271490	256.639383	511.287474	256.147375	5
5	495.292560	248.149918	478.266011	239.636643			P	*472.276575*	236.641925	455.250026	228.128651	454.266010	227.636643	4
6	624.335153	312.671215	607.308604	304.157940	606.324588	303.665932	E	375.223811	188.115543	358.197262	179.602269	357.213246	179.110261	3
7	723.403567	362.205422	706.377018	353.692147	705.393002	353.200139	V	246.181218	123.594247	229.154669	115.080972			2
8							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of VPKGPEVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.3	868.501816	0.002752	VPKGPEVK
10.7	868.513031	-0.008463	LNIGPAIR
8.5	868.513031	-0.008463	VKPREPK
6.2	868.513031	-0.008463	DPKQIIR
5.8	868.501801	0.002767	VIPELNGK
5.8	868.513046	-0.008478	VIRPQPK
5.8	868.501816	0.002752	VITAQPPK
5.8	868.501816	0.002752	VITAQPPK
5.8	868.513046	-0.008478	VLGLQAPR
5.8	868.505844	-0.001276	VLYVFTK

Mascot: http://www.matrixscience.com/

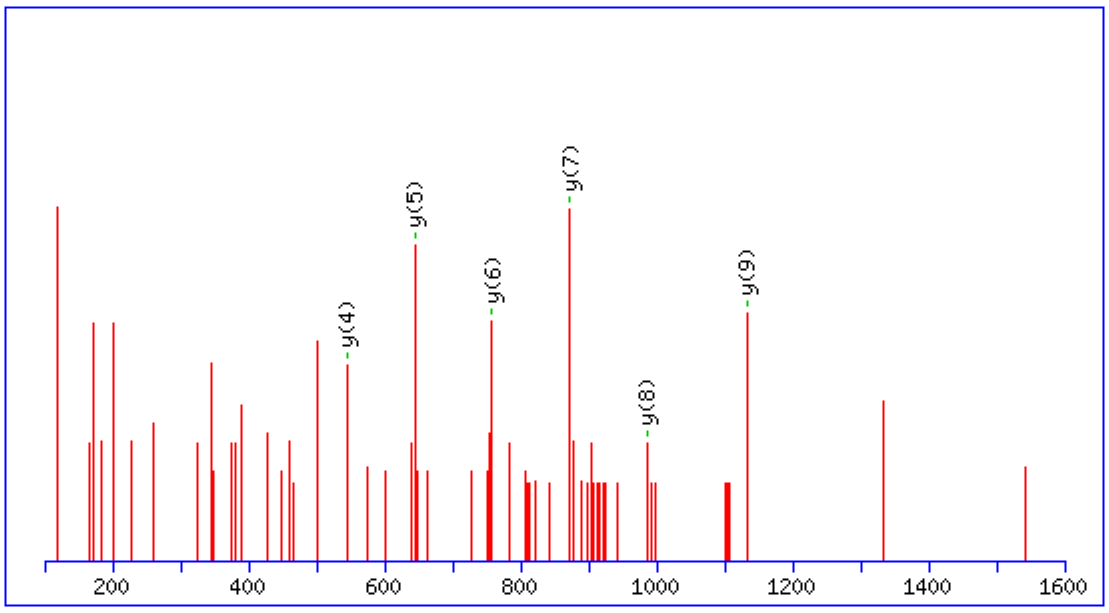
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SLFLDLVELQR**
Found in **ACOX3_HUMAN**, Peroxisomal acyl-coenzyme A oxidase 3 OS=Homo sapiens GN=ACOX3 PE=1 SV=2

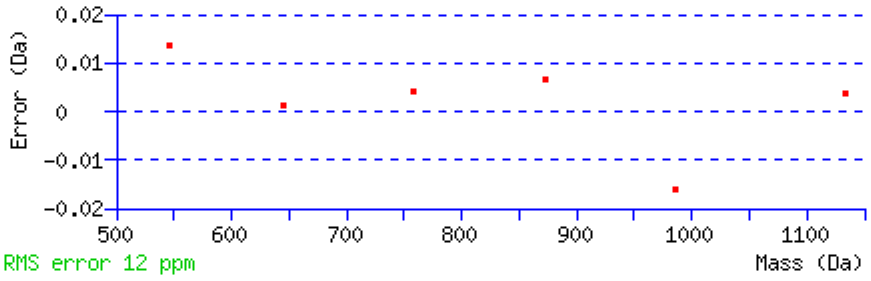
Match to Query 37919: 1331.738688 from(666.876620,2+) rtinseconds(4036) index(59819)
Title: Locus:1.1.1.2914.18
Data file 2011-11-12 - TFD - EP 6-2.mgf

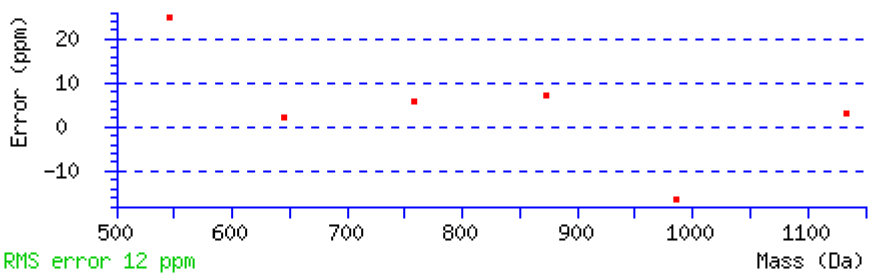
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1331.744888
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 37  Expect: 0.0015
Matches : 6/96 fragment ions using 11 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							11
2	201.123368	101.065322			183.112803	92.060039	L	1245.720150	623.363713	1228.693601	614.850439	1227.709585	614.358430	10
3	348.191782	174.599529			330.181217	165.594246	F	***1132.636086***	566.821681	1115.609537	558.308407	1114.625521	557.816398	9
4	461.275846	231.141561			443.265281	222.136278	L	***985.567672***	493.287474	968.541123	484.774200	967.557107	484.282192	8
5	576.302789	288.655033			558.292224	279.649750	D	***872.483608***	436.745442	855.457059	428.232168	854.473043	427.740160	7
6	689.386853	345.197065			671.376288	336.191782	L	***757.456665***	379.231971	740.430116	370.718696	739.446100	370.226688	6
7	788.455267	394.731271			770.444702	385.725989	V	***644.372601***	322.689939	627.346052	314.176664	626.362036	313.684656	5
8	917.497860	459.252568			899.487295	450.247285	E	***545.304187***	273.155732	528.277638	264.642457	527.293622	264.150449	4
9	1030.581924	515.794600			1012.571359	506.789317	L	416.261594	208.634435	399.235045	200.121160			3
10	1158.640502	579.823889	1141.613953	571.310615	1140.629937	570.818606	Q	303.177530	152.092403	286.150981	143.579129			2
11							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of SLFLDLVELQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.5	1331.744888	-0.006200	SLFLDLVELQR

Mascot: http://www.matrixscience.com/

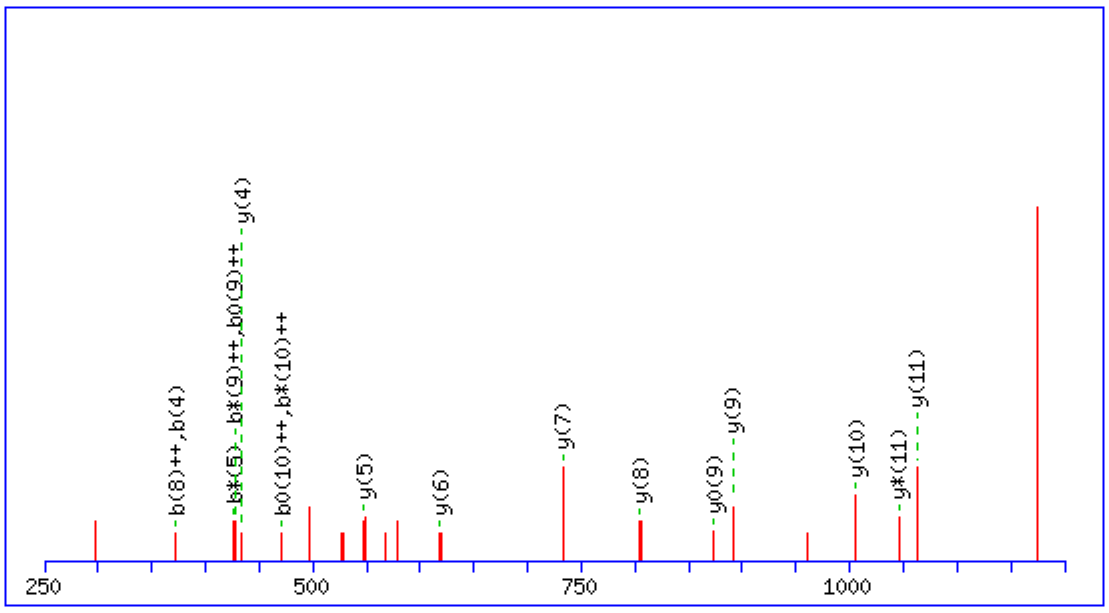
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGNSADALESAK**
Found in **PX11B_HUMAN**, Peroxisomal membrane protein 11B OS=Homo sapiens GN=PEX11B PE=1 SV=1

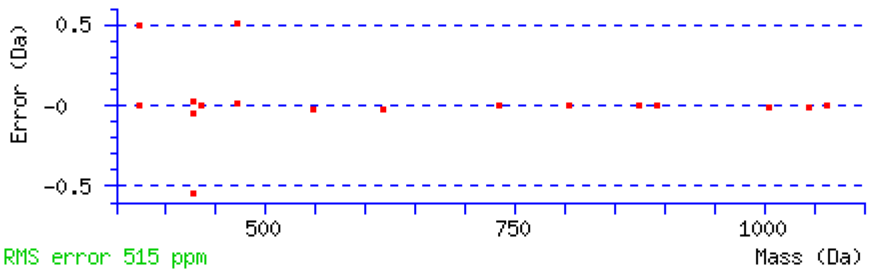
Match to Query 27048: 1174.584668 from(588.299610,2+) rtinseconds(1502) index(8951)
Title: Locus:1.1.1.2157.35
Data file 2011-11-12 - TFD - EP 5-5.mgf

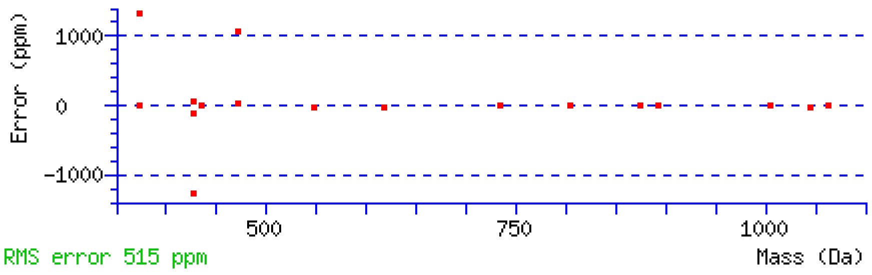
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1174.582947
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 55 **Expect:** 4.1e-005
Matches : 17/118 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							12
2	171.112804	86.060040					G	***1062.506193***	531.756735	1045.479644	523.243460	1044.495628	522.751452	11
3	285.155731	143.081504	268.129182	134.568229			N	***1005.484729***	503.246003	988.458180	494.732728	987.474164	494.240720	10
4	372.187759	186.597517	355.161210	178.084243	354.177194	177.592235	S	***891.441802***	446.224539	874.415253	437.711265	873.431237	437.219257	9
5	443.224873	222.116074	426.198324	213.602800	425.214308	213.110792	A	***804.409774***	402.708525	787.383225	394.195251	786.399209	393.703243	8
6	558.251816	279.629546	541.225267	271.116271	540.241251	270.624263	D	***733.372660***	367.189968	716.346111	358.676694	715.362095	358.184686	7
7	629.288930	315.148103	612.262381	306.634828	611.278365	306.142820	A	***618.345717***	309.676497	601.319168	301.163222	600.335152	300.671214	6
8	742.372994	371.690135	725.346445	363.176860	724.362429	362.684852	L	***547.308603***	274.157940	530.282054	265.644665	529.298038	265.152657	5
9	871.415587	436.211432	854.389038	427.698157	853.405022	427.206149	E	***434.224539***	217.615908	417.197990	209.102633	416.213974	208.610625	4
10	958.447615	479.727445	941.421066	471.214171	940.437050	470.722163	S	305.181946	153.094611	288.155397	144.581337	287.171381	144.089329	3
11	1029.484729	515.246003	1012.458180	506.732728	1011.474164	506.240720	A	218.149918	109.578597	201.123369	101.065323			2
12							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of LGNSADALESAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.1	1174.582947	0.001721	LGNSADALESAK
19.8	1174.576431	0.008237	LGSNAGNKPCK

Mascot: http://www.matrixscience.com/

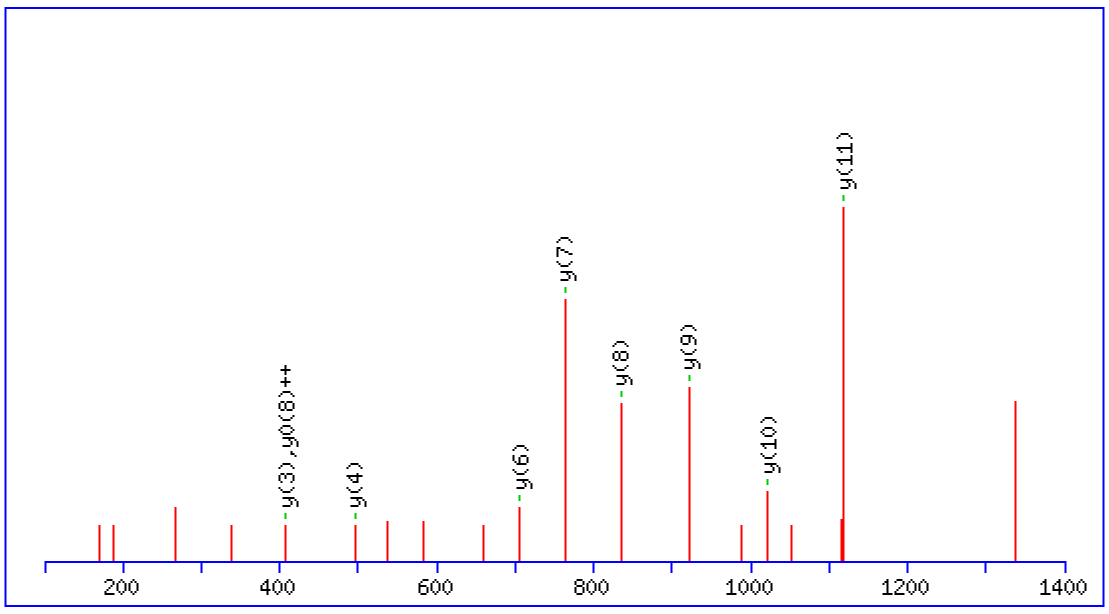
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DTPTSAGPNSFNK**
Found in **PCNP_HUMAN**, PEST proteolytic signal-containing nuclear protein OS=Homo sapiens GN=PCNP PE=1 SV=2

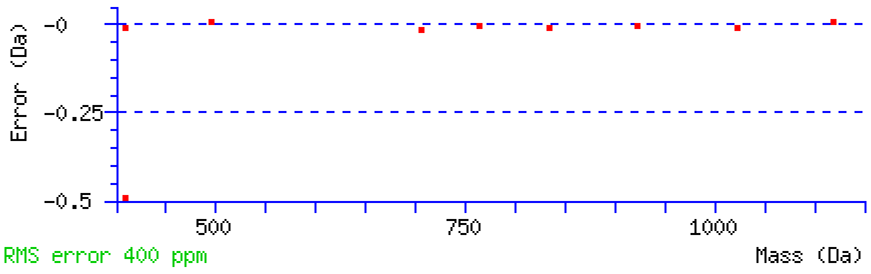
Match to Query 34281: 1334.607608 from(668.311080,2+) rtinseconds(1412) index(5048)
Title: Locus:1.1.1.1994.40
Data file 2011-11-10 - TFD - EP 4-7.mgf

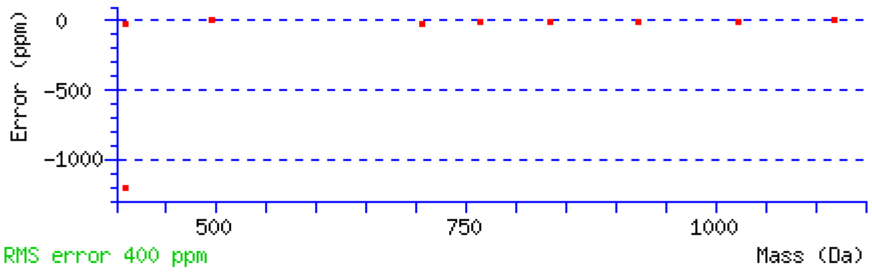
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1334.610260
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 59 **Expect:** 2.7e-006
Matches : 9/122 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.034219	58.520748			98.023654	49.515465	D							13
2	217.081898	109.044587			199.071333	100.039304	T	1220.590592	610.798934	1203.564043	602.285660	1202.580027	601.793652	12
3	314.134662	157.570969			296.124097	148.565687	P	***1119.542913***	560.275095	1102.516364	551.761820	1101.532348	551.269812	11
4	415.182341	208.094809			397.171776	199.089526	T	***1022.490149***	511.748713	1005.463600	503.235438	1004.479584	502.743430	10
5	502.214369	251.610822			484.203804	242.605540	S	***921.442470***	461.224873	904.415921	452.711599	903.431905	452.219591	9
6	573.251483	287.129380			555.240918	278.124097	A	***834.410442***	417.708859	817.383893	409.195585	816.399877	408.703577	8
7	630.272947	315.640112			612.262382	306.634829	G	***763.373328***	382.190302	746.346779	373.677028	745.362763	373.185020	7
8	727.325711	364.166494			709.315146	355.161211	P	***706.351864***	353.679570	689.325315	345.166296	688.341299	344.674288	6
9	841.368638	421.187957	824.342089	412.674683	823.358073	412.182675	N	609.299100	305.153188	592.272551	296.639914	591.288535	296.147906	5
10	928.400666	464.703971	911.374117	456.190697	910.390101	455.698689	S	***495.256173***	248.131724	478.229624	239.618450	477.245608	239.126442	4
11	1075.469080	538.238178	1058.442531	529.724904	1057.458515	529.232896	F	***408.224145***	204.615711	391.197596	196.102436			3
12	1189.512007	595.259642	1172.485458	586.746367	1171.501442	586.254359	N	261.155731	131.081503	244.129182	122.568229			2
13							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of DTPTSAGPNSFNK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
59.4	1334.610260	-0.002652	DTPTSAGPNSFNK
0.0	1334.611099	-0.003491	SEPCLMDWRK

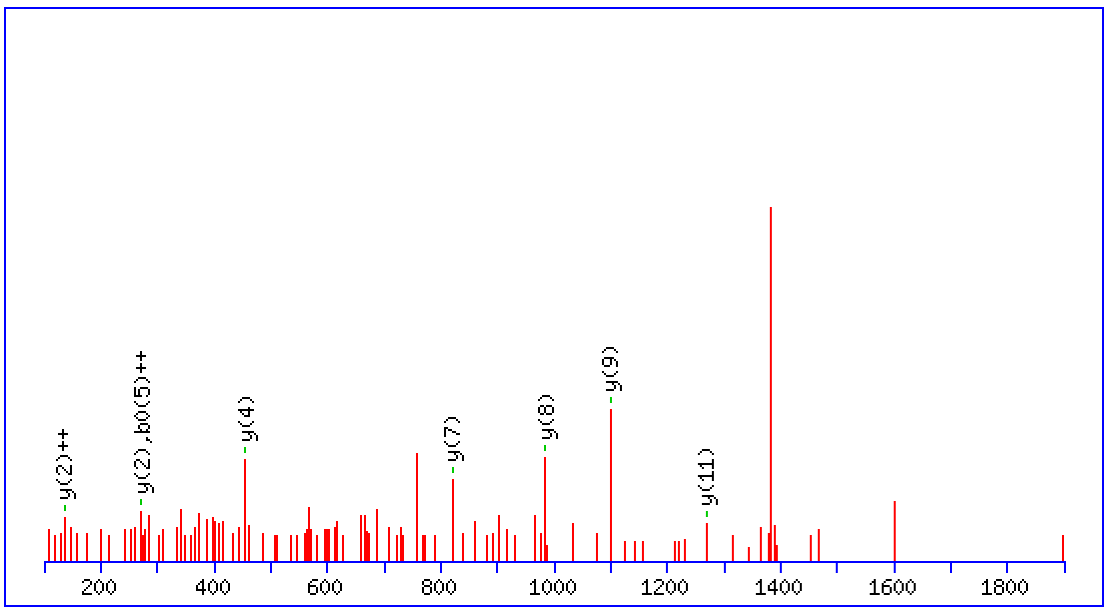
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGLDYSYDLAPR**
Found in **PLBL1_HUMAN**, Phospholipase B-like 1 OS=Homo sapiens GN=PLBD1 PE=1 SV=2

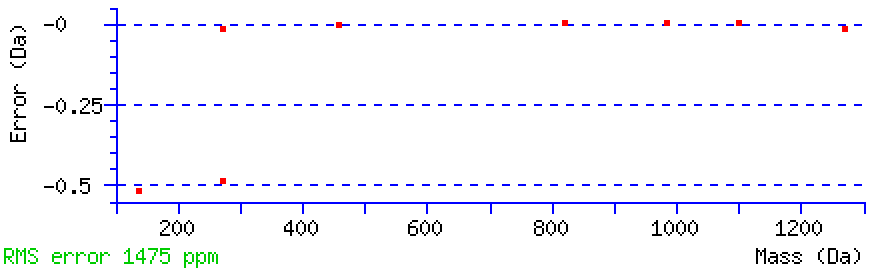
Match to Query 40967: 1381.693468 from(691.854010,2+) rtinseconds(2902) index(40026)
Title: Locus:1.1.1.2400.36
Data file 2011-11-12 - TFD - EP 6-4.mgf

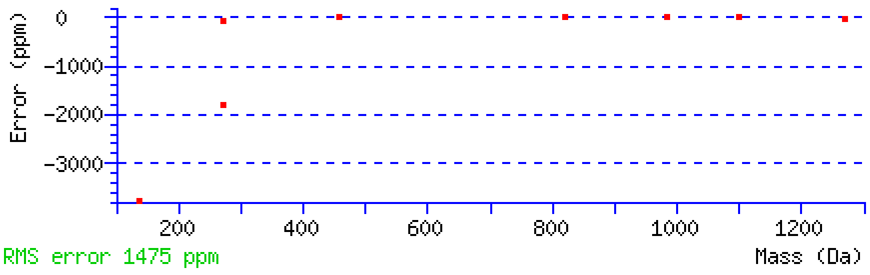
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1381.687759
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.0013
Matches : 8/96 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			**L**							12
2	171.112804	86.060040			**G**	***1269.610994***	635.309135	1252.584445	626.795861	1251.600429	626.303853	11
3	284.196868	142.602072			**L**	1212.589530	606.798403	1195.562981	598.285129	1194.578965	597.793120	10
4	399.223811	200.115544	381.213246	191.110261	**D**	***1099.505466***	550.256371	1082.478917	541.743097	1081.494901	541.251089	9
5	562.287140	281.647208	544.276575	272.641926	**Y**	***984.478523***	492.742900	967.451974	484.229625	966.467958	483.737617	8
6	649.319168	325.163222	631.308603	316.157940	**S**	***821.415194***	411.211235	804.388645	402.697960	803.404629	402.205952	7
7	812.382497	406.694887	794.371932	397.689604	**Y**	734.383166	367.695221	717.356617	359.181946	716.372601	358.689938	6
8	927.409440	464.208358	909.398875	455.203076	**D**	571.319837	286.163557	554.293288	277.650282	553.309272	277.158274	5
9	1040.493504	520.750390	1022.482939	511.745108	**L**	***456.292894***	228.650085	439.266345	220.136810			4
10	1111.530618	556.268947	1093.520053	547.263665	**A**	343.208830	172.108053	326.182281	163.594778			3
11	1208.583382	604.795329	1190.572817	595.790047	**P**	***272.171716***	136.589496	255.145167	128.076221			2
12					**R**	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LGLDYSYDLAPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.3	1381.687759	0.005709	LGLDYSYDLAPR
2.5	1381.702393	-0.008925	VAPGTPADLCVPR
1.9	1381.687759	0.005709	REPSYFEIPTK

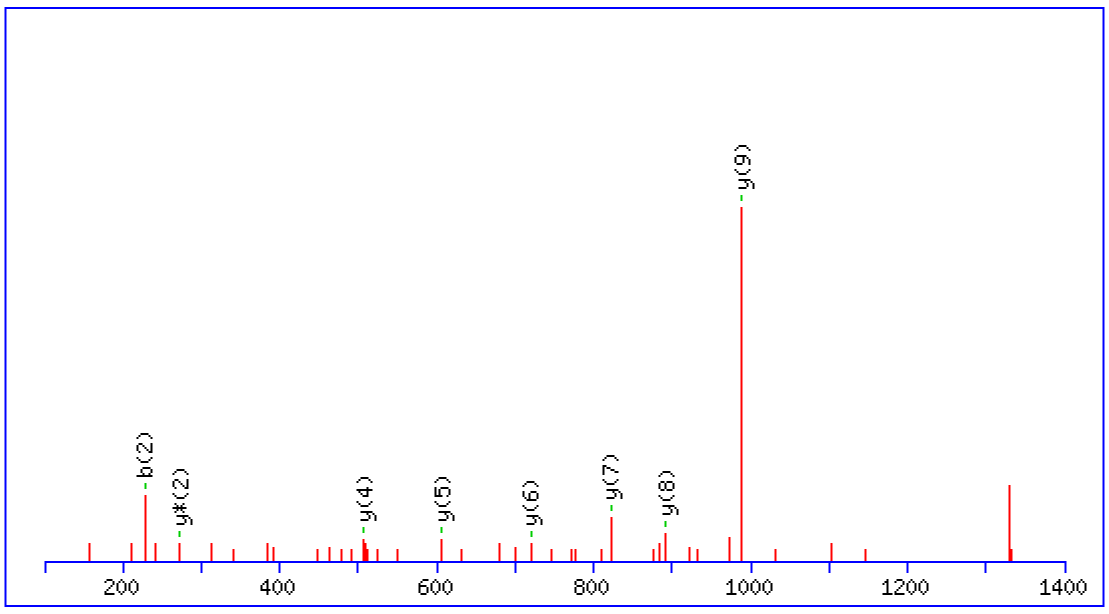
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LNIPATNVFANR**
Found in **SERB_HUMAN**, Phosphoserine phosphatase OS=Homo sapiens GN=PSPH PE=1 SV=2

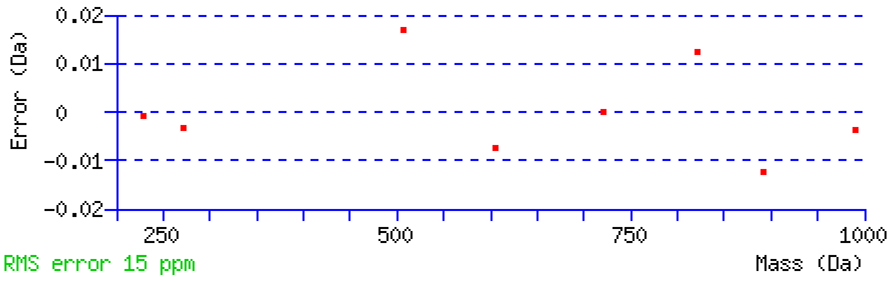
Match to Query 37616: 1328.714648 from(665.364600,2+) rtinseconds(2824) index(36617)
Title: Locus:1.1.1.2389.36
Data file 2011-11-10 - TFD - EP 4-5.mgf

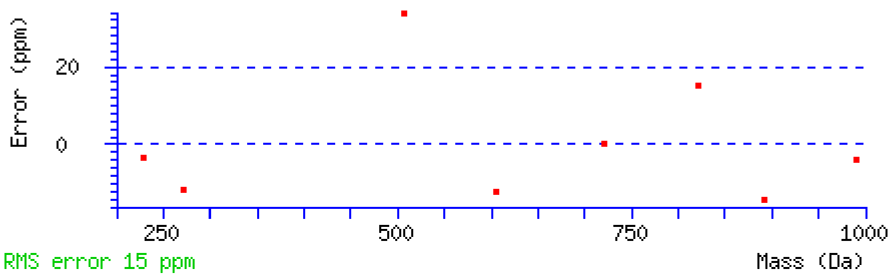
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1328.720062
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 47 **Expect:** 0.00013
Matches : 8/108 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					L							12
2	228.134267	114.570771	211.107718	106.057497			N	1216.643296	608.825286	1199.616747	600.312012	1198.632731	599.820003	11
3	341.218331	171.112803	324.191782	162.599529			I	1102.600369	551.803822	1085.573820	543.290548	1084.589804	542.798540	10
4	438.271095	219.639186	421.244546	211.125911			P	***989.516305***	495.261790	972.489756	486.748516	971.505740	486.256508	9
5	509.308209	255.157742	492.281660	246.644468			A	***892.463541***	446.735408	875.436992	438.222134	874.452976	437.730126	8
6	610.355888	305.681582	593.329339	297.168308	592.345323	296.676300	T	***821.426427***	411.216851	804.399878	402.703577	803.415862	402.211569	7
7	724.398815	362.703046	707.372266	354.189771	706.388250	353.697763	N	***720.378748***	360.693012	703.352199	352.179737			6
8	823.467229	412.237253	806.440680	403.723978	805.456664	403.231970	V	***606.335821***	303.671548	589.309272	295.158274			5
9	970.535643	485.771459	953.509094	477.258185	952.525078	476.766177	F	***507.267407***	254.137341	490.240858	245.624067			4
10	1041.572757	521.290016	1024.546208	512.776742	1023.562192	512.284734	A	360.198993	180.603134	343.172444	172.089860			3
11	1155.615684	578.311480	1138.589135	569.798205	1137.605119	569.306197	N	289.161879	145.084577	272.135330	136.571303			2
12							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LNIPATNVFANR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.4	1328.720062	-0.005414	LNIPATNVFANR
2.6	1328.705688	0.008960	GPLGLRLMMPGR
2.6	1328.705688	0.008960	GPLGLRLMMPGR
2.1	1328.705688	0.008960	GPLGLRLMMPGR

Mascot: http://www.matrixscience.com/

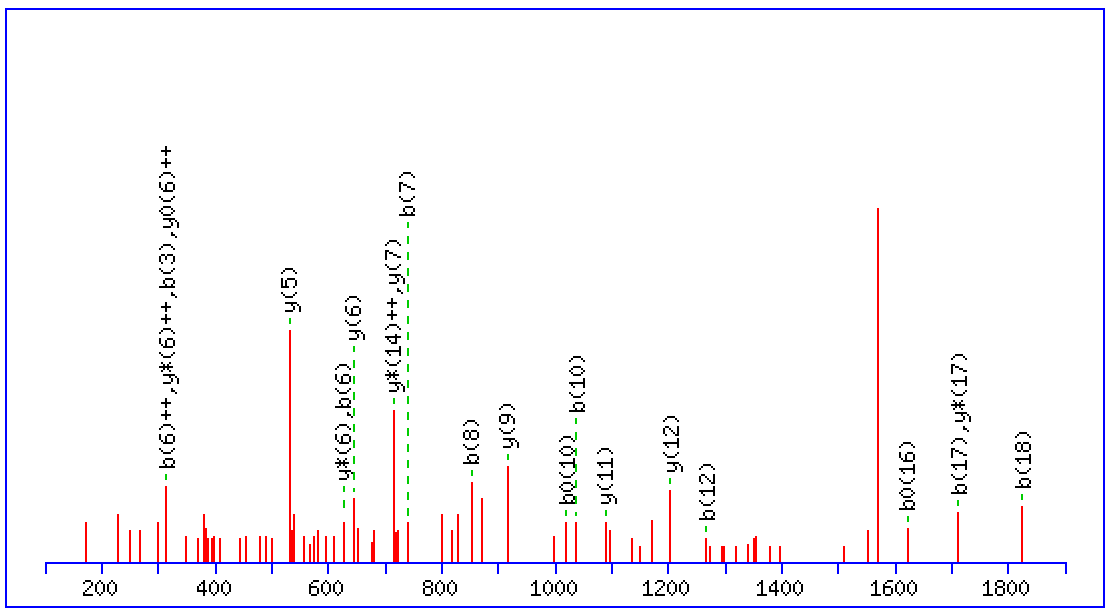
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TVLGQQILGQLDSSSLALPSEAK**
Found in **PKP2_HUMAN**, Plakophilin-2 OS=Homo sapiens GN=PKP2 PE=1 SV=2

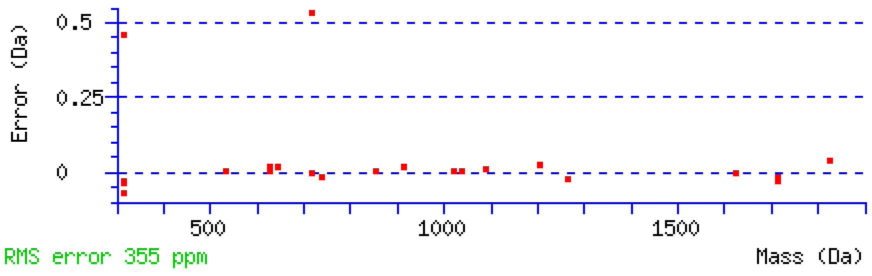
Match to Query 68512: 2354.280792 from(785.767540,3+) rtinseconds(3842) index(56143)
Title: Locus:1.1.1.2942.35
Data file 2011-11-10 - TFD - EP 4-2.mgf

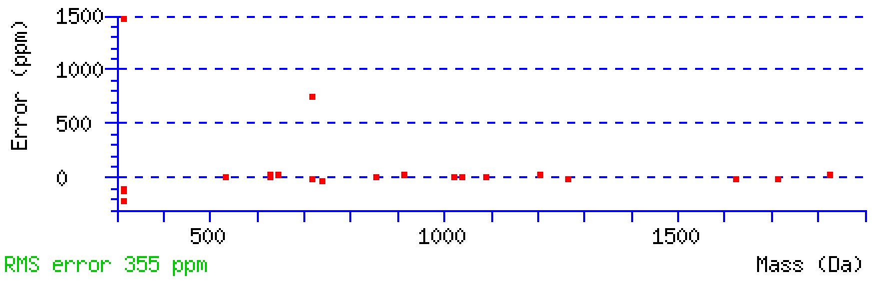
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2354.269287
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 42 **Expect:** 0.00027
Matches : 22/252 fragment ions using 30 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	**T**							**23**
2	201.123369	101.065322			183.112804	92.060040	**V**	2254.228904	1127.618090	2237.202355	1119.104815	2236.218339	1118.612807	**22**
3	***314.207433***	157.607354			296.196868	148.602072	**L**	2155.160490	1078.083883	2138.133941	1069.570608	2137.149925	1069.078600	**21**
4	371.228897	186.118086			353.218332	177.112804	**G**	2042.076426	1021.541851	2025.049877	1013.028577	2024.065861	1012.536569	**20**
5	499.287475	250.147375	482.260926	241.634101	481.276910	241.142093	**Q**	1985.054962	993.031119	1968.028413	984.517845	1967.044397	984.025837	**19**
6	***627.346053***	314.176665	610.319504	305.663390	609.335488	305.171382	**Q**	1856.996384	929.001830	1839.969835	920.488556	1838.985819	919.996548	**18**
7	***740.430117***	370.718697	723.403568	362.205422	722.419552	361.713414	**I**	1728.937806	864.972541	1711.911257	856.459267	1710.927241	855.967259	**17**
8	***853.514181***	427.260729	836.487632	418.747454	835.503616	418.255446	**L**	1615.853742	808.430509	1598.827193	799.917235	1597.843177	799.425227	**16**
9	910.535645	455.771461	893.509096	447.258186	892.525080	446.766178	**G**	1502.769678	751.888477	1485.743129	743.375203	1484.759113	742.883195	**15**
10	***1038.594223***	519.800750	1021.567674	511.287475	1020.583658	510.795467	**Q**	1445.748214	723.377745	1428.721665	714.864471	1427.737649	714.372463	**14**
11	1151.678287	576.342782	1134.651738	567.829507	1133.667722	567.337499	**L**	1317.689636	659.348456	1300.663087	650.835182	1299.679071	650.343174	**13**
12	***1266.705230***	633.856253	1249.678681	625.342979	1248.694665	624.850971	**D**	***1204.605572***	602.806424	1187.579023	594.293150	1186.595007	593.801142	**12**
13	1353.737258	677.372267	1336.710709	668.858993	1335.726693	668.366985	**S**	***1089.578629***	545.292953	1072.552080	536.779678	1071.568064	536.287670	**11**
14	1440.769286	720.888281	1423.742737	712.375007	1422.758721	711.882999	**S**	1002.546601	501.776939	985.520052	493.263664	984.536036	492.771656	**10**
15	1527.801314	764.404295	1510.774765	755.891021	1509.790749	755.399013	**S**	***915.514573***	458.260925	898.488024	449.747650	897.504008	449.255642	**9**
16	1640.885378	820.946327	1623.858829	812.433053	1622.874813	811.941045	**L**	828.482545	414.744911	811.455996	406.231636	810.471980	405.739628	**8**
17	***1711.922492***	856.464884	1694.895943	847.951610	1693.911927	847.459602	**A**	***715.398481***	358.202879	698.371932	349.689604	697.387916	349.197596	**7**
18	***1825.006556***	913.006916	1807.980007	904.493642	1806.995991	904.001634	**L**	***644.361367***	322.684322	627.334818	314.171047	626.350802	313.679039	**6**
19	1922.059320	961.533298	1905.032771	953.020024	1904.048755	952.528016	**P**	***531.277303***	266.142290	514.250754	257.629015	513.266738	257.137007	**5**
20	2009.091348	1005.049312	1992.064799	996.536038	1991.080783	996.044030	**S**	434.224539	217.615908	417.197990	209.102633	416.213974	208.610625	**4**
21	2138.133941	1069.570608	2121.107392	1061.057334	2120.123376	1060.565326	**E**	347.192511	174.099894	330.165962	165.586619	329.181946	165.094611	**3**
22	2209.171055	1105.089166	2192.144506	1096.575891	2191.160490	1096.083883	**A**	218.149918	109.578597	201.123369	101.065323			**2**
23							**K**	147.112804	74.060040	130.086255	65.546765			**1**





NCBI **BLAST** search of TVLGQQILGQLDSSSLALPSEAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.0	2354.269287	0.011505	TVLGQQILGQLDSSSLALPSEAK
1.5	2354.270813	0.009979	EPFSWIKVDLLAPMIIHGIK

Mascot: http://www.matrixscience.com/

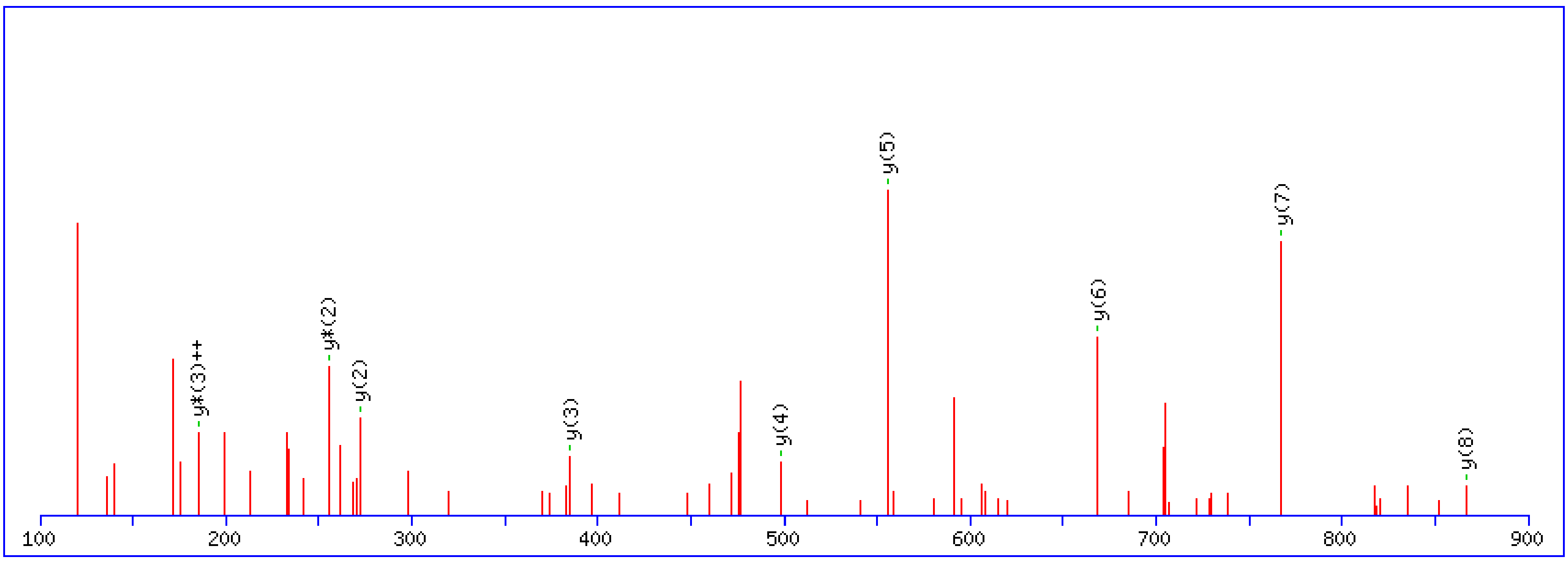
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVVLGLLPR**
Found in **PA1B3_HUMAN**, Platelet-activating factor acetylhydrolase IB subunit gamma OS=Homo sapiens GN=PAFAH1B3 PE=1 SV=1

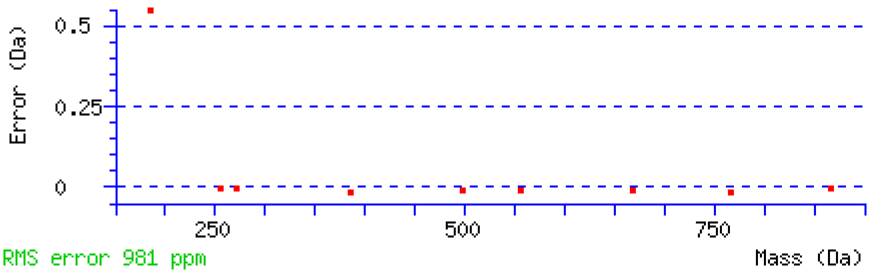
Match to Query 7729: 964.641808 from(483.328180,2+) rtinseconds(2988) index(41175)
Title: Locus:1.1.1.1579.5
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 3.mgf

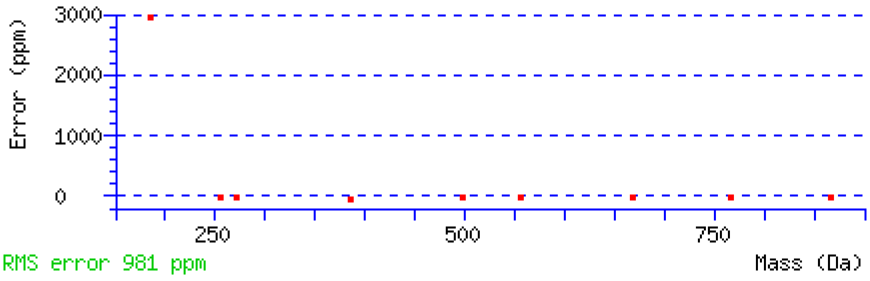
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 964.643341
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.00011
Matches : 9/48 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	100.075690	50.541483	V					9
2	199.144104	100.075690	V	*866.582200*	433.794738	849.555651	425.281464	8
3	298.212518	149.609897	V	*767.513786*	384.260531	750.487237	375.747257	7
4	411.296582	206.151929	L	*668.445372*	334.726324	651.418823	326.213050	6
5	468.318046	234.662661	G	*555.361308*	278.184292	538.334759	269.671018	5
6	581.402110	291.204693	L	*498.339844*	249.673560	481.313295	241.160286	4
7	694.486174	347.746725	L	*385.255780*	193.131528	368.229231	184.618254	3
8	791.538938	396.273107	P	*272.171716*	136.589496	255.145167	128.076222	2
9			R	175.118952	88.063114	158.092403	79.549840	1





NCBI **BLAST** search of VVVLGLLPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.5	964.643341	-0.001533	VVVLGLLPR

Mascot: http://www.matrixscience.com/

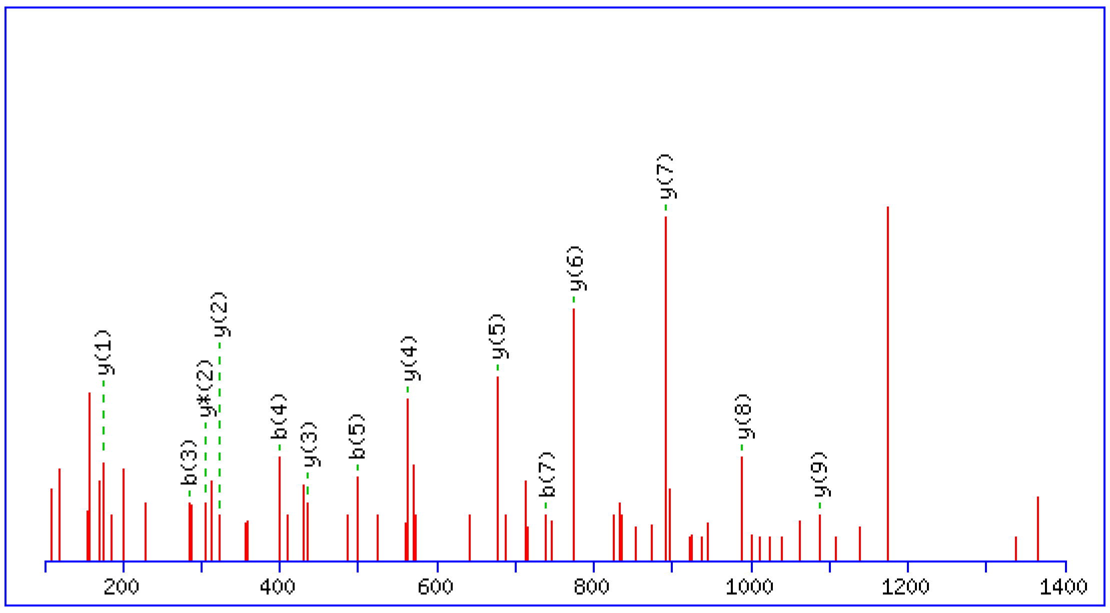
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SPVDVLQIFR**
Found in **PARP4_HUMAN**, Poly [ADP-ribose] polymerase 4 OS=Homo sapiens GN=PARP4 PE=1 SV=3

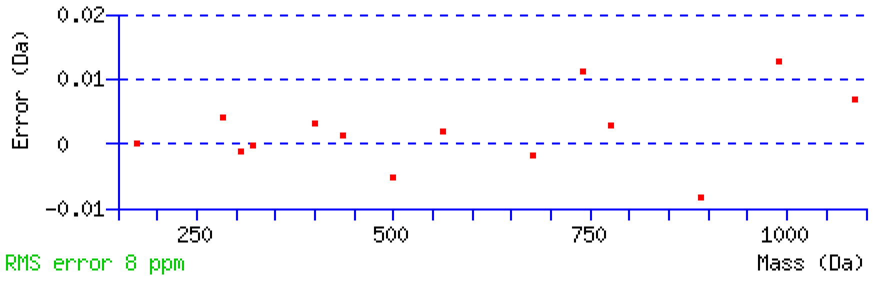
Match to Query 27633: 1172.646448 from(587.330500,2+) rtinseconds(3688) index(54293)
Title: Locus:1.1.1.2706.4
Data file 2011-11-12 - TFD - EP 6-1.mgf

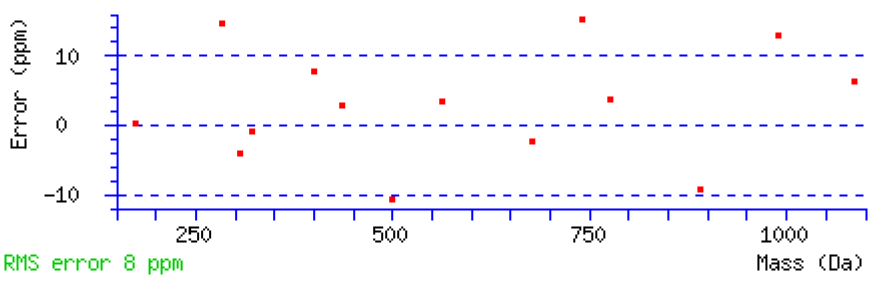
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1172.655365
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 63  Expect: 9.4e-006
Matches : 14/84 fragment ions using 31 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							10
2	185.092068	93.049672			167.081503	84.044389	P	*1086.630607*	543.818942	1069.604058	535.305667	1068.620042	534.813659	9
3	**284.160482**	142.583879			266.149917	133.578597	V	*989.577843*	495.292560	972.551294	486.779285	971.567278	486.287277	8
4	**399.187425**	200.097351			381.176860	191.092068	D	*890.509429*	445.758353	873.482880	437.245078	872.498864	436.753070	7
5	**498.255839**	249.631558			480.245274	240.626275	V	*775.482486*	388.244881	758.455937	379.731607			6
6	611.339903	306.173590			593.329338	297.168307	L	*676.414072*	338.710674	659.387523	330.197400			5
7	**739.398481**	370.202879	722.371932	361.689604	721.387916	361.197596	Q	*563.330008*	282.168642	546.303459	273.655368			4
8	852.482545	426.744911	835.455996	418.231636	834.471980	417.739628	I	*435.271430*	218.139353	418.244881	209.626079			3
9	999.550959	500.279118	982.524410	491.765843	981.540394	491.273835	F	*322.187366*	161.597321	305.160817	153.084047			2
10							R	*175.118952*	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of SPVDVLQIFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
62.9	1172.655365	-0.008917	SPVDVLQIFR
3.0	1172.651321	-0.004873	AIITDSVKNGR
1.0	1172.651321	-0.004873	RIDISPSTLR

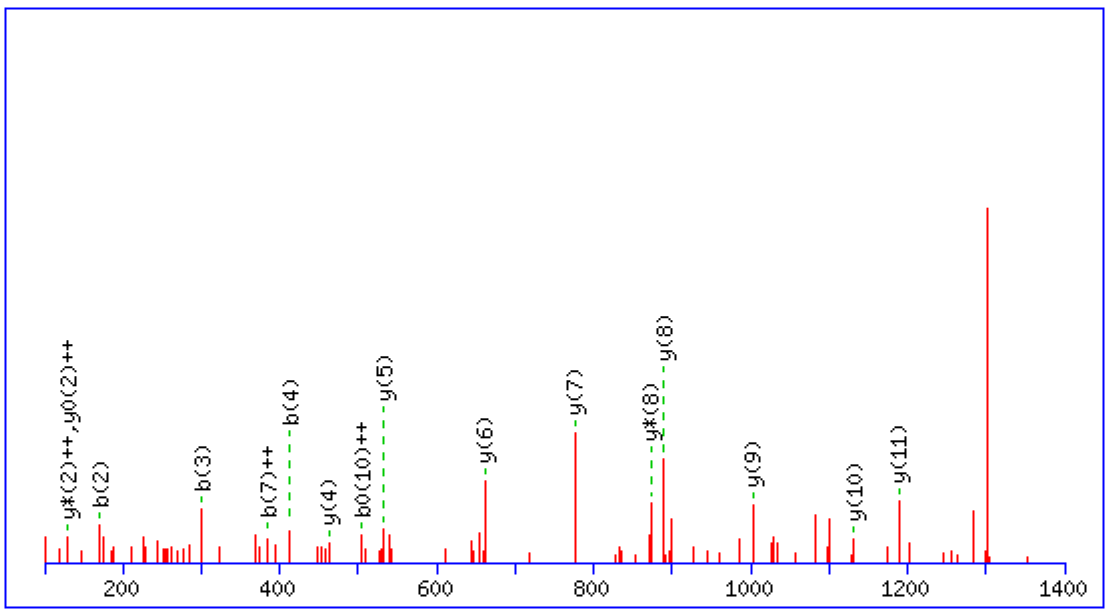
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IGELLDQASVTR**
Found in **ARHL2_HUMAN**, Poly(ADP-ribose) glycohydrolase ARH3 OS=Homo sapiens GN=ADPRHL2 PE=1 SV=1

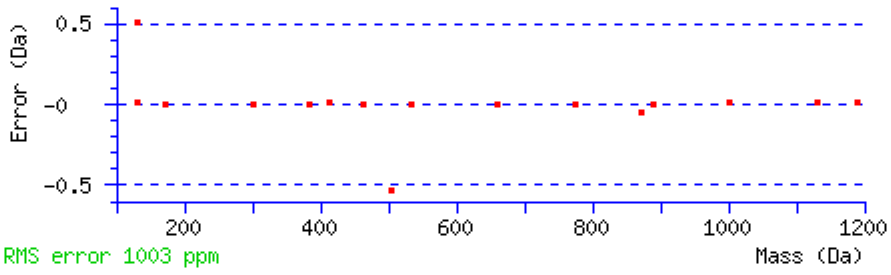
Match to Query 35160: 1300.710928 from(651.362740,2+) rtinseconds(2295) index(27984)
Title: Locus:1.1.1.2304.38
Data file 2011-11-13 - TFD - EP 7-4.mgf

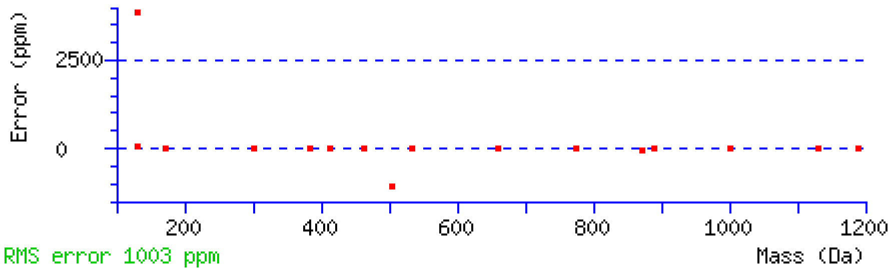
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1300.698669
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 58  Expect: 3.1e-005
Matches : 16/114 fragment ions using 24 most intense peaks   (help)
```

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	114.091340	57.549308					I							12
2	**171.112804**	86.060040					G	***1188.621893***	594.814585	1171.595344	586.301310	1170.611328	585.809302	11
3	**300.155397**	150.581336			282.144832	141.576054	E	***1131.600429***	566.303852	1114.573880	557.790578	1113.589864	557.298570	10
4	**413.239461**	207.123369			395.228896	198.118086	L	***1002.557836***	501.782556	985.531287	493.269281	984.547271	492.777273	9
5	526.323525	263.665401			508.312960	254.660118	L	***889.473772***	445.240524	872.447223	436.727249	871.463207	436.235241	8
6	641.350468	321.178872			623.339903	312.173589	D	***776.389708***	388.698492	759.363159	380.185217	758.379143	379.693209	7
7	769.409046	385.208161	752.382497	376.694887	751.398481	376.202879	Q	***661.362765***	331.185021	644.336216	322.671746	643.352200	322.179738	6
8	840.446160	420.726718	823.419611	412.213443	822.435595	411.721435	A	***533.304187***	267.155732	516.277638	258.642457	515.293622	258.150449	5
9	927.478188	464.242732	910.451639	455.729457	909.467623	455.237449	S	***462.267073***	231.637174	445.240524	223.123900	444.256508	222.631892	4
10	1026.546602	513.776939	1009.520053	505.263664	1008.536037	504.771656	V	375.235045	188.121160	358.208496	179.607886	357.224480	179.115878	3
11	1127.594281	564.300778	1110.567732	555.787504	1109.583716	555.295496	T	276.166631	138.586953	259.140082	130.073679	258.156066	129.581671	2
12							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of IGELLDQASVTR
(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	1300.698669	0.012259	IGELLDQASVTR
8.2	1300.709900	0.001028	KAGRPGTSPLASK
7.2	1300.717941	-0.007013	WILAGVLSWEK
6.3	1300.706039	0.004889	IEAVKLQMEPK
3.8	1300.707397	0.003531	WLLMVNPTRR
3.2	1300.707397	0.003531	WLLMVNPTRR
2.8	1300.706055	0.004873	CLAATDLLLPGK
2.5	1300.706070	0.004858	TTPSGLQIMPLK
2.0	1300.703400	0.007528	TVVCRNVAGGVR
1.9	1300.723816	-0.012888	SVIIPKLDDSSK

Mascot: http://www.matrixscience.com/

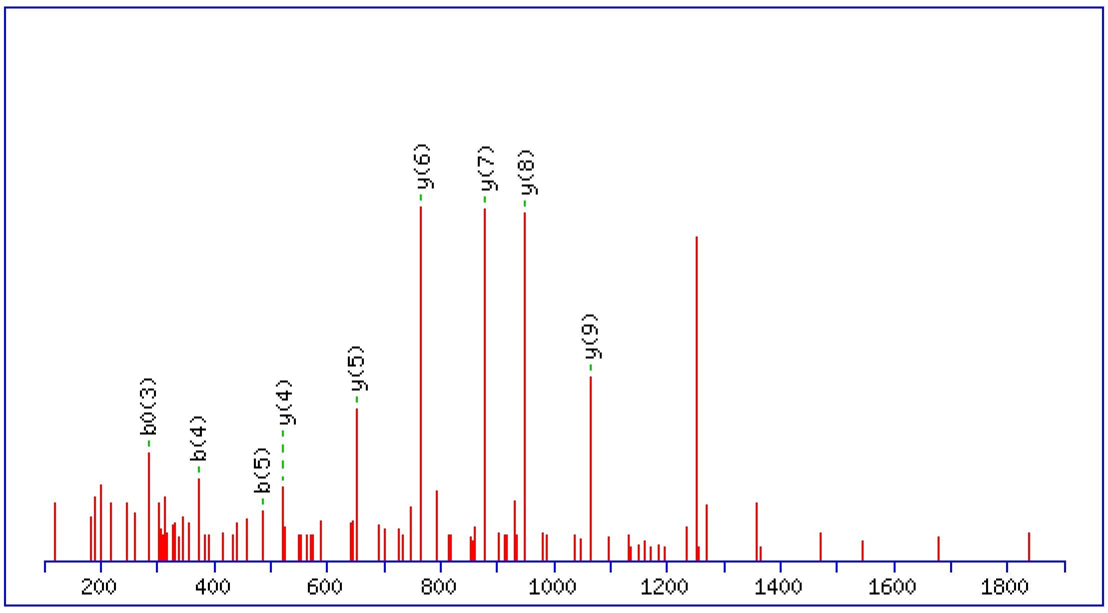
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **TSLALDESLFR**
Found in **PABP2_HUMAN**, Polyadenylate-binding protein 2 OS=Homo sapiens GN=PABPN1 PE=1 SV=3

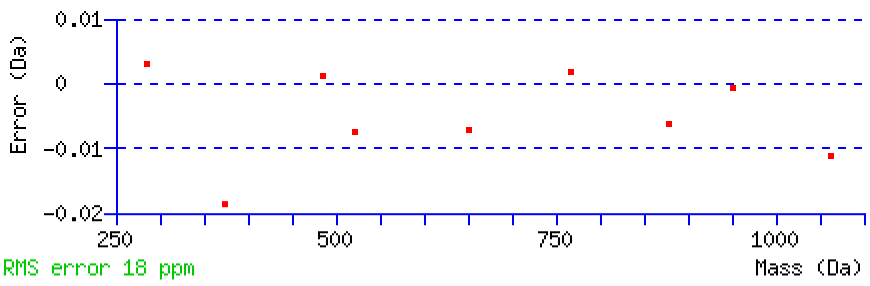
Match to Query 25852: 1250.654028 from(626.334290,2+) rtinseconds(3039) index(42536)
Title: Locus:1.1.1.2645.20
Data file 2011-11-10 - TFD - EP 4-3.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●

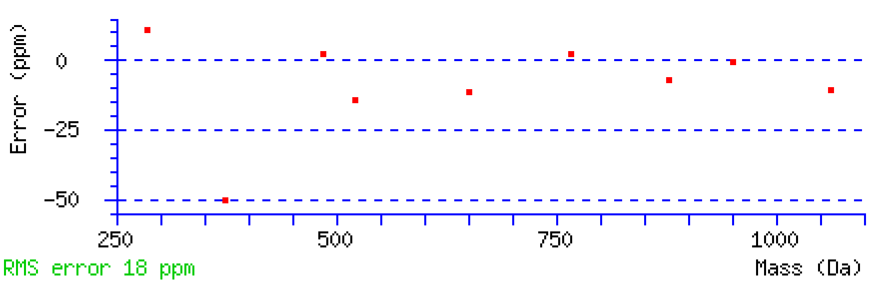


Monoisotopic mass of neutral peptide Mr(calc): 1250.650650
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 51 **Expect:** 0.00025
Matches : 9/94 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116	84.044390	42.525833	T							11
2	189.086983	95.047129	171.076418	86.041847	S	1150.610264	575.808770	1133.583715	567.295496	1132.599699	566.803487	10
3	302.171047	151.589161	284.160482	142.583879	L	***1063.578236***	532.292756	1046.551687	523.779482	1045.567671	523.287474	9
4	**373.208161**	187.107718	355.197596	178.102436	A	***950.494172***	475.750724	933.467623	467.237449	932.483607	466.745441	8
5	**486.292225**	243.649750	468.281660	234.644468	L	***879.457058***	440.232167	862.430509	431.718892	861.446493	431.226884	7
6	601.319168	301.163222	583.308603	292.157940	D	***766.372994***	383.690135	749.346445	375.176860	748.362429	374.684852	6
7	730.361761	365.684519	712.351196	356.679236	E	***651.346051***	326.176664	634.319502	317.663389	633.335486	317.171381	5
8	817.393789	409.200533	799.383224	400.195250	S	***522.303458***	261.655367	505.276909	253.142092	504.292893	252.650084	4
9	930.477853	465.742565	912.467288	456.737282	L	435.271430	218.139353	418.244881	209.626078			3
10	1077.546267	539.276772	1059.535702	530.271489	F	322.187366	161.597321	305.160817	153.084046			2
11					R	175.118952	88.063114	158.092403	79.549839			1



RMS error 18 ppm



RMS error 18 ppm

NCBI **BLAST** search of TSLALDESLFR
(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	1250.650650	0.003378	TSLALDESLFR
1.4	1250.644775	0.009253	RWFLYPPEK

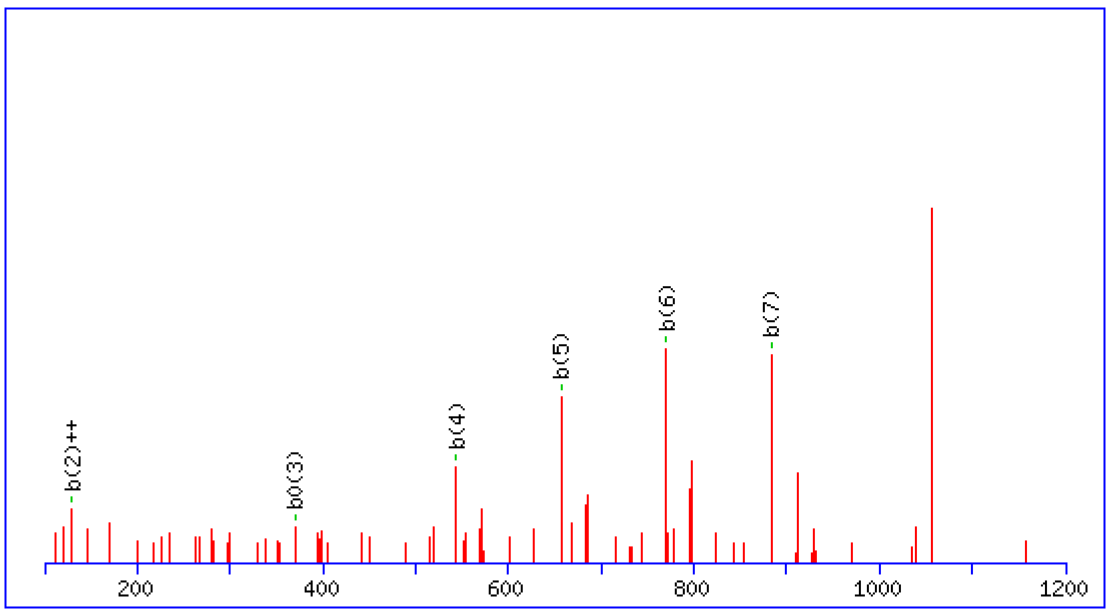
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EEERPLPR**
Found in **KCNA3_HUMAN**, Potassium voltage-gated channel subfamily A member 3 OS=Homo sapiens GN=KCNA3 PE=2 SV=3

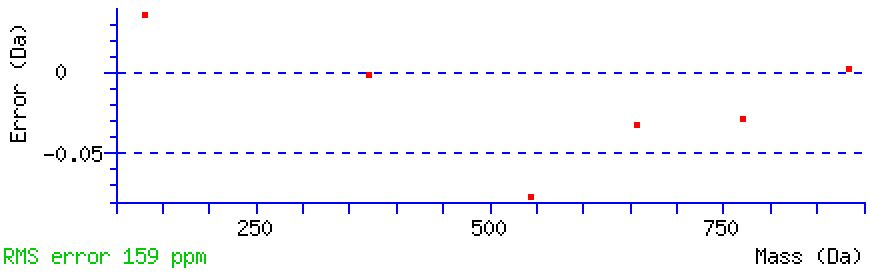
Match to Query 13144: 1056.509848 from(529.262200,2+) rtinseconds(1815) index(18666)
Title: Locus:1.1.1.2206.29
Data file 2011-11-12 - TFD - EP 5-3.mgf

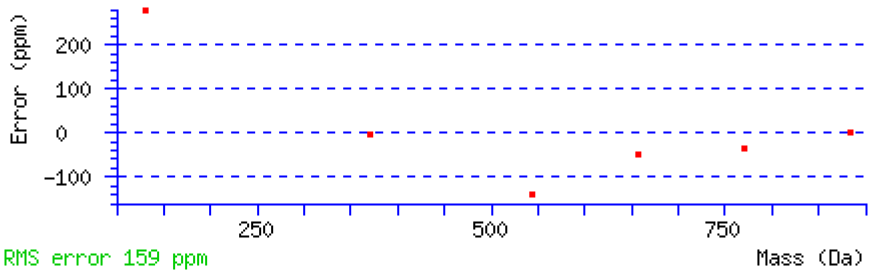
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1056.519958
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P5      : Oxidation (P)
P7      : Oxidation (P)
Ions Score: 36  Expect: 0.0023
Matches : 7/68 fragment ions using 10 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	***130.049869***	65.528572			112.039304	56.523290	E							8
2	259.092462	130.049869			241.081897	121.044587	E	928.484671	464.745974	911.458122	456.232699	910.474106	455.740691	7
3	388.135055	194.571166			370.124490	185.565883	E	799.442078	400.224677	782.415529	391.711403	781.431513	391.219395	6
4	***544.236166***	272.621721	527.209617	264.108447	526.225601	263.616439	R	670.399485	335.703381	653.372936	327.190106			5
5	***657.283845***	329.145561	640.257296	320.632286	639.273280	320.140278	P	514.298374	257.652825	497.271825	249.139551			4
6	***770.367909***	385.687593	753.341360	377.174318	752.357344	376.682310	L	401.250695	201.128986	384.224146	192.615711			3
7	***883.415588***	442.211432	866.389039	433.698158	865.405023	433.206150	P	288.166631	144.586954	271.140082	136.073679			2
8							R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of EEERPLPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.0	1056.519958	-0.010110	EEERPLPR
19.9	1056.508743	0.001105	GEIDEPPLR
19.9	1056.508743	0.001105	LATEEPPPR
19.8	1056.519974	-0.010126	EVEQNGIPR
13.1	1056.508728	0.001120	QAELQDEPK
10.3	1056.508743	0.001105	QDSPAGELPK
9.6	1056.519974	-0.010126	DAAAPSQPLR
9.5	1056.519974	-0.010126	QLEGNDPLR
9.4	1056.519989	-0.010141	EVTTPPNQR
8.7	1056.508743	0.001105	EDSPLPDLR

Mascot: http://www.matrixscience.com/

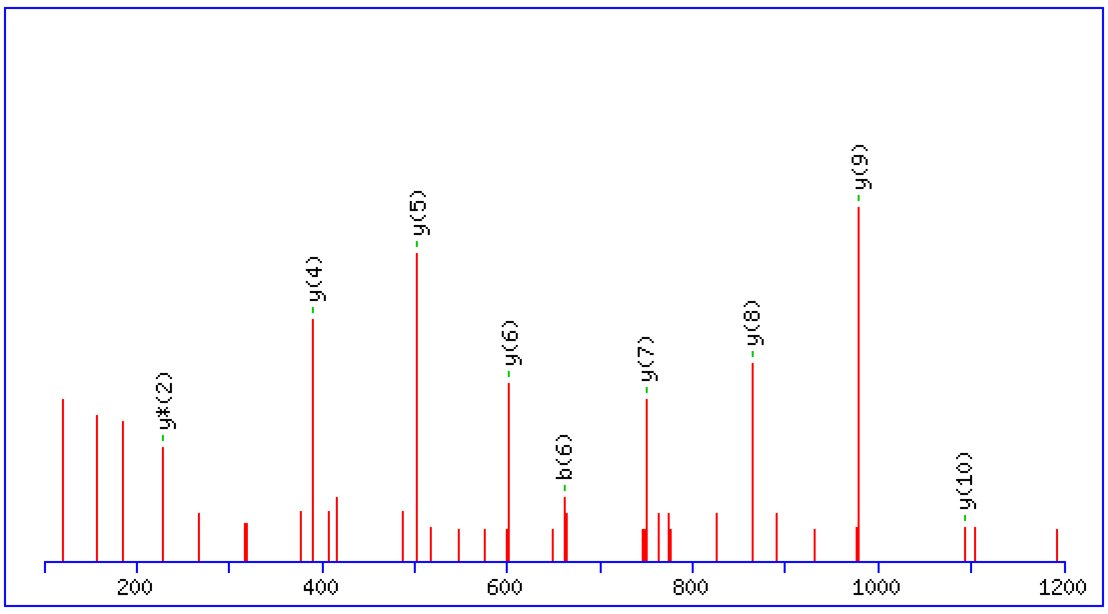
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALDDFVLGSAR**
Found in **PRAF2_HUMAN**, PRA1 family protein 2 OS=Homo sapiens GN=PRAF2 PE=1 SV=1

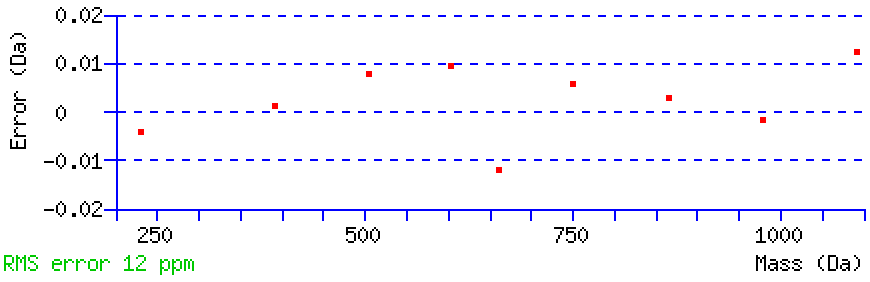
Match to Query 32554: 1162.596968 from(582.305760,2+) rtinseconds(2893) index(37445)
Title: Locus:1.1.1.2359.22
Data file 2011-11-10 - TFD - EP 4-6.mgf

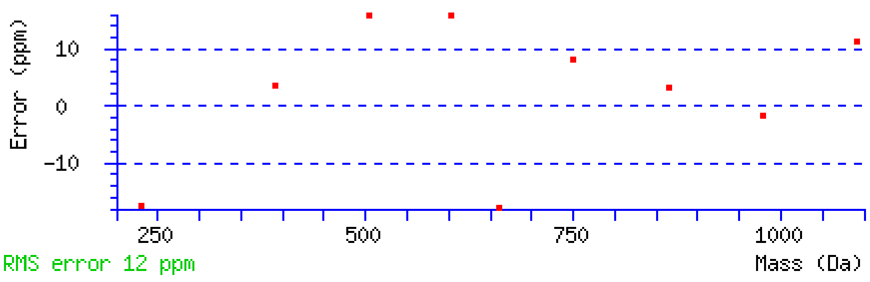
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1200] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1162.598236
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 65  Expect: 3.4e-006
Matches : 9/92 fragment ions using 10 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			A							11
2	185.128454	93.067865			L	***1092.568400***	546.787838	1075.541851	538.274564	1074.557835	537.782556	10
3	300.155397	150.581336	282.144832	141.576054	D	***979.484336***	490.245806	962.457787	481.732532	961.473771	481.240524	9
4	415.182340	208.094808	397.171775	199.089526	D	***864.457393***	432.732335	847.430844	424.219060	846.446828	423.727052	8
5	562.250754	281.629015	544.240189	272.623733	F	***749.430450***	375.218863	732.403901	366.705589	731.419885	366.213581	7
6	661.319168	331.163222	643.308603	322.157940	V	***602.362036***	301.684656	585.335487	293.171382	584.351471	292.679374	6
7	774.403232	387.705254	756.392667	378.699972	L	***503.293622***	252.150449	486.267073	243.637175	485.283057	243.145167	5
8	831.424696	416.215986	813.414131	407.210704	G	***390.209558***	195.608417	373.183009	187.095143	372.198993	186.603135	4
9	918.456724	459.732000	900.446159	450.726718	S	333.188094	167.097685	316.161545	158.584410	315.177529	158.092402	3
10	989.493838	495.250557	971.483273	486.245274	A	246.156066	123.581671	229.129517	115.068397			2
11					R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of ALDDFVLGSAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
64.7	1162.598236	-0.001268	ALDDFVLGSAR
6.2	1162.588333	0.008635	AIDSFPRWR
6.2	1162.586990	0.009978	SITLFPDENK
4.8	1162.598206	-0.001238	IATEAIENFR

Mascot: http://www.matrixscience.com/

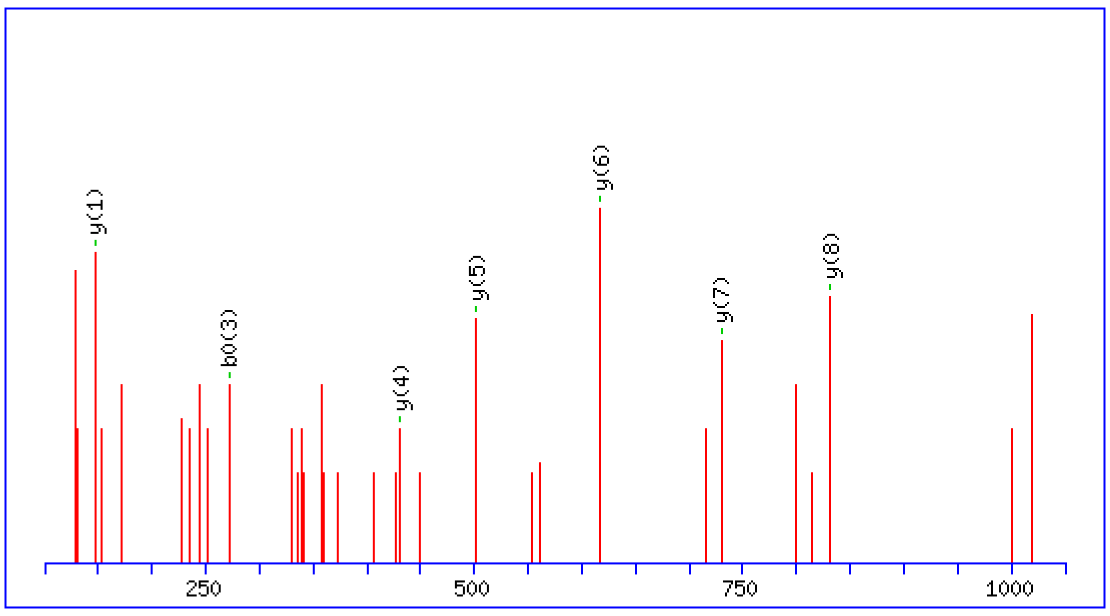
Mascot Search Results

Peptide View

MS/MS Fragmentation of **STTLDAGNIK**
Found in **PR40A_HUMAN**, Pre-mRNA-processing factor 40 homolog A OS=Homo sapiens GN=PRPF40A PE=1 SV=2

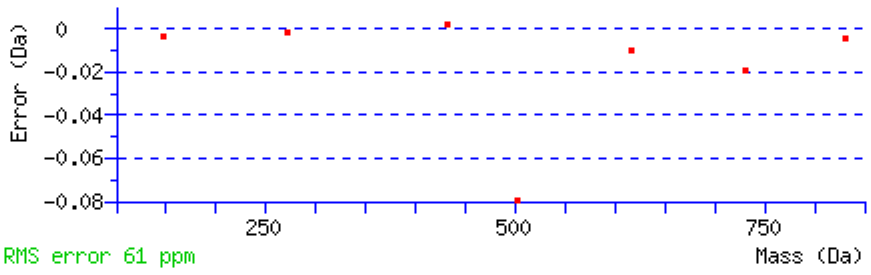
Match to Query 285857: 1018.526668 from(510.270610,2+) rtinseconds(1399) index(251309)
Title: Locus:1.1.1.977.10
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

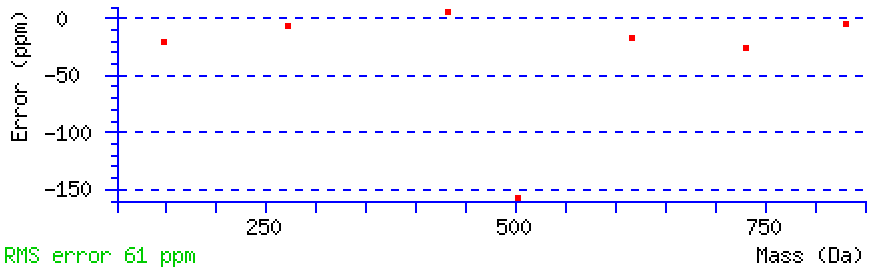
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1018.529480
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.0035
Matches : 7/84 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							10
2	189.086983	95.047129			171.076418	86.041847	T	932.504738	466.756007	915.478189	458.242733	914.494173	457.750725	9
3	290.134662	145.570969			272.124097	136.565687	T	***831.457059***	416.232168	814.430510	407.718893	813.446494	407.226885	8
4	403.218726	202.113001			385.208161	193.107719	L	***730.409380***	365.708328	713.382831	357.195054	712.398815	356.703046	7
5	518.245669	259.626473			500.235104	250.621190	D	***617.325316***	309.166296	600.298767	300.653022	599.314751	300.161014	6
6	589.282783	295.145030			571.272218	286.139747	A	***502.298373***	251.652824	485.271824	243.139550			5
7	646.304247	323.655762			628.293682	314.650479	G	***431.261259***	216.134267	414.234710	207.620993			4
8	760.347174	380.677225	743.320625	372.163951	742.336609	371.671943	N	374.239795	187.623535	357.213246	179.110261			3
9	873.431238	437.219257	856.404689	428.705983	855.420673	428.213975	I	260.196868	130.602072	243.170319	122.088798			2
10							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of STTLDAGNIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.8	1018.529480	-0.002812	STTLDAGNIK
16.4	1018.522949	0.003719	MGTKAQVER
15.7	1018.529465	-0.002797	QEKTGLESK
12.7	1018.529510	-0.002842	STVISGPGTGK
8.8	1018.536850	-0.010182	EQMLLLEK
7.1	1018.529480	-0.002812	SPSVSLSQSK
6.1	1018.529465	-0.002797	ESSTKPDKK
5.6	1018.529480	-0.002812	SKAGVTPESK
5.2	1018.529480	-0.002812	DSLGPTKSSK
5.0	1018.529465	-0.002797	TSEAAVKEGK

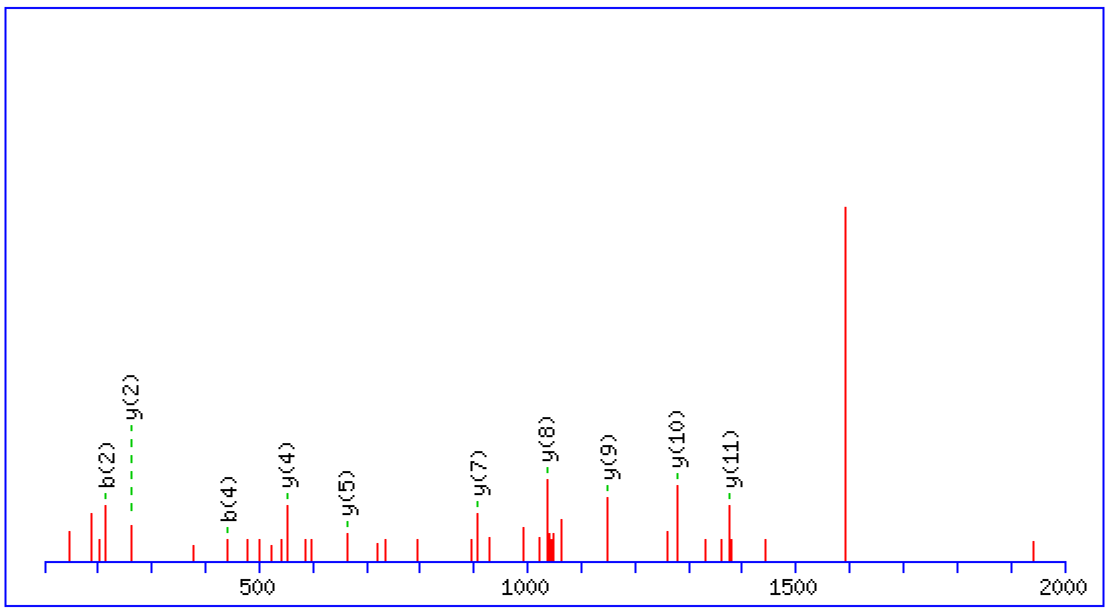
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TIVQLENEIYQIK**
Found in **SPF27_HUMAN**, Pre-mRNA-splicing factor SPF27 OS=Homo sapiens GN=BCAS2 PE=1 SV=1

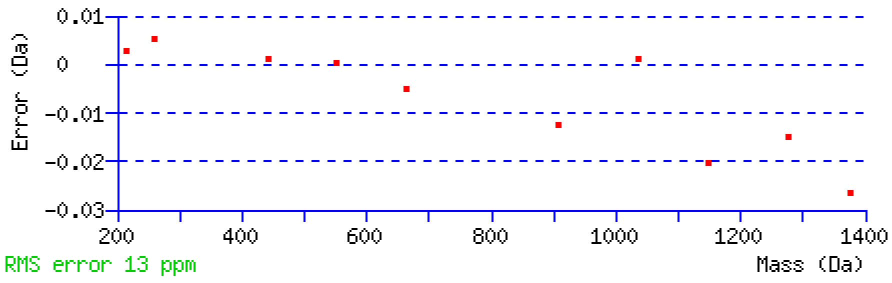
Match to Query 46129: 1589.860748 from(795.937650,2+) rtinseconds(3470) index(47864)
Title: Locus:1.1.1.2737.44
Data file 2011-11-13 - TFD - EP 7-5.mgf

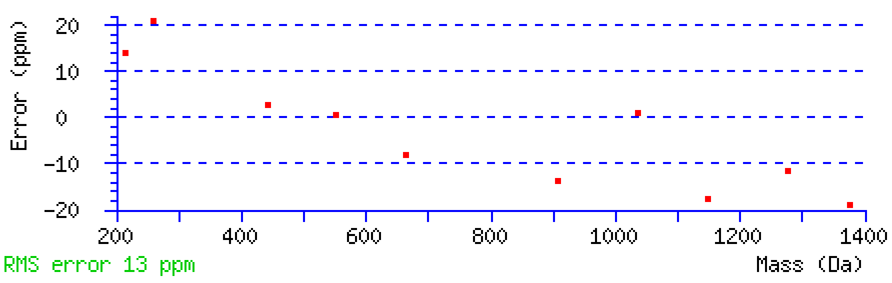
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1589.866440
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 66 **Expect:** 7.3e-007
Matches : 10/128 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							13
2	**215.139019**	108.073147			197.128454	99.067865	I	1489.826072	745.416674	1472.799523	736.903400	1471.815507	736.411392	12
3	314.207433	157.607354			296.196868	148.602072	V	***1376.742008***	688.874642	1359.715459	680.361368	1358.731443	679.869360	11
4	**442.266011**	221.636643	425.239462	213.123369	424.255446	212.631361	Q	***1277.673594***	639.340435	1260.647045	630.827161	1259.663029	630.335153	10
5	555.350075	278.178676	538.323526	269.665401	537.339510	269.173393	L	***1149.615016***	575.311146	1132.588467	566.797872	1131.604451	566.305863	9
6	684.392668	342.699972	667.366119	334.186698	666.382103	333.694690	E	***1036.530952***	518.769114	1019.504403	510.255840	1018.520387	509.763832	8
7	798.435595	399.721436	781.409046	391.208161	780.425030	390.716153	N	***907.488359***	454.247818	890.461810	445.734543	889.477794	445.242535	7
8	927.478188	464.242732	910.451639	455.729458	909.467623	455.237450	E	793.445432	397.226354	776.418883	388.713080	775.434867	388.221072	6
9	1040.562252	520.784764	1023.535703	512.271489	1022.551687	511.779481	I	***664.402839***	332.705058	647.376290	324.191783			5
10	1203.625581	602.316429	1186.599032	593.803154	1185.615016	593.311146	Y	***551.318775***	276.163026	534.292226	267.649751			4
11	1331.684159	666.345718	1314.657610	657.832443	1313.673594	657.340435	Q	388.255446	194.631361	371.228897	186.118087			3
12	1444.768223	722.887750	1427.741674	714.374475	1426.757658	713.882467	I	***260.196868***	130.602072	243.170319	122.088797			2
13							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of TIVQLENEIYQIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
66.2	1589.866440	-0.005692	TIVQLENEIYQIK
0.8	1589.867783	-0.007035	ASQARLHYLSGFIK
0.5	1589.859924	0.000824	LSLQELTWKMSVR
0.4	1589.866409	-0.005661	EKLALALENEGYIK

Mascot: http://www.matrixscience.com/

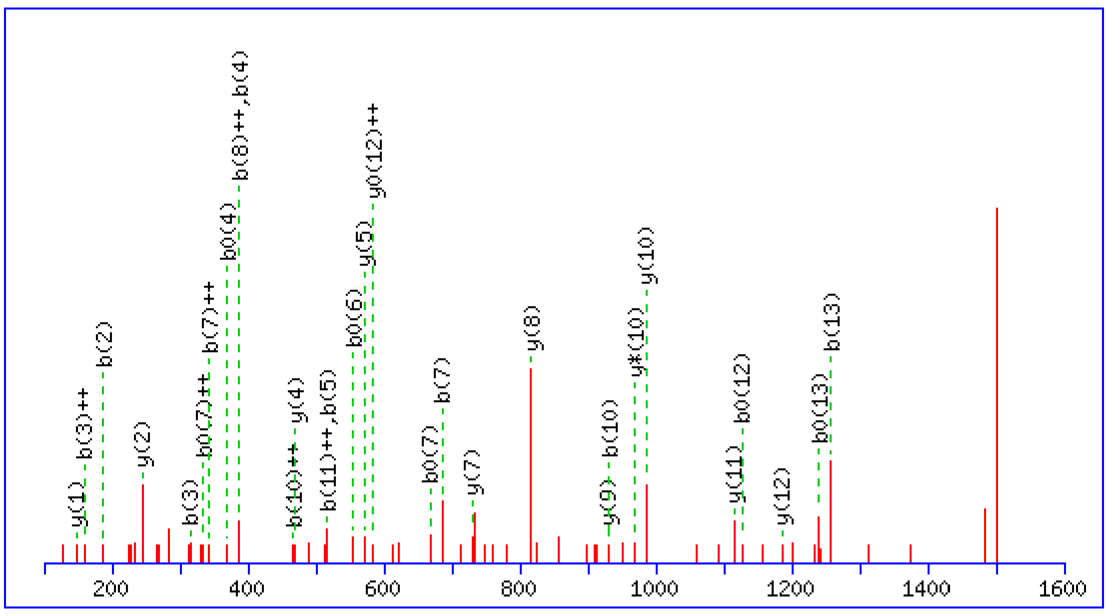
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DAEAEGLSGTTLLPK**
Found in **PRAF1_HUMAN**, Prenylated Rab acceptor protein 1 OS=Homo sapiens GN=RABAC1 PE=1 SV=1

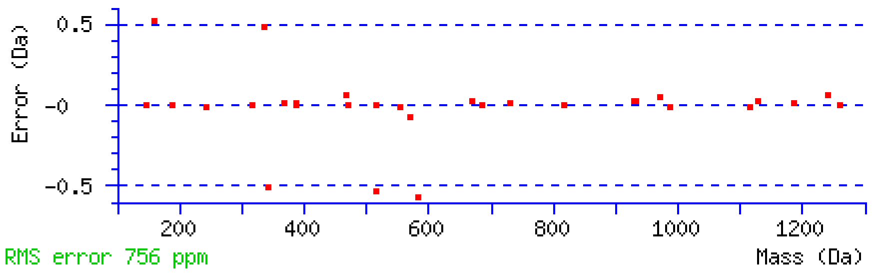
Match to Query 45281: 1500.770068 from(751.392310,2+) rtinseconds(2647) index(33095)
Title: Locus:1.1.1.2160.42
Data file 2011-11-12 - TFD - EP 6-6.mgf

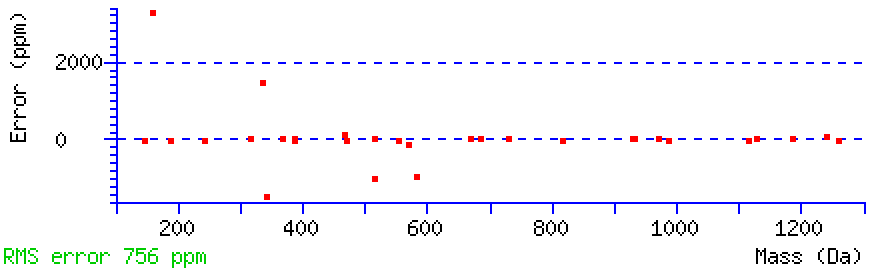
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1500.767136
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 58 **Expect:** 2e-005
Matches : 30/132 fragment ions using 56 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.034219	58.520748	98.023654	49.515465	D							15
2	**187.071333**	94.039304	169.060768	85.034022	A	1386.747488	693.877382	1369.720939	685.364108	1368.736923	684.872099	14
3	**316.113926**	**158.560601**	298.103361	149.555319	E	1315.710374	658.358825	1298.683825	649.845551	1297.699809	649.353543	13
4	**387.151040**	194.079158	369.140475	185.073876	A	***1186.667781***	593.837529	1169.641232	585.324254	1168.657216	584.832246	12
5	**516.193633**	258.600455	498.183068	249.595172	E	***1115.630667***	558.318972	1098.604118	549.805697	1097.620102	549.313689	11
6	573.215097	287.111187	555.204532	278.105904	G	***986.588074***	493.797675	969.561525	485.284401	968.577509	484.792393	10
7	**686.299161**	**343.653219**	668.288596	334.647936	L	***929.566610***	465.286943	912.540061	456.773668	911.556045	456.281660	9
8	773.331189	**387.169233**	755.320624	378.163950	S	***816.482546***	408.744911	799.455997	400.231636	798.471981	399.739628	8
9	830.352653	415.679965	812.342088	406.674682	G	***729.450518***	365.228897	712.423969	356.715622	711.439953	356.223615	7
10	**931.400332**	**466.203804**	913.389767	457.198522	T	672.429054	336.718165	655.402505	328.204890	654.418489	327.712882	6
11	1032.448011	**516.727644**	1014.437446	507.722361	T	***571.381375***	286.194325	554.354826	277.681051	553.370810	277.189043	5
12	1145.532075	573.269676	1127.521510	564.264393	L	***470.333696***	235.670486	453.307147	227.157211			4
13	**1258.616139**	629.811708	1240.605574	620.806425	L	357.249632	179.128454	340.223083	170.615179			3
14	1355.668903	678.338090	1337.658338	669.332807	P	***244.165568***	122.586422	227.139019	114.073148			2
15					K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of DAEAEGLSGTTLLPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.4	1500.767136	0.002932	DAEAEGLSGTTLLPK
9.4	1500.760620	0.009448	GIEPTGNMVKQPAK
7.3	1500.760620	0.009448	GIEPTGNMVKQPAK
4.2	1500.779709	-0.009641	ERPTSPAPHRPPK
1.8	1500.760620	0.009448	GIEPTGNMVKQPAK
1.5	1500.771835	-0.001767	RENIVGDAMEVLR
0.2	1500.779724	-0.009656	RHRPSPPATPPPK
0.2	1500.779724	-0.009656	RHRPSPPATPPPK

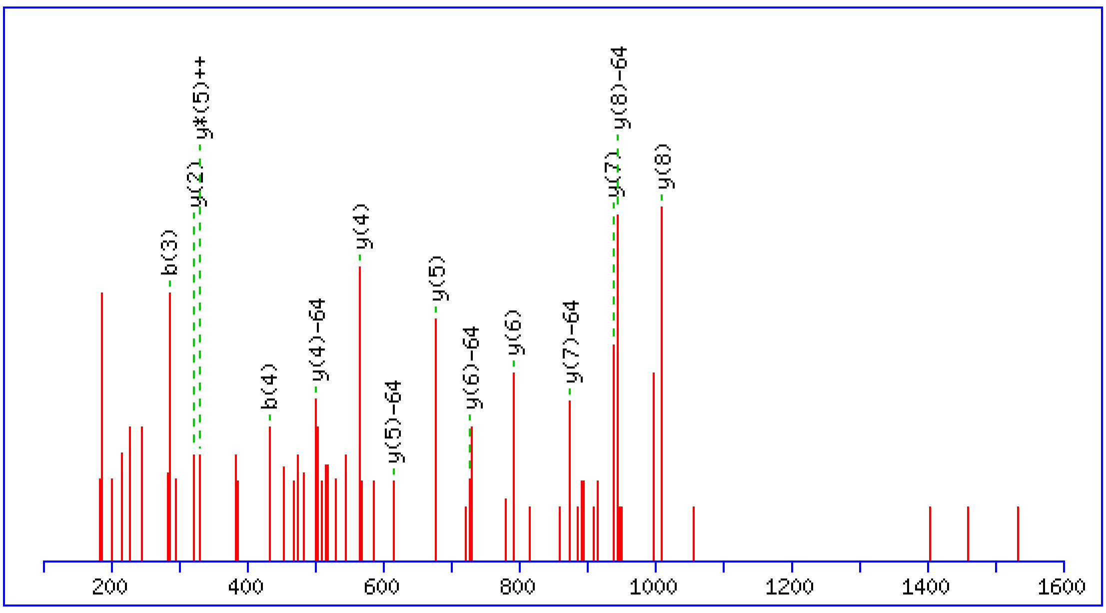
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TIAFLLPMFR**
Found in **DDX46_HUMAN**, Probable ATP-dependent RNA helicase DDX46 OS=Homo sapiens GN=DDX46 PE=1 SV=2

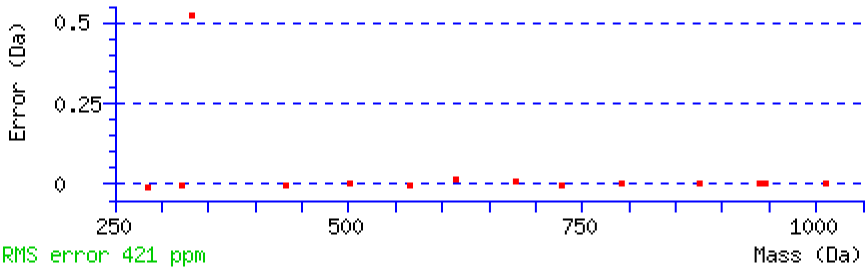
Match to Query 30804: 1223.666308 from(612.840430,2+) rtinseconds(3797) index(55639)
Title: Locus:1.1.1.2837.17
Data file 2011-11-14 - TFD - EP 8-1.mgf

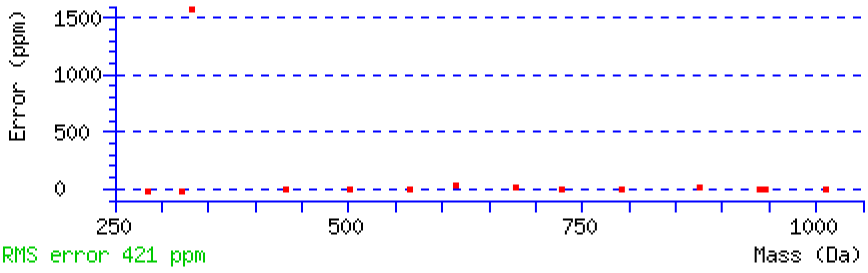
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1223.673645
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M8 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 31 **Expect:** 0.0059
Matches : 14/108 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	102.054955	51.531116	84.044390	42.525833	T					10
2	215.139019	108.073147	197.128454	99.067865	I	1123.633250	562.320263	1106.606701	553.806989	9
3	**286.176133**	143.591704	268.165568	134.586422	A	***1010.549186***	505.778231	993.522637	497.264957	8
4	**433.244547**	217.125911	415.233982	208.120629	F	***939.512072***	470.259674	922.485523	461.746400	7
5	546.328611	273.667944	528.318046	264.662661	L	***792.443658***	396.725467	775.417109	388.212193	6
6	659.412675	330.209976	641.402110	321.204693	L	***679.359594***	340.183435	662.333045	331.670161	5
7	756.465439	378.736358	738.454874	369.731075	P	***566.275530***	283.641403	549.248981	275.128129	4
8	903.500839	452.254058	885.490274	443.248775	M	469.222766	235.115021	452.196217	226.601746	3
9	1050.569253	525.788265	1032.558688	516.782982	F	***322.187366***	161.597321	305.160817	153.084047	2
10					R	175.118952	88.063114	158.092403	79.549839	1





NCBI **BLAST** search of TIAFLLPMFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.2	1223.673645	-0.007337	TIAFLLPMFR
22.4	1223.673645	-0.007337	TIAFLLPMFR

Mascot: http://www.matrixscience.com/

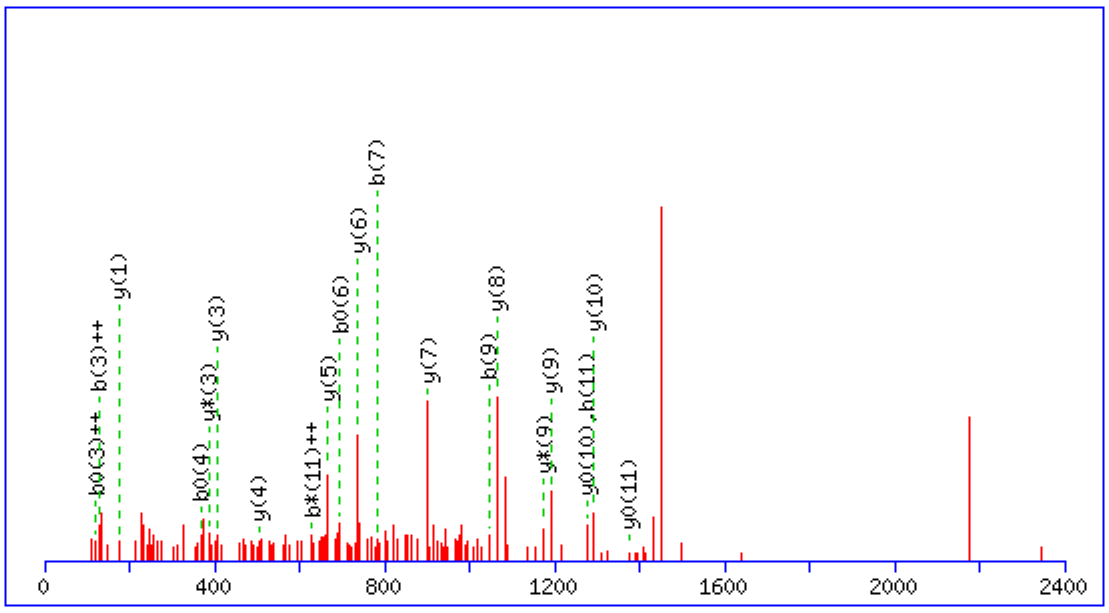
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GVTQYYAYVTER**
Found in **DDX6_HUMAN**, Probable ATP-dependent RNA helicase DDX6 OS=Homo sapiens GN=DDX6 PE=1 SV=2

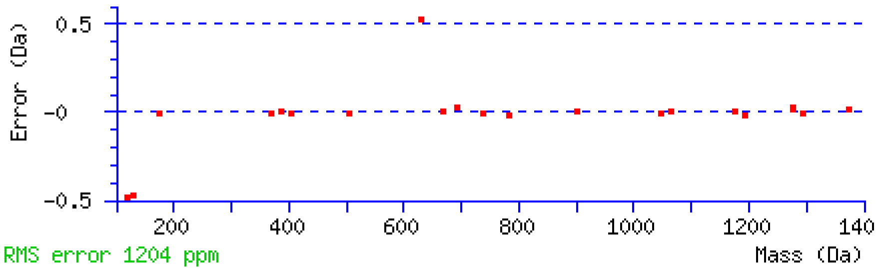
Match to Query 38954: 1448.694408 from(725.354480,2+) rtinseconds(2645) index(35059)
Title: Locus:1.1.1.2495.43
Data file 2011-11-10 - TFD - EP 4-3.mgf

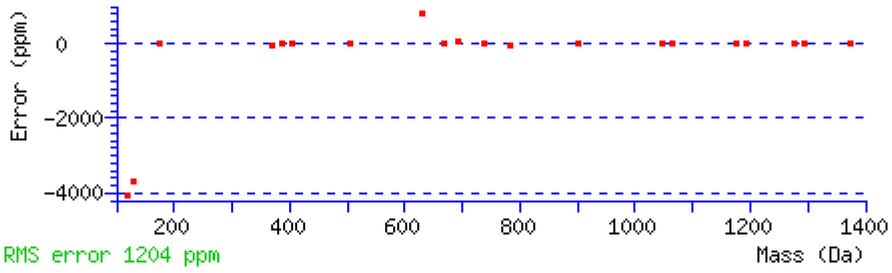
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1448.693588
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.0032
Matches : 21/120 fragment ions using 67 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	58.028740	29.518008					G							12
2	157.097154	79.052215					V	1392.679410	696.843343	1375.652861	688.330069	1374.668845	687.838061	11
3	258.144833	129.576055			240.134268	120.570772	T	***1293.610996***	647.309136	1276.584447	638.795862	1275.600431	638.303854	10
4	386.203411	193.605344	369.176862	185.092069	368.192846	184.600061	Q	***1192.563317***	596.785297	1175.536768	588.272022	1174.552752	587.780014	9
5	549.266740	275.137008	532.240191	266.623734	531.256175	266.131726	Y	***1064.504739***	532.756008	1047.478190	524.242733	1046.494174	523.750725	8
6	712.330069	356.668673	695.303520	348.155398	694.319504	347.663390	Y	***901.441410***	451.224343	884.414861	442.711069	883.430845	442.219061	7
7	**783.367183**	392.187230	766.340634	383.673955	765.356618	383.181947	A	***738.378081***	369.692679	721.351532	361.179404	720.367516	360.687396	6
8	946.430512	473.718894	929.403963	465.205620	928.419947	464.713612	Y	***667.340967***	334.174122	650.314418	325.660847	649.330402	325.168839	5
9	**1045.498926**	523.253101	1028.472377	514.739827	1027.488361	514.247819	V	***504.277638***	252.642457	487.251089	244.129183	486.267073	243.637175	4
10	1146.546605	573.776941	1129.520056	565.263666	1128.536040	564.771658	T	***405.209224***	203.108250	388.182675	194.594976	387.198659	194.102968	3
11	**1275.589198**	638.298237	1258.562649	629.784963	1257.578633	629.292955	E	304.161545	152.584411	287.134996	144.071136	286.150980	143.579128	2
12							R	***175.118952***	88.063114	158.092403	79.549839			1



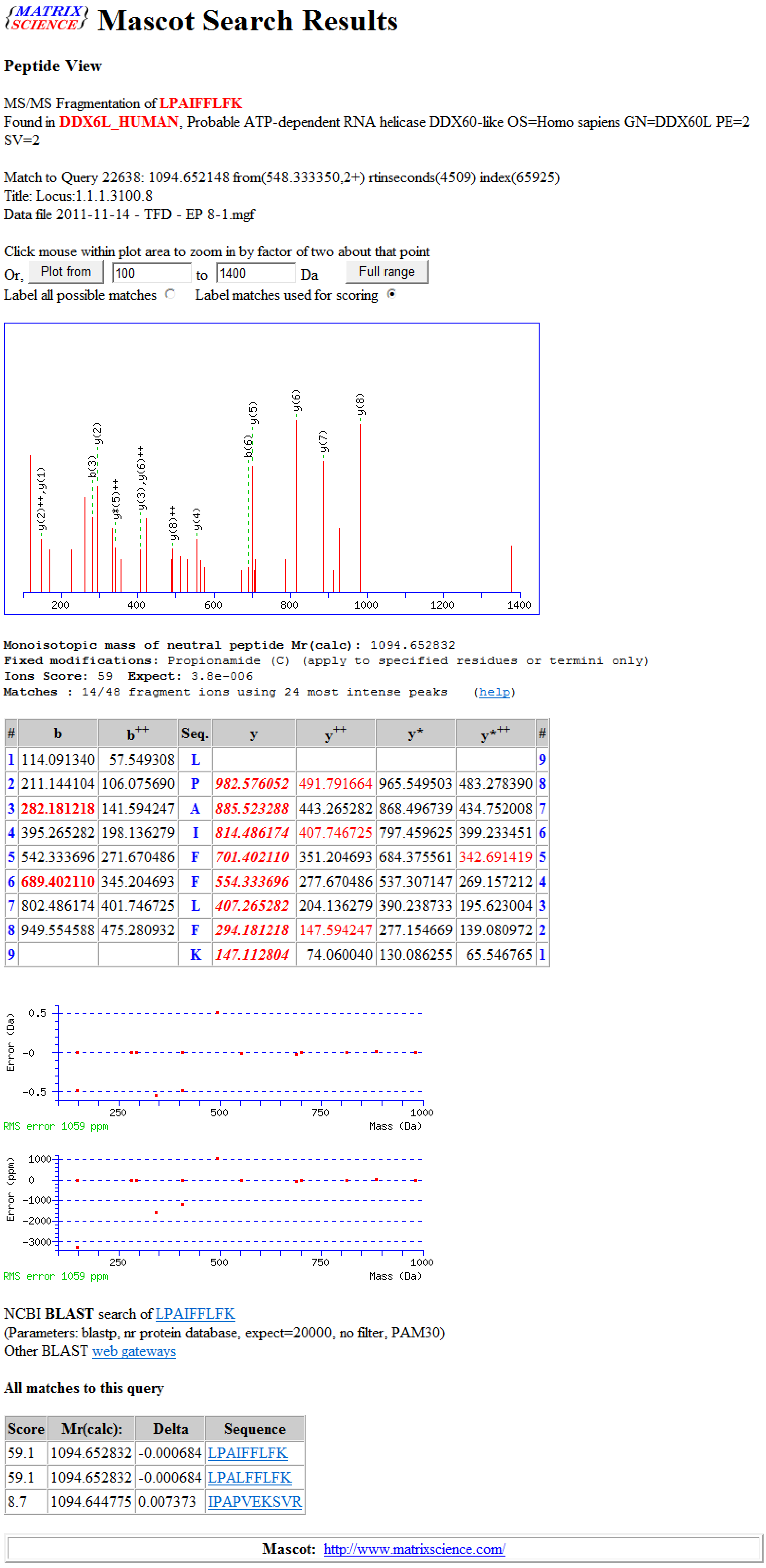


NCBI **BLAST** search of GVTQYYAYVTER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.9	1448.693588	0.000820	GVTQYYAYVTER
0.3	1448.685547	0.008861	QKSPAQSDSTTQR

Mascot: http://www.matrixscience.com/



{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LPAIFFLFK**
Found in **DDX6L_HUMAN**, Probable ATP-dependent RNA helicase DDX60-like OS=Homo sapiens GN=DDX60L PE=2 SV=2

Match to Query 22638: 1094.652148 from(548.333350,2+) rtinseconds(4509) index(65925)
Title: Locus:1.1.1.3100.8
Data file 2011-11-14 - TFD - EP 8-1.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
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1094.652832
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 59 **Expect:** 3.8e-006
Matches : 14/48 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	Seq.	y	y^{++}	y^*	y^{*++}	#
1	114.091340	57.549308	L					9
2	211.144104	106.075690	P	***982.576052***	491.791664	965.549503	483.278390	8
3	**282.181218**	141.594247	A	***885.523288***	443.265282	868.496739	434.752008	7
4	395.265282	198.136279	I	***814.486174***	407.746725	797.459625	399.233451	6
5	542.333696	271.670486	F	***701.402110***	351.204693	684.375561	342.691419	5
6	**689.402110**	345.204693	F	***554.333696***	277.670486	537.307147	269.157212	4
7	802.486174	401.746725	L	***407.265282***	204.136279	390.238733	195.623004	3
8	949.554588	475.280932	F	***294.181218***	147.594247	277.154669	139.080972	2
9			K	***147.112804***	74.060040	130.086255	65.546765	1

RMS error 1059 ppm

RMS error 1059 ppm

NCBI **BLAST** search of LPAIFFLFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
59.1	1094.652832	-0.000684	LPAIFFLFK
59.1	1094.652832	-0.000684	LPALFFLFK
8.7	1094.644775	0.007373	IPAPVEKSVR

Mascot: http://www.matrixscience.com/

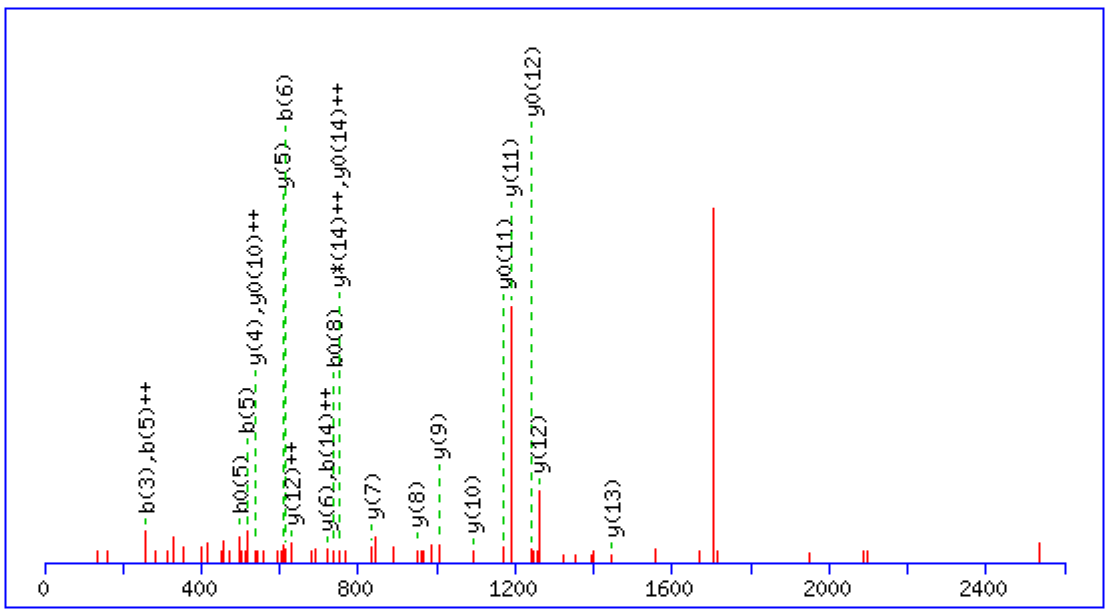
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SVAWAPSGNLLATCSR**
Found in **CIAO1_HUMAN**, Probable cytosolic iron-sulfur protein assembly protein CIAO1 OS=Homo sapiens GN=CIAO1 PE=1 SV=1

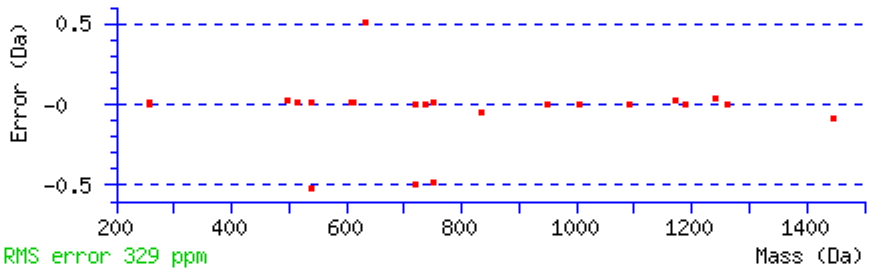
Match to Query 54833: 1702.850168 from(852.432360,2+) rtinseconds(2898) index(39565)
Title: Locus:1.1.1.2444.46
Data file 2011-11-10 - TFD - EP 3-4.mgf

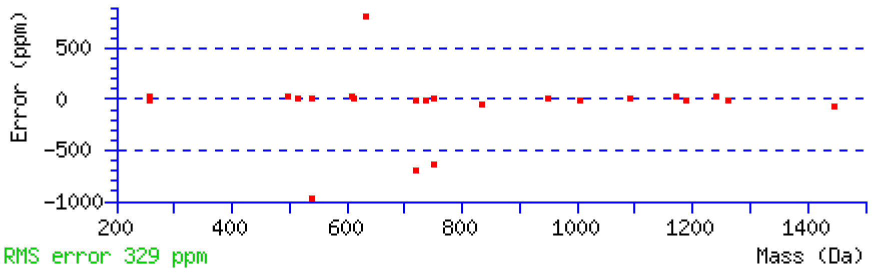
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1702.846069
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 48  Expect: 8.6e-005
Matches : 23/162 fragment ions using 48 most intense peaks   (help)
```

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							16
2	187.107718	94.057497			169.097153	85.052214	V	1616.821338	808.914307	1599.794789	800.401033	1598.810773	799.909025	15
3	**258.144832**	129.576054			240.134267	120.570772	A	1517.752924	759.380100	1500.726375	750.866826	1499.742359	750.374818	14
4	444.224145	222.615711			426.213580	213.610428	W	***1446.715810***	723.861543	1429.689261	715.348269	1428.705245	714.856261	13
5	**515.261259**	258.134268			497.250694	249.128985	A	***1260.636497***	630.821887	1243.609948	622.308612	1242.625932	621.816604	12
6	**612.314023**	306.660650			594.303458	297.655367	P	***1189.599383***	595.303330	1172.572834	586.790055	1171.588818	586.298047	11
7	699.346051	350.176664			681.335486	341.171381	S	***1092.546619***	546.776948	1075.520070	538.263673	1074.536054	537.771665	10
8	756.367515	378.687396			738.356950	369.682113	G	***1005.514591***	503.260934	988.488042	494.747659	987.504026	494.255651	9
9	870.410442	435.708859	853.383893	427.195585	852.399877	426.703577	N	***948.493127***	474.750202	931.466578	466.236927	930.482562	465.744919	8
10	983.494506	492.250891	966.467957	483.737617	965.483941	483.245609	L	***834.450200***	417.728738	817.423651	409.215464	816.439635	408.723456	7
11	1096.578570	548.792923	1079.552021	540.279649	1078.568005	539.787641	L	***721.366136***	361.186706	704.339587	352.673432	703.355571	352.181424	6
12	1167.615684	584.311480	1150.589135	575.798206	1149.605119	575.306198	A	***608.282072***	304.644674	591.255523	296.131400	590.271507	295.639392	5
13	1268.663363	634.835320	1251.636814	626.322045	1250.652798	625.830037	T	***537.244958***	269.126117	520.218409	260.612843	519.234393	260.120835	4
14	1442.709662	721.858469	1425.683113	713.345195	1424.699097	712.853187	C	436.197279	218.602278	419.170730	210.089003	418.186714	209.596995	3
15	1529.741690	765.374483	1512.715141	756.861209	1511.731125	756.369201	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
16							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of SVAWAPSGNLLATCSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.3	1702.846069	0.004099	SVAWAPSGNLLATCSR
4.6	1702.855957	-0.005789	VASALPGMENVQEKSK
2.5	1702.863815	-0.013647	EQYILATQQNNLPR
0.2	1702.849426	0.000742	ALAKMMGGAGPGSSLEAR

Mascot: http://www.matrixscience.com/

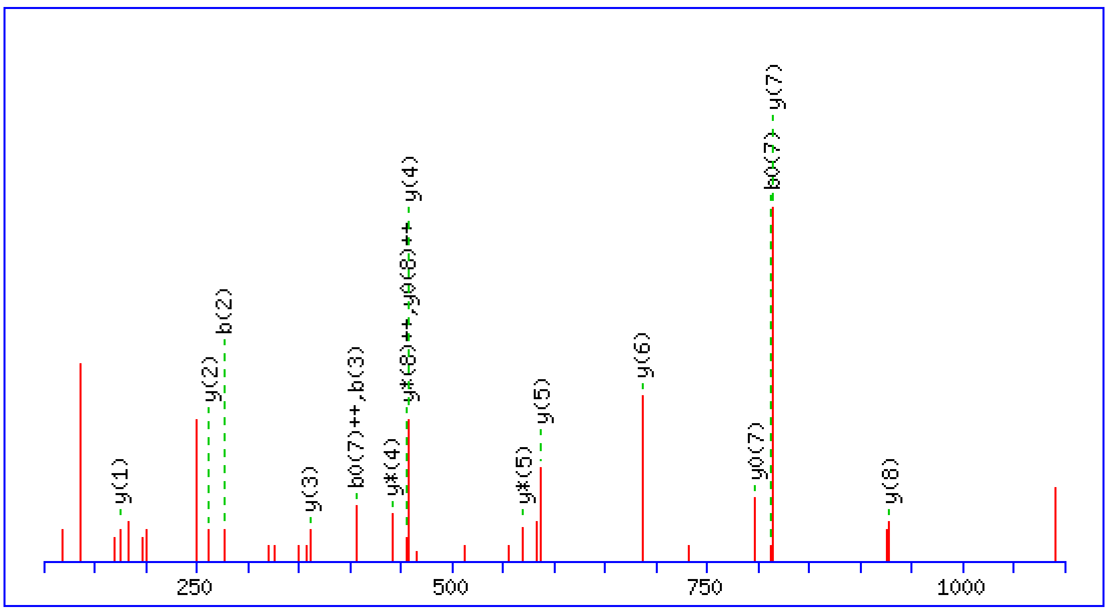
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YLEVEPVSR**
Found in **ERG28_HUMAN**, Probable ergosterol biosynthetic protein 28 OS=Homo sapiens GN=C14orf1 PE=1 SV=1

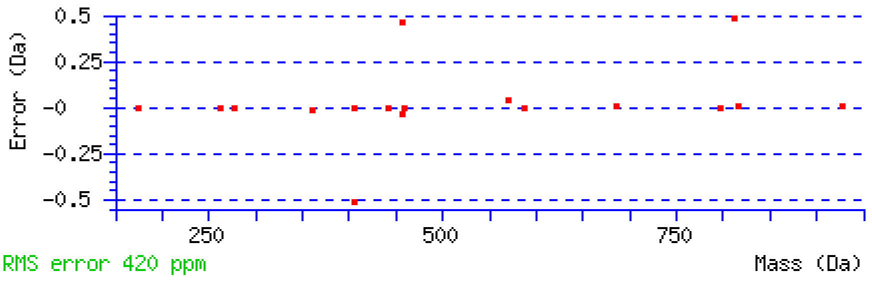
Match to Query 20771: 1090.564428 from(546.289490,2+) rtinseconds(1938) index(15228)
Title: Locus:1.1.1.2189.25
Data file 2011-11-13 - TFD - EP 7-7.mgf

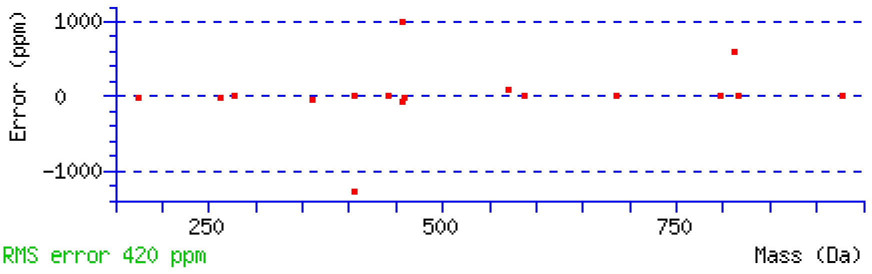
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1090.565857
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 71  Expect: 1.1e-006
Matches : 17/74 fragment ions using 21 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.070605	82.538940			Y							9
2	**277.154669**	139.080973			L	***928.509822***	464.758549	911.483273	456.245274	910.499257	455.753267	8
3	**406.197262**	203.602269	388.186697	194.596987	E	***815.425758***	408.216517	798.399209	399.703243	797.415193	399.211235	7
4	505.265676	253.136476	487.255111	244.131194	V	***686.383165***	343.695221	669.356616	335.181946	668.372600	334.689938	6
5	634.308269	317.657773	616.297704	308.652490	E	***587.314751***	294.161014	570.288202	285.647739	569.304186	285.155731	5
6	731.361033	366.184155	713.350468	357.178872	P	***458.272158***	229.639717	441.245609	221.126442	440.261593	220.634434	4
7	830.429447	415.718362	812.418882	406.713079	V	***361.219394***	181.113335	344.192845	172.600060	343.208829	172.108052	3
8	917.461475	459.234376	899.450910	450.229093	S	***262.150980***	131.579128	245.124431	123.065853	244.140415	122.573845	2
9					R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of YLEVEPVSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
70.8	1090.565857	-0.001429	YLEVEPVSR
14.7	1090.569229	-0.004801	VLSGPMEKAK
12.7	1090.559326	0.005102	YLPALQGCR
5.3	1090.555969	0.008459	YLFVEHQR
4.1	1090.555969	0.008459	YLFHEVQR
2.3	1090.573944	-0.009516	VARIMVCGR
2.2	1090.567184	-0.002756	YNARFPPAR
1.9	1090.565857	-0.001429	YDGPIEILR

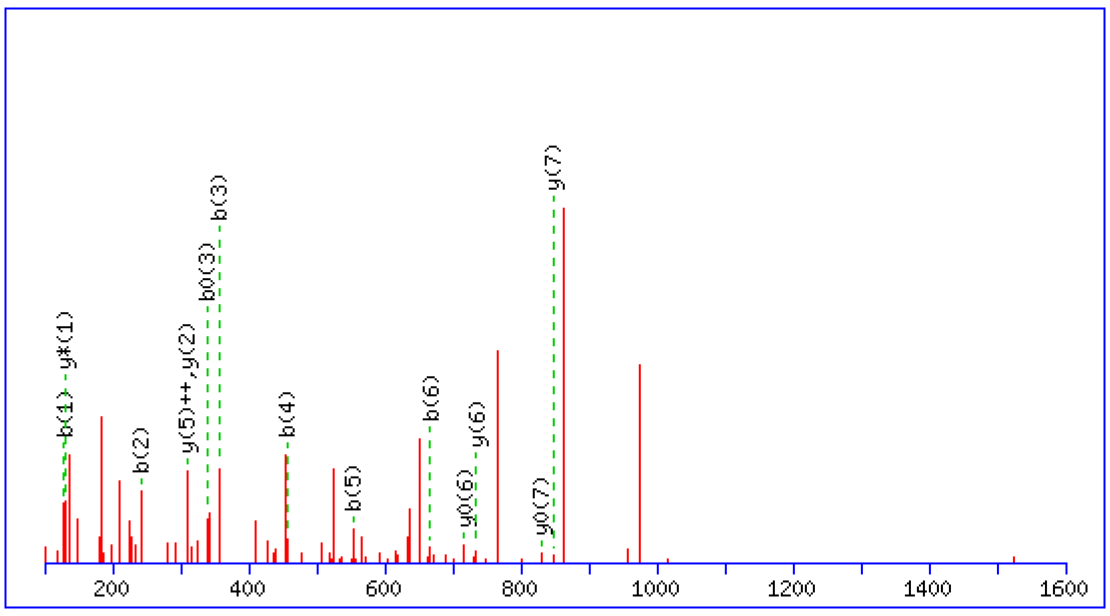
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KPDVPLYK**
Found in **ASH1L_HUMAN**, Probable histone-lysine N-methyltransferase ASH1L OS=Homo sapiens GN=ASH1L PE=1 SV=2

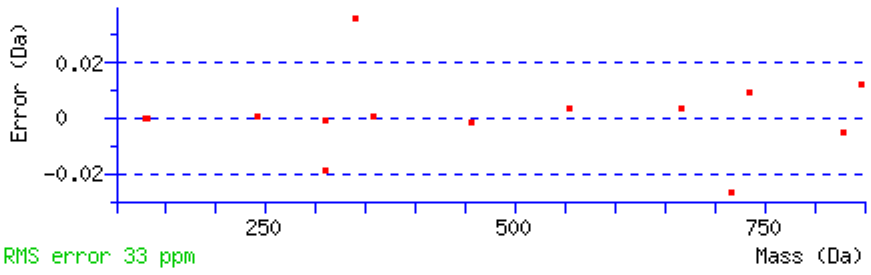
Match to Query 13397: 974.545668 from(488.280110,2+) rtinseconds(2208) index(26940)
Title: Locus:1.1.1.2168.11
Data file 2011-11-10 - TFD - EP 4-4.mgf

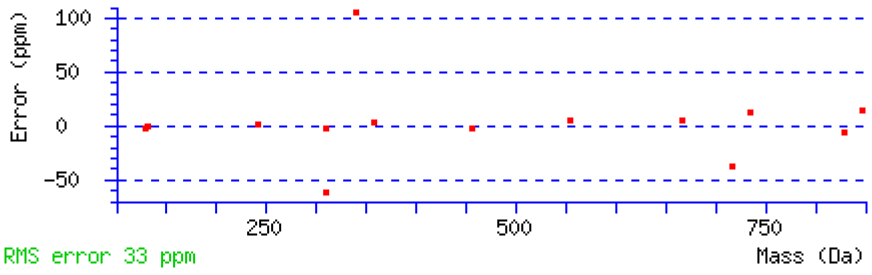
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 974.543671
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P2      : Oxidation (P)
Ions Score: 36  Expect: 0.0024
Matches : 15/70 fragment ions using 33 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	***129.102239***	65.054757	112.075690	56.541483			K							8
2	***242.149918***	121.578597	225.123369	113.065322			P	**847.455997**	424.231637	830.429448	415.718362	829.445432	415.226354	7
3	***357.176861***	179.092068	340.150312	170.578794	339.166296	170.086786	D	**734.408318**	367.707797	717.381769	359.194523	716.397753	358.702515	6
4	***456.245275***	228.626275	439.218726	220.113001	438.234710	219.620993	V	619.381375	310.194326	602.354826	301.681051			5
5	***553.298039***	277.152658	536.271490	268.639383	535.287474	268.147375	P	520.312961	260.660119	503.286412	252.146844			4
6	***666.382103***	333.694690	649.355554	325.181415	648.371538	324.689407	L	423.260197	212.133736	406.233648	203.620462			3
7	***829.445432***	415.226354	812.418883	406.713079	811.434867	406.221071	Y	**310.176133**	155.591704	293.149584	147.078430			2
8							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of KPDVPLYK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.4	974.543671	0.001997	LPLQDVYK
36.2	974.543671	0.001997	KPDVPLYK
22.6	974.543671	0.001997	QLDVLYPK
21.0	974.547043	-0.001375	MPIVDKLK
20.2	974.543686	0.001982	QLDFLPVK
19.5	974.543671	0.001997	QDVYLLPK
17.4	974.554916	-0.009248	TVRVPYPK
16.6	974.554901	-0.009233	KLDFPALR
14.1	974.543671	0.001997	KPDVPLYK
13.6	974.543671	0.001997	INLPDFLK

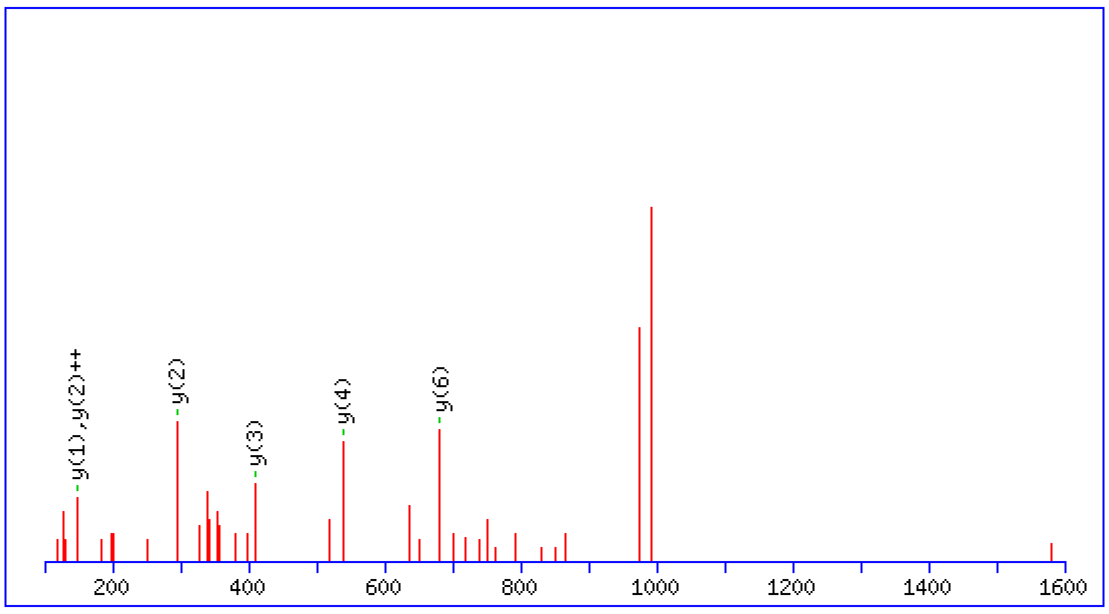
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LKDWPSGEDFK**
Found in **JHD2C_HUMAN**, Probable JmjC domain-containing histone demethylation protein 2C OS=Homo sapiens GN=JMJD1C PE=1 SV=2

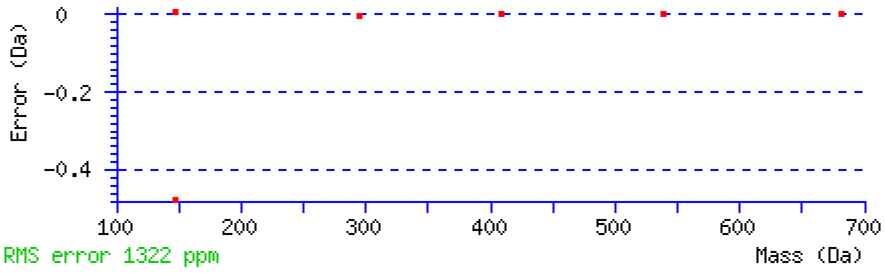
Match to Query 663738: 1320.634008 from(661.324280,2+) rtinseconds(2279) index(760703)
Title: Locus:1.1.1.1214.33
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

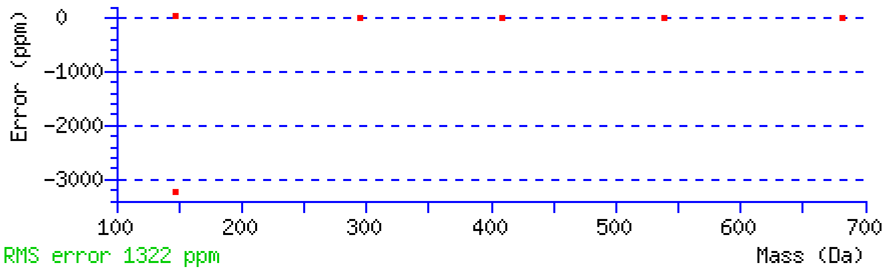
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1320.635010
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.0039
Matches : 6/110 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							11
2	242.186303	121.596790	225.159754	113.083515			K	1208.558229	604.782753	1191.531680	596.269478	1190.547664	595.777470	10
3	357.213246	179.110261	340.186697	170.596987	339.202681	170.104979	D	1080.463266	540.735271	1063.436717	532.221997	1062.452701	531.729989	9
4	543.292559	272.149918	526.266010	263.636643	525.281994	263.144635	W	965.436323	483.221800	948.409774	474.708525	947.425758	474.216517	8
5	640.345323	320.676300	623.318774	312.163025	622.334758	311.671017	P	779.357010	390.182143	762.330461	381.668869	761.346445	381.176861	7
6	727.377351	364.192314	710.350802	355.679039	709.366786	355.187031	S	***682.304246***	341.655761	665.277697	333.142487	664.293681	332.650479	6
7	784.398815	392.703046	767.372266	384.189771	766.388250	383.697763	G	595.272218	298.139747	578.245669	289.626473	577.261653	289.134465	5
8	913.441408	457.224342	896.414859	448.711068	895.430843	448.219060	E	***538.250754***	269.629015	521.224205	261.115741	520.240189	260.623733	4
9	1028.468351	514.737814	1011.441802	506.224539	1010.457786	505.732531	D	***409.208161***	205.107719	392.181612	196.594444	391.197596	196.102436	3
10	1175.536765	588.272021	1158.510216	579.758746	1157.526200	579.266738	F	***294.181218***	147.594247	277.154669	139.080973			2
11							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of LKDWPSGEDFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.8	1320.635010	-0.001002	LKDWPSGEDFK
5.8	1320.635712	-0.001704	RVSPPSCPPHR
5.7	1320.638397	-0.004389	TPQPPPPSPPMK
4.5	1320.627136	0.006872	MDPPSEIYPLK
3.3	1320.627136	0.006872	MDPPSEIYPLK
2.5	1320.627136	0.006872	MDPPSEIYPLK
1.3	1320.623123	0.010885	GVAINMVTEEDK
1.1	1320.642242	-0.008234	PGQPPPSSGTPQR

Mascot: http://www.matrixscience.com/

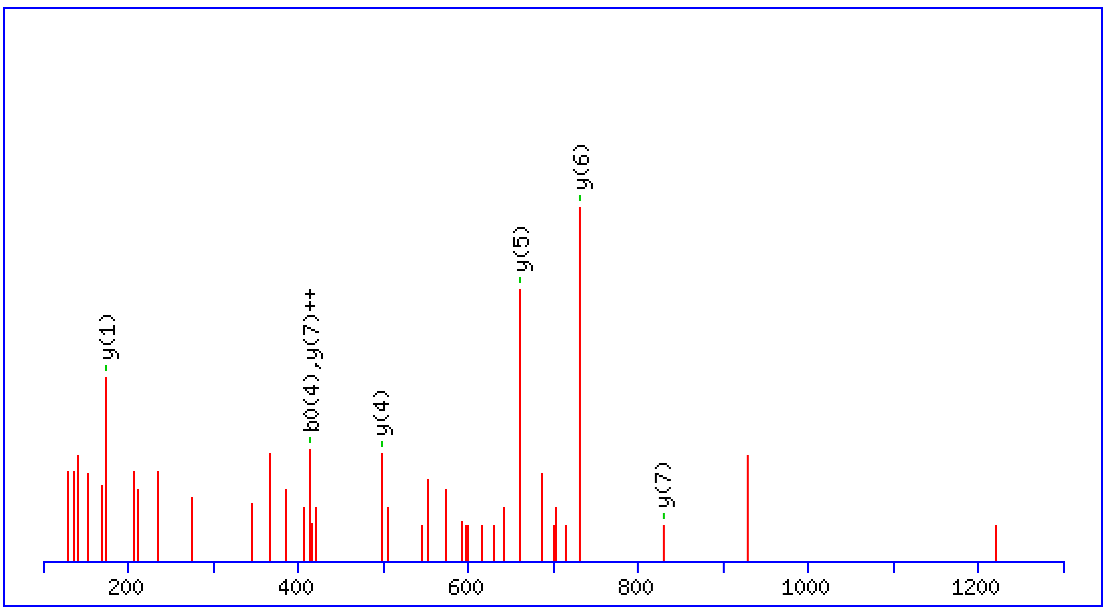
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TPAYIPIR**
Found in **GT251_HUMAN**, Procollagen galactosyltransferase 1 OS=Homo sapiens GN=GLT25D1 PE=1 SV=1

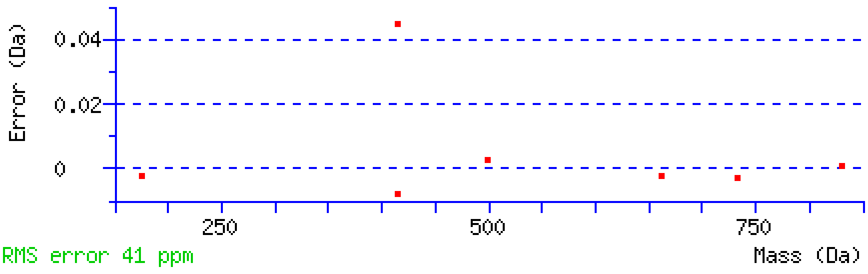
Match to Query 10557: 929.532988 from(465.773770,2+) rtinseconds(2069) index(23731)
Title: Locus:1.1.1.2230.14
Data file 2011-11-10 - TFD - EP 3-2.mgf

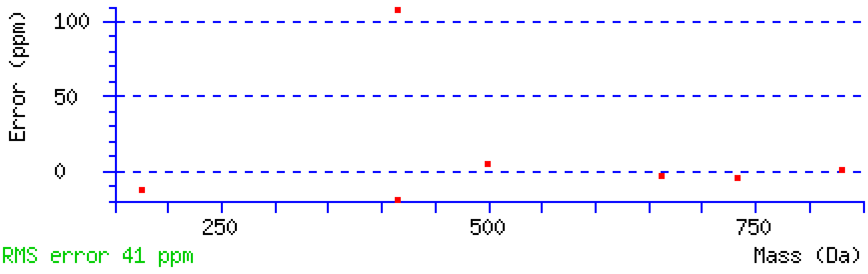
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 929.533432
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 37 **Expect:** 0.0021
Matches : 7/56 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	102.054955	51.531116	84.044390	42.525833	T					8
2	199.107719	100.057497	181.097154	91.052215	P	***829.493051***	415.250164	812.466502	406.736889	7
3	270.144833	135.576055	252.134268	126.570772	A	***732.440287***	366.723782	715.413738	358.210507	6
4	433.208162	217.107719	415.197597	208.102437	Y	***661.403173***	331.205225	644.376624	322.691950	5
5	546.292226	273.649751	528.281661	264.644469	I	***498.339844***	249.673560	481.313295	241.160286	4
6	643.344990	322.176133	625.334425	313.170851	P	385.255780	193.131528	368.229231	184.618254	3
7	756.429054	378.718165	738.418489	369.712883	I	288.203016	144.605146	271.176467	136.091872	2
8					R	***175.118952***	88.063114	158.092403	79.549840	1





NCBI **BLAST** search of TPAYIPIR
(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	929.533432	-0.000444	TPAYIPIR
10.7	929.529434	0.003554	VVATNTLGR
10.2	929.536804	-0.003816	LLSPLMTR
2.9	929.540649	-0.007661	LRAQSVTR
1.9	929.536819	-0.003831	MVVLSLPR
0.8	929.540649	-0.007661	RPSLKTGR
0.8	929.529419	0.003569	TSINGLLGR

Mascot: http://www.matrixscience.com/

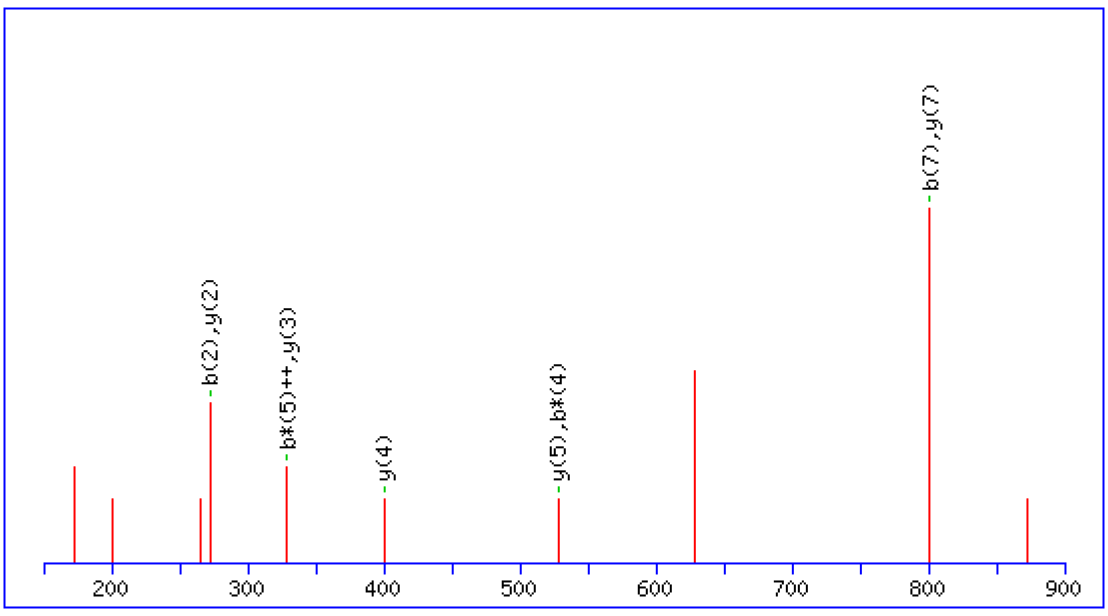
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DRCPQAGPR**
Found in **PRR16_HUMAN**, Proline-rich protein 16 OS=Homo sapiens GN=PRR16 PE=2 SV=1

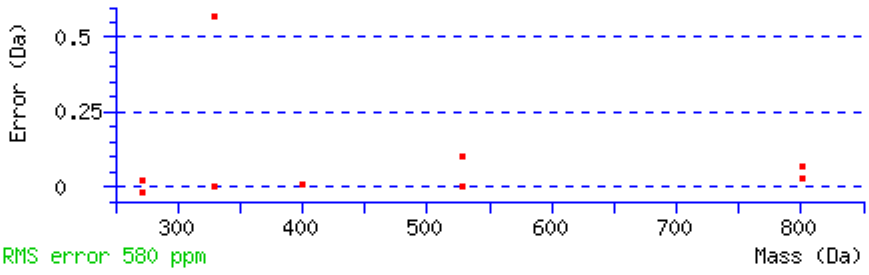
Match to Query 356413: 1071.495588 from(536.755070,2+) rtinseconds(1061) index(77773)
Title: Locus:1.1.1.1258.22
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

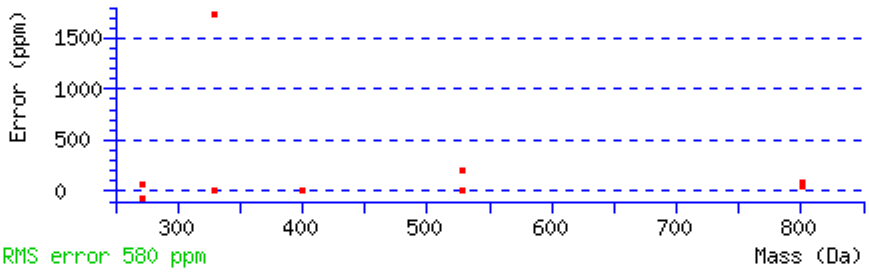
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1071.487976
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
P4 : Oxidation (P)
Ions Score: 45 **Expect:** 0.00028
Matches : 9/78 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	116.034219	58.520748			98.023654	49.515465	D					9
2	**272.135330**	136.571303	255.108781	128.058029	254.124765	127.566021	R	957.468311	479.237794	940.441762	470.724519	8
3	432.165979	216.586628	415.139430	208.073353	414.155414	207.581345	C	***801.367200***	401.187238	784.340651	392.673964	7
4	545.213658	273.110467	528.187109	264.597193	527.203093	264.105185	P	641.336551	321.171914	624.310002	312.658639	6
5	673.272236	337.139756	656.245687	328.626482	655.261671	328.134474	Q	***528.288872***	264.648074	511.262323	256.134800	5
6	744.309350	372.658313	727.282801	364.145039	726.298785	363.653031	A	***400.230294***	200.618785	383.203745	192.105510	4
7	**801.330814**	401.169045	784.304265	392.655771	783.320249	392.163763	G	***329.193180***	165.100228	312.166631	156.586953	3
8	898.383578	449.695427	881.357029	441.182153	880.373013	440.690145	P	***272.171716***	136.589496	255.145167	128.076221	2
9							R	175.118952	88.063114	158.092403	79.549839	1





NCBI **BLAST** search of DRCPQAGPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.3	1071.487976	0.007612	DRCPQAGPR
21.1	1071.501892	-0.006304	ISAGPSHVAAM
15.3	1071.490646	0.004942	VTAEEAPQPM
12.5	1071.494690	0.000898	SPALVYPFM
5.5	1071.501877	-0.006289	MEVAPEQPR
5.5	1071.501877	-0.006289	MEVAPEQPR
4.4	1071.487976	0.007612	DRCPQAGPR
4.4	1071.501907	-0.006319	GDMPPSVTPR
4.4	1071.501907	-0.006319	GDMPPSVTPR
3.8	1071.501907	-0.006319	GDMPPSVTPR

Mascot: http://www.matrixscience.com/

{MATRIX SCIENCE}

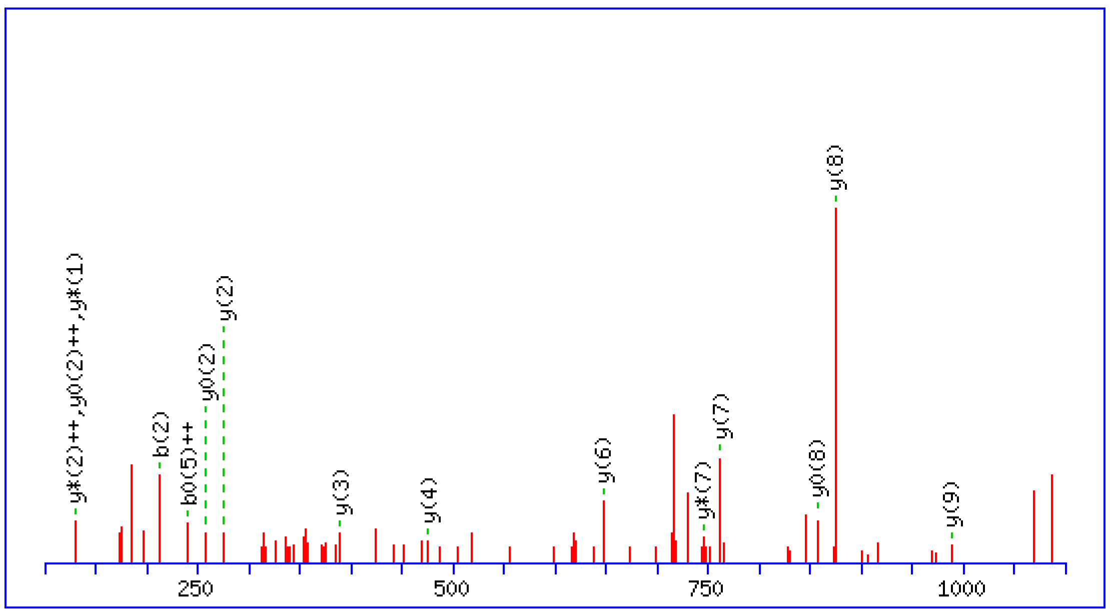
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VILDGNSLEK**
Found in **PTGR2_HUMAN**, Prostaglandin reductase 2 OS=Homo sapiens GN=PTGR2 PE=1 SV=1

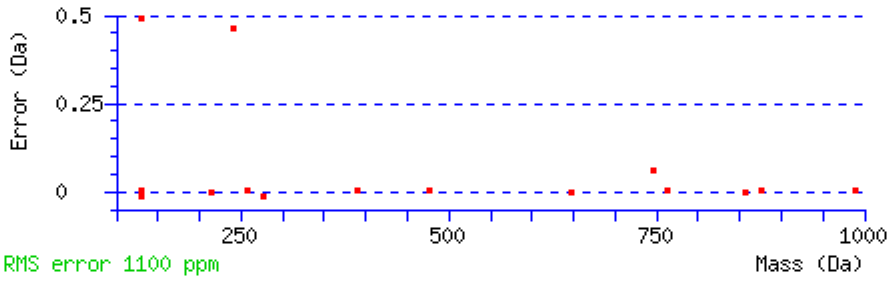
Match to Query 22316: 1086.588468 from(544.301510,2+) rtinseconds(1916) index(20996)
Title: Locus:1.1.1.2073.27
Data file 2011-11-10 - TFD - EP 3-4.mgf

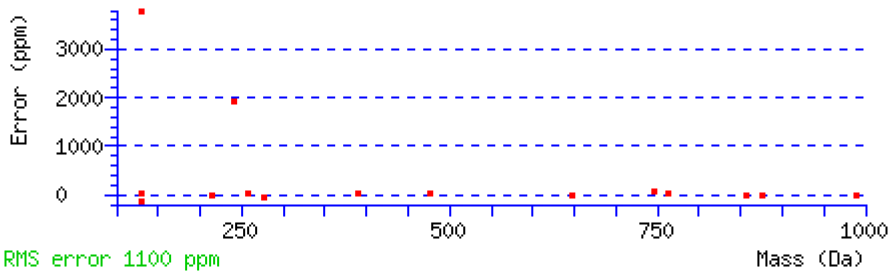
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1086.592072
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.0029
Matches : 15/90 fragment ions using 28 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							10
2	213.159754	107.083515					I	***988.530951***	494.769114	971.504402	486.255839	970.520386	485.763831	9
3	326.243818	163.625547					L	***875.446887***	438.227082	858.420338	429.713807	857.436322	429.221799	8
4	441.270761	221.139018			423.260196	212.133736	D	***762.362823***	381.685050	745.336274	373.171775	744.352258	372.679767	7
5	498.292225	249.649750			480.281660	240.644468	G	***647.335880***	324.171578	630.309331	315.658304	629.325315	315.166296	6
6	612.335152	306.671214	595.308603	298.157940	594.324587	297.665932	N	590.314416	295.660846	573.287867	287.147572	572.303851	286.655564	5
7	699.367180	350.187228	682.340631	341.673953	681.356615	341.181945	S	***476.271489***	238.639382	459.244940	230.126108	458.260924	229.634100	4
8	812.451244	406.729260	795.424695	398.215985	794.440679	397.723977	L	***389.239461***	195.123369	372.212912	186.610094	371.228896	186.118086	3
9	941.493837	471.250557	924.467288	462.737282	923.483272	462.245274	E	***276.155397***	138.581336	259.128848	130.068062	258.144832	129.576054	2
10							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of VILDGNSLEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.0	1086.592072	-0.003604	VILDGNSLEK
9.6	1086.596771	-0.008303	VLRICEQR
7.7	1086.585556	0.002912	LGADVCAVLR
6.2	1086.592056	-0.003588	KEVINEVEK
4.3	1086.592087	-0.003619	IQDLLVDSGK
4.3	1086.592056	-0.003588	AVKAPESLEK
3.1	1086.592072	-0.003604	LQQTLEEVK
2.2	1086.592072	-0.003604	KLLDGPSTEK
0.8	1086.596100	-0.007632	EPLFLDLPK
0.2	1086.589600	-0.001132	LVPMTVFHK

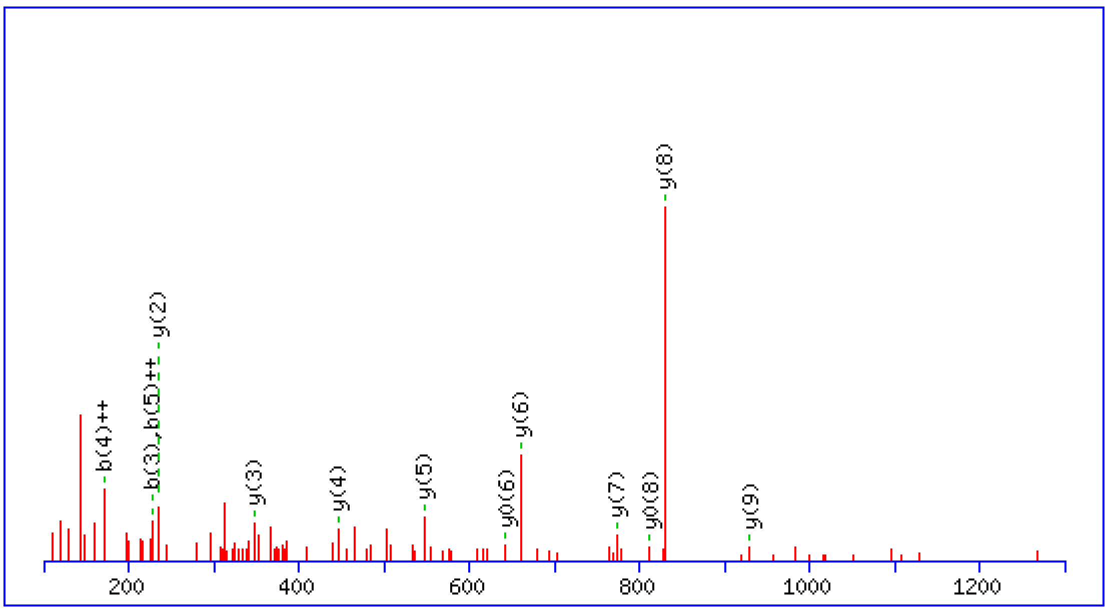
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AVGLLTVISK**
Found in **PSCA_HUMAN**, Prostate stem cell antigen OS=Homo sapiens GN=PSCA PE=1 SV=1

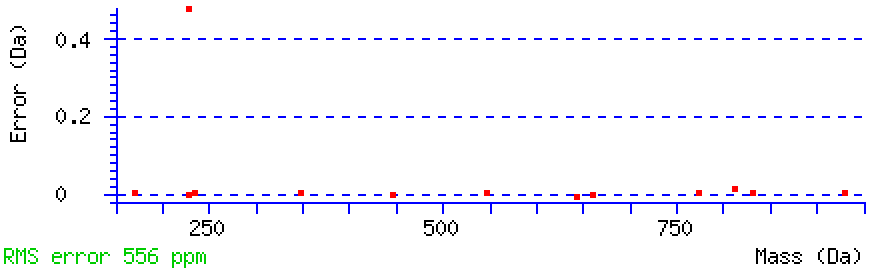
Match to Query 15325: 999.634068 from(500.824310,2+) rtinseconds(2866) index(38758)
Title: Locus:1.1.1.2520.12
Data file 2011-11-13 - TFD - EP 7-4.mgf

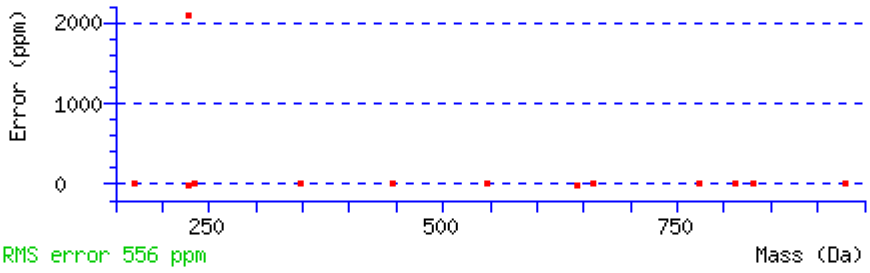
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 999.632828
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 71 **Expect:** 9.8e-008
Matches : 14/78 fragment ions using 18 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	72.044390	36.525833			A							10
2	**171.112804**	86.060040			V	***929.602995***	465.305136	912.576446	456.791861	911.592430	456.299853	9
3	**228.134268**	114.570772			G	***830.534581***	415.770929	813.508032	407.257654	812.524016	406.765646	8
4	341.218332	**171.112804**			L	***773.513117***	387.260197	756.486568	378.746922	755.502552	378.254914	7
5	454.302396	**227.654836**			L	***660.429053***	330.718165	643.402504	322.204890	642.418488	321.712882	6
6	555.350075	278.178676	537.339510	269.173393	T	***547.344989***	274.176133	530.318440	265.662858	529.334424	265.170850	5
7	654.418489	327.712883	636.407924	318.707600	V	***446.297310***	223.652293	429.270761	215.139018	428.286745	214.647010	4
8	767.502553	384.254915	749.491988	375.249632	I	***347.228896***	174.118086	330.202347	165.604811	329.218331	165.112803	3
9	854.534581	427.770929	836.524016	418.765646	S	***234.144832***	117.576054	217.118283	109.062779	216.134267	108.570771	2
10					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of AVGLLTVISK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
71.0	999.632828	0.001240	AVGLLTVISK
5.1	999.644028	-0.009960	RLAIISSLK

Mascot: http://www.matrixscience.com/

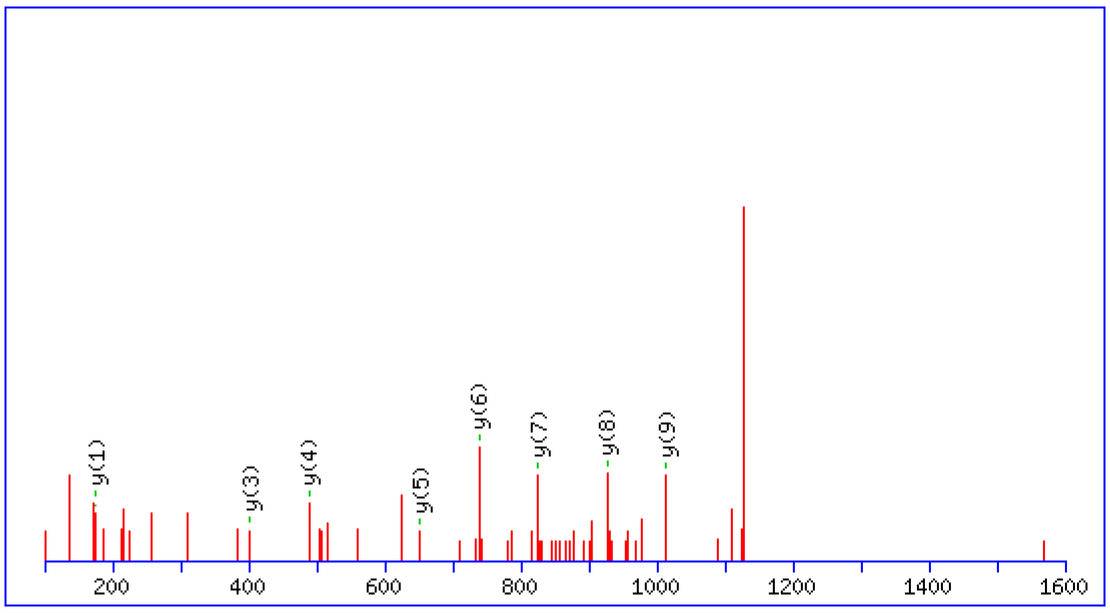
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSTSSYSQVR**
Found in **PSME4_HUMAN**, Proteasome activator complex subunit 4 OS=Homo sapiens GN=PSME4 PE=1 SV=2

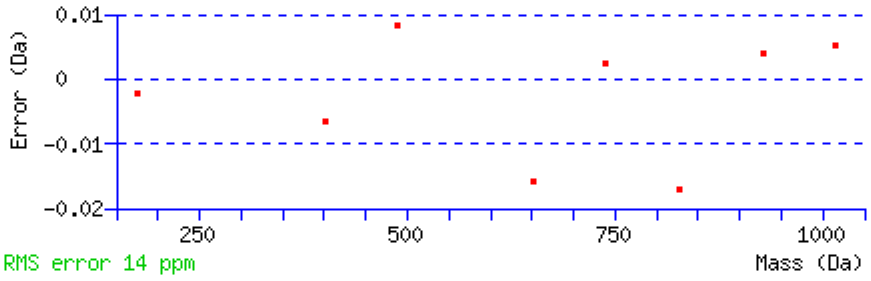
Match to Query 24932: 1126.572308 from(564.293430,2+) rtinseconds(1443) index(11433)
Title: Locus:1.1.1.1902.38
Data file 2011-11-10 - TFD - EP 4-1.mgf

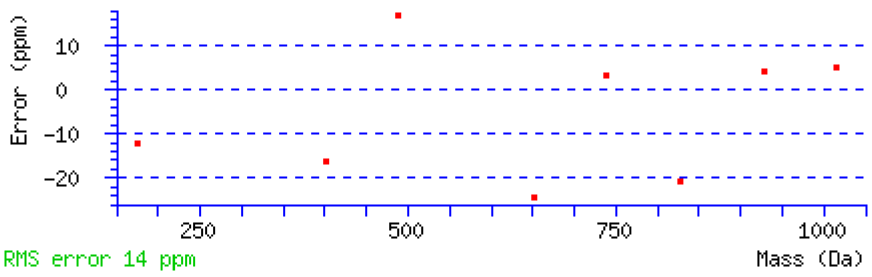
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1126.561844
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.00095
Matches : 8/86 fragment ions using 28 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							10
2	201.123368	101.065322			183.112803	92.060039	S	*1014.485064*	507.746170	997.458515	499.232896	996.474499	498.740888	9
3	302.171047	151.589161			284.160482	142.583879	T	*927.453036*	464.230156	910.426487	455.716882	909.442471	455.224874	8
4	389.203075	195.105175			371.192510	186.099893	S	*826.405357*	413.706317	809.378808	405.193042	808.394792	404.701034	7
5	476.235103	238.621189			458.224538	229.615907	S	*739.373329*	370.190303	722.346780	361.677028	721.362764	361.185020	6
6	639.298432	320.152854			621.287867	311.147572	Y	*652.341301*	326.674289	635.314752	318.161014	634.330736	317.669006	5
7	726.330460	363.668868			708.319895	354.663586	S	*489.277972*	245.142624	472.251423	236.629349	471.267407	236.137341	4
8	854.389038	427.698157	837.362489	419.184883	836.378473	418.692875	Q	*402.245944*	201.626610	385.219395	193.113336			3
9	953.457452	477.232364	936.430903	468.719090	935.446887	468.227082	V	274.187366	137.597321	257.160817	129.084047			2
10							R	*175.118952*	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of LSTSSYSQVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.3	1126.561844	0.010464	LSTSSYSQVR
6.6	1126.561874	0.010434	TSPPPTPVQR
6.6	1126.561874	0.010434	TSPPPTPVQR

Mascot: http://www.matrixscience.com/

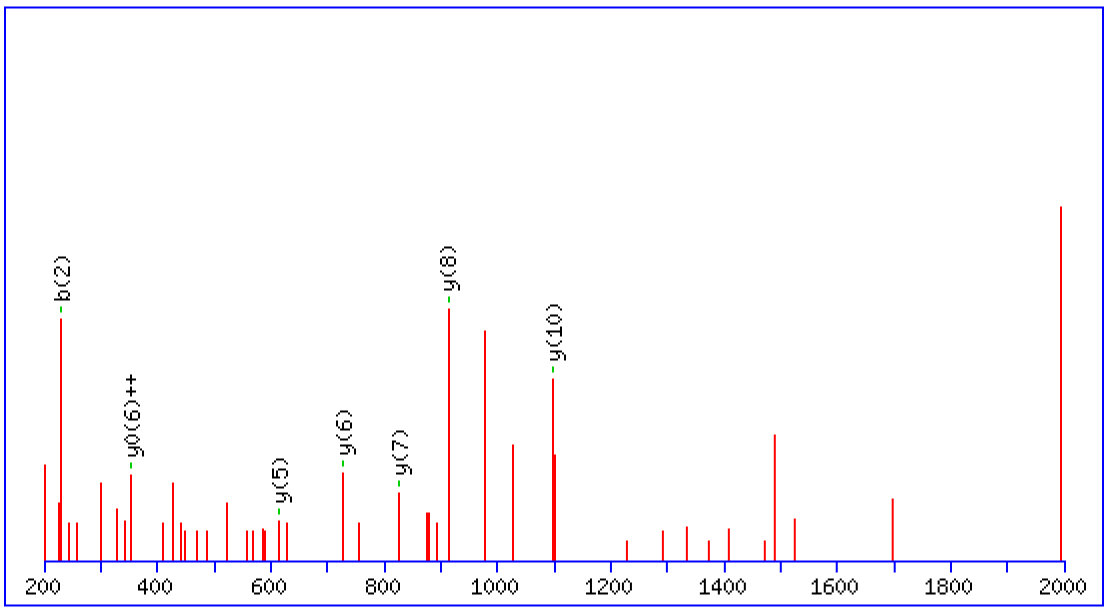
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TEALSVIELLLK**
Found in **ECM29_HUMAN**, Proteasome-associated protein ECM29 homolog OS=Homo sapiens GN=ECM29 PE=1 SV=2

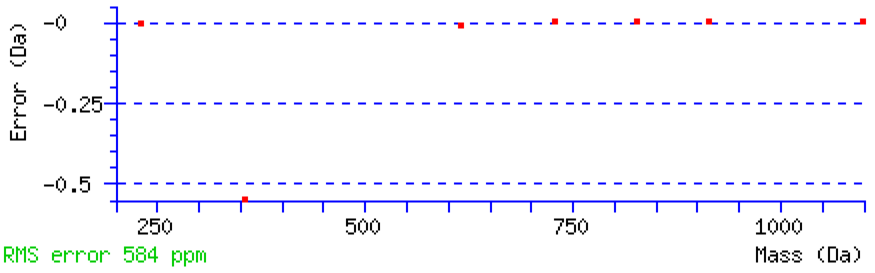
Match to Query 37564: 1327.801068 from(664.907810,2+) rtinseconds(4534) index(68465)
Title: Locus:1.1.1.3018.22
Data file 2011-11-12 - TFD - EP 6-1.mgf

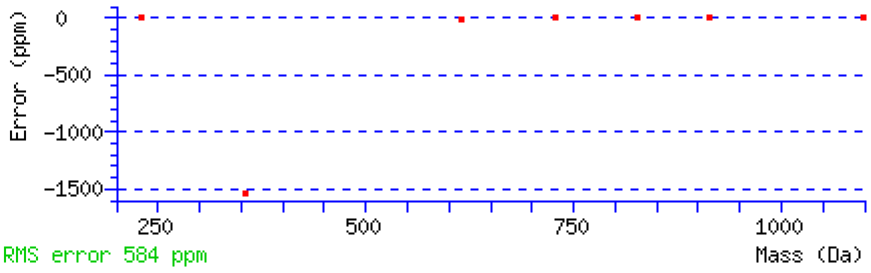
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1327.796234
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.00076
Matches : 7/102 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116	84.044390	42.525833	**T**							**12**
2	231.097548	116.052412	213.086983	107.047130	**E**	1227.755866	614.381571	1210.729317	605.868297	1209.745301	605.376288	**11**
3	302.134662	151.570969	284.124097	142.565687	**A**	***1098.713273***	549.860275	1081.686724	541.347000	1080.702708	540.854992	**10**
4	415.218726	208.113001	397.208161	199.107719	**L**	1027.676159	514.341718	1010.649610	505.828443	1009.665594	505.336435	**9**
5	502.250754	251.629015	484.240189	242.623732	**S**	***914.592095***	457.799686	897.565546	449.286411	896.581530	448.794403	**8**
6	601.319168	301.163222	583.308603	292.157940	**V**	***827.560067***	414.283672	810.533518	405.770397	809.549502	405.278389	**7**
7	714.403232	357.705254	696.392667	348.699972	**I**	***728.491653***	364.749465	711.465104	356.236190	710.481088	355.744182	**6**
8	843.445825	422.226551	825.435260	413.221268	**E**	***615.407589***	308.207433	598.381040	299.694158	597.397024	299.202150	**5**
9	956.529889	478.768583	938.519324	469.763300	**L**	486.364996	243.686136	469.338447	235.172861			**4**
10	1069.613953	535.310615	1051.603388	526.305332	**L**	373.280932	187.144104	356.254383	178.630829			**3**
11	1182.698017	591.852646	1164.687452	582.847364	**L**	260.196868	130.602072	243.170319	122.088797			**2**
12					**K**	147.112804	74.060040	130.086255	65.546765			**1**





NCBI **BLAST** search of TEALSVIELLLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.2	1327.796234	0.004834	TEALSVIELLLK

Mascot: http://www.matrixscience.com/

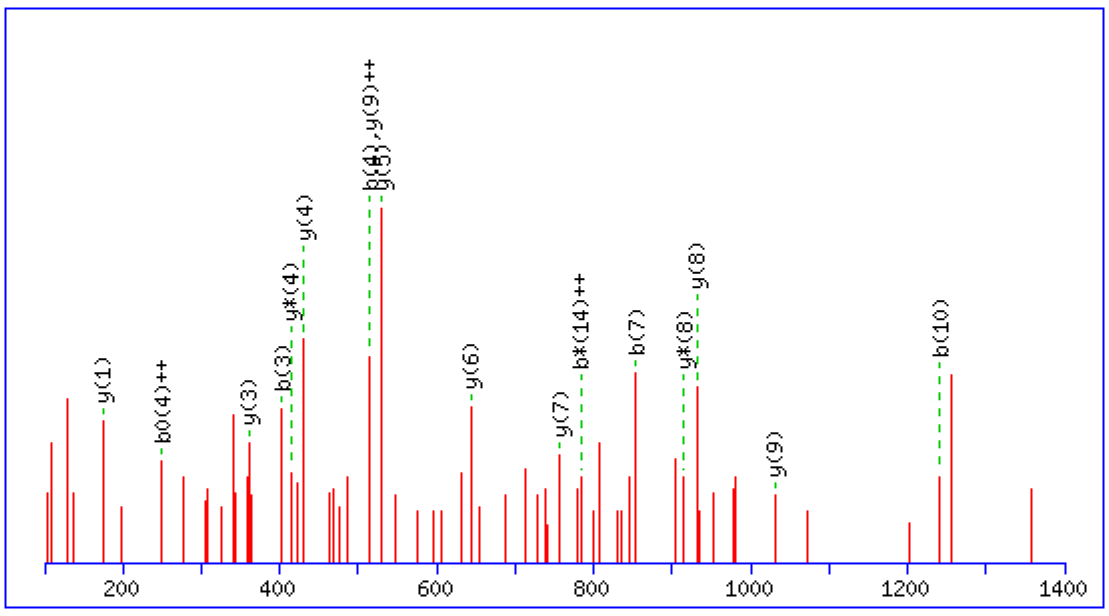
Mascot Search Results

Peptide View

MS/MS Fragmentation of **HTYLPLEVCNIVAGQR**
Found in **AGO1_HUMAN**, Protein argonaute-1 OS=Homo sapiens GN=EIF2C1 PE=1 SV=3

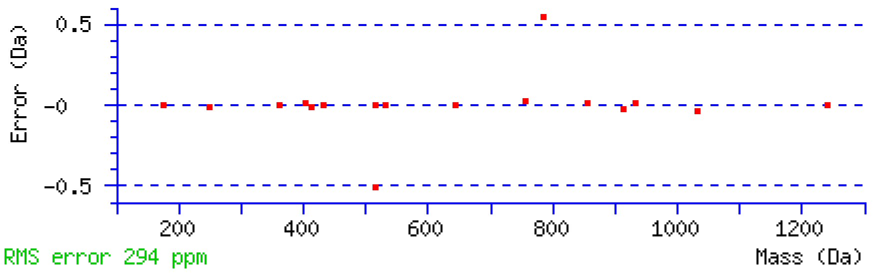
Match to Query 57640: 1882.962522 from(628.661450,3+) rtinseconds(3163) index(42893)
Title: Locus:1.1.1.2655.32
Data file 2011-11-14 - TFD - EP 7-2.mgf

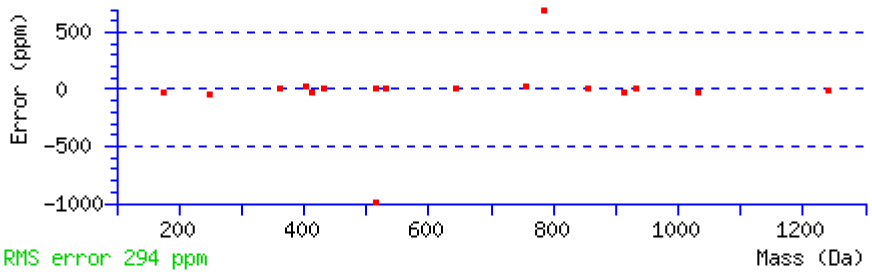
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1882.972336
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 40 **Expect:** 0.00071
Matches : 17/142 fragment ions using 32 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	138.066188	69.536732					H							16
2	239.113867	120.060571			221.103302	111.055289	T	1746.920719	873.963998	1729.894170	865.450723	1728.910154	864.958715	15
3	**402.177196**	201.592236			384.166631	192.586953	Y	1645.873040	823.440158	1628.846491	814.926884	1627.862475	814.434875	14
4	**515.261260**	258.134268			497.250695	249.128986	L	1482.809711	741.908493	1465.783162	733.395219	1464.799146	732.903211	13
5	612.314024	306.660650			594.303459	297.655368	P	1369.725647	685.366462	1352.699098	676.853187	1351.715082	676.361179	12
6	725.398088	363.202682			707.387523	354.197400	L	1272.672883	636.840080	1255.646334	628.326805	1254.662318	627.834797	11
7	**854.440681**	427.723979			836.430116	418.718696	E	1159.588819	580.298047	1142.562270	571.784773	1141.578254	571.292765	10
8	953.509095	477.258186			935.498530	468.252903	V	***1030.546226***	515.776751	1013.519677	507.263476			9
9	1127.555394	564.281335			1109.544829	555.276052	C	***931.477812***	466.242544	914.451263	457.729269			8
10	**1241.598321**	621.302798	1224.571772	612.789524	1223.587756	612.297516	N	***757.431513***	379.219395	740.404964	370.706120			7
11	1354.682385	677.844830	1337.655836	669.331556	1336.671820	668.839548	I	***643.388586***	322.197931	626.362037	313.684657			6
12	1453.750799	727.379037	1436.724250	718.865763	1435.740234	718.373755	V	***530.304522***	265.655899	513.277973	257.142625			5
13	1524.787913	762.897594	1507.761364	754.384320	1506.777348	753.892312	A	***431.236108***	216.121692	414.209559	207.608417			4
14	1581.809377	791.408326	1564.782828	782.895052	1563.798812	782.403044	G	***360.198994***	180.603135	343.172445	172.089860			3
15	1709.867955	855.437615	1692.841406	846.924341	1691.857390	846.432333	Q	303.177530	152.092403	286.150981	143.579129			2
16							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of HTYLPLEVCNIVAGQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.0	1882.972336	-0.009814	HTYLPLEVCNIVAGQR
6.0	1882.957047	0.005475	AEAEKVSAMLDHSNLIR
3.6	1882.963608	-0.001086	ELPSLSPAPDTGLSPSKR
1.2	1882.979553	-0.017031	MAGVRPDNVAEVVAGARR
0.3	1882.979553	-0.017031	MAGVRPDNVAEVVAGARR

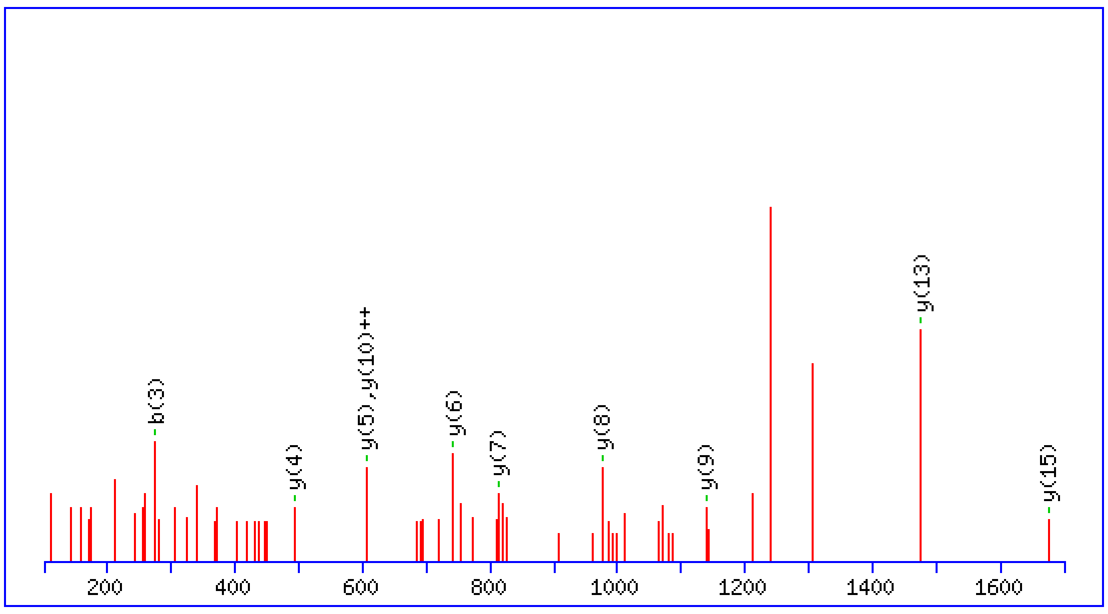
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SVSIPAPAYYAHLVAFR**
Found in **AGO2_HUMAN**, Protein argonaute-2 OS=Homo sapiens GN=EIF2C2 PE=1 SV=3

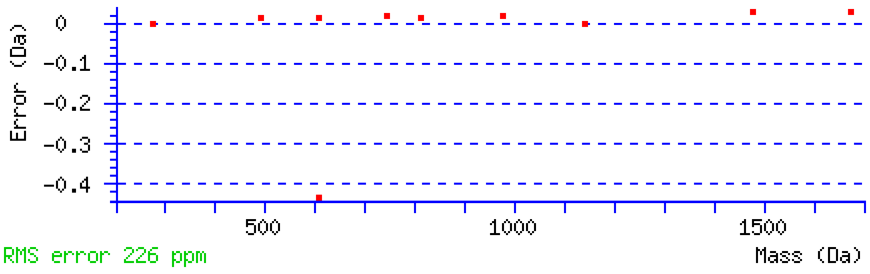
Match to Query 59957: 1860.985332 from(621.335720,3+) rtinseconds(3489) index(50202)
Title: Locus:1.1.1.2760.15
Data file 2011-11-10 - TFD - EP 3-2.mgf

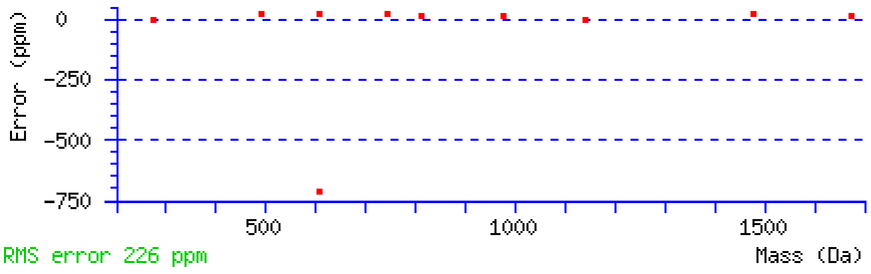
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1860.988632
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 51  Expect: 7.1e-005
Matches : 10/132 fragment ions using 14 most intense peaks   (help)
```

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	S							17
2	187.107718	94.057497	169.097153	85.052214	V	1774.963904	887.985590	1757.937355	879.472316	1756.953339	878.980307	16
3	274.139746	137.573511	256.129181	128.568229	S	***1675.895490***	838.451383	1658.868941	829.938109	1657.884925	829.446101	15
4	387.223810	194.115543	369.213245	185.110261	I	1588.863462	794.935369	1571.836913	786.422095			14
5	484.276574	242.641925	466.266009	233.636643	P	***1475.779398***	738.393337	1458.752849	729.880063			13
6	555.313688	278.160482	537.303123	269.155200	A	1378.726634	689.866955	1361.700085	681.353681			12
7	652.366452	326.686864	634.355887	317.681582	P	1307.689520	654.348398	1290.662971	645.835124			11
8	723.403566	362.205421	705.393001	353.200139	A	1210.636756	605.822016	1193.610207	597.308742			10
9	886.466895	443.737086	868.456330	434.731803	Y	***1139.599642***	570.303459	1122.573093	561.790185			9
10	1049.530224	525.268750	1031.519659	516.263468	Y	***976.536313***	488.771795	959.509764	480.258520			8
11	1120.567338	560.787307	1102.556773	551.782025	A	***813.472984***	407.240130	796.446435	398.726856			7
12	1257.626250	629.316763	1239.615685	620.311481	H	***742.435870***	371.721573	725.409321	363.208299			6
13	1370.710314	685.858795	1352.699749	676.853512	L	***605.376958***	303.192117	588.350409	294.678843			5
14	1469.778728	735.393002	1451.768163	726.387720	V	***492.292894***	246.650085	475.266345	238.136811			4
15	1540.815842	770.911559	1522.805277	761.906276	A	393.224480	197.115878	376.197931	188.602603			3
16	1687.884256	844.445766	1669.873691	835.440484	F	322.187366	161.597321	305.160817	153.084047			2
17					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of SVSIPAPAYYAHLVAFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
50.8	1860.988632	-0.003300	SVSIPAPAYYAHLVAFR

Mascot: http://www.matrixscience.com/

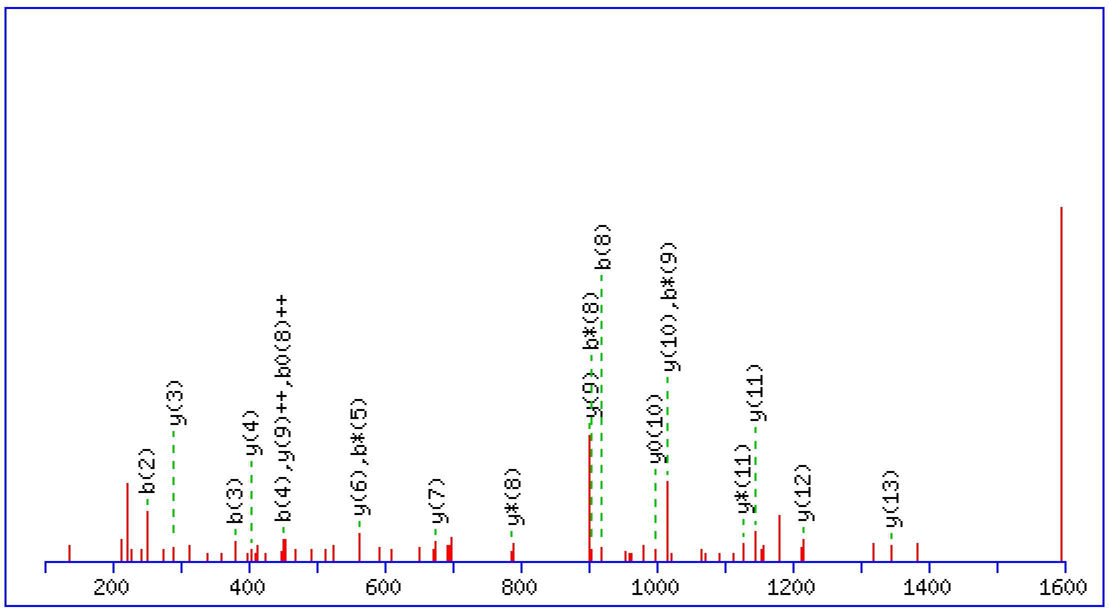
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SYEAQDPEIASLSGK**
Found in **C10_HUMAN**, Protein C10 OS=Homo sapiens GN=C12orf57 PE=1 SV=1

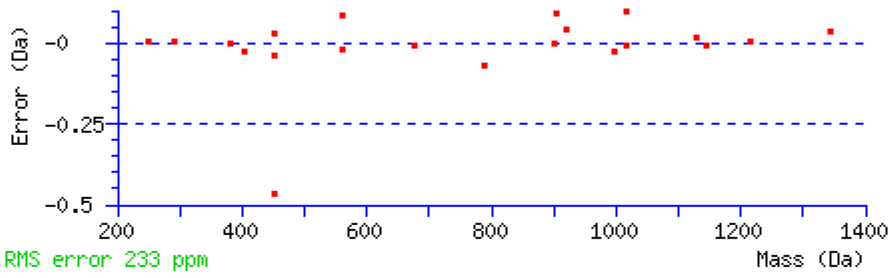
Match to Query 42202: 1593.759268 from(797.886910,2+) rtinseconds(2244) index(21700)
Title: Locus:1.1.1.2185.28
Data file 2011-11-12 - TFD - EP 6-7.mgf

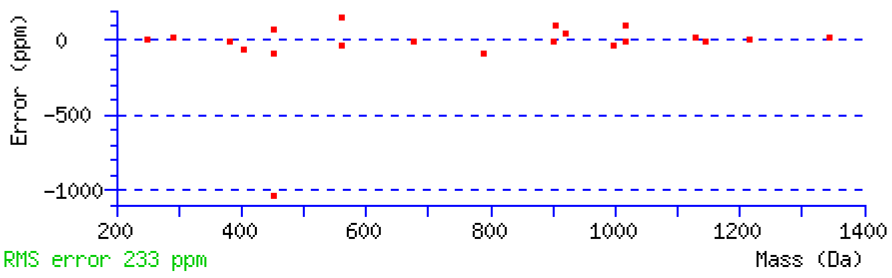
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1593.752197
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 53  Expect: 6.6e-005
Matches : 21/156 fragment ions using 36 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							15
2	**251.102633**	126.054954			233.092068	117.049672	Y	1507.727480	754.367378	1490.700931	745.854104	1489.716915	745.362096	14
3	**380.145226**	190.576251			362.134661	181.570969	E	***1344.664151***	672.835714	1327.637602	664.322439	1326.653586	663.830431	13
4	**451.182340**	226.094808			433.171775	217.089526	A	***1215.621558***	608.314417	1198.595009	599.801143	1197.610993	599.309135	12
5	579.240918	290.124097	562.214369	281.610823	561.230353	281.118815	Q	***1144.584444***	572.795860	1127.557895	564.282586	1126.573879	563.790578	11
6	694.267861	347.637569	677.241312	339.124294	676.257296	338.632286	D	***1016.525866***	508.766571	999.499317	500.253297	998.515301	499.761289	10
7	791.320625	396.163951	774.294076	387.650676	773.310060	387.158668	P	***901.498923***	451.253100	884.472374	442.739825	883.488358	442.247817	9
8	**920.363218**	460.685247	903.336669	452.171973	902.352653	451.679965	E	804.446159	402.726718	787.419610	394.213443	786.435594	393.721435	8
9	1033.447282	517.227279	1016.420733	508.714005	1015.436717	508.221997	I	***675.403566***	338.205421	658.377017	329.692147	657.393001	329.200139	7
10	1104.484396	552.745836	1087.457847	544.232562	1086.473831	543.740554	A	***562.319502***	281.663389	545.292953	273.150115	544.308937	272.658107	6
11	1191.516424	596.261850	1174.489875	587.748576	1173.505859	587.256568	S	491.282388	246.144832	474.255839	237.631557	473.271823	237.139549	5
12	1304.600488	652.803882	1287.573939	644.290608	1286.589923	643.798600	L	***404.250360***	202.628818	387.223811	194.115543	386.239795	193.623535	4
13	1391.632516	696.319896	1374.605967	687.806622	1373.621951	687.314614	S	***291.166296***	146.086786	274.139747	137.573512	273.155731	137.081504	3
14	1448.653980	724.830628	1431.627431	716.317354	1430.643415	715.825346	G	204.134268	102.570772	187.107719	94.057497			2
15							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of SYEAQDPEIASLSGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.6	1593.752197	0.007071	SYEAQDPEIASLSGK

Mascot: http://www.matrixscience.com/

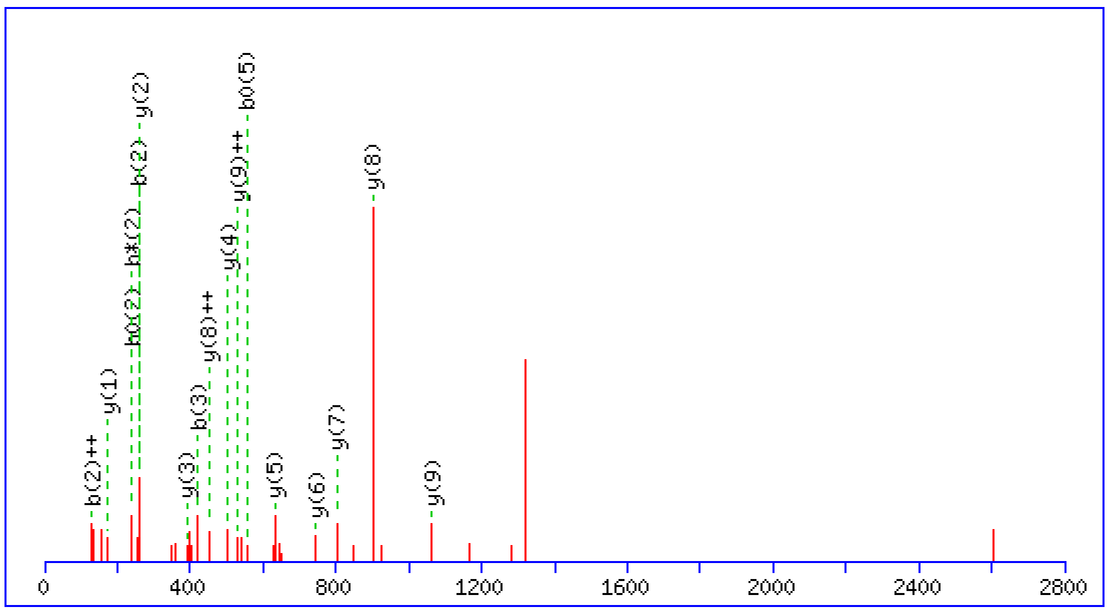
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EQYPGIEIESR**
Found in **CQ037_HUMAN**, Protein C17orf37 OS=Homo sapiens GN=C17orf37 PE=1 SV=1

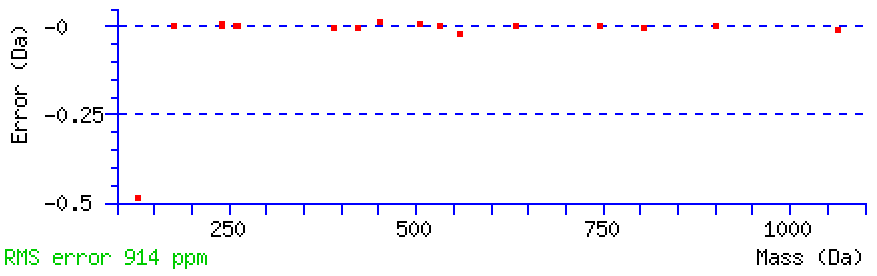
Match to Query 33520: 1319.636768 from(660.825660,2+) rtinseconds(2235) index(19537)
Title: Locus:1.1.1.2307.36
Data file 2011-11-10 - TFD - EP 4-7.mgf

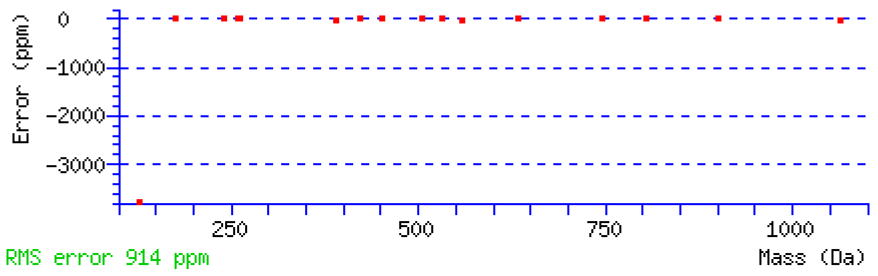
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1319.635712
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 70  Expect: 1.2e-006
Matches : 17/116 fragment ions using 29 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	E							11
2	**258.108447**	129.557862	241.081898	121.044587	240.097882	120.552579	Q	1191.600429	596.303853	1174.573880	587.790578	1173.589864	587.298570	10
3	**421.171776**	211.089526	404.145227	202.576252	403.161211	202.084244	Y	***1063.541851***	532.274564	1046.515302	523.761289	1045.531286	523.269281	9
4	518.224540	259.615908	501.197991	251.102634	500.213975	250.610626	P	***900.478522***	450.742899	883.451973	442.229625	882.467957	441.737617	8
5	575.246004	288.126640	558.219455	279.613366	557.235439	279.121358	G	***803.425758***	402.216517	786.399209	393.703243	785.415193	393.211235	7
6	688.330068	344.668672	671.303519	336.155398	670.319503	335.663390	I	***746.404294***	373.705785	729.377745	365.192511	728.393729	364.700503	6
7	817.372661	409.189969	800.346112	400.676694	799.362096	400.184686	E	***633.320230***	317.163753	616.293681	308.650479	615.309665	308.158471	5
8	930.456725	465.732001	913.430176	457.218726	912.446160	456.726718	I	***504.277637***	252.642457	487.251088	244.129182	486.267072	243.637174	4
9	1059.499318	530.253297	1042.472769	521.740023	1041.488753	521.248015	E	***391.193573***	196.100425	374.167024	187.587150	373.183008	187.095142	3
10	1146.531346	573.769311	1129.504797	565.256037	1128.520781	564.764029	S	***262.150980***	131.579128	245.124431	123.065854	244.140415	122.573846	2
11							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of EQYPGIEIESR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
69.8	1319.635712	0.001056	EQYPGIEIESR
11.0	1319.640442	-0.003674	RPSWMVDNKR
4.7	1319.627884	0.008884	KIDPVTMDPEK
3.2	1319.640457	-0.003689	MGDKPPGFRGSR
2.9	1319.646957	-0.010189	GLSQEQLNEFR
2.1	1319.646942	-0.010174	EQGNIYKPNNK
2.0	1319.639084	-0.002316	LEIMSAQEIDR
1.0	1319.639114	-0.002346	LDQPMTEIVSR

Mascot: http://www.matrixscience.com/

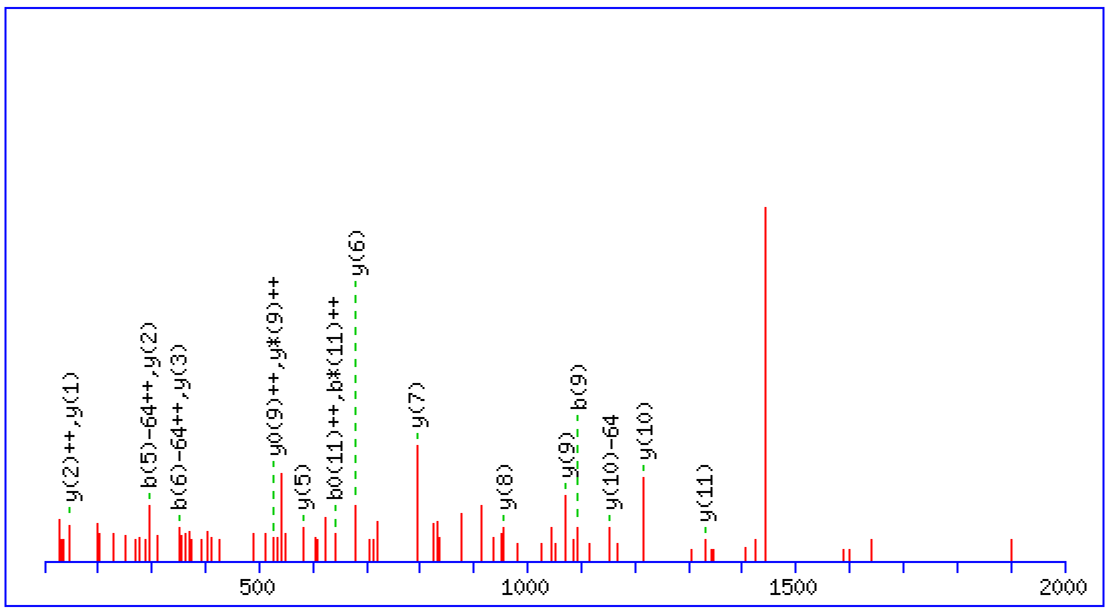
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LIMNYLVTEGFK**
Found in **CT011_HUMAN**, Protein C20orf11 OS=Homo sapiens GN=C20orf11 PE=1 SV=1

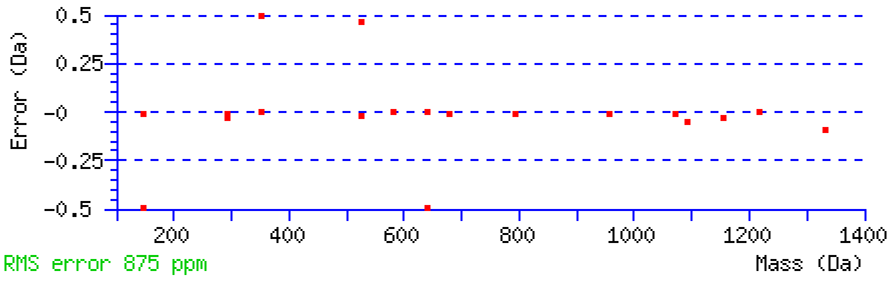
Match to Query 43811: 1442.755908 from(722.385230,2+) rtinseconds(3009) index(40240)
Title: Locus:1.1.1.2466.40
Data file 2011-11-14 - TFD - EP 8-5.mgf

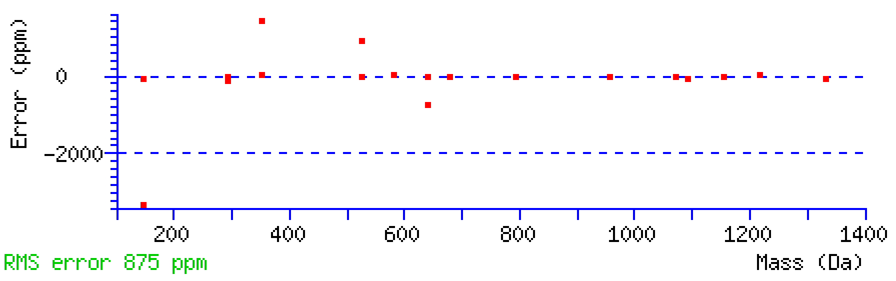
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1442.747925
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M3 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 52 **Expect:** 2.9e-005
Matches : 19/160 fragment ions using 37 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					L							12
2	227.175404	114.091340					I	*1330.671152*	665.839214	1313.644603	657.325940	1312.660587	656.833932	11
3	374.210804	187.609040					M	*1217.587088*	609.297182	1200.560539	600.783908	1199.576523	600.291900	10
4	488.253731	244.630504	471.227182	236.117229			N	*1070.551688*	535.779482	1053.525139	527.266208	1052.541123	526.774200	9
5	651.317060	326.162168	634.290511	317.648894			Y	*956.508761*	478.758019	939.482212	470.244744	938.498196	469.752736	8
6	764.401124	382.704200	747.374575	374.190926			L	*793.445432*	397.226354	776.418883	388.713079	775.434867	388.221071	7
7	863.469538	432.238407	846.442989	423.725133			V	*680.361368*	340.684322	663.334819	332.171047	662.350803	331.679039	6
8	964.517217	482.762247	947.490668	474.248972	946.506652	473.756964	T	*581.292954*	291.150115	564.266405	282.636841	563.282389	282.144833	5
9	1093.559810	547.283543	1076.533261	538.770269	1075.549245	538.278260	E	480.245275	240.626275	463.218726	232.113001	462.234710	231.620993	4
10	1150.581274	575.794275	1133.554725	567.281001	1132.570709	566.788992	G	*351.202682*	176.104979	334.176133	167.591704			3
11	1297.649688	649.328482	1280.623139	640.815208	1279.639123	640.323199	F	*294.181218*	147.594247	277.154669	139.080973			2
12							K	*147.112804*	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of LIMNYLVTEGFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.2	1442.747925	0.007983	LIMNYLVTEGFK
3.8	1442.743896	0.012012	ILGPLAPEMIDSR
3.3	1442.751755	0.004153	ESHRLPVDIAYK
0.7	1442.743896	0.012012	ILGPLAPEMIDSR

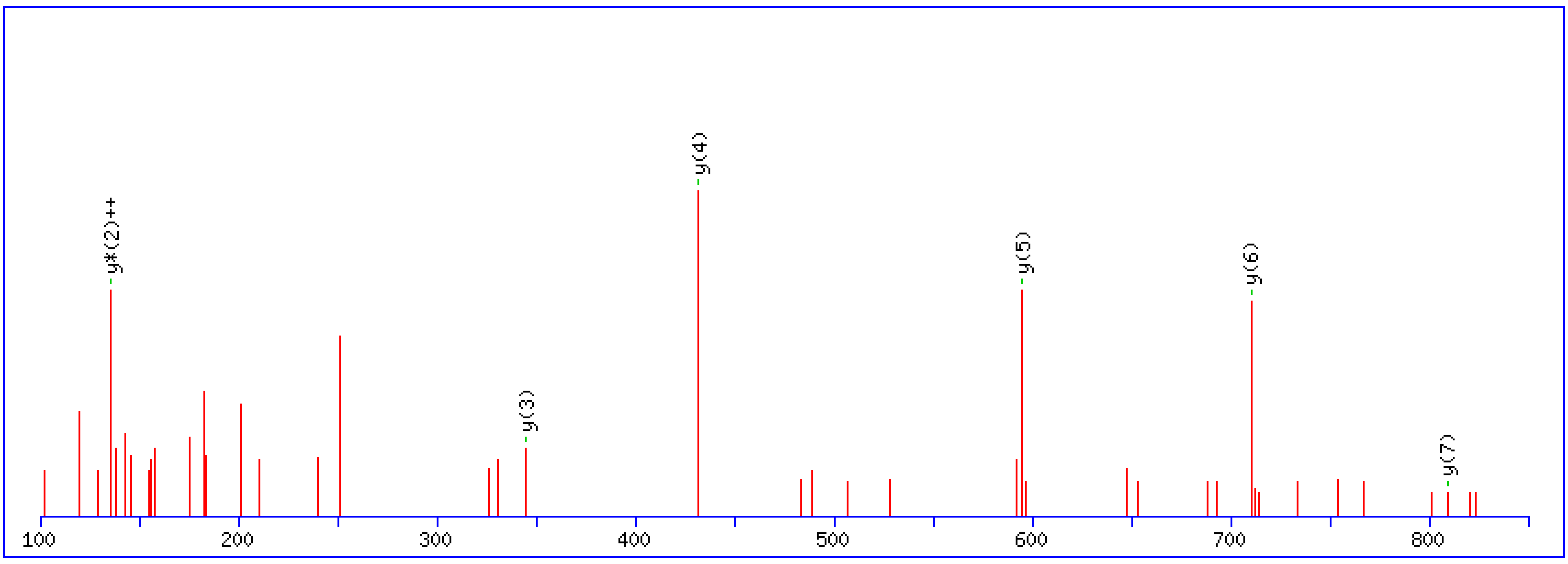
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EVDYSGLR**
Found in **CDV3_HUMAN**, Protein CDV3 homolog OS=Homo sapiens GN=CDV3 PE=1 SV=1

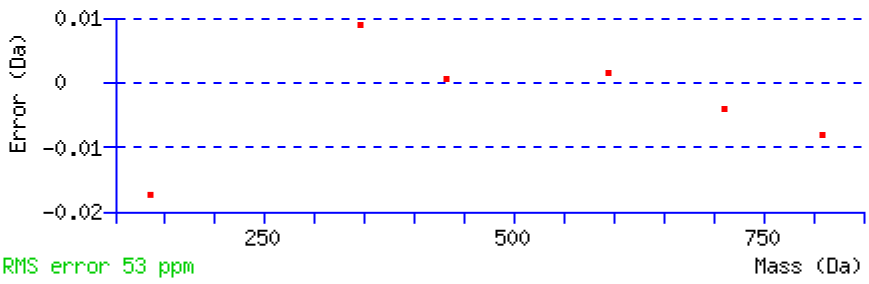
Match to Query 5676: 937.457508 from(469.736030,2+) rtinseconds(1473) index(12719)
Title: Locus:1.1.1.944.10
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 2.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●

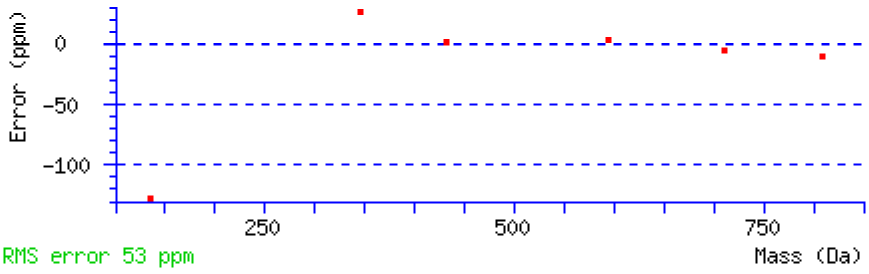


Monoisotopic mass of neutral peptide Mr(calc): 937.450500
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.00024
Matches : 6/64 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572	112.039304	56.523290	E							8
2	229.118283	115.062780	211.107718	106.057497	V	***809.415194***	405.211235	792.388645	396.697961	791.404629	396.205953	7
3	344.145226	172.576251	326.134661	163.570969	D	***710.346780***	355.677028	693.320231	347.163754	692.336215	346.671746	6
4	507.208555	254.107916	489.197990	245.102633	Y	***595.319837***	298.163557	578.293288	289.650282	577.309272	289.158274	5
5	594.240583	297.623930	576.230018	288.618647	S	***432.256508***	216.631892	415.229959	208.118618	414.245943	207.626610	4
6	651.262047	326.134662	633.251482	317.129379	G	***345.224480***	173.115878	328.197931	164.602604			3
7	764.346111	382.676694	746.335546	373.671411	L	288.203016	144.605146	271.176467	136.091872			2
8					R	175.118952	88.063114	158.092403	79.549840			1



RMS error 53 ppm



RMS error 53 ppm

NCBI **BLAST** search of EVDYSGLR
(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	937.450500	0.007008	EVDYSGLR
2.5	937.461746	-0.004238	DIIHDPGR

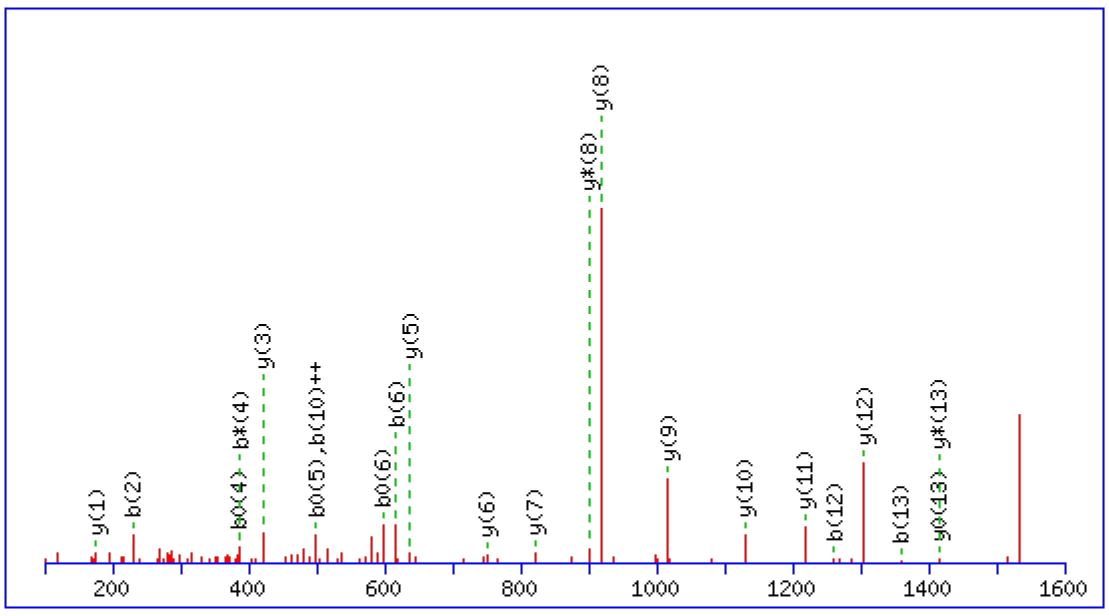
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TQSSLVPALTDFVR**
Found in **CUTA_HUMAN**, Protein CutA OS=Homo sapiens GN=CUTA PE=1 SV=2

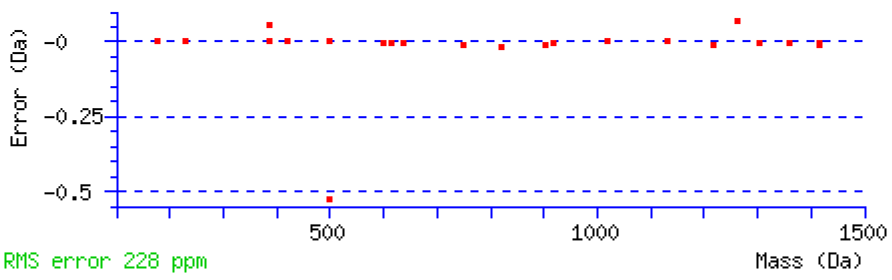
Match to Query 41178: 1532.818308 from(767.416430,2+) rtinseconds(3631) index(40708)
Title: Locus:1.1.1.2714.11
Data file 2011-11-12 - TFD - EP 6-7.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●

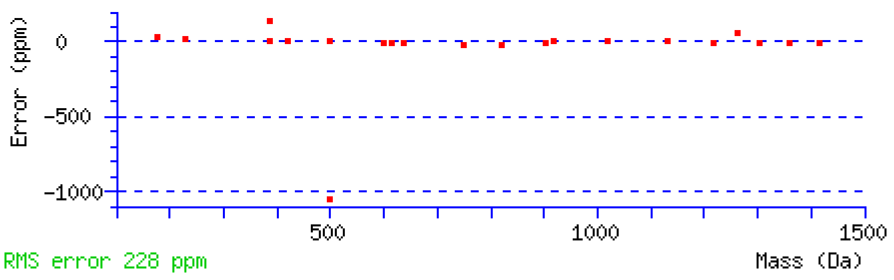


Monoisotopic mass of neutral peptide Mr(calc): 1532.819870
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 89 **Expect:** 1.2e-008
Matches : 22/148 fragment ions using 28 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							14
2	**230.113533**	115.560405	213.086984	107.047130	212.102968	106.555122	Q	1432.779456	716.893366	1415.752907	708.380092	1414.768891	707.888084	13
3	317.145561	159.076418	300.119012	150.563144	299.134996	150.071136	S	***1304.720878***	652.864077	1287.694329	644.350803	1286.710313	643.858795	12
4	404.177589	202.592432	387.151040	194.079158	386.167024	193.587150	S	***1217.688850***	609.348063	1200.662301	600.834789	1199.678285	600.342781	11
5	517.261653	259.134465	500.235104	250.621190	499.251088	250.129182	L	***1130.656822***	565.832049	1113.630273	557.318775	1112.646257	556.826767	10
6	**616.330067**	308.668672	599.303518	300.155397	598.319502	299.663389	V	***1017.572758***	509.290017	1000.546209	500.776743	999.562193	500.284735	9
7	713.382831	357.195054	696.356282	348.681779	695.372266	348.189771	P	***918.504344***	459.755810	901.477795	451.242536	900.493779	450.750528	8
8	784.419945	392.713611	767.393396	384.200336	766.409380	383.708328	A	***821.451580***	411.229428	804.425031	402.716154	803.441015	402.224146	7
9	897.504009	449.255643	880.477460	440.742368	879.493444	440.250360	L	***750.414466***	375.710871	733.387917	367.197597	732.403901	366.705589	6
10	998.551688	499.779482	981.525139	491.266208	980.541123	490.774200	T	***637.330402***	319.168839	620.303853	310.655565	619.319837	310.163557	5
11	1113.578631	557.292954	1096.552082	548.779679	1095.568066	548.287671	D	536.282723	268.645000	519.256174	260.131725	518.272158	259.639717	4
12	**1260.647045**	630.827161	1243.620496	622.313886	1242.636480	621.821878	F	***421.255780***	211.131528	404.229231	202.618254			3
13	**1359.715459**	680.361368	1342.688910	671.848093	1341.704894	671.356085	V	274.187366	137.597321	257.160817	129.084047			2
14							R	***175.118952***	88.063114	158.092403	79.549839			1



RMS error 228 ppm



RMS error 228 ppm

NCBI **BLAST** search of TQSSLVPALTDFVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
89.2	1532.819870	-0.001562	TQSSLVPALTDFVR
11.0	1532.816681	0.001627	LMDAVMLQLTRAR
7.5	1532.816681	0.001627	LMDAVMLQLTRAR
7.0	1532.819839	-0.001531	GLIEGKSDPYALVR
6.2	1532.823853	-0.005545	IYYTGKYQSLGIK
4.1	1532.813309	0.004999	ARTMALYNPIPVR
3.0	1532.808594	0.009714	ALPEPLPAPPEDKK
3.0	1532.808594	0.009714	ALPEPLPAPPEDKK
2.9	1532.808594	0.009714	ALPEPLPAPPEDKK
2.1	1532.816666	0.001642	ELILMRNLMNVR

Mascot: http://www.matrixscience.com/

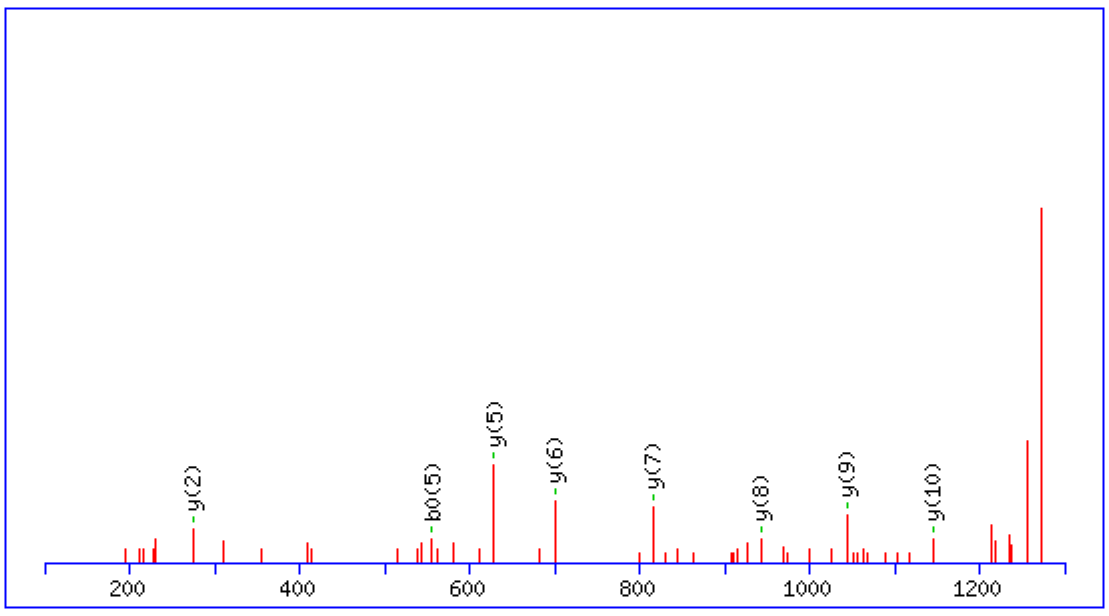
{MATRIX}{SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QTTQDAPEEVR**
Found in **CWC15_HUMAN**, Protein CWC15 homolog OS=Homo sapiens GN=CWC15 PE=1 SV=2

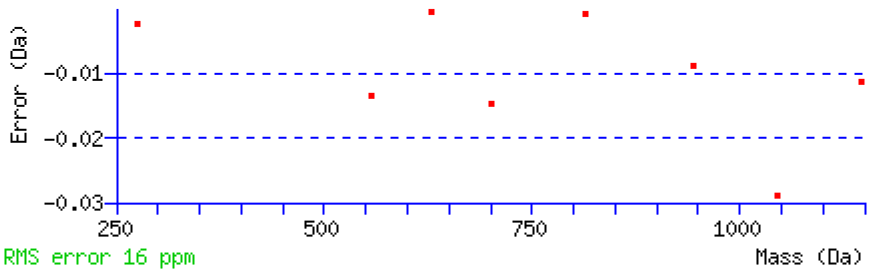
Match to Query 608605: 1272.599568 from(637.307060,2+) rtinseconds(1056) index(244830)
Title: Locus:1.1.1.843.33
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

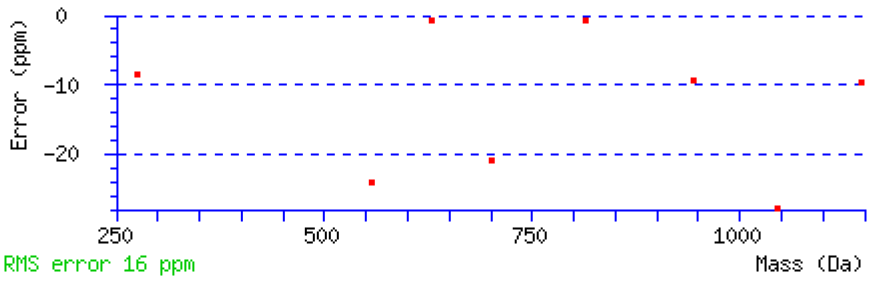
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1300] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1272.594604
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 58 **Expect:** 1.1e-005
Matches : 8/114 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	129.065854	65.036565	112.039305	56.523291			Q							11
2	230.113533	115.560405	213.086984	107.047130	212.102968	106.555122	T	***1145.543309***	573.275292	1128.516760	564.762018	1127.532744	564.270010	10
3	331.161212	166.084244	314.134663	157.570970	313.150647	157.078962	T	***1044.495630***	522.751453	1027.469081	514.238179	1026.485065	513.746171	9
4	459.219790	230.113533	442.193241	221.600259	441.209225	221.108251	Q	***943.447951***	472.227614	926.421402	463.714339	925.437386	463.222331	8
5	574.246733	287.627005	557.220184	279.113730	556.236168	278.621722	D	***815.389373***	408.198325	798.362824	399.685050	797.378808	399.193042	7
6	645.283847	323.145562	628.257298	314.632287	627.273282	314.140279	A	***700.362430***	350.684853	683.335881	342.171579	682.351865	341.679571	6
7	742.336611	371.671944	725.310062	363.158669	724.326046	362.666661	P	***629.325316***	315.166296	612.298767	306.653022	611.314751	306.161014	5
8	871.379204	436.193240	854.352655	427.679966	853.368639	427.187958	E	532.272552	266.639914	515.246003	258.126640	514.261987	257.634632	4
9	1000.421797	500.714537	983.395248	492.201262	982.411232	491.709254	E	403.229959	202.118617	386.203410	193.605343	385.219394	193.113335	3
10	1099.490211	550.248744	1082.463662	541.735469	1081.479646	541.243461	V	***274.187366***	137.597321	257.160817	129.084046			2
11							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of QTTQDAPEEVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.4	1272.594604	0.004964	QTTQDAPEEVR
5.2	1272.603348	-0.003780	ICKGDHWTTR
5.1	1272.602005	-0.002437	GLCVLGEDNAPL
4.6	1272.594604	0.004964	QTKDAQGPDDAK
0.5	1272.599503	0.000065	SIFCPLMSFR
0.1	1272.594604	0.004964	QSPTSKAPNTQD
0.1	1272.596146	0.003422	KWPPPCAFTPG
0.1	1272.596146	0.003422	KWPPPCAFTPG
0.1	1272.596146	0.003422	KWPPPCAFTPG
0.1	1272.592102	0.007466	QCLEWDPAVR

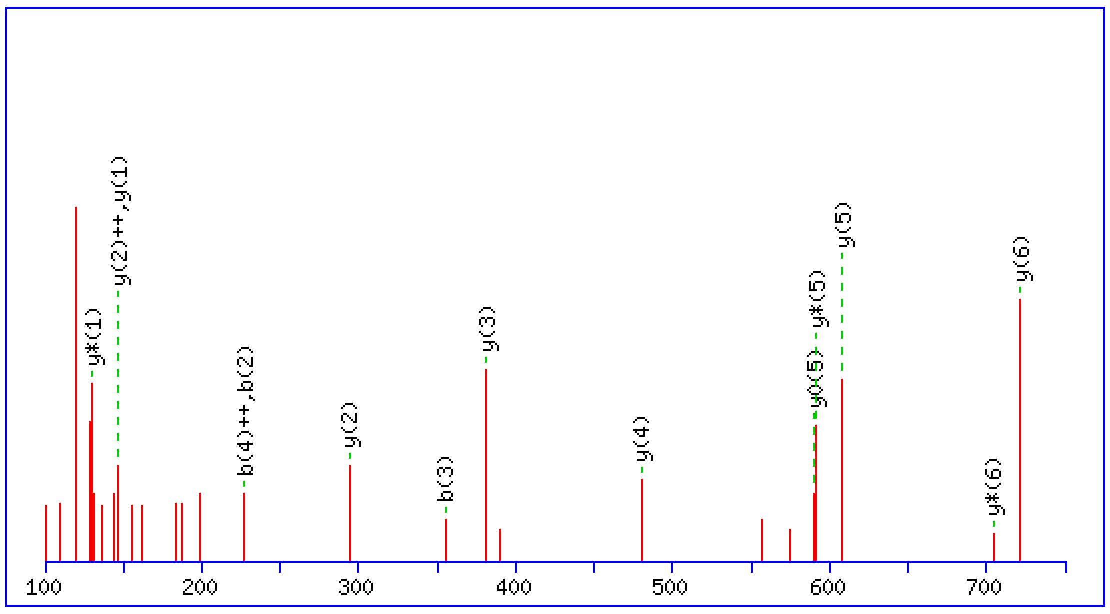
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILKVSMK**
Found in **DLK1_HUMAN**, Protein delta homolog 1 OS=Homo sapiens GN=DLK1 PE=1 SV=3

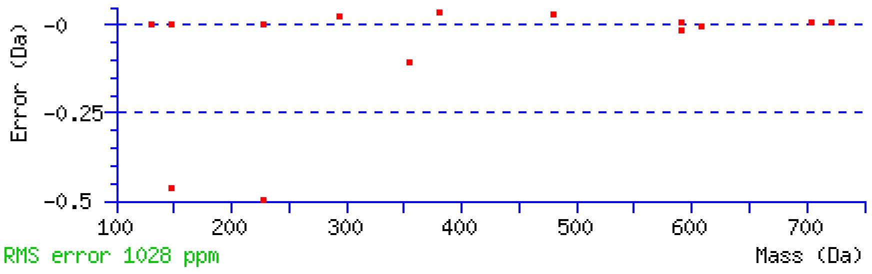
Match to Query 2968: 833.501668 from(417.758110,2+) rtinseconds(2262) index(27350)
Title: Locus:1.1.1.2292.4
Data file 2011-11-13 - TFD - EP 7-4.mgf

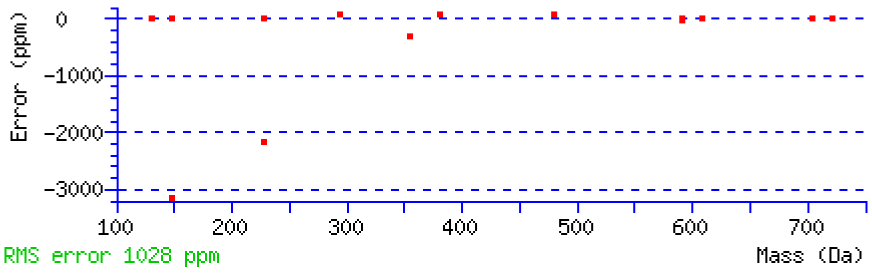
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 833.504440
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M6      : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 51  Expect: 2.5e-005
Matches : 14/90 fragment ions using 18 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					**I**							7
2	**227.175404**	114.091340					**L**	***721.427673***	361.217475	704.401124	352.704200	703.417108	352.212192	6
3	**355.270367**	178.138822	338.243818	169.625547			**K**	***608.343609***	304.675443	591.317060	296.162168	590.333044	295.670160	5
4	454.338781	227.673029	437.312232	219.159754			**V**	***480.248646***	240.627961	463.222097	232.114687	462.238081	231.622679	4
5	541.370809	271.189043	524.344260	262.675768	523.360244	262.183760	**S**	***381.180232***	191.093754	364.153683	182.580480	363.169667	182.088472	3
6	688.406209	344.706743	671.379660	336.193468	670.395644	335.701460	**M**	***294.148204***	147.577740	277.121655	139.064465			2
7							**K**	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of ILKVSMK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.3	833.504440	-0.002772	ILKVSMK
51.3	833.501083	0.000585	ILQVSFK
22.3	833.504440	-0.002772	LIKSMVK
10.0	833.504440	-0.002772	ILMSKVK
10.0	833.501083	0.000585	LPSFKVK
9.1	833.501083	0.000585	KPLSVFK
7.5	833.501083	0.000585	INLTVFK
3.8	833.501068	0.000600	KLFEGLK
0.9	833.501068	0.000600	FIKGEIK

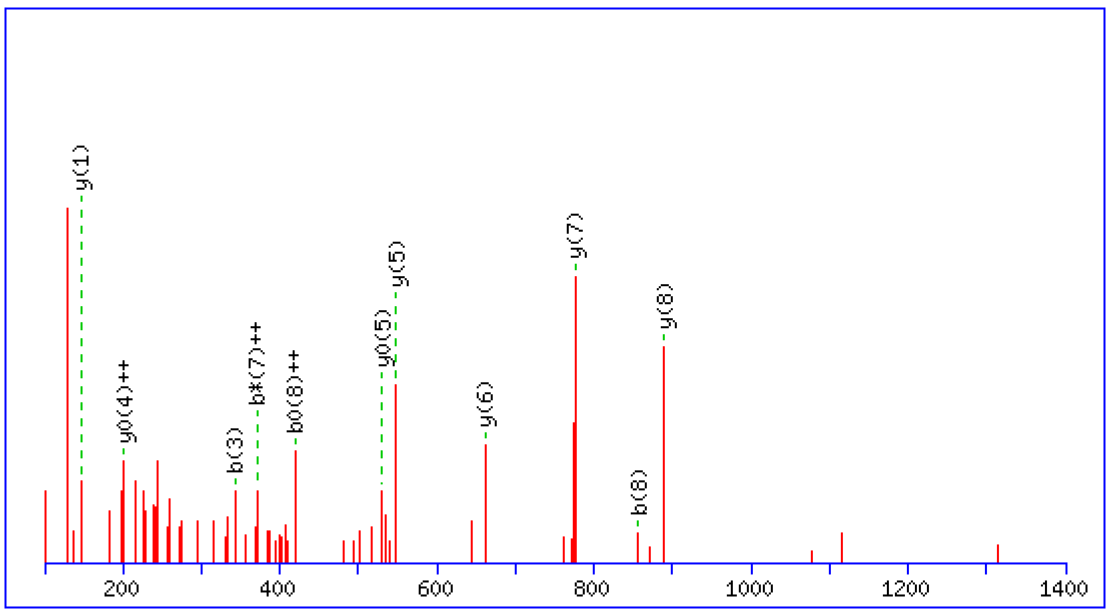
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LPDLKSSVK**
Found in **DLN1_HUMAN**, Protein DLN-1 OS=Homo sapiens GN=C10orf140 PE=2 SV=1

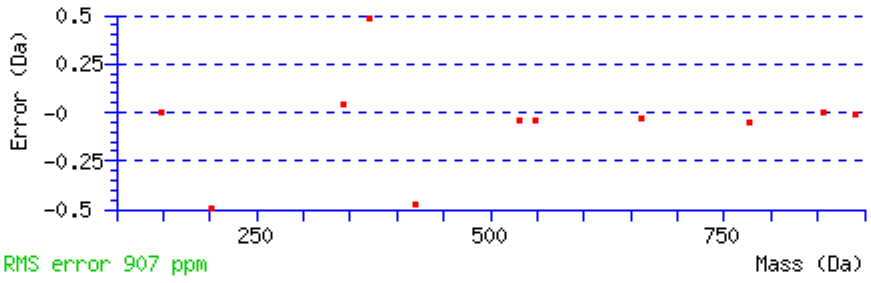
Match to Query 10532: 1001.577068 from(501.795810,2+) rtinseconds(1935) index(21535)
Title: Locus:1.1.1.2225.19
Data file 2011-11-10 - TFD - EP 4-3.mgf

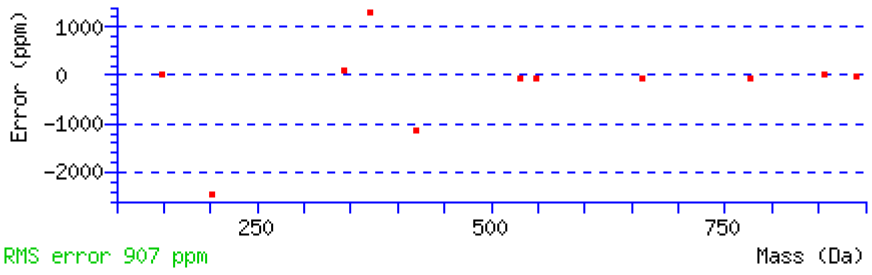
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1400] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1001.575699
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P2      : Oxidation (P)
Ions Score: 34  Expect: 0.003
Matches : 11/80 fragment ions using 16 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							9
2	227.139019	114.073147					P	*889.498923*	445.253100	872.472374	436.739825	871.488358	436.247817	8
3	**342.165962**	171.586619			324.155397	162.581336	D	*776.451244*	388.729260	759.424695	380.215986	758.440679	379.723978	7
4	455.250026	228.128651			437.239461	219.123369	L	*661.424301*	331.215789	644.397752	322.702514	643.413736	322.210506	6
5	583.344989	292.176133	566.318440	283.662858	565.334424	283.170850	K	*548.340237*	274.673757	531.313688	266.160482	530.329672	265.668474	5
6	670.377017	335.692147	653.350468	327.178872	652.366452	326.686864	S	420.245274	210.626275	403.218725	202.113000	402.234709	201.620992	4
7	757.409045	379.208161	740.382496	370.694886	739.398480	370.202878	S	333.213246	167.110261	316.186697	158.596986	315.202681	158.104978	3
8	**856.477459**	428.742368	839.450910	420.229093	838.466894	419.737085	V	246.181218	123.594247	229.154669	115.080972			2
9							K	*147.112804*	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of LPDLKSSVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.8	1001.575699	0.001369	LPDLKSSVK
32.2	1001.575699	0.001369	LIDIVSSQK
10.0	1001.575699	0.001369	LPSSVEVKK
9.0	1001.580399	-0.003331	ILSGGRMLR
8.7	1001.575684	0.001384	IDVASIKEK
8.0	1001.586929	-0.009861	LSNNTKVVK
7.0	1001.586929	-0.009861	ISPATTLRK
6.1	1001.575684	0.001384	EPILSTAKK
5.6	1001.575699	0.001369	VEELVTGKK
5.2	1001.586914	-0.009846	IESLGLRSK

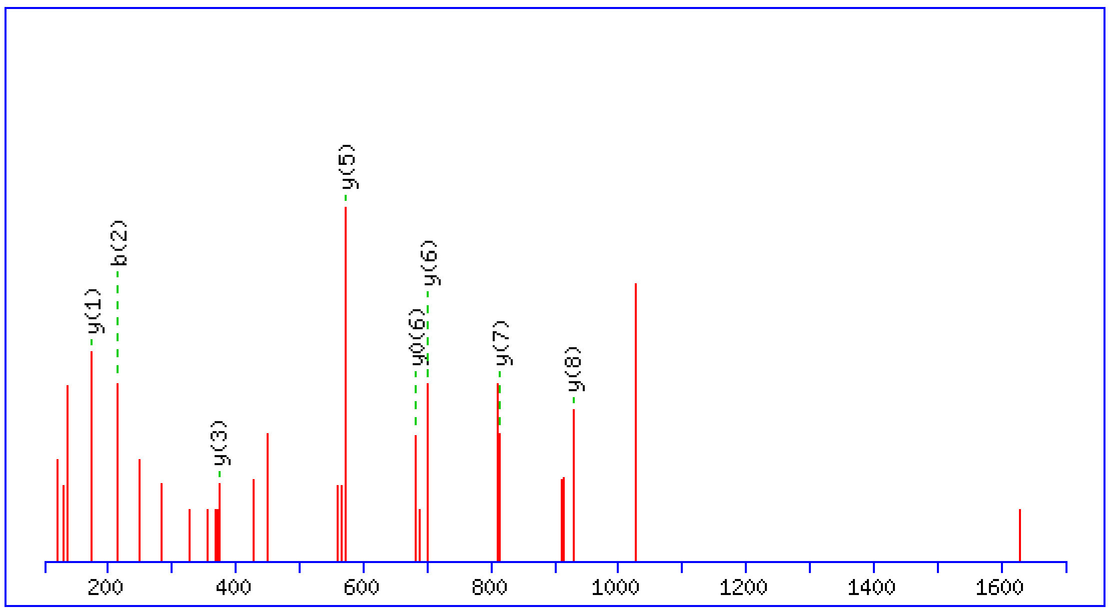
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **VDLQSLPTR**
Found in **DPY30_HUMAN**, Protein dpy-30 homolog OS=Homo sapiens GN=DPY30 PE=1 SV=1

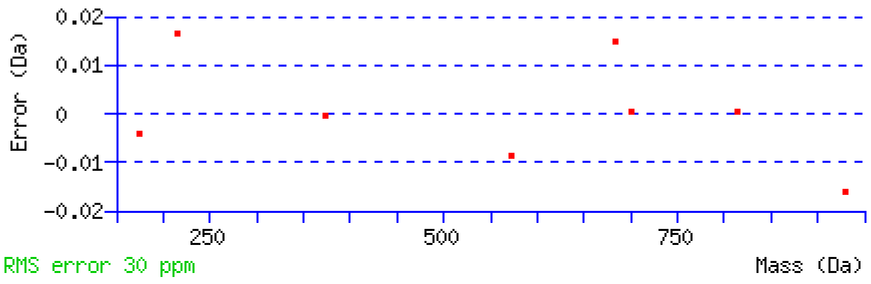
Match to Query 297265: 1027.572008 from(514.793280,2+) rtinseconds(1999) index(511877)
Title: Locus:1.1.1.1094.10
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

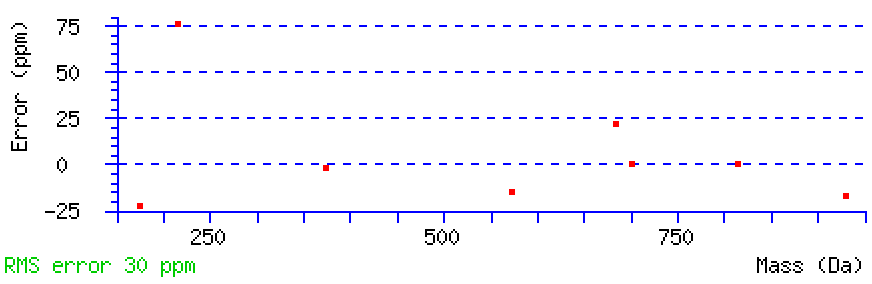
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1027.566208
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 34 **Expect:** 0.0049
Matches : 8/86 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					**V**							9
2	215.102633	108.054954			197.092068	99.049672	**D**	***929.505072***	465.256174	912.478523	456.742900	911.494507	456.250892	8
3	328.186697	164.596986			310.176132	155.591704	**L**	***814.478129***	407.742703	797.451580	399.229428	796.467564	398.737420	7
4	456.245275	228.626275	439.218726	220.113001	438.234710	219.620993	**Q**	***701.394065***	351.200671	684.367516	342.687396	683.383500	342.195388	6
5	543.277303	272.142290	526.250754	263.629015	525.266738	263.137007	**S**	***573.335487***	287.171382	556.308938	278.658107	555.324922	278.166099	5
6	656.361367	328.684322	639.334818	320.171047	638.350802	319.679039	**L**	486.303459	243.655368	469.276910	235.142093	468.292894	234.650085	4
7	753.414131	377.210704	736.387582	368.697429	735.403566	368.205421	**P**	***373.219395***	187.113336	356.192846	178.600061	355.208830	178.108053	3
8	854.461810	427.734543	837.435261	419.221269	836.451245	418.729261	**T**	276.166631	138.586954	259.140082	130.073679	258.156066	129.581671	2
9							**R**	***175.118952***	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of VDLQSLPTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.8	1027.566208	0.005800	VDLQSLPTR
8.6	1027.577408	-0.005400	VENIRLER
8.2	1027.581467	-0.009459	IPQTVLWR
6.8	1027.566193	0.005815	LLTLPNGER
5.6	1027.570236	0.001772	TLITPGPWK
5.6	1027.570236	0.001772	TLITPGPWK
2.4	1027.566193	0.005815	VALLEDVNR
2.1	1027.566208	0.005800	VLAVTDSPAR
2.0	1027.577423	-0.005415	VQIRLEDR
0.9	1027.566193	0.005815	TLEAQLTPR

Mascot: http://www.matrixscience.com/

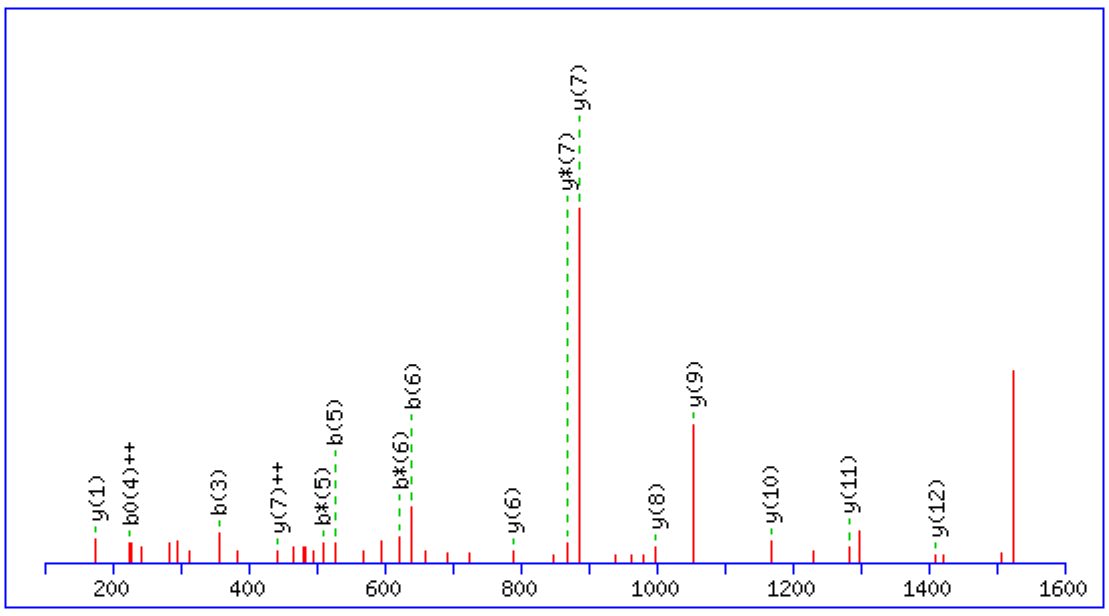
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LENLGIPEEELLR**
Found in **NC2B_HUMAN**, Protein Dr1 OS=Homo sapiens GN=DR1 PE=1 SV=1

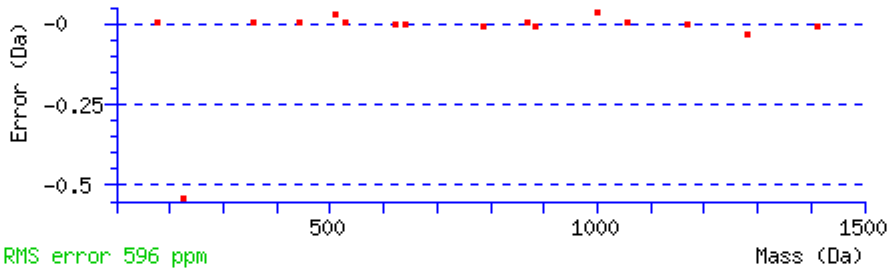
Match to Query 50929: 1523.816508 from(762.915530,2+) rtinseconds(3294) index(44565)
Title: Locus:1.1.1.2509.27
Data file 2011-11-10 - TFD - EP 4-6.mgf

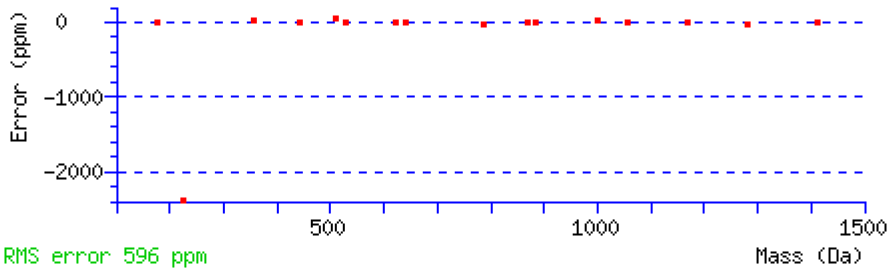
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1523.819473
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 57 **Expect:** 2e-005
Matches : 16/132 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							13
2	243.133933	122.070605			225.123368	113.065322	E	***1411.742735***	706.375006	1394.716186	697.861731	1393.732170	697.369723	12
3	**357.176860**	179.092068	340.150311	170.578794	339.166295	170.086786	N	***1282.700142***	641.853709	1265.673593	633.340435	1264.689577	632.848426	11
4	470.260924	235.634100	453.234375	227.120826	452.250359	226.628818	L	***1168.657215***	584.832246	1151.630666	576.318971	1150.646650	575.826963	10
5	**527.282388**	264.144832	510.255839	255.631558	509.271823	255.139550	G	***1055.573151***	528.290213	1038.546602	519.776939	1037.562586	519.284931	9
6	**640.366452**	320.686864	623.339903	312.173590	622.355887	311.681582	I	***998.551687***	499.779481	981.525138	491.266207	980.541122	490.774199	8
7	737.419216	369.213246	720.392667	360.699972	719.408651	360.207964	P	***885.467623***	443.237449	868.441074	434.724175	867.457058	434.232167	7
8	866.461809	433.734543	849.435260	425.221268	848.451244	424.729260	E	***788.414859***	394.711067	771.388310	386.197793	770.404294	385.705785	6
9	995.504402	498.255839	978.477853	489.742565	977.493837	489.250557	E	659.372266	330.189771	642.345717	321.676496	641.361701	321.184488	5
10	1124.546995	562.777136	1107.520446	554.263861	1106.536430	553.771853	E	530.329673	265.668474	513.303124	257.155200	512.319108	256.663192	4
11	1237.631059	619.319168	1220.604510	610.805893	1219.620494	610.313885	L	401.287080	201.147178	384.260531	192.633903			3
12	1350.715123	675.861200	1333.688574	667.347925	1332.704558	666.855917	L	288.203016	144.605146	271.176467	136.091871			2
13							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LENLGIPEEELLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.8	1523.819473	-0.002965	LENLGIPEEELLR
15.3	1523.820847	-0.004339	LLGWLRGEPGAPSR
15.3	1523.820847	-0.004339	LLGWLRGEPGAPSR
13.0	1523.830795	-0.014287	LPGSVGTPLPGVQVR
9.5	1523.820847	-0.004339	KDPIGPLEHRPLH
6.0	1523.805603	0.010905	LPRATPATAPGTSPR
4.7	1523.824219	-0.007711	LLRPGQPMSPQLR
4.4	1523.820831	-0.004323	IPLARHAFEEGLR
4.2	1523.809616	0.006892	LLFQPDQNAPPIR
4.1	1523.805603	0.010905	LPRATPATAPGTSPR

Mascot: http://www.matrixscience.com/

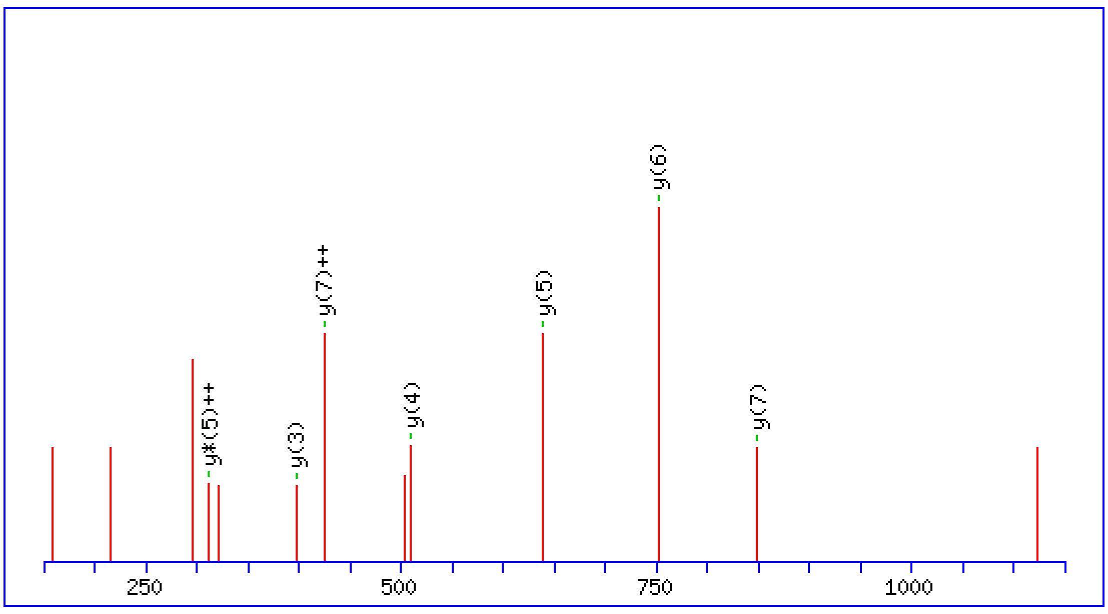
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IPIEPHPK**
Found in **F123A_HUMAN**, Protein FAM123A OS=Homo sapiens GN=FAM123A PE=2 SV=3

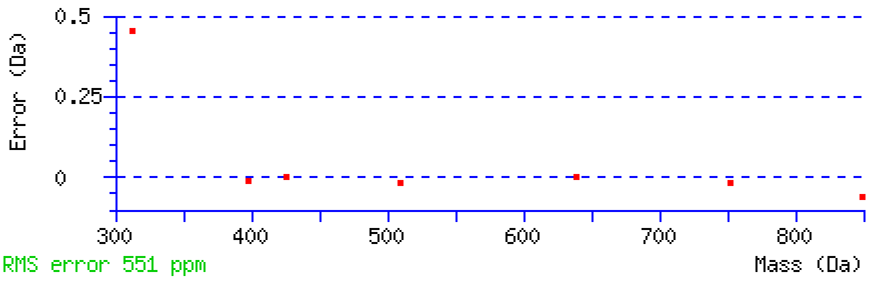
Match to Query 210229: 961.521708 from(481.768130,2+) rtinseconds(1991) index(755295)
Title: Locus:1.1.1.1103.15
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 150 to 1150 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●

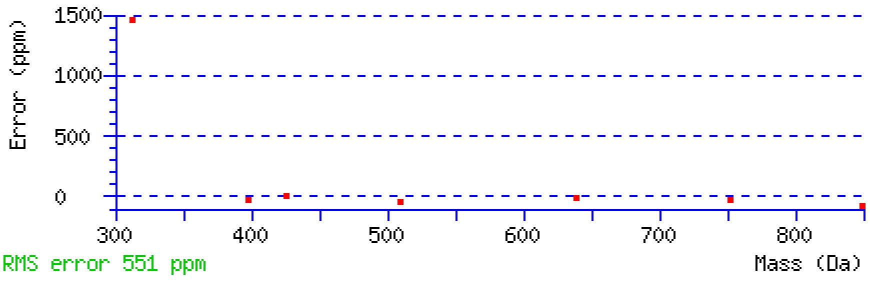


```
Monoisotopic mass of neutral peptide Mr(calc): 961.523270
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
P5      : Oxidation (P)
P7      : Oxidation (P)
Ions Score: 35  Expect: 0.0029
Matches : 7/56 fragment ions using 11 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							8
2	211.144104	106.075690			P	***849.446495***	425.226886	832.419946	416.713611	831.435930	416.221603	7
3	324.228168	162.617722			I	***752.393731***	376.700504	735.367182	368.187229	734.383166	367.695221	6
4	453.270761	227.139018	435.260196	218.133736	E	***639.309667***	320.158472	622.283118	311.645197	621.299102	311.153189	5
5	566.318440	283.662858	548.307875	274.657576	P	***510.267074***	255.637175	493.240525	247.123900			4
6	703.377352	352.192314	685.366787	343.187031	H	***397.219395***	199.113335	380.192846	190.600061			3
7	816.425031	408.716154	798.414466	399.710871	P	260.160483	130.583879	243.133934	122.070605			2
8					K	147.112804	74.060040	130.086255	65.546765			1



RMS error 551 ppm



RMS error 551 ppm

NCBI **BLAST** search of IPIEPHPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.1	961.523270	-0.001562	IPIEPHPK
27.6	961.523254	-0.001546	LPLETAYR
13.9	961.515411	0.006297	TLIEVMPK
13.7	961.519241	0.002467	LGDSSLSRK
11.9	961.526642	-0.004934	LLIPSTRM
11.6	961.515396	0.006312	MLLSLPEK
11.1	961.526627	-0.004919	MSLLNKPK
8.9	961.515381	0.006327	LAMEELIK
8.0	961.530670	-0.008962	LTLPLFGAM
5.8	961.523270	-0.001562	IPIEPHPK

Mascot: http://www.matrixscience.com/

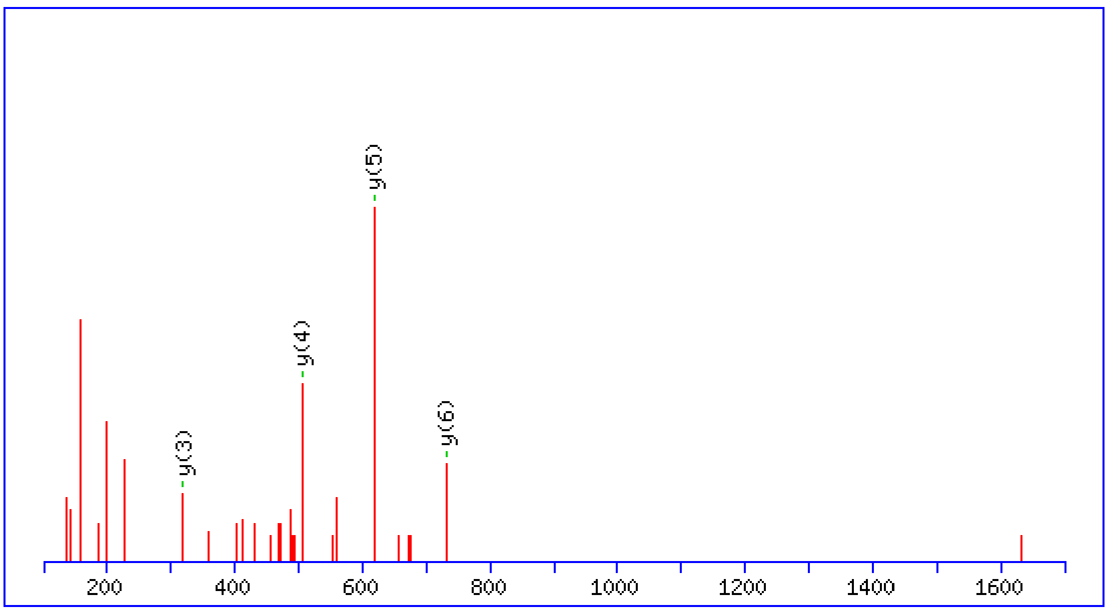
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILIWSGR**
Found in **F162A_HUMAN**, Protein FAM162A OS=Homo sapiens GN=FAM162A PE=1 SV=2

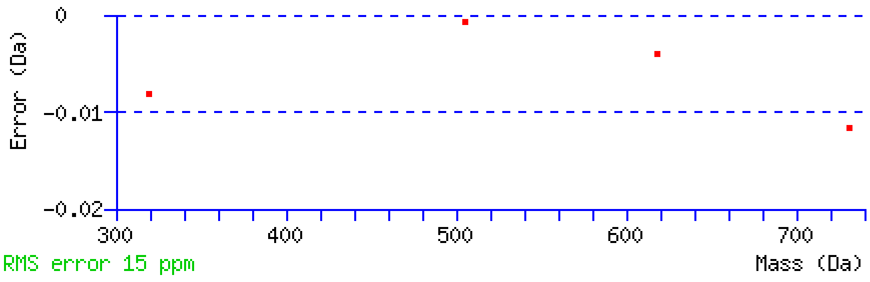
Match to Query 3929: 843.497468 from(422.756010,2+) rtinseconds(2574) index(31930)
Title: Locus:1.1.1.2132.4
Data file 2011-11-12 - TFD - EP 6-6.mgf

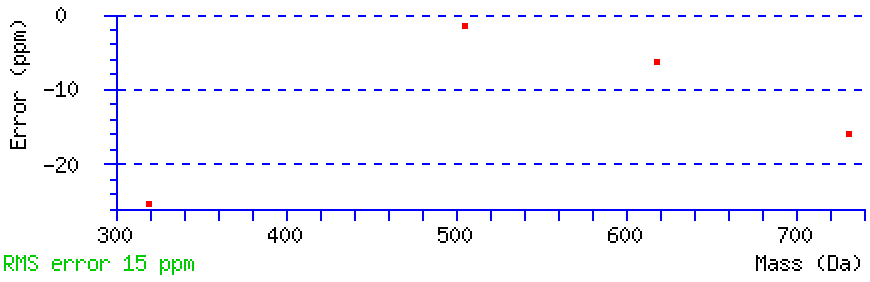
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 843.496658
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 34 **Expect:** 0.0036
Matches : 4/48 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							7
2	227.175404	114.091340			L	*731.419885*	366.213581	714.393336	357.700306	713.409320	357.208298	6
3	340.259468	170.633372			I	*618.335821*	309.671549	601.309272	301.158274	600.325256	300.666266	5
4	526.338781	263.673029			W	*505.251757*	253.129517	488.225208	244.616242	487.241192	244.124234	4
5	613.370809	307.189043	595.360244	298.183760	S	*319.172444*	160.089860	302.145895	151.576586	301.161879	151.084578	3
6	670.392273	335.699775	652.381708	326.694492	G	232.140416	116.573846	215.113867	108.060572			2
7					R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of ILIWSGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.8	843.496658	0.000810	ILIWSGR
15.9	843.500015	-0.002547	LPIRMAK
6.4	843.500015	-0.002547	ILRSPMK
6.4	843.492630	0.004838	ILTDARR
6.4	843.492630	0.004838	ILTRGER
6.4	843.496643	0.000825	ILWKER
6.4	843.492630	0.004838	IPSRSLR
6.4	843.492630	0.004838	LISPSRR
6.4	843.492630	0.004838	LPSIRSR
1.6	843.496658	0.000810	ILAFPQR

Mascot: http://www.matrixscience.com/

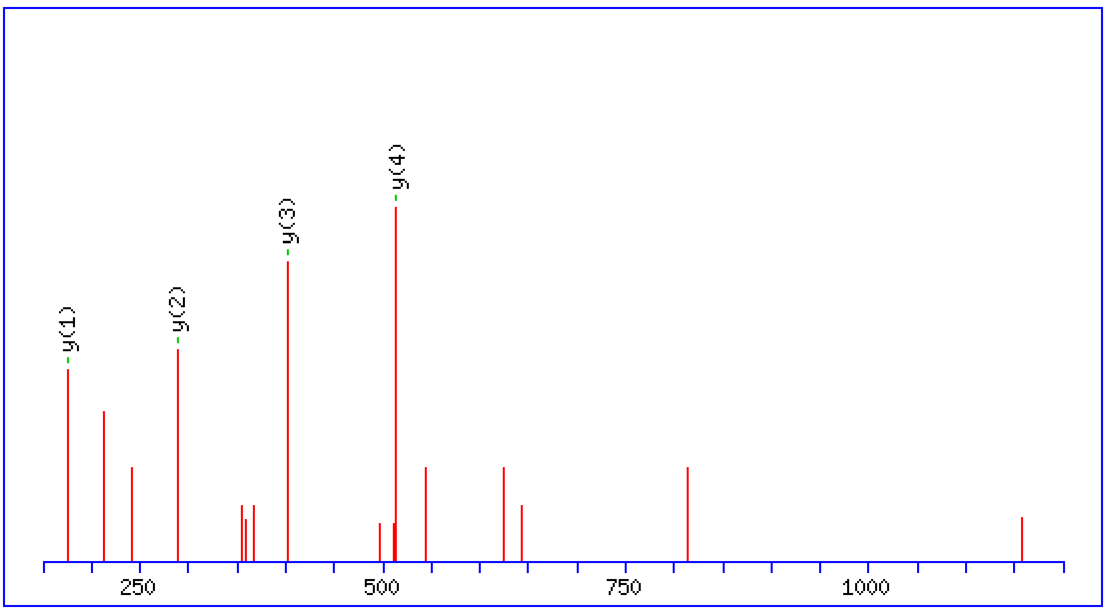
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EGLLPLR**
Found in **F179A_HUMAN**, Protein FAM179A OS=Homo sapiens GN=FAM179A PE=2 SV=2

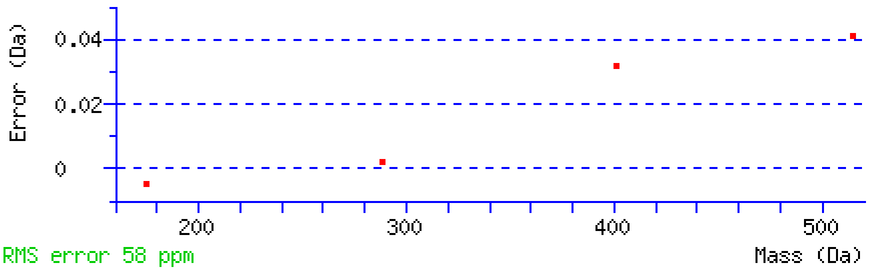
Match to Query 1124: 812.478148 from(407.246350,2+) rtinseconds(1892) index(17508)
Title: Locus:1.1.1.1993.3
Data file 2011-11-14 - TFD - EP 8-6.mgf

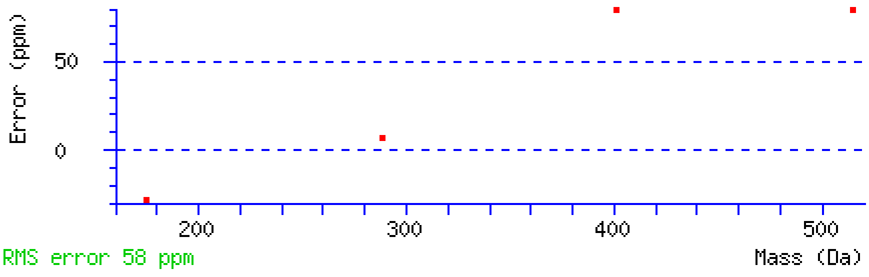
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 812.475586
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P5 : Oxidation (P)
Ions Score: 35 **Expect:** 0.0013
Matches : 4/48 fragment ions using 5 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	130.049869	65.528572	112.039304	56.523290	E					7
2	187.071333	94.039305	169.060768	85.034022	G	684.440287	342.723782	667.413738	334.210507	6
3	300.155397	150.581336	282.144832	141.576054	L	627.418823	314.213050	610.392274	305.699775	5
4	413.239461	207.123369	395.228896	198.118086	L	***514.334759***	257.671018	497.308210	249.157743	4
5	526.287140	263.647208	508.276575	254.641926	P	***401.250695***	201.128985	384.224146	192.615711	3
6	639.371204	320.189240	621.360639	311.183958	L	***288.203016***	144.605146	271.176467	136.091871	2
7					R	***175.118952***	88.063114	158.092403	79.549839	1





NCBI **BLAST** search of EGLLPLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.3	812.475586	0.002562	EGLLPLR
18.7	812.475586	0.002562	APEVLLR
18.7	812.475601	0.002547	TLTPPLR
2.5	812.475586	0.002562	ILSVEPR
2.5	812.475601	0.002547	TVLVPER
1.7	812.475601	0.002547	DIVPTLR
1.7	812.475601	0.002547	DPVLTLR
1.7	812.475586	0.002562	EVLPAIR
1.7	812.475586	0.002562	IAPEVLR
1.7	812.475601	0.002547	IPSLVPR

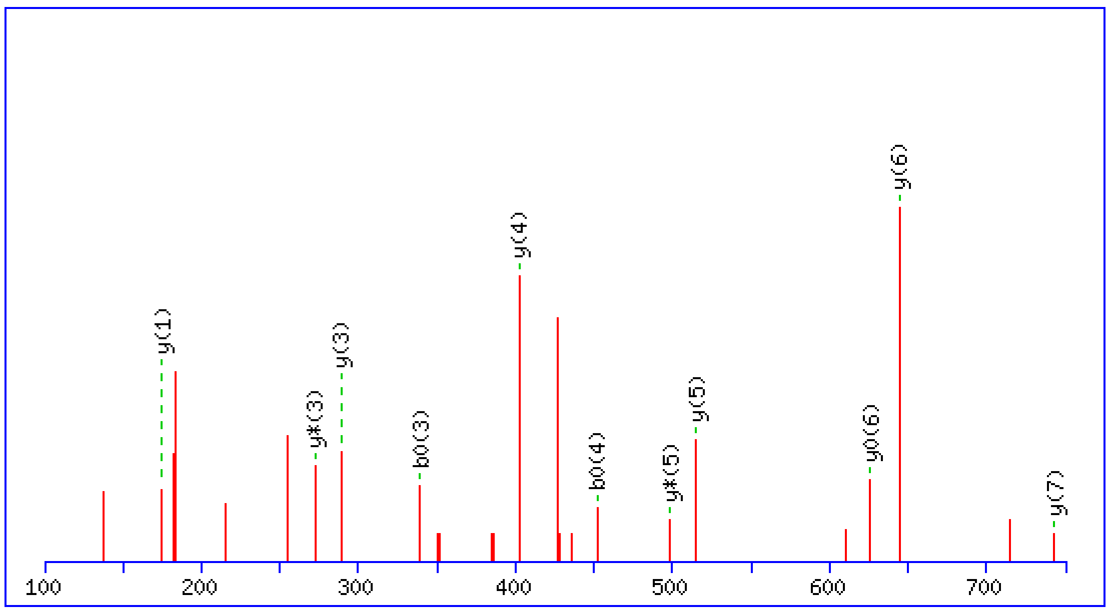
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QVEILGGR**
Found in **F186B_HUMAN**, Protein FAM186B OS=Homo sapiens GN=FAM186B PE=2 SV=2

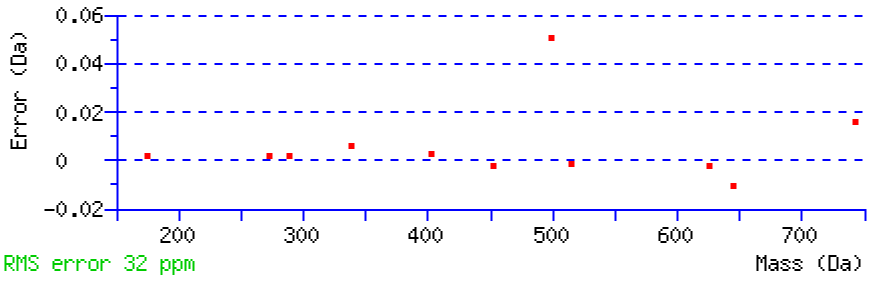
Match to Query 89453: 870.494428 from(436.254490,2+) rtinseconds(1610) index(504451)
Title: Locus:1.1.1.943.9
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

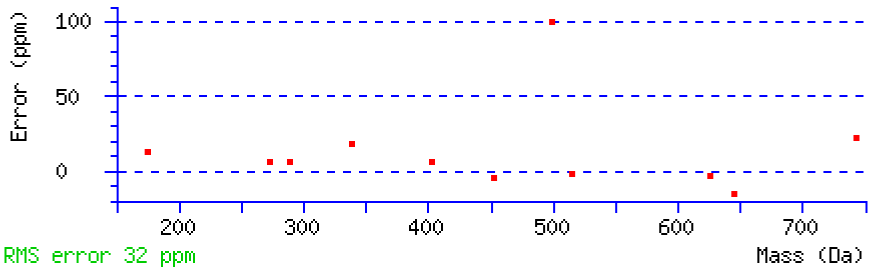
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 870.492310
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 46 **Expect:** 0.00046
Matches : 11/70 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	129.065854	65.036565	112.039305	56.523291			**Q**							8
2	228.134268	114.570772	211.107719	106.057498			**V**	***743.441015***	372.224146	726.414466	363.710871	725.430450	363.218863	7
3	357.176861	179.092069	340.150312	170.578794	339.166296	170.086786	**E**	***644.372601***	322.689939	627.346052	314.176664	626.362036	313.684656	6
4	470.260925	235.634101	453.234376	227.120826	452.250360	226.628818	**I**	***515.330008***	258.168642	498.303459	249.655368			5
5	583.344989	292.176133	566.318440	283.662858	565.334424	283.170850	**L**	***402.245944***	201.626610	385.219395	193.113336			4
6	640.366453	320.686865	623.339904	312.173590	622.355888	311.681582	**G**	***289.161880***	145.084578	272.135331	136.571304			3
7	697.387917	349.197597	680.361368	340.684322	679.377352	340.192314	**G**	232.140416	116.573846	215.113867	108.060572			2
8							**R**	***175.118952***	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of QVEILGGR
(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	870.492310	0.002118	QVEILGGR
46.2	870.492294	0.002134	QVEILNR
29.2	870.492294	0.002134	QEVLINR
17.2	870.492325	0.002103	AVSVPLGGR
12.0	870.492310	0.002118	VKSSTPPR
9.5	870.485764	0.008664	KPSMRPR
9.5	870.492325	0.002103	KTTPGVPR
9.3	870.492294	0.002134	NLEQVLR
9.3	870.492294	0.002134	NLEVQLR
9.2	870.492310	0.002118	KSVSTPPR

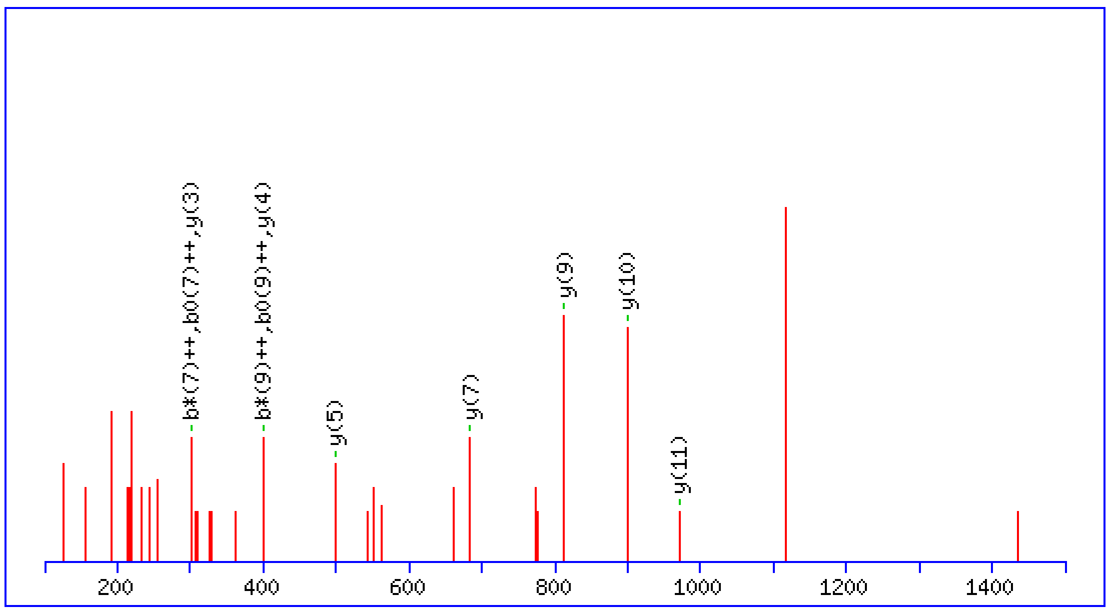
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MASGAANVVGPK**
Found in **FAM3C_HUMAN**, Protein FAM3C OS=Homo sapiens GN=FAM3C PE=1 SV=1

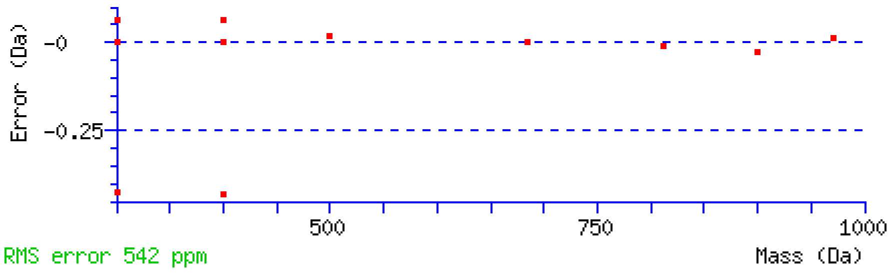
Match to Query 24460: 1116.558208 from(559.286380,2+) rtinseconds(1062) index(3306)
Title: Locus:1.1.1.1718.33
Data file 2011-11-10 - TFD - EP 4-5.mgf

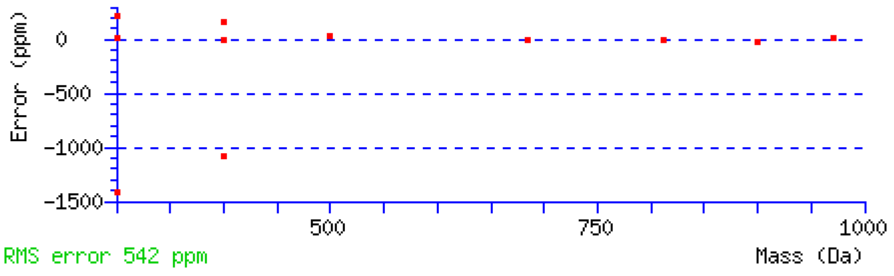
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1116.559738
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 67 **Expect:** 7.8e-006
Matches : 11/148 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.042676	74.524976					M							12
2	219.079790	110.043533					A	***970.531621***	485.769449	953.505072	477.256174	952.521056	476.764166	11
3	306.111818	153.559547			288.101253	144.554264	S	***899.494507***	450.250892	882.467958	441.737617	881.483942	441.245609	10
4	363.133282	182.070279			345.122717	173.064996	G	***812.462479***	406.734878	795.435930	398.221603			9
5	434.170396	217.588836			416.159831	208.583553	A	755.441015	378.224146	738.414466	369.710871			8
6	505.207510	253.107393			487.196945	244.102110	A	***684.403901***	342.705589	667.377352	334.192314			7
7	619.250437	310.128856	602.223888	301.615582	601.239872	301.123574	N	613.366787	307.187032	596.340238	298.673757			6
8	718.318851	359.663063	701.292302	351.149789	700.308286	350.657781	V	***499.323860***	250.165568	482.297311	241.652294			5
9	817.387265	409.197270	800.360716	400.683996	799.376700	400.191988	V	***400.255446***	200.631361	383.228897	192.118087			4
10	874.408729	437.708002	857.382180	429.194728	856.398164	428.702720	G	***301.187032***	151.097154	284.160483	142.583880			3
11	971.461493	486.234384	954.434944	477.721110	953.450928	477.229102	P	244.165568	122.586422	227.139019	114.073148			2
12							K	147.112804	74.060040	130.086255	65.546766			1





NCBI **BLAST** search of MASGAANVVGPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
66.6	1116.559738	-0.001530	MASGAANVVGPK
0.5	1116.559753	-0.001545	MAAPVVTAPGR

Mascot: http://www.matrixscience.com/

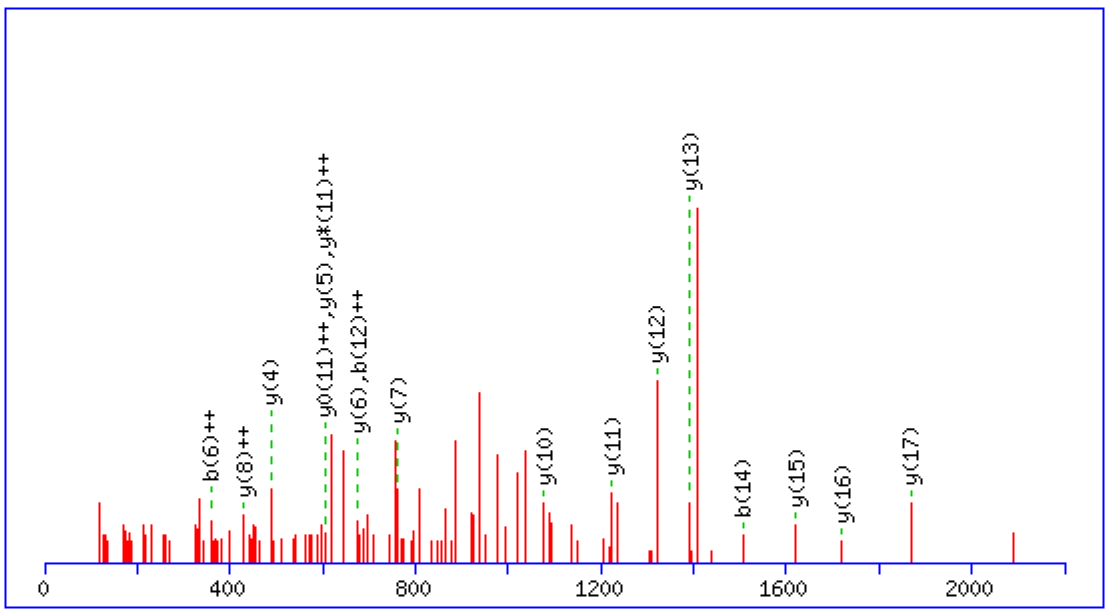
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EIFTNLAPFSEVSADGEKR**
Found in **FA45A_HUMAN**, Protein FAM45A OS=Homo sapiens GN=FAM45A PE=2 SV=1

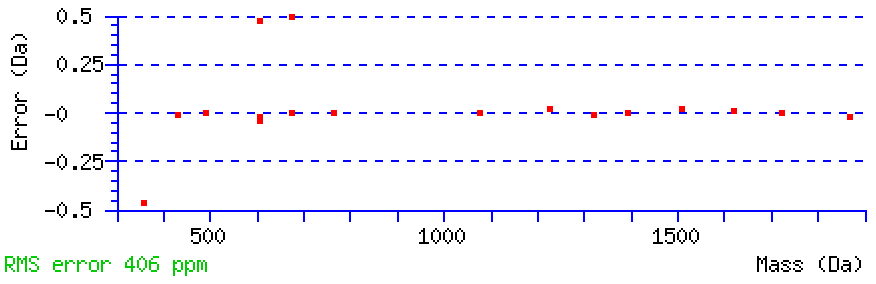
Match to Query 66235: 2109.032202 from(704.018010,3+) rtinseconds(3123) index(44208)
Title: Locus:1.1.1.2513.29
Data file 2011-11-10 - TFD - EP 4-4.mgf

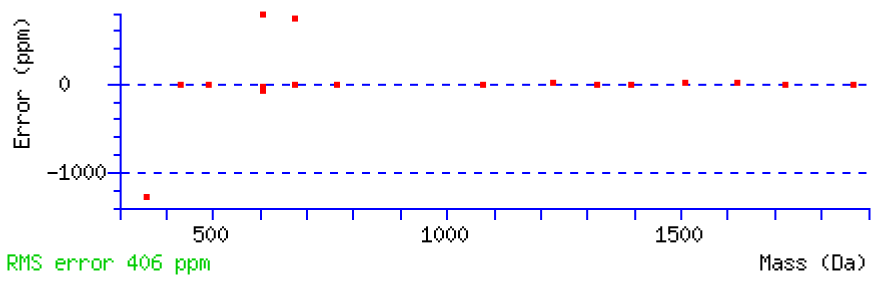
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2109.037827
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 36  Expect: 0.00056
Matches : 17/204 fragment ions using 45 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	E							19
2	243.133933	122.070605			225.123368	113.065322	I	1981.002532	991.004904	1963.975983	982.491630	1962.991967	981.999622	18
3	390.202347	195.604811			372.191782	186.599529	F	***1867.918468***	934.462872	1850.891919	925.949598	1849.907903	925.457590	17
4	491.250026	246.128651			473.239461	237.123369	T	***1720.850054***	860.928665	1703.823505	852.415391	1702.839489	851.923383	16
5	605.292953	303.150115	588.266404	294.636840	587.282388	294.144832	N	***1619.802375***	810.404826	1602.775826	801.891551	1601.791810	801.399543	15
6	718.377017	359.692147	701.350468	351.178872	700.366452	350.686864	L	1505.759448	753.383362	1488.732899	744.870088	1487.748883	744.378080	14
7	789.414131	395.210704	772.387582	386.697429	771.403566	386.205421	A	***1392.675384***	696.841330	1375.648835	688.328056	1374.664819	687.836048	13
8	886.466895	443.737086	869.440346	435.223811	868.456330	434.731803	P	***1321.638270***	661.322773	1304.611721	652.809499	1303.627705	652.317491	12
9	1033.535309	517.271293	1016.508760	508.758018	1015.524744	508.266010	F	***1224.585506***	612.796391	1207.558957	604.283117	1206.574941	603.791109	11
10	1120.567337	560.787307	1103.540788	552.274032	1102.556772	551.782024	S	***1077.517092***	539.262184	1060.490543	530.748910	1059.506527	530.256902	10
11	1249.609930	625.308603	1232.583381	616.795329	1231.599365	616.303321	E	990.485064	495.746170	973.458515	487.232896	972.474499	486.740888	9
12	1348.678344	674.842810	1331.651795	666.329536	1330.667779	665.837528	V	861.442471	431.224874	844.415922	422.711599	843.431906	422.219591	8
13	1435.710372	718.358824	1418.683823	709.845550	1417.699807	709.353542	S	***762.374057***	381.690667	745.347508	373.177392	744.363492	372.685384	7
14	1506.747486	753.877381	1489.720937	745.364107	1488.736921	744.872099	A	***675.342029***	338.174652	658.315480	329.661378	657.331464	329.169370	6
15	1621.774429	811.390853	1604.747880	802.877578	1603.763864	802.385570	D	***604.304915***	302.656095	587.278366	294.142821	586.294350	293.650813	5
16	1678.795893	839.901585	1661.769344	831.388310	1660.785328	830.896302	G	***489.277972***	245.142624	472.251423	236.629349	471.267407	236.137341	4
17	1807.838486	904.422881	1790.811937	895.909607	1789.827921	895.417599	E	432.256508	216.631892	415.229959	208.118617	414.245943	207.626609	3
18	1935.933449	968.470363	1918.906900	959.957088	1917.922884	959.465080	K	303.213915	152.110595	286.187366	143.597321			2
19							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of EIFTNLAPFSEVSADGEKR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.1	2109.037827	-0.005625	EIFTNLAPFSEVSADGEKR
1.4	2109.029984	0.002218	TPPECVLTPLPPSADDNLK

Mascot: http://www.matrixscience.com/

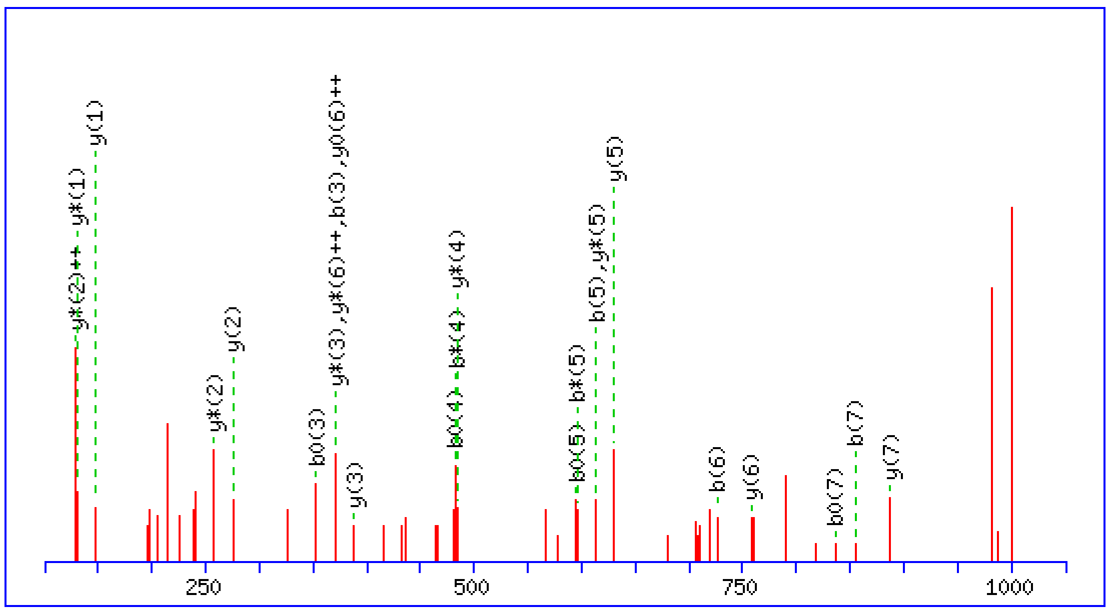
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IEKELLQK**
Found in **FA81A_HUMAN**, Protein FAM81A OS=Homo sapiens GN=FAM81A PE=2 SV=3

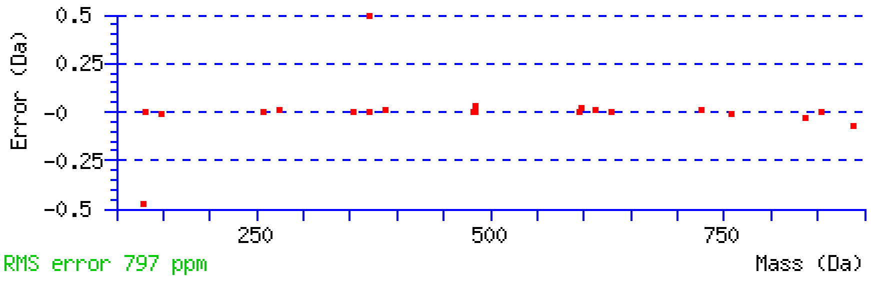
Match to Query 11407: 999.599108 from(500.806830,2+) rtinseconds(1596) index(4000)
Title: Locus:1.1.1.2264.12
Data file 2011-11-13 - TFD - EP 7-8.mgf

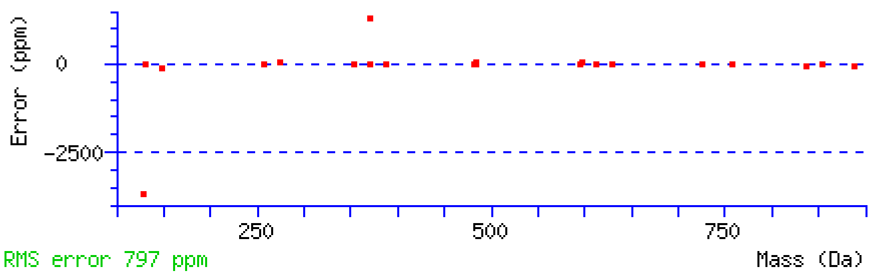
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 999.596405
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 38  Expect: 0.0011
Matches : 24/70 fragment ions using 33 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					**I**							8
2	243.133933	122.070605			225.123368	113.065322	**E**	***887.519659***	444.263468	870.493110	435.750193	869.509094	435.258185	7
3	**371.228896**	186.118086	354.202347	177.604812	353.218331	177.112804	**K**	***758.477066***	379.742171	741.450517	371.228897	740.466501	370.736889	6
4	500.271489	250.639383	483.244940	242.126108	482.260924	241.634100	**E**	***630.382103***	315.694690	613.355554	307.181415	612.371538	306.689407	5
5	**613.355553**	307.181415	596.329004	298.668140	595.344988	298.176132	**L**	501.339510	251.173393	484.312961	242.660119			4
6	**726.439617**	363.723447	709.413068	355.210172	708.429052	354.718164	**L**	***388.255446***	194.631361	371.228897	186.118087			3
7	**854.498195**	427.752736	837.471646	419.239461	836.487630	418.747453	**Q**	***275.171382***	138.089329	258.144833	129.576055			2
8							**K**	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of IEKELLQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.6	999.596405	0.002703	EQLELLKK
42.5	999.596405	0.002703	QLELEIKK
38.4	999.596405	0.002703	IEKELLQK
33.2	999.596405	0.002703	ELKELIQK
25.1	999.596405	0.002703	LQELEKIK
21.1	999.596405	0.002703	LQELKIEK
20.8	999.607651	-0.008543	LLRTELQK
17.6	999.596405	0.002703	ELQILKEK
17.4	999.596405	0.002703	EEIAVALKK
15.9	999.596405	0.002703	EKEILQIK

Mascot: http://www.matrixscience.com/

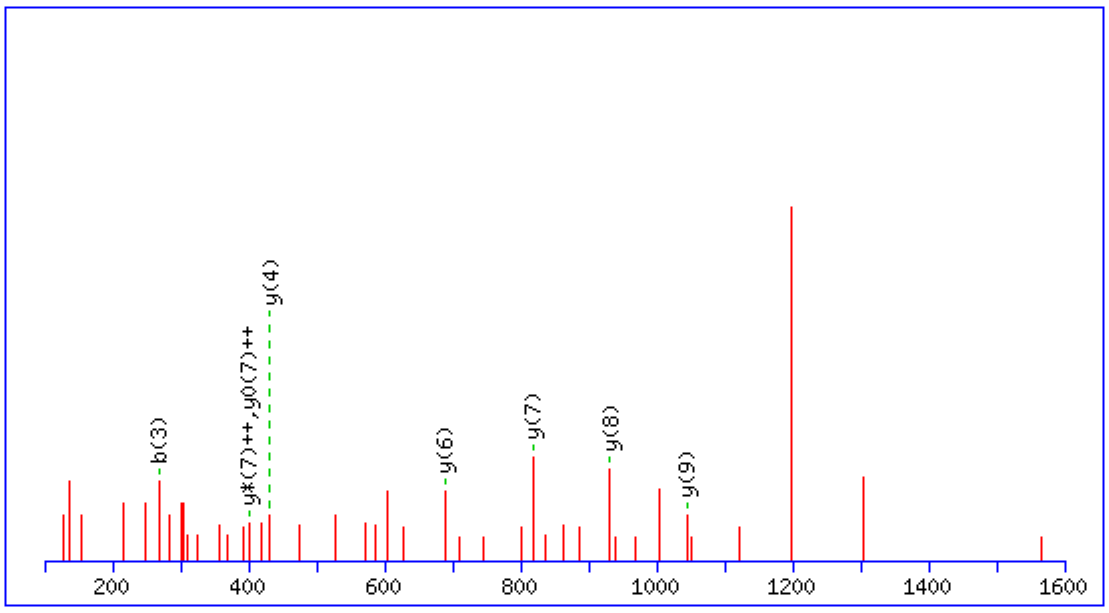
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GPLLEEQALTK**
Found in **FA98B_HUMAN**, Protein FAM98B OS=Homo sapiens GN=FAM98B PE=1 SV=1

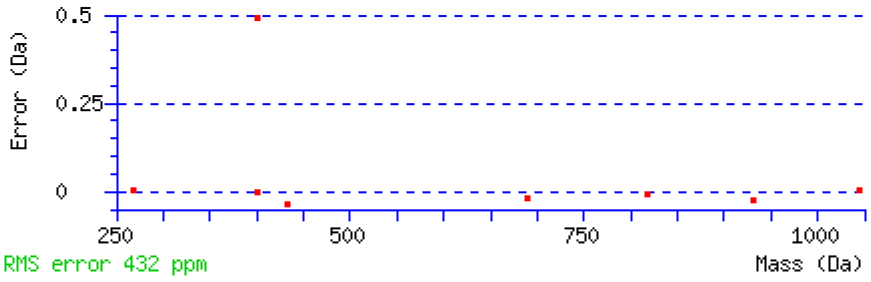
Match to Query 518483: 1197.651328 from(599.832940,2+) rtinseconds(2223) index(759646)
Title: Locus:1.1.1.1192.27
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

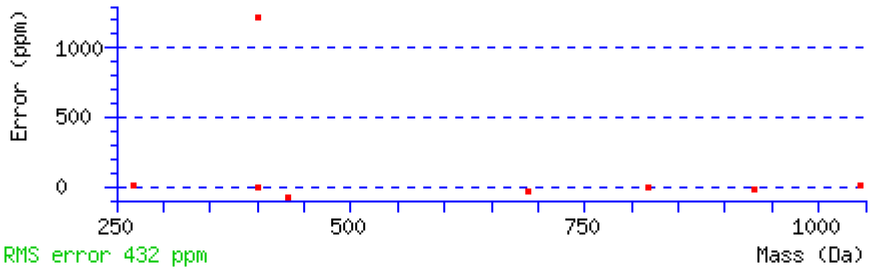
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1197.660477
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.011
Matches : 8/98 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							11
2	155.081504	78.044390					P	1141.646317	571.326797	1124.619768	562.813522	1123.635752	562.321514	10
3	268.165568	134.586422					L	***1044.593553***	522.800415	1027.567004	514.287140	1026.582988	513.795132	9
4	381.249632	191.128454					L	***931.509489***	466.258383	914.482940	457.745108	913.498924	457.253100	8
5	510.292225	255.649751			492.281660	246.644468	E	***818.425425***	409.716351	801.398876	401.203076	800.414860	400.711068	7
6	639.334818	320.171047			621.324253	311.165765	E	***689.382832***	345.195054	672.356283	336.681780	671.372267	336.189772	6
7	767.393396	384.200336	750.366847	375.687062	749.382831	375.195054	Q	560.340239	280.673758	543.313690	272.160483	542.329674	271.668475	5
8	838.430510	419.718893	821.403961	411.205619	820.419945	410.713611	A	***432.281661***	216.644468	415.255112	208.131194	414.271096	207.639186	4
9	951.514574	476.260925	934.488025	467.747651	933.504009	467.255643	L	361.244547	181.125912	344.217998	172.612637	343.233982	172.120629	3
10	1052.562253	526.784765	1035.535704	518.271490	1034.551688	517.779482	T	248.160483	124.583879	231.133934	116.070605	230.149918	115.578597	2
11							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of GPLLEEQALTK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.1	1197.660477	-0.009149	GPLLEEQALTK

Mascot: http://www.matrixscience.com/

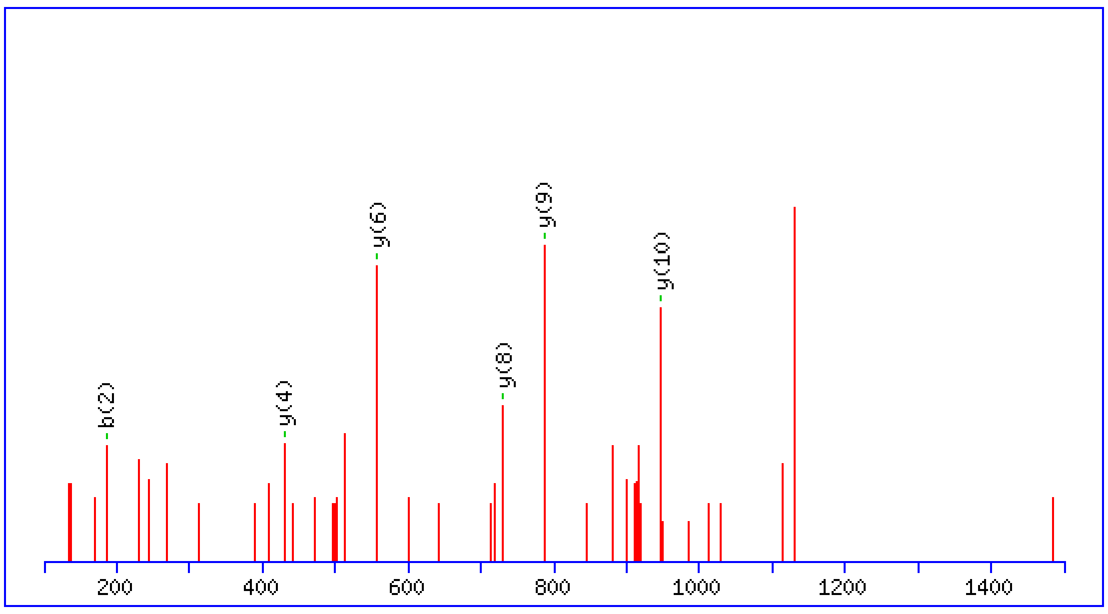
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALCGGDGAAALR**
Found in **FA98C_HUMAN**, Protein FAM98C OS=Homo sapiens GN=FAM98C PE=2 SV=1

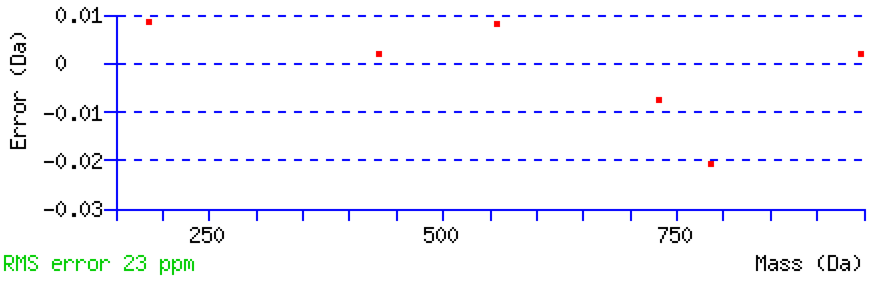
Match to Query 432625: 1130.551948 from(566.283250,2+) rtinseconds(1552) index(421300)
Title: Locus:1.1.1.931.25
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

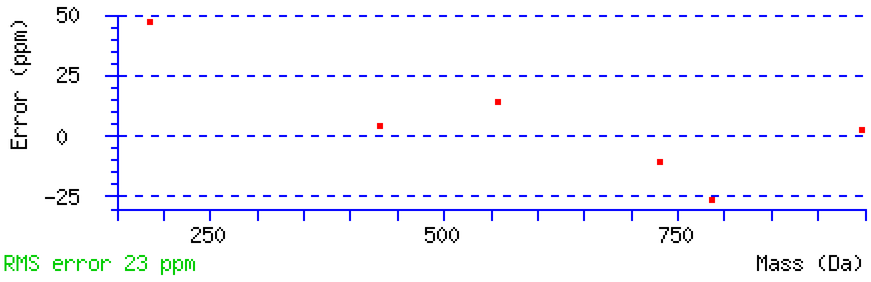
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1500] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1130.550232
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.0027
Matches : 6/88 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			A							12
2	185.128454	93.067865			L	1060.520406	530.763841	1043.493857	522.250567	1042.509841	521.758559	11
3	345.159103	173.083190			C	*947.436342*	474.221809	930.409793	465.708535	929.425777	465.216527	10
4	402.180567	201.593921			G	*787.405693*	394.206485	770.379144	385.693210	769.395128	385.201202	9
5	459.202031	230.104653			G	*730.384229*	365.695753	713.357680	357.182478	712.373664	356.690470	8
6	574.228974	287.618125	556.218409	278.612843	D	673.362765	337.185021	656.336216	328.671746	655.352200	328.179738	7
7	631.250438	316.128857	613.239873	307.123575	G	*558.335822*	279.671549	541.309273	271.158275			6
8	702.287552	351.647414	684.276987	342.642132	A	501.314358	251.160817	484.287809	242.647542			5
9	773.324666	387.165971	755.314101	378.160688	A	*430.277244*	215.642260	413.250695	207.128986			4
10	844.361780	422.684528	826.351215	413.679245	A	359.240130	180.123703	342.213581	171.610429			3
11	957.445844	479.226560	939.435279	470.221277	L	288.203016	144.605146	271.176467	136.091872			2
12					R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of ALCGGDGAAALR
(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	1130.550232	0.001716	ALCGGDGAAALR
4.0	1130.546387	0.005561	MAAKQPPPLM
4.0	1130.546387	0.005561	MAAKQPPPLM
4.0	1130.546387	0.005561	MAAKQPPPLM
3.7	1130.550217	0.001731	MAAAAAAGSGTPR
2.6	1130.546387	0.005561	MAAKQPPPLM
1.8	1130.556763	-0.004815	SDAAGDIVDIR

Mascot: http://www.matrixscience.com/

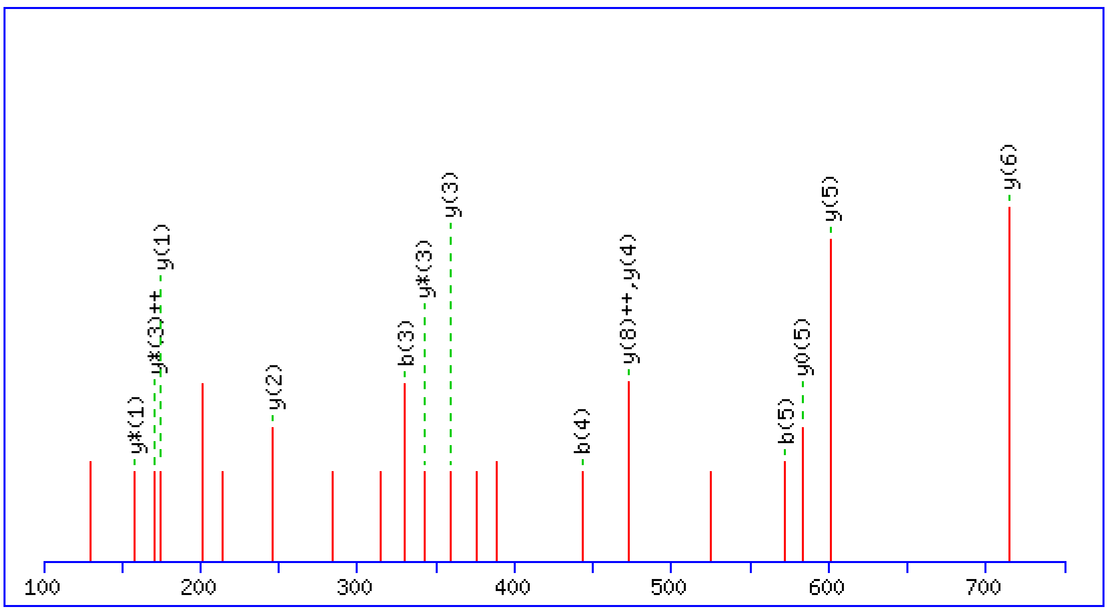
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TDLIELLAR**
Found in **FRYL_HUMAN**, Protein furry homolog-like OS=Homo sapiens GN=FRYL PE=1 SV=2

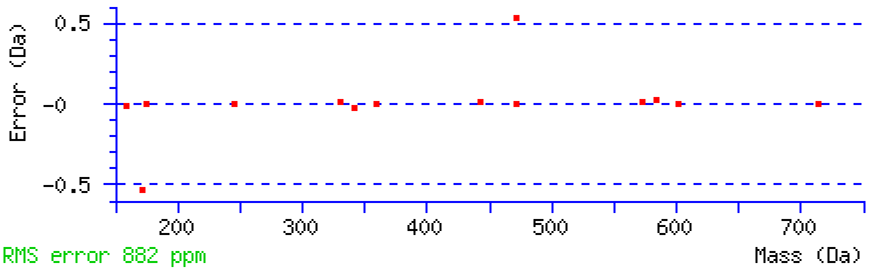
Match to Query 18314: 1042.605528 from(522.310040,2+) rtinseconds(3619) index(51963)
Title: Locus:1.1.1.2791.5
Data file 2011-11-10 - TFD - EP 3-1.mgf

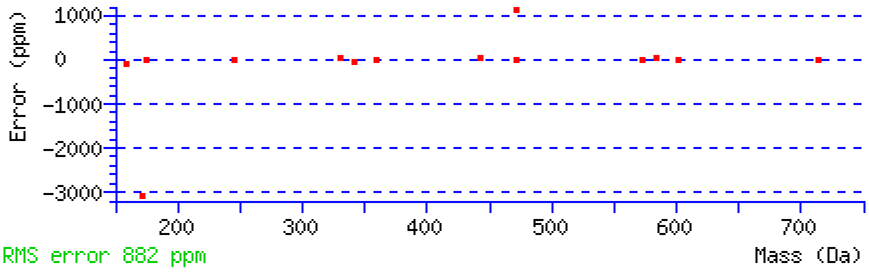
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [750] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1042.602234
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 44 **Expect:** 0.00051
Matches : 14/72 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116	84.044390	42.525833	T							9
2	217.081898	109.044587	199.071333	100.039304	D	942.561858	471.784567	925.535309	463.271293	924.551293	462.779285	8
3	**330.165962**	165.586619	312.155397	156.581336	L	827.534915	414.271096	810.508366	405.757821	809.524350	405.265813	7
4	**443.250026**	222.128651	425.239461	213.123369	I	***714.450851***	357.729064	697.424302	349.215789	696.440286	348.723781	6
5	**572.292619**	286.649948	554.282054	277.644665	E	***601.366787***	301.187032	584.340238	292.673757	583.356222	292.181749	5
6	685.376683	343.191980	667.366118	334.186697	L	***472.324194***	236.665735	455.297645	228.152460			4
7	798.460747	399.734012	780.450182	390.728729	L	***359.240130***	180.123703	342.213581	171.610428			3
8	869.497861	435.252569	851.487296	426.247286	A	***246.156066***	123.581671	229.129517	115.068396			2
9					R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of TDLIELLAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.0	1042.602234	0.003294	TDLIELLAR
10.8	1042.613464	-0.007936	ASEALKVVAR
7.5	1042.595703	0.009825	MPTLKANIR
6.4	1042.613495	-0.007967	VQGVSLTALR
6.0	1042.613480	-0.007952	ATKPAVTLAR
4.0	1042.606934	-0.001406	LRLQCLAR
2.9	1042.603577	0.001951	TLWARLQR
2.4	1042.613480	-0.007952	VVDSIRNLK
1.8	1042.602249	0.003279	VTASLLGAPSK
1.3	1042.613510	-0.007982	TGGVPIRTVK

Mascot: http://www.matrixscience.com/

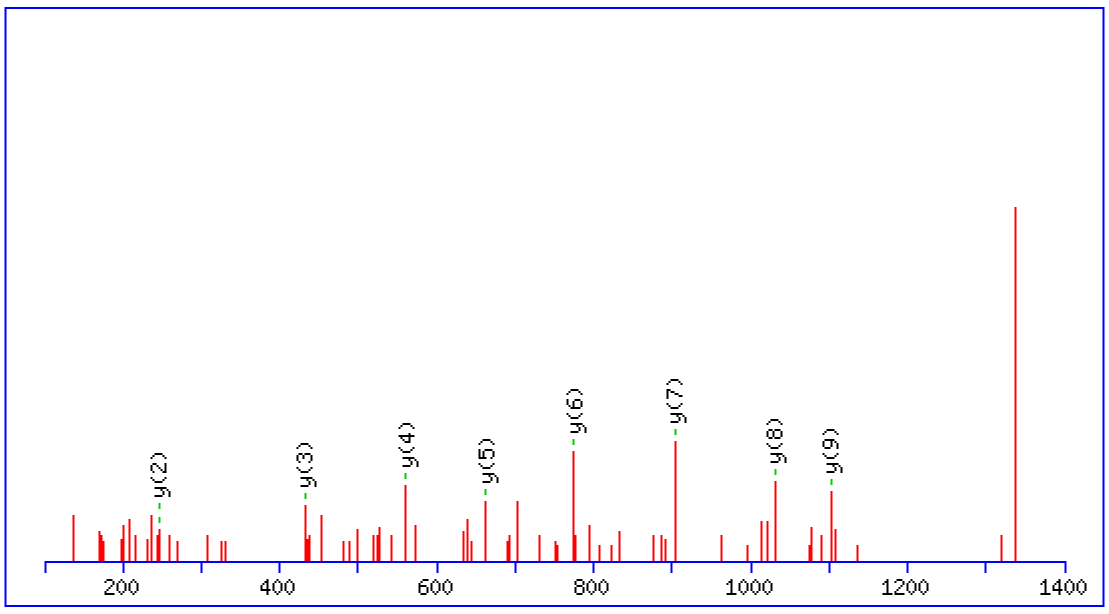
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AYAQQLTEWAR**
Found in **PACN2_HUMAN**, Protein kinase C and casein kinase substrate in neurons protein 2 OS=Homo sapiens GN=PACSIN2 PE=1 SV=2

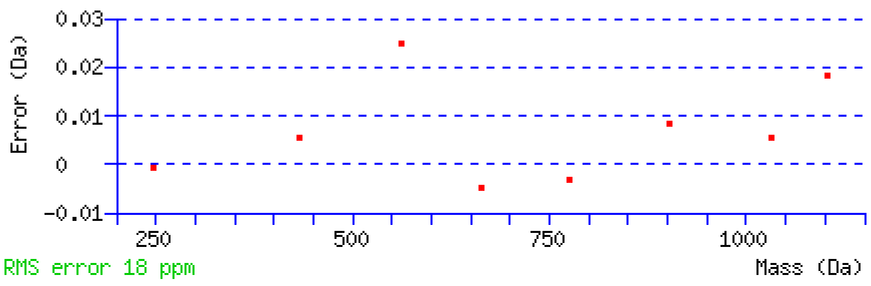
Match to Query 35712: 1335.658568 from(668.836560,2+) rtinseconds(2656) index(35783)
Title: Locus:1.1.1.2430.38
Data file 2011-11-10 - TFD - EP 3-3.mgf

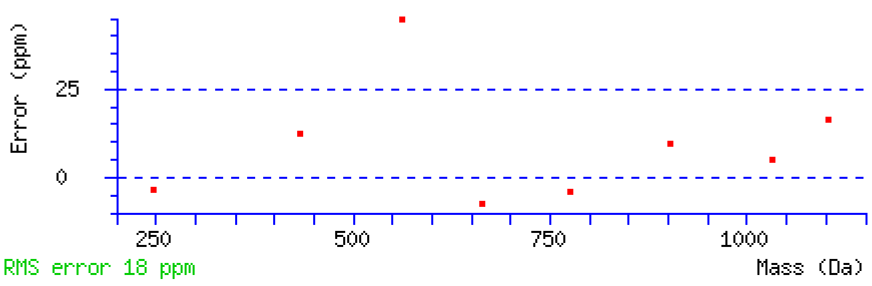
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1335.657120
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 67  Expect: 2.3e-006
Matches : 8/96 fragment ions using 12 most intense peaks   (help)
```

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	72.044390	36.525833					A							11
2	235.107719	118.057498					Y	1265.627314	633.317295	1248.600765	624.804021	1247.616749	624.312013	10
3	306.144833	153.576055					A	***1102.563985***	551.785631	1085.537436	543.272356	1084.553420	542.780348	9
4	434.203411	217.605344	417.176862	209.092069			Q	***1031.526871***	516.267074	1014.500322	507.753799	1013.516306	507.261791	8
5	562.261989	281.634633	545.235440	273.121358			Q	***903.468293***	452.237785	886.441744	443.724510	885.457728	443.232502	7
6	675.346053	338.176665	658.319504	329.663390			L	***775.409715***	388.208496	758.383166	379.695221	757.399150	379.203213	6
7	776.393732	388.700504	759.367183	380.187230	758.383167	379.695222	T	***662.325651***	331.666464	645.299102	323.153189	644.315086	322.661181	5
8	905.436325	453.221801	888.409776	444.708526	887.425760	444.216518	E	***561.277972***	281.142624	544.251423	272.629349	543.267407	272.137341	4
9	1091.515638	546.261457	1074.489089	537.748183	1073.505073	537.256175	W	***432.235379***	216.621327	415.208830	208.108053			3
10	1162.552752	581.780014	1145.526203	573.266740	1144.542187	572.774732	A	***246.156066***	123.581671	229.129517	115.068396			2
11							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of AYAQQLTEWAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
67.5	1335.657120	0.001448	AYAQQLTEWAR
9.2	1335.645248	0.013320	DLSNNTMSLSVR
5.3	1335.667892	-0.009324	FLNEMIAPVMR
4.9	1335.660507	-0.001939	EAGLQMFGQLAR
0.5	1335.659164	-0.000596	SLDMDSIIAEVK

Mascot: http://www.matrixscience.com/

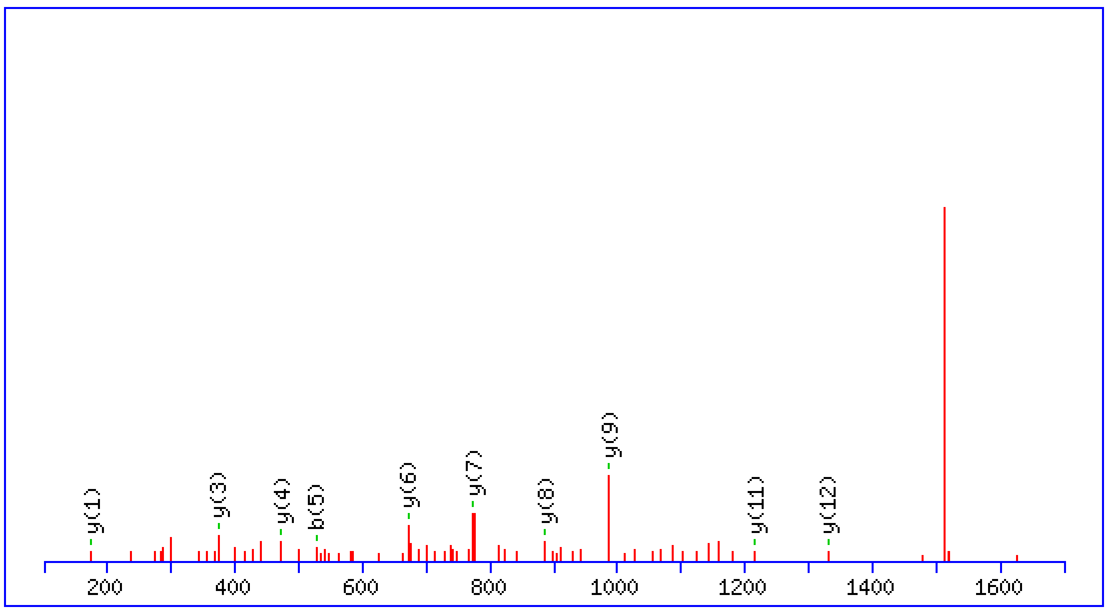
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SPDEVTLTSIVPTR**
Found in **PACN3_HUMAN**, Protein kinase C and casein kinase substrate in neurons protein 3 OS=Homo sapiens GN=PACSIN3 PE=1 SV=2

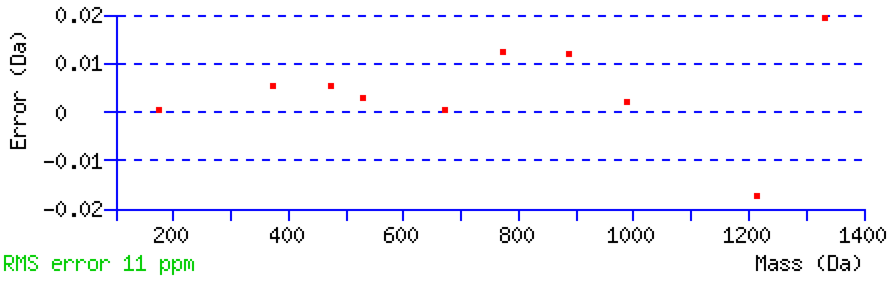
Match to Query 45590: 1513.794228 from(757.904390,2+) rtinseconds(2798) index(38024)
Title: Locus:1.1.1.2613.42
Data file 2011-11-13 - TFD - EP 7-3.mgf

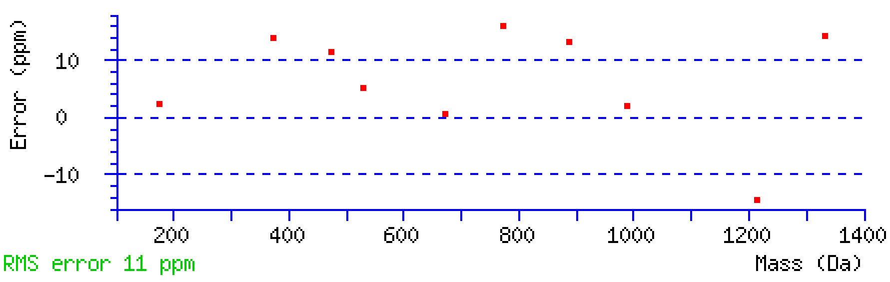
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1513.798798
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 74 **Expect:** 2.2e-007
Matches : 10/128 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	**S**							14
2	185.092068	93.049672	167.081503	84.044389	**P**	1427.774037	714.390657	1410.747488	705.877382	1409.763472	705.385374	13
3	300.119011	150.563144	282.108446	141.557861	**D**	***1330.721273***	665.864275	1313.694724	657.351000	1312.710708	656.858992	12
4	429.161604	215.084440	411.151039	206.079158	**E**	***1215.694330***	608.350803	1198.667781	599.837529	1197.683765	599.345521	11
5	528.230018	264.618647	510.219453	255.613365	**V**	1086.651737	543.829507	1069.625188	535.316232	1068.641172	534.824224	10
6	629.277697	315.142487	611.267132	306.137204	**T**	***987.583323***	494.295300	970.556774	485.782025	969.572758	485.290017	9
7	742.361761	371.684519	724.351196	362.679236	**L**	***886.535644***	443.771460	869.509095	435.258186	868.525079	434.766178	8
8	843.409440	422.208358	825.398875	413.203076	**T**	***773.451580***	387.229428	756.425031	378.716154	755.441015	378.224146	7
9	930.441468	465.724372	912.430903	456.719090	**S**	***672.403901***	336.705589	655.377352	328.192314	654.393336	327.700306	6
10	1043.525532	522.266404	1025.514967	513.261122	**I**	585.371873	293.189575	568.345324	284.676300	567.361308	284.184292	5
11	1142.593946	571.800611	1124.583381	562.795329	**V**	***472.287809***	236.647543	455.261260	228.134268	454.277244	227.642260	4
12	1239.646710	620.326993	1221.636145	611.321711	**P**	***373.219395***	187.113335	356.192846	178.600061	355.208830	178.108053	3
13	1340.694389	670.850833	1322.683824	661.845550	**T**	276.166631	138.586953	259.140082	130.073679	258.156066	129.581671	2
14					**R**	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of SPDEVTLTSIVPTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
74.5	1513.798798	-0.004570	SPDEVTLTSIVPTR
3.5	1513.788864	0.005364	QSWGLENEALIVR

Mascot: http://www.matrixscience.com/

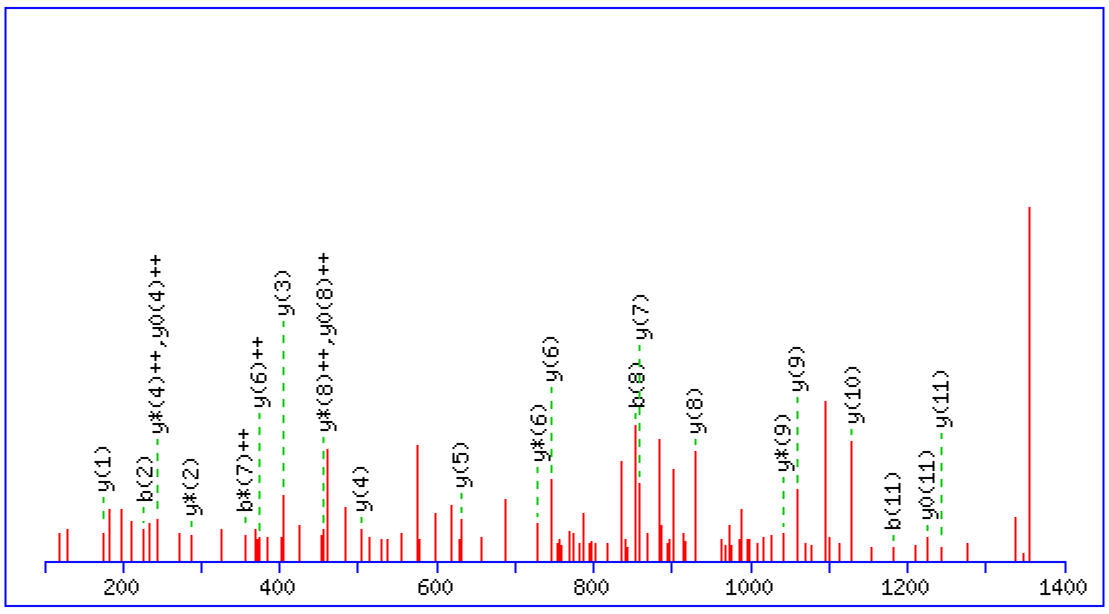
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLAEALNQVTQR**
Found in **KPCD_HUMAN**, Protein kinase C delta type OS=Homo sapiens GN=PRKCD PE=1 SV=2

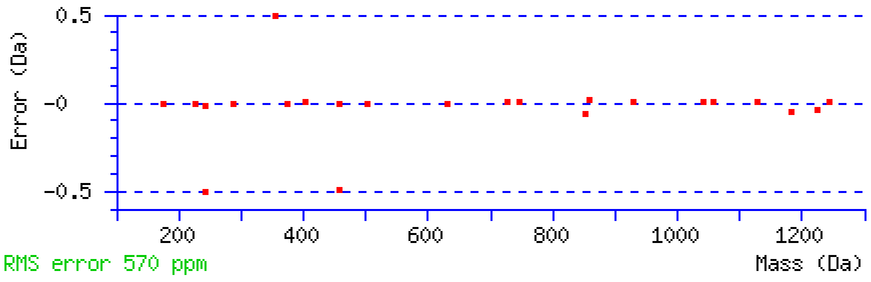
Match to Query 37282: 1354.756788 from(678.385670,2+) rtinseconds(2608) index(30485)
Title: Locus:1.1.1.2632.38
Data file 2011-11-12 - TFD - EP 5-2.mgf

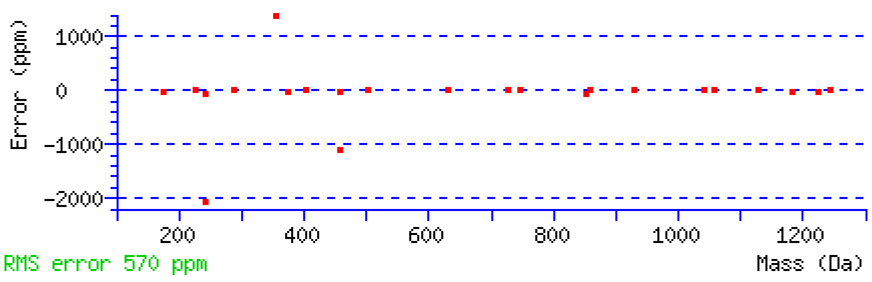
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1354.756836
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 39   Expect: 0.00094
Matches : 23/110 fragment ions using 68 most intense peaks   (help)
```

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					L							12
2	**227.175404**	114.091340					L	***1242.680077***	621.843677	1225.653528	613.330402	1224.669512	612.838394	11
3	298.212518	149.609897					A	***1129.596013***	565.301644	1112.569464	556.788370	1111.585448	556.296362	10
4	427.255111	214.131193			409.244546	205.125911	E	***1058.558899***	529.783087	1041.532350	521.269813	1040.548334	520.777805	9
5	498.292225	249.649750			480.281660	240.644468	A	***929.516306***	465.261791	912.489757	456.748516	911.505741	456.256508	8
6	611.376289	306.191783			593.365724	297.186500	L	***858.479192***	429.743234	841.452643	421.229959	840.468627	420.737951	7
7	725.419216	363.213246	708.392667	354.699972	707.408651	354.207964	N	***745.395128***	373.201202	728.368579	364.687927	727.384563	364.195919	6
8	**853.477794**	427.242535	836.451245	418.729261	835.467229	418.237253	Q	***631.352201***	316.179738	614.325652	307.666464	613.341636	307.174456	5
9	952.546208	476.776742	935.519659	468.263467	934.535643	467.771459	V	***503.293623***	252.150449	486.267074	243.637175	485.283058	243.145167	4
10	1053.593887	527.300582	1036.567338	518.787307	1035.583322	518.295299	T	***404.225209***	202.616242	387.198660	194.102968	386.214644	193.610960	3
11	**1181.652465**	591.329870	1164.625916	582.816596	1163.641900	582.324588	Q	303.177530	152.092403	286.150981	143.579128			2
12							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LLAEALNQVTQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.3	1354.756836	-0.000048	LLAEALNQVTQR
6.8	1354.745605	0.011183	LLAAIDDIDRPK
0.3	1354.745651	0.011137	VVPQVETVDTLR

Mascot: http://www.matrixscience.com/

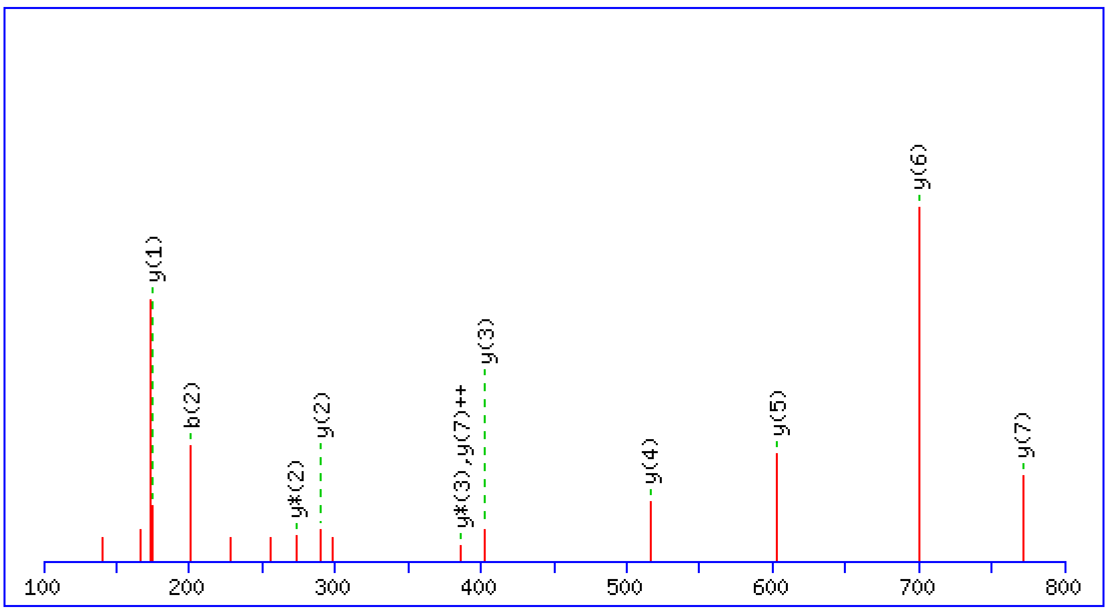
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SLAPSLLDR**
Found in **KISHA_HUMAN**, Protein kish-A OS=Homo sapiens GN=TMEM167A PE=2 SV=1

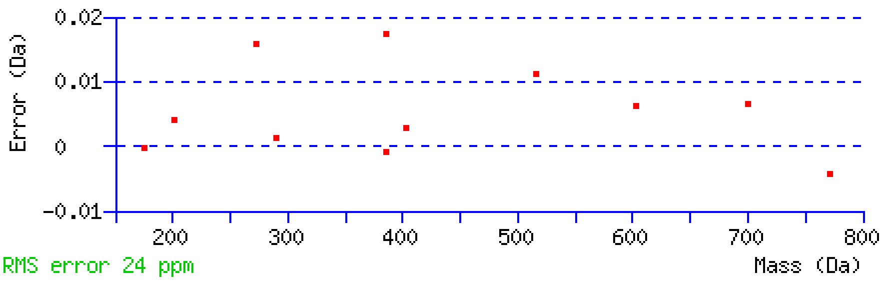
Match to Query 10415: 970.549708 from(486.282130,2+) rtinseconds(2317) index(13589)
Title: Locus:1.1.1.2606.15
Data file 2011-11-14 - TFD - EP 8-8.mgf

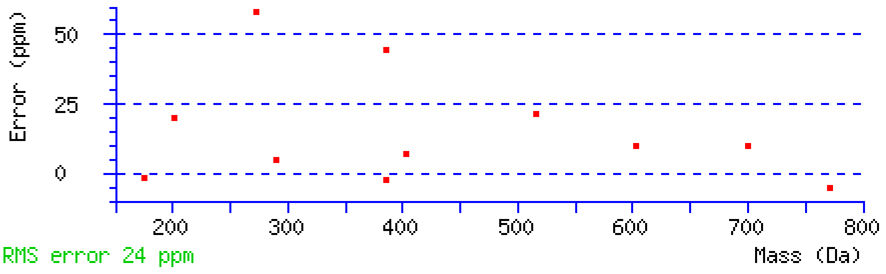
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 970.544724
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 67  Expect: 2.6e-006
Matches : 11/78 fragment ions using 12 most intense peaks   (help)
```

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	S							9
2	201.123368	101.065322	183.112803	92.060039	L	884.519993	442.763635	867.493444	434.250360	866.509428	433.758352	8
3	272.160482	136.583879	254.149917	127.578596	A	***771.435929***	386.221603	754.409380	377.708328	753.425364	377.216320	7
4	369.213246	185.110261	351.202681	176.104978	P	***700.398815***	350.703046	683.372266	342.189771	682.388250	341.697763	6
5	456.245274	228.626275	438.234709	219.620992	S	***603.346051***	302.176664	586.319502	293.663389	585.335486	293.171381	5
6	569.329338	285.168307	551.318773	276.163025	L	***516.314023***	258.660650	499.287474	250.147375	498.303458	249.655367	4
7	682.413402	341.710339	664.402837	332.705057	L	***403.229959***	202.118617	386.203410	193.605343	385.219394	193.113335	3
8	797.440345	399.223811	779.429780	390.218528	D	***290.145895***	145.576585	273.119346	137.063311	272.135330	136.571303	2
9					R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of SLAPSLLDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
66.9	970.544724	0.004984	SLAPSLLDR
13.0	970.544724	0.004984	AEILSPLGR
6.8	970.544739	0.004969	SLSPILPGR
5.0	970.555954	-0.006246	QAVEAAKVR
5.0	970.555969	-0.006261	SVRIIDPR
3.7	970.544739	0.004969	SPGSPLLLR
1.7	970.544739	0.004969	GTIIPAQQK
1.6	970.544739	0.004969	SSPSPVILR
1.4	970.555954	-0.006246	DRLGLEIR
1.3	970.555969	-0.006261	SALGGGKLPR

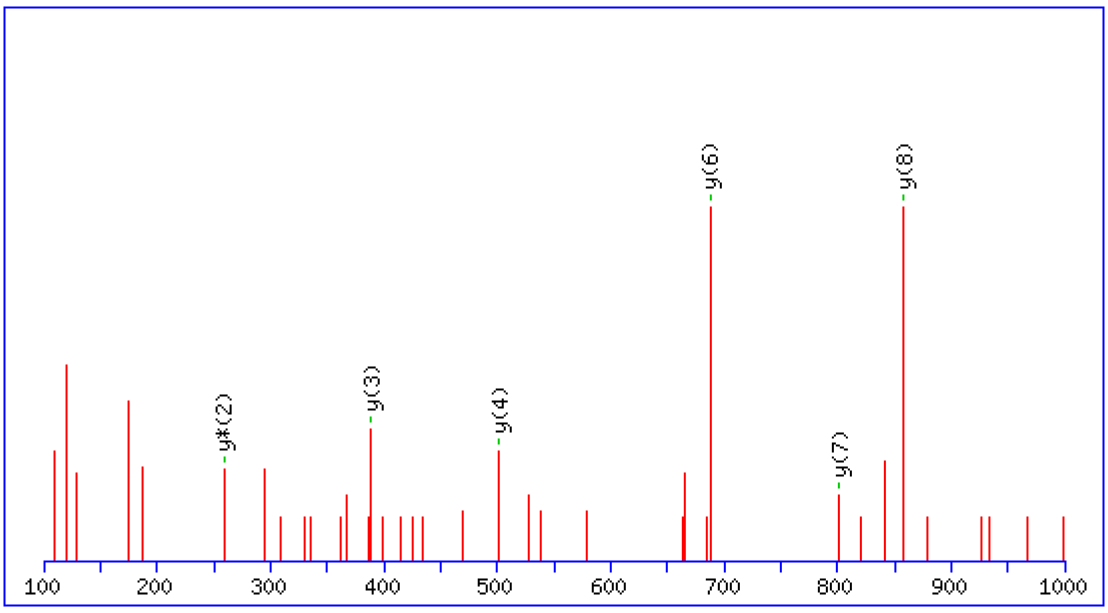
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IGIGELITR**
Found in **K0664_HUMAN**, Protein KIAA0664 OS=Homo sapiens GN=KIAA0664 PE=1 SV=2

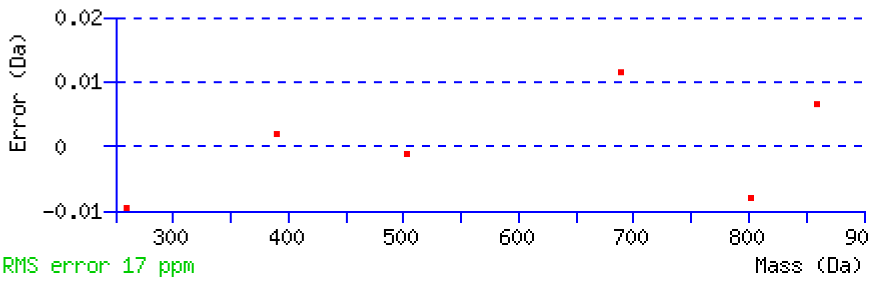
Match to Query 12946: 970.584728 from(486.299640,2+) rtinseconds(2786) index(36568)
Title: Locus:1.1.1.2483.9
Data file 2011-11-10 - TFD - EP 3-1.mgf

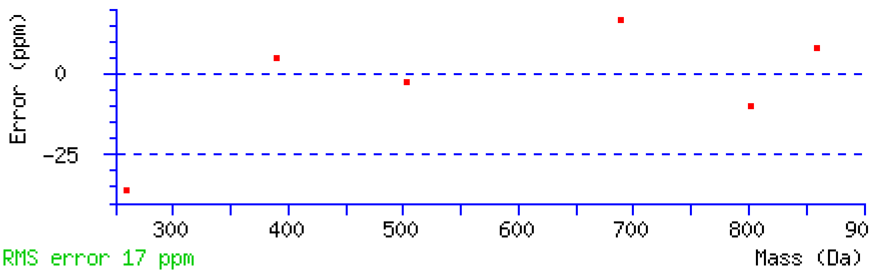
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 970.581116
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 38  Expect: 0.0015
Matches : 6/70 fragment ions using 9 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							9
2	171.112804	86.060040			G	***858.504344***	429.755810	841.477795	421.242536	840.493779	420.750528	8
3	284.196868	142.602072			I	***801.482880***	401.245078	784.456331	392.731804	783.472315	392.239796	7
4	341.218332	171.112804			G	***688.398816***	344.703046	671.372267	336.189772	670.388251	335.697764	6
5	470.260925	235.634100	452.250360	226.628818	E	631.377352	316.192314	614.350803	307.679040	613.366787	307.187032	5
6	583.344989	292.176133	565.334424	283.170850	L	***502.334759***	251.671017	485.308210	243.157743	484.324194	242.665735	4
7	696.429053	348.718165	678.418488	339.712882	I	***389.250695***	195.128985	372.224146	186.615711	371.240130	186.123703	3
8	797.476732	399.242004	779.466167	390.236722	T	276.166631	138.586953	259.140082	130.073679	258.156066	129.581671	2
9					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of IGIGELITR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.5	970.581116	0.003612	IGIGELITR
9.8	970.592346	-0.007618	LLRSPTLR
4.5	970.581116	0.003612	LEVLQLTR
1.4	970.592361	-0.007633	LAVGVKATGR
0.1	970.581116	0.003612	LDLAAVTLR

Mascot: http://www.matrixscience.com/

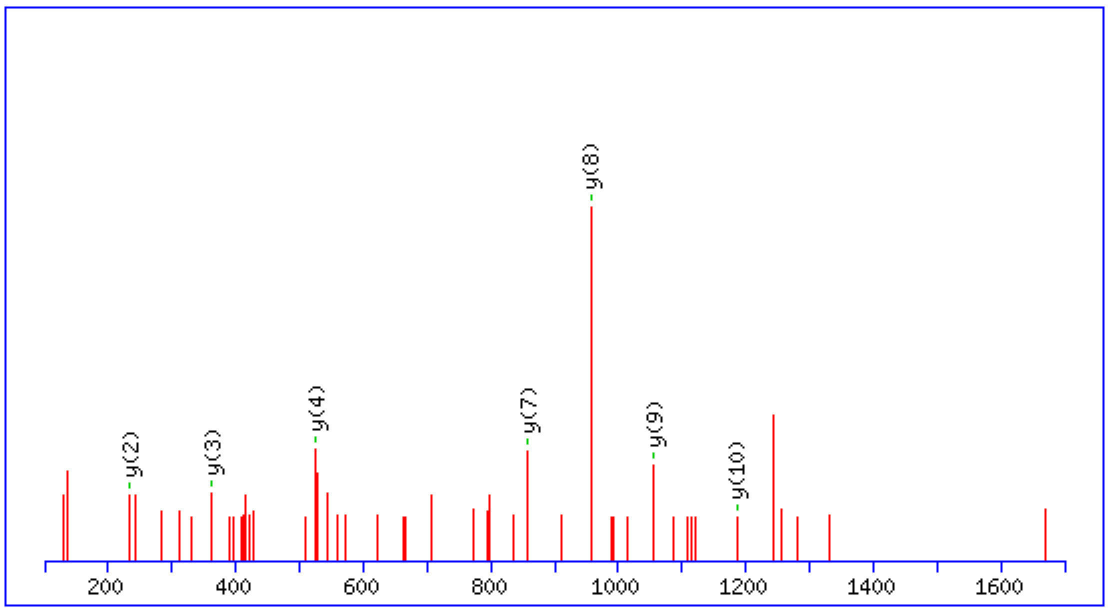
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LQGEVVAFDYQSK**
Found in **LSM12_HUMAN**, Protein LSM12 homolog OS=Homo sapiens GN=LSM12 PE=1 SV=2

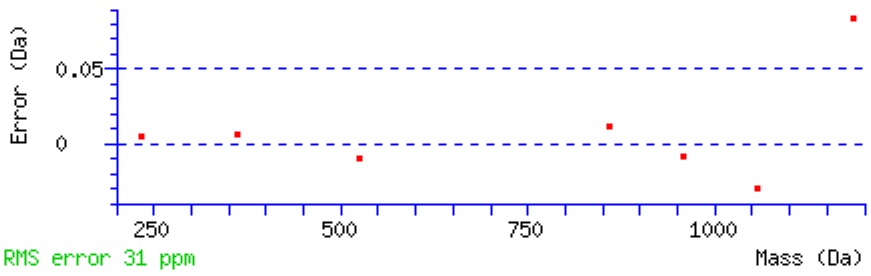
Match to Query 40037: 1482.739108 from(742.376830,2+) rtinseconds(2470) index(26678)
Title: Locus:1.1.1.2561.48
Data file 2011-11-10 - TFD - EP 3-5.mgf

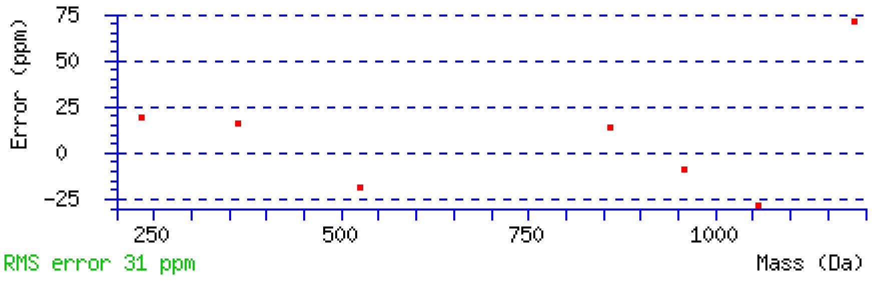
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1700] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1482.735458
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 46  Expect: 0.00018
Matches : 7/134 fragment ions using 12 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.091340	57.549308					L							13
2	242.149918	121.578597	225.123369	113.065323			Q	1370.658673	685.832975	1353.632124	677.319700	1352.648108	676.827692	12
3	299.171382	150.089329	282.144833	141.576055			G	1242.600095	621.803686	1225.573546	613.290411	1224.589530	612.798403	11
4	428.213975	214.610626	411.187426	206.097351	410.203410	205.605343	E	***1185.578631***	593.292954	1168.552082	584.779679	1167.568066	584.287671	10
5	527.282389	264.144833	510.255840	255.631558	509.271824	255.139550	V	***1056.536038***	528.771657	1039.509489	520.258383	1038.525473	519.766375	9
6	626.350803	313.679040	609.324254	305.165765	608.340238	304.673757	V	***957.467624***	479.237450	940.441075	470.724176	939.457059	470.232168	8
7	697.387917	349.197597	680.361368	340.684322	679.377352	340.192314	A	***858.399210***	429.703243	841.372661	421.189969	840.388645	420.697961	7
8	844.456331	422.731804	827.429782	414.218529	826.445766	413.726521	F	787.362096	394.184686	770.335547	385.671412	769.351531	385.179404	6
9	959.483274	480.245275	942.456725	471.732000	941.472709	471.239992	D	640.293682	320.650479	623.267133	312.137205	622.283117	311.645197	5
10	1122.546603	561.776940	1105.520054	553.263665	1104.536038	552.771657	Y	***525.266739***	263.137008	508.240190	254.623733	507.256174	254.131725	4
11	1250.605181	625.806229	1233.578632	617.292954	1232.594616	616.800946	Q	***362.203410***	181.605343	345.176861	173.092069	344.192845	172.600061	3
12	1337.637209	669.322243	1320.610660	660.808968	1319.626644	660.316960	S	***234.144832***	117.576054	217.118283	109.062780	216.134267	108.570772	2
13							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of LQGEVVAFDYQSK
(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	1482.735458	0.003650	LQGEVVAFDYQSK

Mascot: http://www.matrixscience.com/

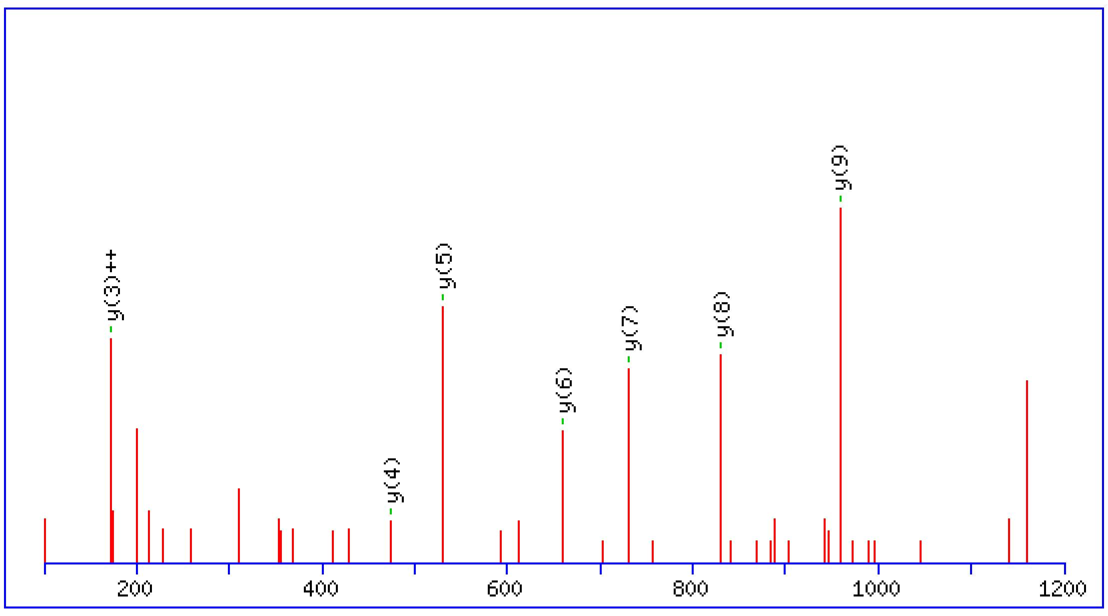
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TVEVAEGEAVR**
Found in **LYRIC_HUMAN**, Protein LYRIC OS=Homo sapiens GN=MTDH PE=1 SV=2

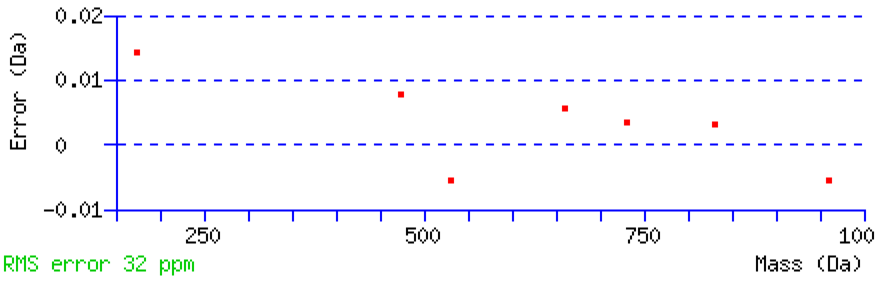
Match to Query 469188: 1158.584468 from(580.299510,2+) rtinseconds(1454) index(337024)
Title: Locus:1.1.1.890.29
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

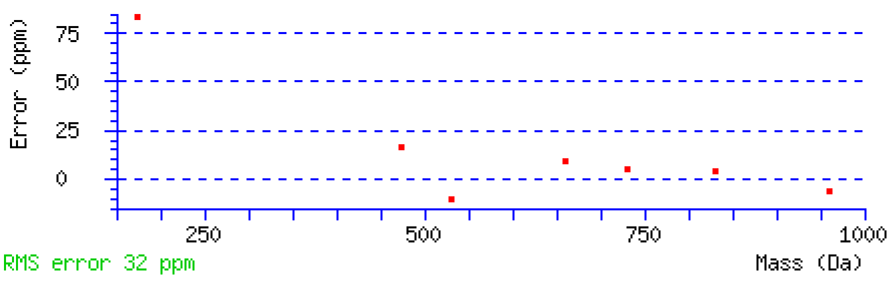
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1158.588058
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 46  Expect: 0.00045
Matches : 7/94 fragment ions using 11 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116	84.044390	42.525833	T							11
2	201.123369	101.065322	183.112804	92.060040	V	1058.547665	529.777471	1041.521116	521.264196	1040.537100	520.772188	10
3	330.165962	165.586619	312.155397	156.581336	E	***959.479251***	480.243264	942.452702	471.729989	941.468686	471.237981	9
4	429.234376	215.120826	411.223811	206.115544	V	***830.436658***	415.721967	813.410109	407.208693	812.426093	406.716685	8
5	500.271490	250.639383	482.260925	241.634101	A	***731.368244***	366.187760	714.341695	357.674486	713.357679	357.182478	7
6	629.314083	315.160680	611.303518	306.155397	E	***660.331130***	330.669203	643.304581	322.155929	642.320565	321.663921	6
7	686.335547	343.671412	668.324982	334.666129	G	***531.288537***	266.147907	514.261988	257.634632	513.277972	257.142624	5
8	815.378140	408.192708	797.367575	399.187426	E	***474.267073***	237.637174	457.240524	229.123900	456.256508	228.631892	4
9	886.415254	443.711265	868.404689	434.705983	A	345.224480	173.115878	328.197931	164.602603			3
10	985.483668	493.245472	967.473103	484.240190	V	274.187366	137.597321	257.160817	129.084046			2
11					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of TVEVAEGEAVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.6	1158.588058	-0.003590	TVEVAEGEAVR
10.7	1158.574326	0.010142	NVSKISFFAM
6.8	1158.574127	0.010341	GSGAGELGRAER
6.5	1158.588043	-0.003575	LSGVEEELQR
1.4	1158.588043	-0.003575	VNKAQEDDLK
1.1	1158.595444	-0.010976	VLGKPKPEEM
1.1	1158.595444	-0.010976	VLGKPKPEEM
0.5	1158.585556	-0.001088	LHCAFASLPK
0.3	1158.578125	0.006343	EAEWREALR

Mascot: http://www.matrixscience.com/

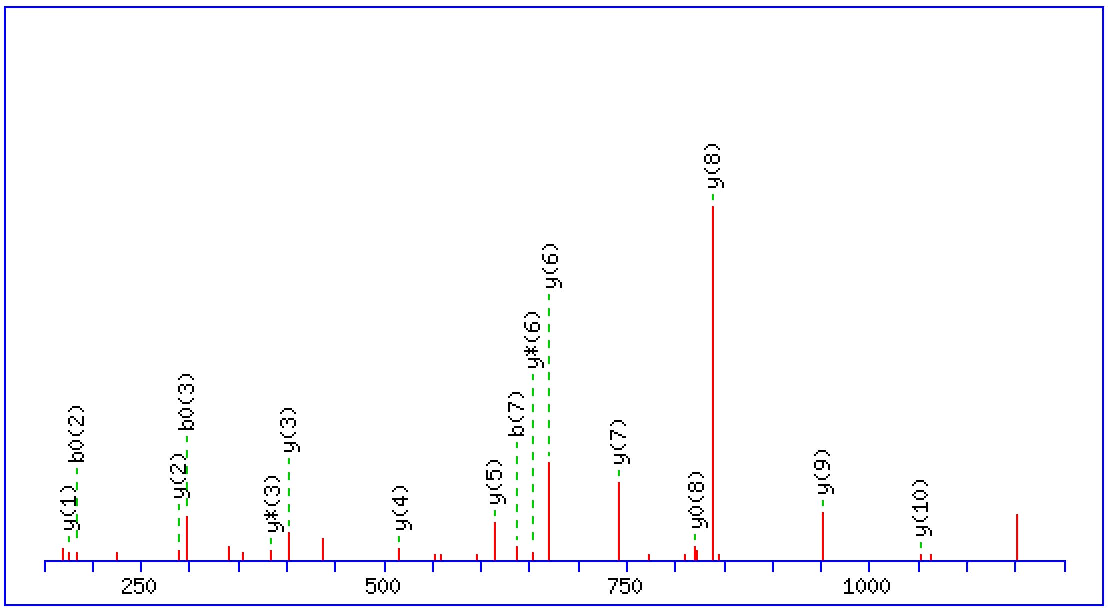
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VTLPAGPDILR**
Found in **MAL2_HUMAN**, Protein MAL2 OS=Homo sapiens GN=MAL2 PE=1 SV=1

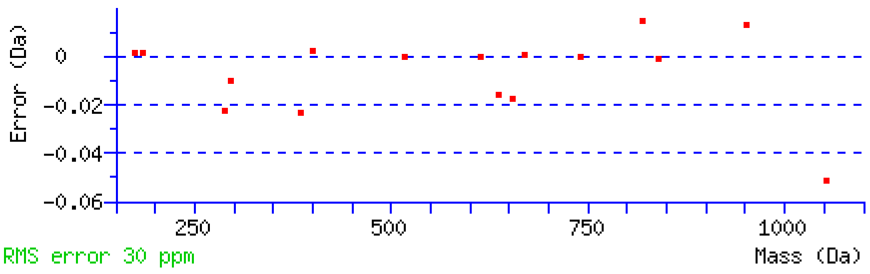
Match to Query 26614: 1150.674748 from(576.344650,2+) rtinseconds(2781) index(34078)
Title: Locus:1.1.1.2328.24
Data file 2011-11-10 - TFD - EP 3-6.mgf

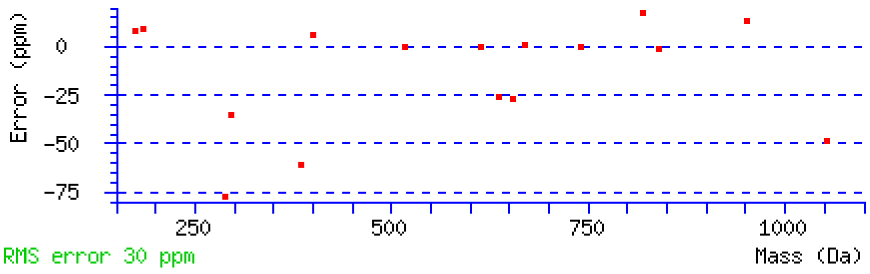
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1150.671005
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 86  Expect: 9.1e-009
Matches : 16/92 fragment ions using 23 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483			V							11
2	201.123369	101.065322	183.112804	92.060040	T	***1052.609872***	526.808574	1035.583323	518.295300	1034.599307	517.803292	10
3	314.207433	157.607354	296.196868	148.602072	L	***951.562193***	476.284735	934.535644	467.771460	933.551628	467.279452	9
4	411.260197	206.133737	393.249632	197.128454	P	***838.478129***	419.742703	821.451580	411.229428	820.467564	410.737420	8
5	482.297311	241.652293	464.286746	232.647011	A	***741.425365***	371.216321	724.398816	362.703046	723.414800	362.211038	7
6	539.318775	270.163026	521.308210	261.157743	G	***670.388251***	335.697764	653.361702	327.184489	652.377686	326.692481	6
7	636.371539	318.689408	618.360974	309.684125	P	***613.366787***	307.187032	596.340238	298.673757	595.356222	298.181749	5
8	751.398482	376.202879	733.387917	367.197597	D	***516.314023***	258.660650	499.287474	250.147375	498.303458	249.655367	4
9	864.482546	432.744911	846.471981	423.739629	I	***401.287080***	201.147178	384.260531	192.633903			3
10	977.566610	489.286943	959.556045	480.281661	L	***288.203016***	144.605146	271.176467	136.091871			2
11					R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of VTLPAGPDILR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
85.6	1150.671005	0.003743	VTLPAGPDILR
5.4	1150.682205	-0.007457	ILNPNKAPLR
3.1	1150.682220	-0.007472	SPARLLPLPR

Mascot: http://www.matrixscience.com/

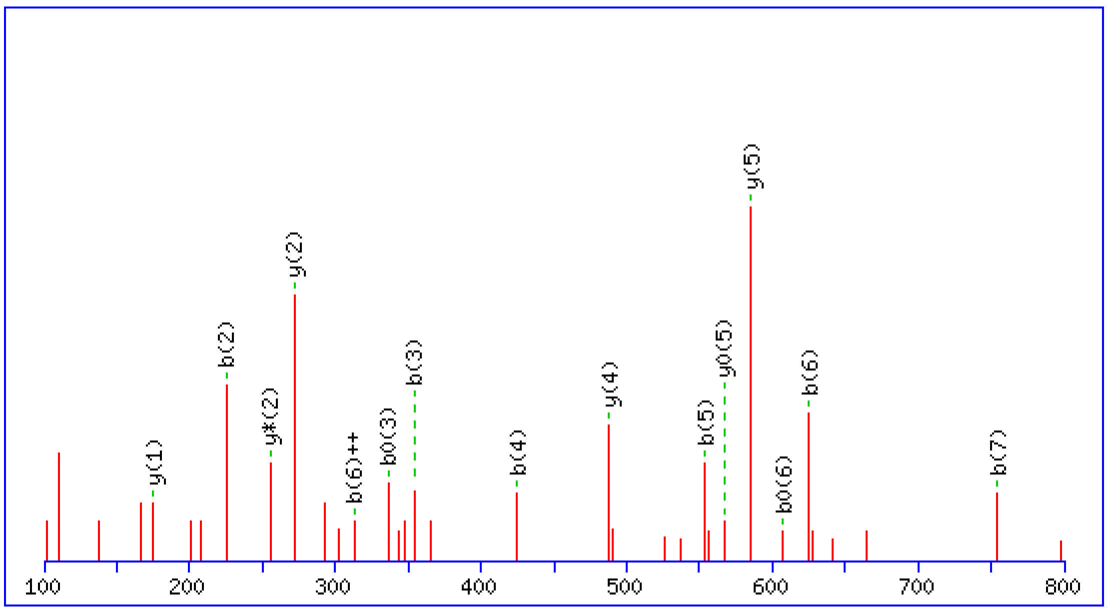
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SHEAEAEPSEPR**
Found in **MANBL_HUMAN**, Protein MANBAL OS=Homo sapiens GN=MANBAL PE=1 SV=1

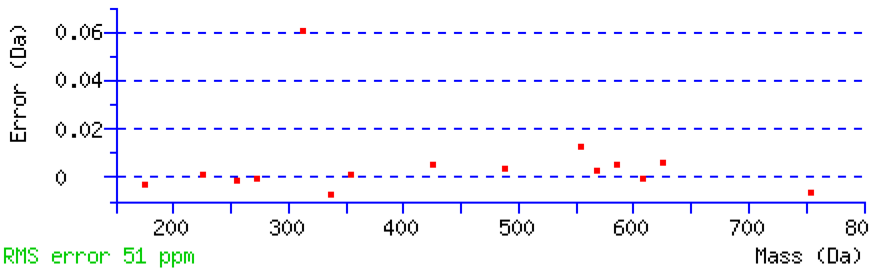
Match to Query 682785: 1337.586162 from(446.869330,3+) rtinseconds(820) index(409314)
Title: Locus:1.1.1.646.6
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

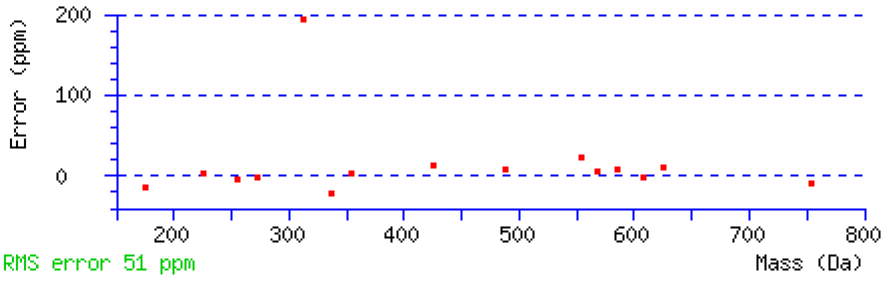
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1337.584732
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 50  Expect: 2.2e-005
Matches : 15/106 fragment ions using 20 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	S							12
2	***225.098216***	113.052746	207.087651	104.047463	H	1251.560020	626.283648	1234.533471	617.770374	1233.549455	617.278366	11
3	***354.140809***	177.574042	336.130244	168.568760	E	1114.501108	557.754192	1097.474559	549.240918	1096.490543	548.748910	10
4	***425.177923***	213.092600	407.167358	204.087317	A	985.458515	493.232896	968.431966	484.719621	967.447950	484.227613	9
5	***554.220516***	277.613896	536.209951	268.608614	E	914.421401	457.714339	897.394852	449.201064	896.410836	448.709056	8
6	***625.257630***	313.132453	607.247065	304.127171	A	785.378808	393.193042	768.352259	384.679768	767.368243	384.187760	7
7	***754.300223***	377.653750	736.289658	368.648467	E	714.341694	357.674485	697.315145	349.161211	696.331129	348.669203	6
8	851.352987	426.180132	833.342422	417.174849	P	***585.299101***	293.153189	568.272552	284.639914	567.288536	284.147906	5
9	938.385015	469.696146	920.374450	460.690863	S	***488.246337***	244.626807	471.219788	236.113532	470.235772	235.621524	4
10	1067.427608	534.217442	1049.417043	525.212160	E	401.214309	201.110793	384.187760	192.597518	383.203744	192.105510	3
11	1164.480372	582.743824	1146.469807	573.738542	P	***272.171716***	136.589496	255.145167	128.076221			2
12					R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of SHEAEAEPSEPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.8	1337.584732	0.001430	SHEAEAEPSEPR
0.2	1337.584778	0.001384	SPSPAGGGSSPYSR

Mascot: http://www.matrixscience.com/

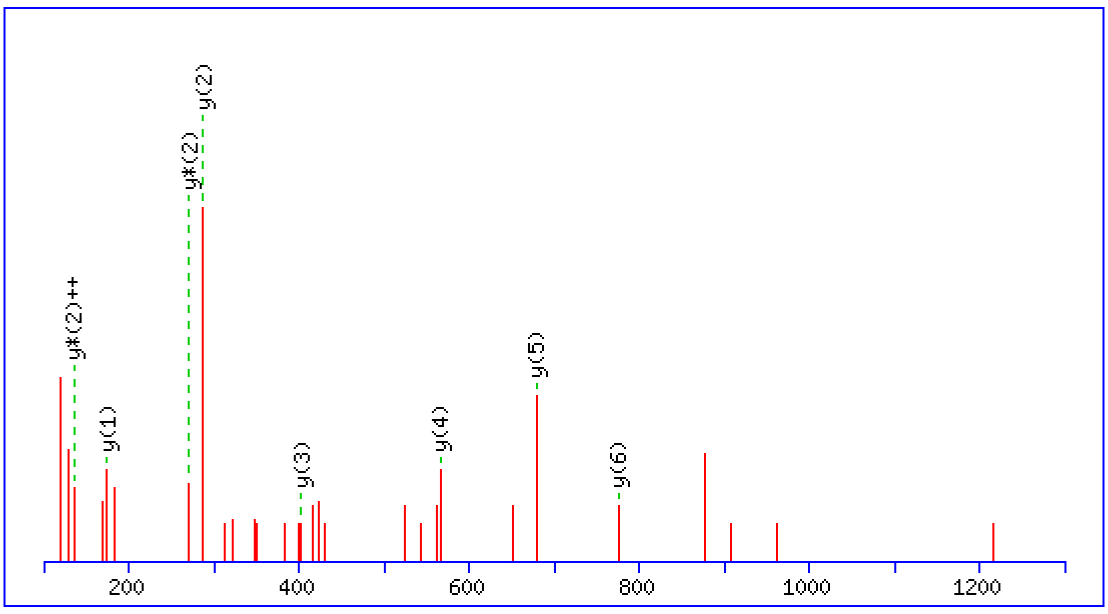
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TPLYDLR**
Found in **MEMO1_HUMAN**, Protein MEMO1 OS=Homo sapiens GN=MEMO1 PE=1 SV=1

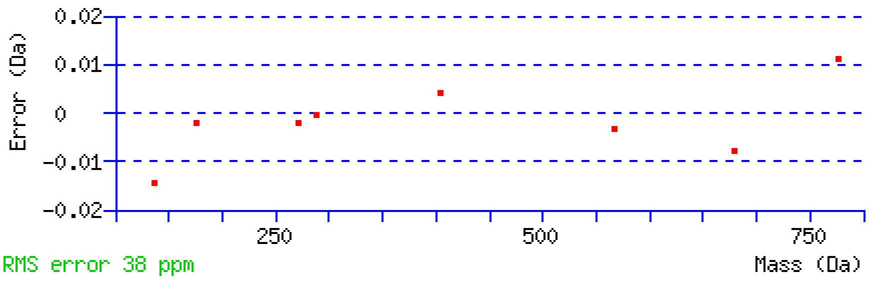
Match to Query 6129: 876.463528 from(439.239040,2+) rtinseconds(2126) index(24973)
Title: Locus:1.1.1.2153.4
Data file 2011-11-10 - TFD - EP 3-4.mgf

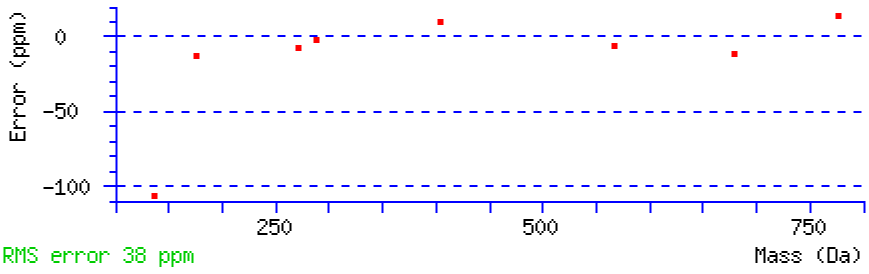
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 876.470505
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 32  Expect: 0.0072
Matches : 8/56 fragment ions using 25 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116	84.044390	42.525833	**T**							7
2	199.107719	100.057497	181.097154	91.052215	**P**	*776.430116*	388.718696	759.403567	380.205422	758.419551	379.713414	6
3	312.191783	156.599529	294.181218	147.594247	**L**	*679.377352*	340.192314	662.350803	331.679039	661.366787	331.187031	5
4	475.255112	238.131194	457.244547	229.125912	**Y**	*566.293288*	283.650282	549.266739	275.137008	548.282723	274.645000	4
5	590.282055	295.644666	572.271490	286.639383	**D**	*403.229959*	202.118617	386.203410	193.605343	385.219394	193.113335	3
6	703.366119	352.186698	685.355554	343.181415	**L**	*288.203016*	144.605146	271.176467	136.091871			2
7					**R**	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of TPLYDLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.1	876.470505	-0.006977	TPLYDLR
8.6	876.459946	0.003582	TNMARIR
7.4	876.470490	-0.006962	AFEIELR
7.2	876.470505	-0.006977	FLPSELR
4.1	876.470490	-0.006962	AYLPLER
0.4	876.467331	-0.003803	CLKCLR
0.2	876.459946	0.003582	GASMRSLR
0.1	876.455231	0.008297	SLSEDAKK
0.1	876.462677	0.000851	VVVVESVM

Mascot: http://www.matrixscience.com/

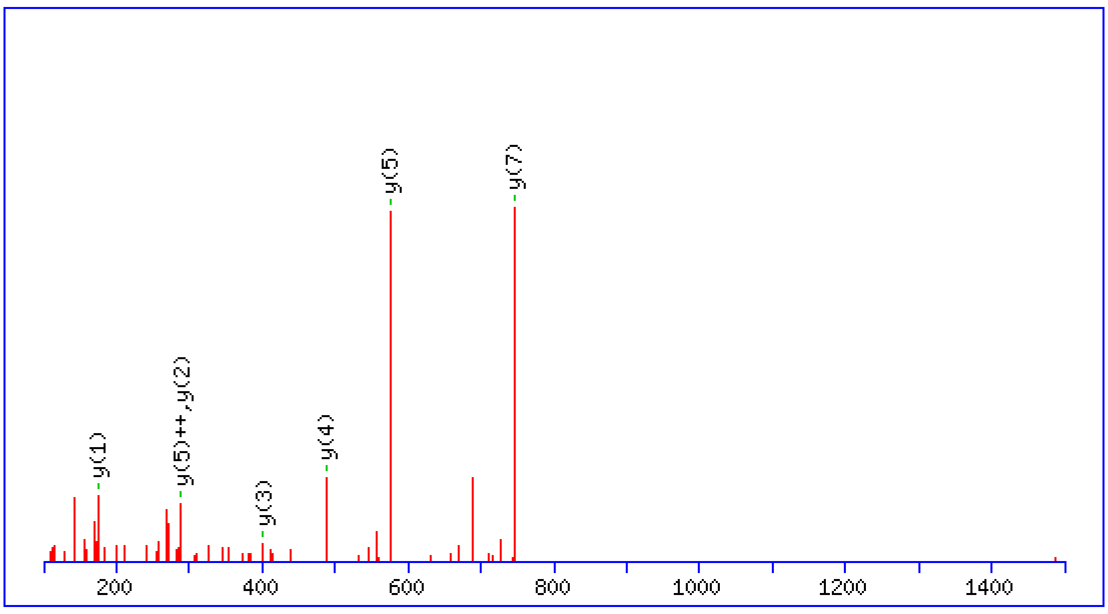
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LAVSSLLR**
Found in **MON2_HUMAN**, Protein MON2 homolog OS=Homo sapiens GN=MON2 PE=1 SV=2

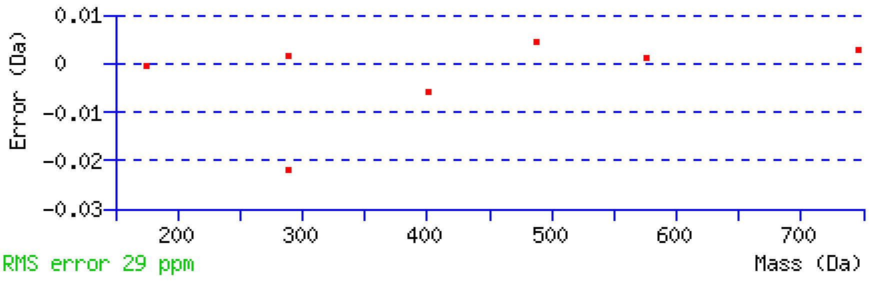
Match to Query 4456: 857.533808 from(429.774180,2+) rtinseconds(2755) index(35663)
Title: Locus:1.1.1.2484.4
Data file 2011-11-14 - TFD - EP 7-1.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●

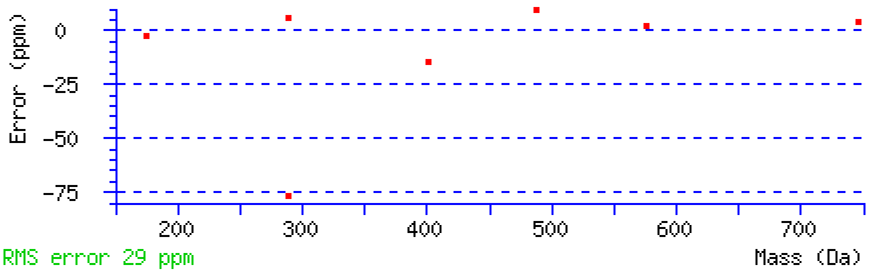


Monoisotopic mass of neutral peptide Mr(calc): 857.533432
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 62 **Expect:** 3.3e-006
Matches : 7/58 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							8
2	185.128454	93.067865			A	*745.456664*	373.231970	728.430115	364.718696	727.446099	364.226688	7
3	284.196868	142.602072			V	674.419550	337.713413	657.393001	329.200139	656.408985	328.708131	6
4	371.228896	186.118086	353.218331	177.112804	S	*575.351136*	288.179206	558.324587	279.665932	557.340571	279.173924	5
5	458.260924	229.634100	440.250359	220.628818	S	*488.319108*	244.663192	471.292559	236.149918	470.308543	235.657910	4
6	571.344988	286.176132	553.334423	277.170850	L	*401.287080*	201.147178	384.260531	192.633904			3
7	684.429052	342.718164	666.418487	333.712882	L	*288.203016*	144.605146	271.176467	136.091872			2
8					R	*175.118952*	88.063114	158.092403	79.549840			1



RMS error 29 ppm



RMS error 29 ppm

NCBI **BLAST** search of LAVSSLLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
83.9	857.533432	0.000376	LGISSLIR
61.9	857.533432	0.000376	LAVSSLLR
26.3	857.533432	0.000376	IEKTVIR
22.3	857.533417	0.000391	EIKSLLR
22.3	857.533417	0.000391	EKLSLIR
18.2	857.533432	0.000376	LVALLSSR
13.9	857.533417	0.000391	LLSKELR
13.2	857.533432	0.000376	IKTVELR
13.2	857.533417	0.000391	LELSKLR
13.2	857.533432	0.000376	LKVTELR

Mascot: http://www.matrixscience.com/

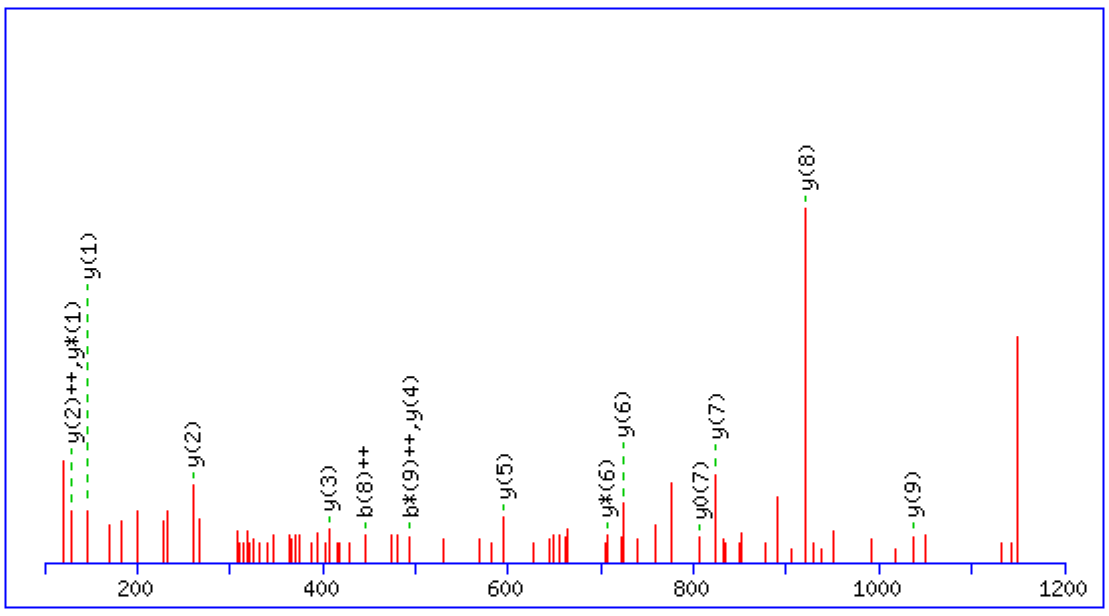
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LDPTQTSFLK**
Found in **NDRG2_HUMAN**, Protein NDRG2 OS=Homo sapiens GN=NDRG2 PE=1 SV=2

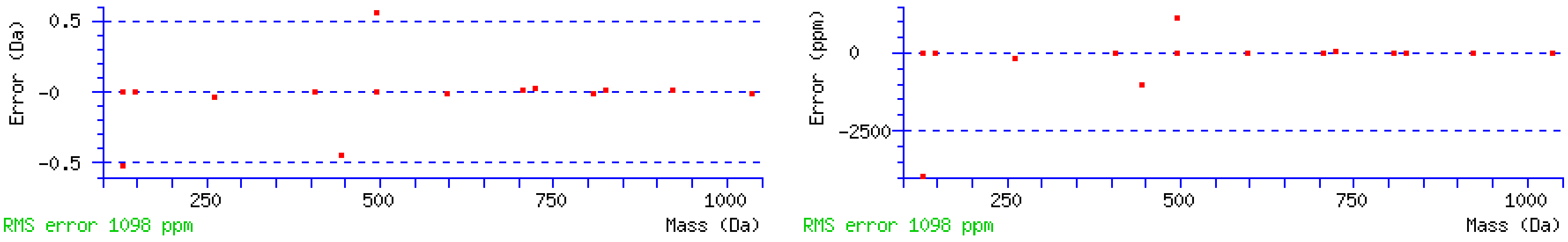
Match to Query 26306: 1148.610288 from(575.312420,2+) rtinseconds(2323) index(28165)
Title: Locus:1.1.1.2301.29
Data file 2011-11-12 - TFD - EP 5-4.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1148.607742
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 45  Expect: 0.00035
Matches : 15/92 fragment ions using 40 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							10
2	229.118283	115.062779			211.107718	106.057497	D	***1036.530953***	518.769115	1019.504404	510.255840	1018.520388	509.763832	9
3	326.171047	163.589161			308.160482	154.583879	P	***921.504010***	461.255643	904.477461	452.742369	903.493445	452.250361	8
4	427.218726	214.113001			409.208161	205.107719	T	***824.451246***	412.729261	807.424697	404.215987	806.440681	403.723979	7
5	555.277304	278.142290	538.250755	269.629016	537.266739	269.137008	Q	***723.403567***	362.205422	706.377018	353.692147	705.393002	353.200139	6
6	656.324983	328.666130	639.298434	320.152855	638.314418	319.660847	T	***595.344989***	298.176133	578.318440	289.662858	577.334424	289.170850	5
7	743.357011	372.182144	726.330462	363.668869	725.346446	363.176861	S	***494.297310***	247.652293	477.270761	239.139018	476.286745	238.647010	4
8	890.425425	445.716351	873.398876	437.203076	872.414860	436.711068	F	***407.265282***	204.136279	390.238733	195.623004			3
9	1003.509489	502.258383	986.482940	493.745108	985.498924	493.253100	L	***260.196868***	130.602072	243.170319	122.088798			2
10							K	***147.112804***	74.060040	130.086255	65.546765			1



NCBI **BLAST** search of LDPTQTSFLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.9	1148.607742	0.002546	LDPTQTSFLK
16.7	1148.607727	0.002561	LLFDQDASLK
7.6	1148.607727	0.002561	LVNEVTEFAK
4.8	1148.604553	0.005735	LMMNLLRDK
3.7	1148.611115	-0.000827	LLVTASMPGTK
3.2	1148.618958	-0.008670	IQRETDFLK
3.0	1148.607727	0.002561	IISPSFDNIK
2.8	1148.619812	-0.009524	MLLLCRWK
2.3	1148.607712	0.002576	EQLYTPASLK
1.3	1148.603699	0.006589	SQSSSSVLINK

Mascot: http://www.matrixscience.com/

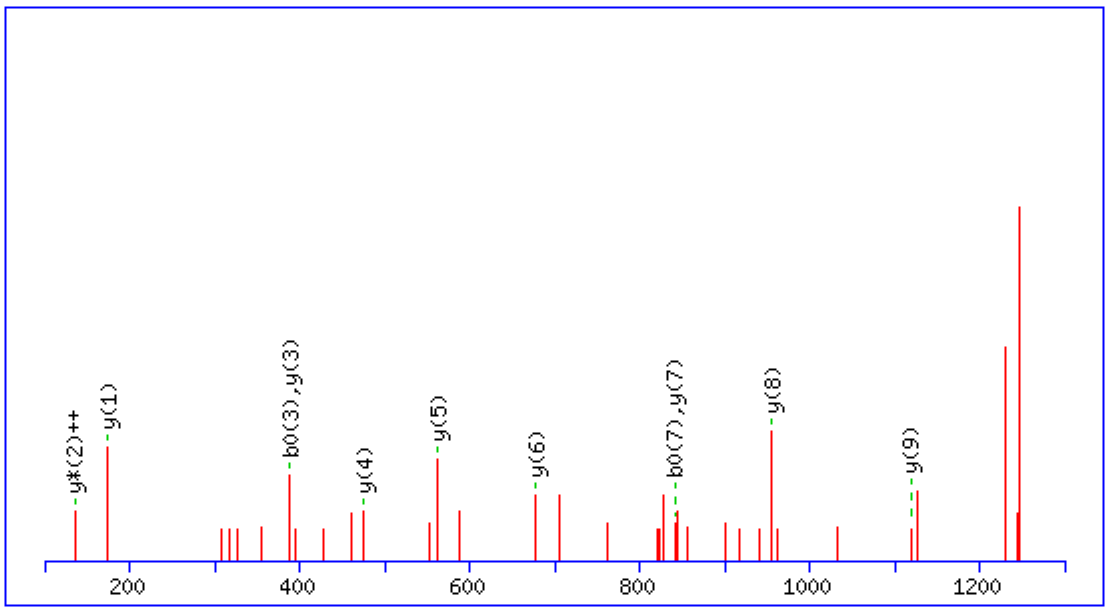
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QYDYDSSTIR**
Found in **NIBAN_HUMAN**, Protein Niban OS=Homo sapiens GN=FAM129A PE=1 SV=1

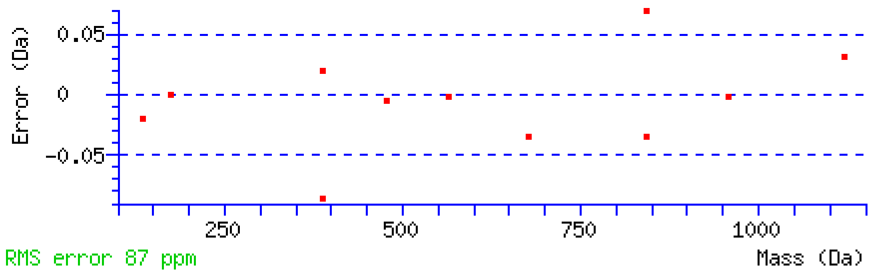
Match to Query 577512: 1246.553828 from(624.284190,2+) rtinseconds(1637) index(504972)
Title: Locus:1.1.1.953.30
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

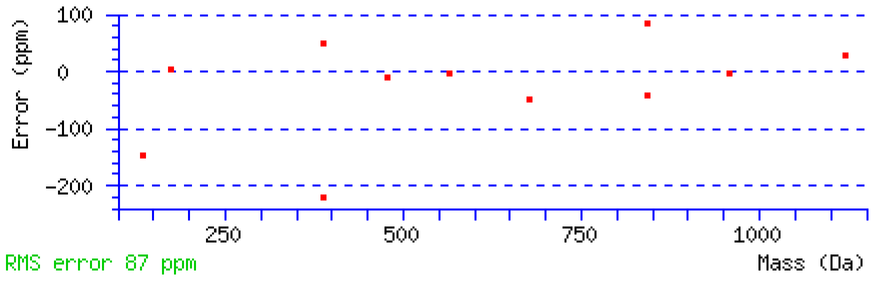
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1246.546585
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 50 **Expect:** 6e-005
Matches : 11/100 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	129.065854	65.036565	112.039305	56.523291			Q							10
2	292.129183	146.568230	275.102634	138.054955			Y	*1119.495295*	560.251285	1102.468746	551.738011	1101.484730	551.246003	9
3	407.156126	204.081701	390.129577	195.568427	389.145561	195.076419	D	*956.431966*	478.719621	939.405417	470.206347	938.421401	469.714339	8
4	570.219455	285.613366	553.192906	277.100091	552.208890	276.608083	Y	*841.405023*	421.206150	824.378474	412.692875	823.394458	412.200867	7
5	685.246398	343.126837	668.219849	334.613563	667.235833	334.121555	D	*678.341694*	339.674485	661.315145	331.161210	660.331129	330.669202	6
6	772.278426	386.642851	755.251877	378.129577	754.267861	377.637569	S	*563.314751*	282.161014	546.288202	273.647739	545.304186	273.155731	5
7	859.310454	430.158865	842.283905	421.645591	841.299889	421.153583	S	*476.282723*	238.644999	459.256174	230.131725	458.272158	229.639717	4
8	960.358133	480.682705	943.331584	472.169430	942.347568	471.677422	T	*389.250695*	195.128985	372.224146	186.615711	371.240130	186.123703	3
9	1073.442197	537.224737	1056.415648	528.711462	1055.431632	528.219454	I	288.203016	144.605146	271.176467	136.091871			2
10							R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of QYDYDSSTIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.7	1246.546585	0.007243	QYDYDSSTIR
4.6	1246.565201	-0.011373	IQTYAEYMGR

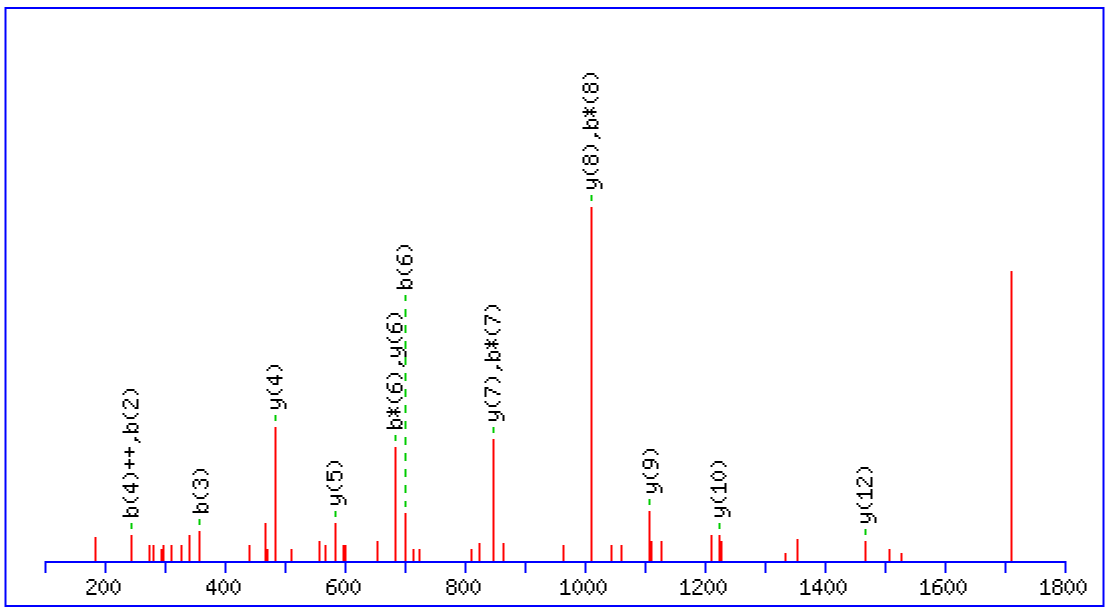
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GWDENVYYTVPLVR**
Found in **NIPS1_HUMAN**, Protein NipSnap homolog 1 OS=Homo sapiens GN=NIPSNAP1 PE=1 SV=1

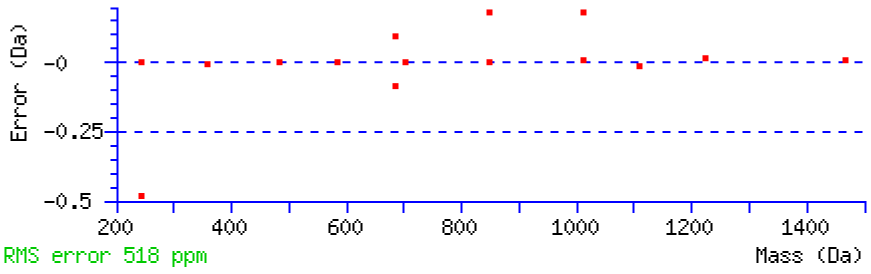
Match to Query 52412: 1709.845208 from(855.929880,2+) rtinseconds(3349) index(46346)
Title: Locus:1.1.1.2596.34
Data file 2011-11-14 - TFD - EP 8-5.mgf

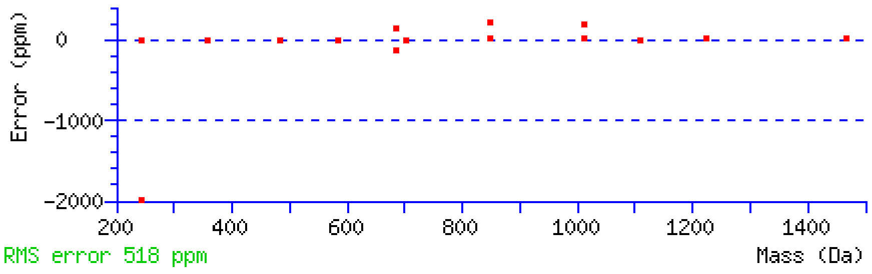
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1709.841324
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 67 **Expect:** 2.3e-006
Matches : 15/134 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							14
2	**244.108053**	122.557665					W	1653.827135	827.417206	1636.800586	818.903931	1635.816570	818.411923	13
3	**359.134996**	180.071136			341.124431	171.065854	D	***1467.747822***	734.377549	1450.721273	725.864275	1449.737257	725.372267	12
4	488.177589	244.592433			470.167024	235.587150	E	1352.720879	676.864078	1335.694330	668.350803	1334.710314	667.858795	11
5	602.220516	301.613896	585.193967	293.100622	584.209951	292.608614	N	***1223.678286***	612.342781	1206.651737	603.829507	1205.667721	603.337499	10
6	**701.288930**	351.148103	684.262381	342.634829	683.278365	342.142821	V	***1109.635359***	555.321318	1092.608810	546.808043	1091.624794	546.316035	9
7	864.352259	432.679768	847.325710	424.166493	846.341694	423.674485	Y	***1010.566945***	505.787111	993.540396	497.273836	992.556380	496.781828	8
8	1027.415588	514.211432	1010.389039	505.698158	1009.405023	505.206150	Y	***847.503616***	424.255446	830.477067	415.742172	829.493051	415.250164	7
9	1128.463267	564.735272	1111.436718	556.221997	1110.452702	555.729989	T	***684.440287***	342.723782	667.413738	334.210507	666.429722	333.718499	6
10	1227.531681	614.269479	1210.505132	605.756204	1209.521116	605.264196	V	***583.392608***	292.199942	566.366059	283.686668			5
11	1324.584445	662.795861	1307.557896	654.282586	1306.573880	653.790578	P	***484.324194***	242.665735	467.297645	234.152460			4
12	1437.668509	719.337893	1420.641960	710.824618	1419.657944	710.332610	L	387.271430	194.139353	370.244881	185.626078			3
13	1536.736923	768.872100	1519.710374	760.358825	1518.726358	759.866817	V	274.187366	137.597321	257.160817	129.084047			2
14							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of GWDENVYYTVPLVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
66.8	1709.841324	0.003884	GWDENVYYTVPLVR
2.6	1709.840652	0.004556	FVKINNSTNEGMNVK
2.5	1709.851425	-0.006217	LRALMDMMGGVLEVK

Mascot: http://www.matrixscience.com/

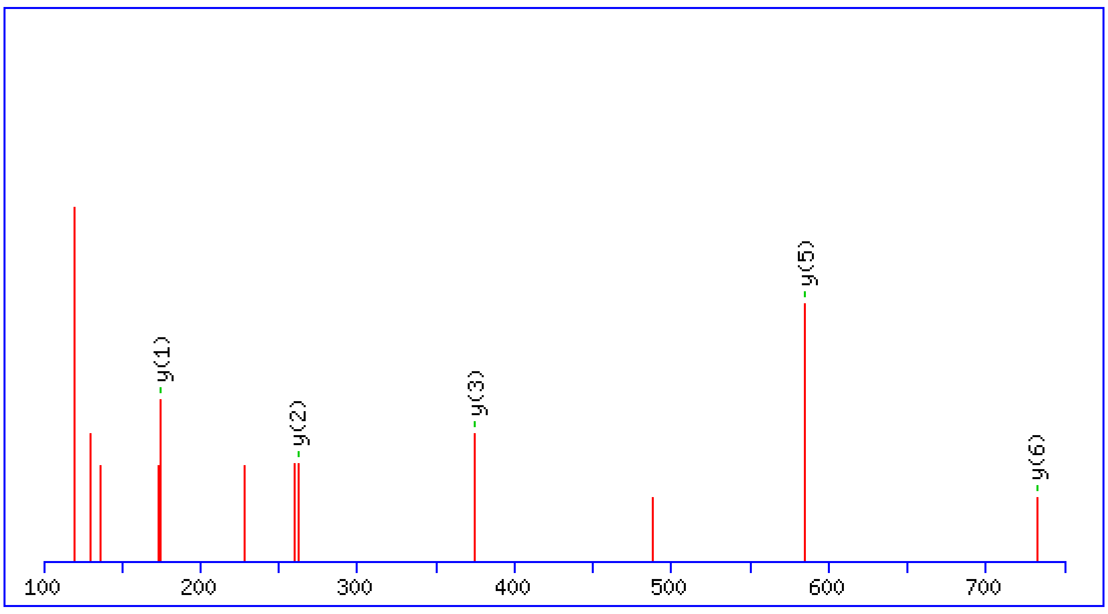
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LFLPLSR**
Found in **NLRC3_HUMAN**, Protein NLRC3 OS=Homo sapiens GN=NLRC3 PE=2 SV=2

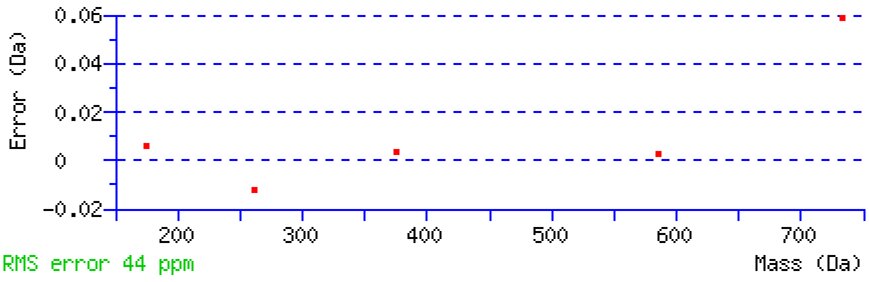
Match to Query 3266: 844.514668 from(423.264610,2+) rtinseconds(1954) index(16943)
Title: Locus:1.1.1.2367.7
Data file 2011-11-10 - TFD - EP 3-5.mgf

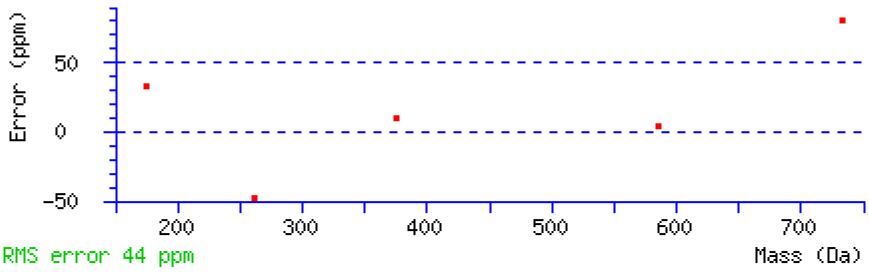
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 844.517059
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.00068
Matches : 5/48 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							7
2	261.159754	131.083515			F	*732.440286*	366.723781	715.413737	358.210507	714.429721	357.718499	6
3	374.243818	187.625547			L	*585.371872*	293.189574	568.345323	284.676300	567.361307	284.184292	5
4	471.296582	236.151929			P	472.287808	236.647542	455.261259	228.134268	454.277243	227.642260	4
5	584.380646	292.693961			L	*375.235044*	188.121160	358.208495	179.607886	357.224479	179.115878	3
6	671.412674	336.209975	653.402109	327.204693	S	*262.150980*	131.579128	245.124431	123.065854	244.140415	122.573846	2
7					R	*175.118952*	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of LFLPLSR
(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	844.517059	-0.002391	LFLPLSR
16.8	844.509186	0.005482	LILMDLK
14.6	844.509201	0.005467	LMVPLLK
13.1	844.513031	0.001637	LVKAATSR
11.1	844.513031	0.001637	LLTKQSR
10.7	844.513016	0.001652	AAIKSLSR
10.7	844.513031	0.001637	KTLQLSR
9.9	844.513031	0.001637	IQTLKSR
2.2	844.509201	0.005467	LVLPMIK
0.5	844.513031	0.001637	LLTKTNR

Mascot: http://www.matrixscience.com/

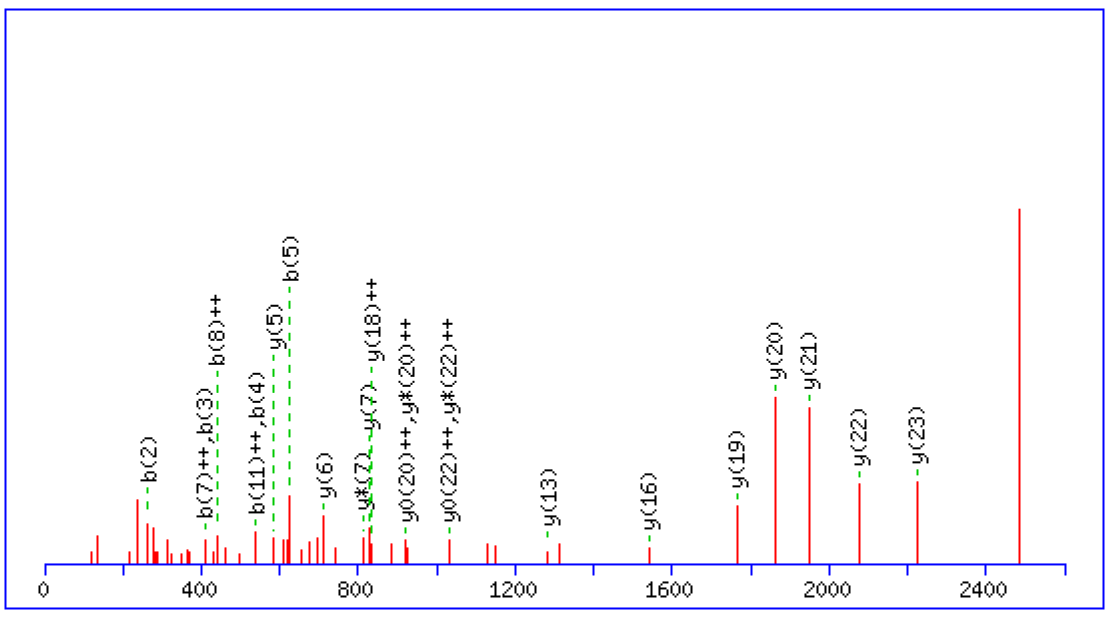
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VYFQSPPGAAGEGPGGADDEGPVRR**
Found in **PP14B_HUMAN**, Protein phosphatase 1 regulatory subunit 14B OS=Homo sapiens GN=PPP1R14B PE=1 SV=3

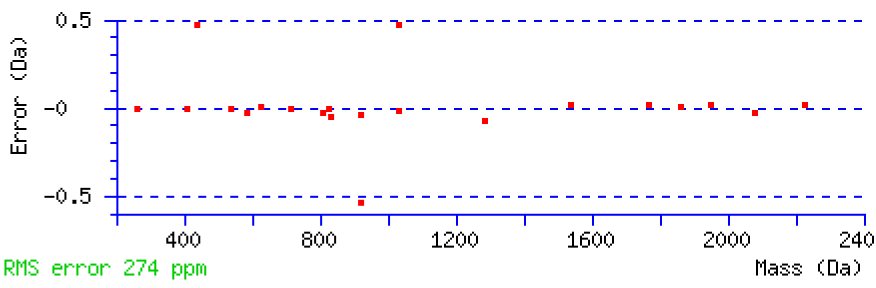
Match to Query 59962: 2485.158522 from(829.393450,3+) rtinseconds(2181) index(24298)
Title: Locus:1.1.1.2087.51
Data file 2011-11-10 - TFD - EP 4-6.mgf

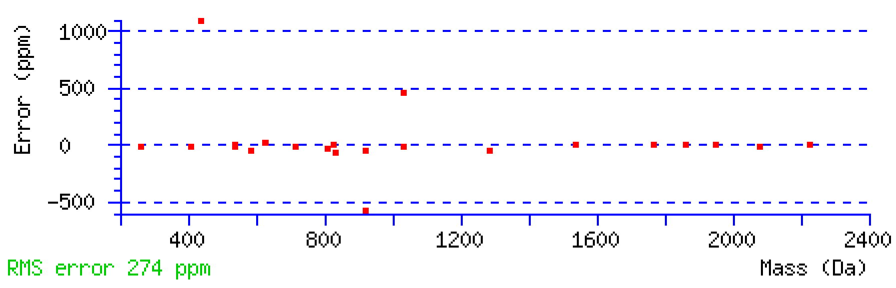
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2485.162231
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 61 **Expect:** 7.9e-006
Matches : 23/264 fragment ions using 29 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							25
2	**263.139019**	132.073148					Y	2387.101080	1194.054178	2370.074531	1185.540903	2369.090515	1185.048895	24
3	**410.207433**	205.607354					F	***2224.037751***	1112.522513	2207.011202	1104.009239	2206.027186	1103.517231	23
4	**538.266011**	269.636644	521.239462	261.123369			Q	***2076.969337***	1038.988306	2059.942788	1030.475032	2058.958772	1029.983024	22
5	**625.298039**	313.152658	608.271490	304.639383	607.287474	304.147375	S	***1948.910759***	974.959017	1931.884210	966.445743	1930.900194	965.953735	21
6	722.350803	361.679040	705.324254	353.165765	704.340238	352.673757	P	***1861.878731***	931.443003	1844.852182	922.929729	1843.868166	922.437721	20
7	819.403567	**410.205422**	802.377018	401.692147	801.393002	401.200139	P	***1764.825967***	882.916621	1747.799418	874.403347	1746.815402	873.911339	19
8	876.425031	**438.716154**	859.398482	430.202879	858.414466	429.710871	G	1667.773203	834.390239	1650.746654	825.876965	1649.762638	825.384957	18
9	947.462145	474.234711	930.435596	465.721436	929.451580	465.229428	A	1610.751739	805.879507	1593.725190	797.366233	1592.741174	796.874225	17
10	1018.499259	509.753268	1001.472710	501.239993	1000.488694	500.747985	A	***1539.714625***	770.360950	1522.688076	761.847676	1521.704060	761.355668	16
11	1075.520723	**538.264000**	1058.494174	529.750725	1057.510158	529.258717	G	1468.677511	734.842393	1451.650962	726.329119	1450.666946	725.837111	15
12	1204.563316	602.785296	1187.536767	594.272022	1186.552751	593.780014	E	1411.656047	706.331661	1394.629498	697.818387	1393.645482	697.326379	14
13	1261.584780	631.296028	1244.558231	622.782754	1243.574215	622.290745	G	***1282.613454***	641.810365	1265.586905	633.297090	1264.602889	632.805082	13
14	1358.637544	679.822410	1341.610995	671.309136	1340.626979	670.817127	P	1225.591990	613.299633	1208.565441	604.786358	1207.581425	604.294350	12
15	1415.659008	708.333142	1398.632459	699.819867	1397.648443	699.327859	G	1128.539226	564.773251	1111.512677	556.259976	1110.528661	555.767968	11
16	1472.680472	736.843874	1455.653923	728.330599	1454.669907	727.838591	G	1071.517762	536.262519	1054.491213	527.749244	1053.507197	527.257236	10
17	1543.717586	772.362431	1526.691037	763.849156	1525.707021	763.357148	A	1014.496298	507.751787	997.469749	499.238512	996.485733	498.746504	9
18	1658.744529	829.875902	1641.717980	821.362628	1640.733964	820.870620	D	943.459184	472.233230	926.432635	463.719955	925.448619	463.227947	8
19	1773.771472	887.389374	1756.744923	878.876100	1755.760907	878.384091	D	***828.432241***	414.719758	811.405692	406.206484	810.421676	405.714476	7
20	1902.814065	951.910670	1885.787516	943.397396	1884.803500	942.905388	E	***713.405298***	357.206287	696.378749	348.693012	695.394733	348.201004	6
21	1959.835529	980.421402	1942.808980	971.908128	1941.824964	971.416120	G	***584.362705***	292.684990	567.336156	284.171716			5
22	2056.888293	1028.947784	2039.861744	1020.434510	2038.877728	1019.942502	P	527.341241	264.174258	510.314692	255.660984			4
23	2155.956707	1078.481991	2138.930158	1069.968717	2137.946142	1069.476709	V	430.288477	215.647876	413.261928	207.134602			3
24	2312.057818	1156.532547	2295.031269	1148.019272	2294.047253	1147.527264	R	331.220063	166.113669	314.193514	157.600395			2
25							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of VYFQSPPGAAGEGPGGADDEGPVRR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
60.6	2485.162231	-0.003709	VYFQSPPGAAGEGPGGADDEGPVRR
6.5	2485.176117	-0.017595	YKTTNQSTEFLSFQDASSLYR
5.8	2485.175522	-0.017000	GVLEAPDTQVNPVGSVSVDCGPSR
3.7	2485.136627	0.021895	CGVPDMRPPPPSAPPSPPGPPPR
0.6	2485.136627	0.021895	CGVPDMRPPPPSAPPSPPGPPPR
0.1	2485.136627	0.021895	CGVPDMRPPPPSAPPSPPGPPPR

Mascot: http://www.matrixscience.com/

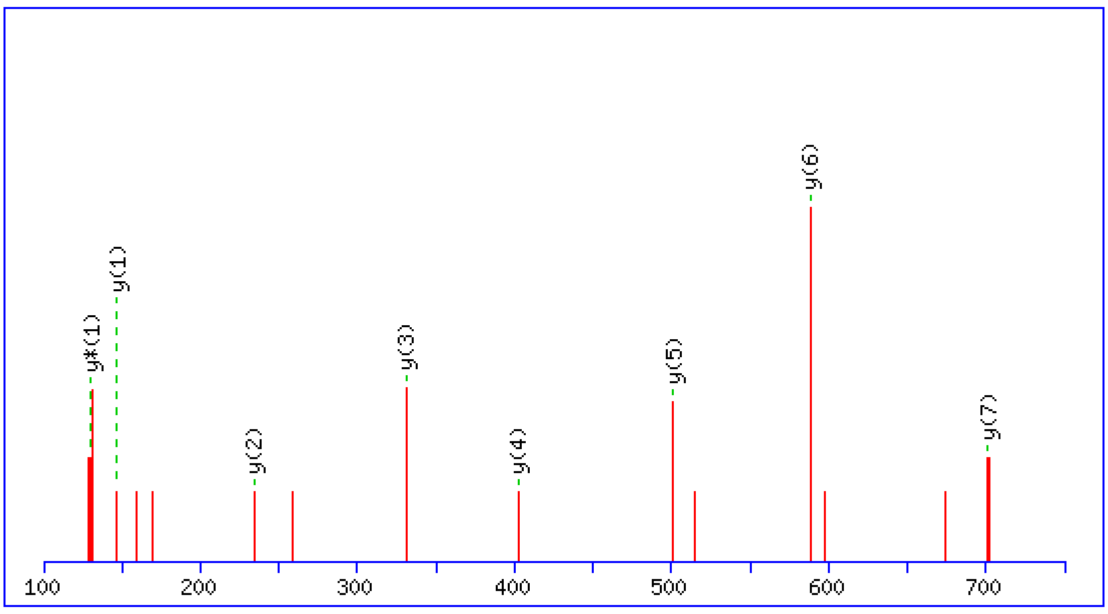
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SALSVAPSK**
Found in **QIL1_HUMAN**, Protein QIL1 OS=Homo sapiens GN=QIL1 PE=1 SV=1

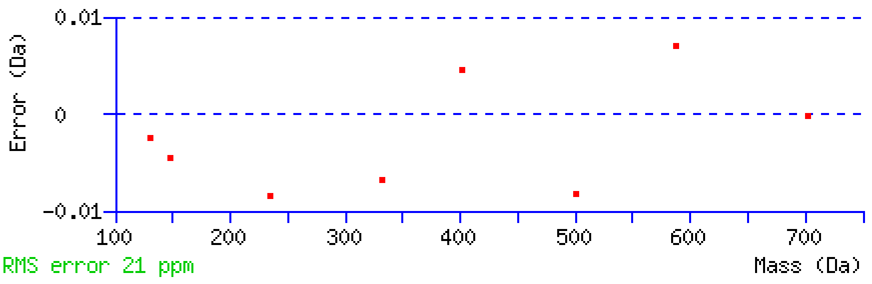
Match to Query 75510: 858.482908 from(430.248730,2+) rtinseconds(1214) index(247819)
Title: Locus:1.1.1.905.3
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●

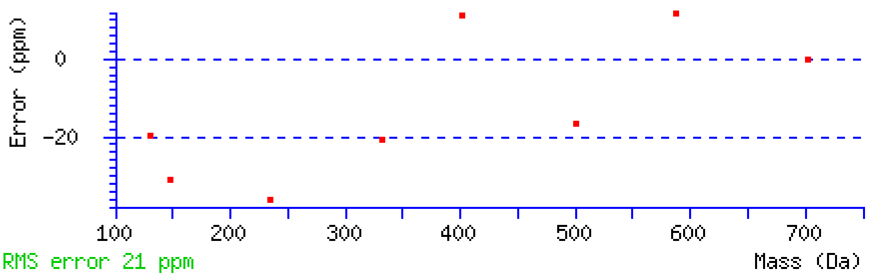


Monoisotopic mass of neutral peptide Mr(calc): 858.481064
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 54 **Expect:** 5.3e-005
Matches : 8/78 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	S							9
2	159.076418	80.041847	141.065853	71.036564	A	772.456330	386.731803	755.429781	378.218529	754.445765	377.726521	8
3	272.160482	136.583879	254.149917	127.578597	L	***701.419216***	351.213246	684.392667	342.699972	683.408651	342.207964	7
4	359.192510	180.099893	341.181945	171.094611	S	***588.335152***	294.671214	571.308603	286.157940	570.324587	285.665932	6
5	458.260924	229.634100	440.250359	220.628818	V	***501.303124***	251.155200	484.276575	242.641926	483.292559	242.149918	5
6	529.298038	265.152657	511.287473	256.147375	A	***402.234710***	201.620993	385.208161	193.107719	384.224145	192.615711	4
7	626.350802	313.679039	608.340237	304.673757	P	***331.197596***	166.102436	314.171047	157.589161	313.187031	157.097153	3
8	713.382830	357.195053	695.372265	348.189771	S	***234.144832***	117.576054	217.118283	109.062779	216.134267	108.570771	2
9					K	***147.112804***	74.060040	130.086255	65.546765			1



RMS error 21 ppm



RMS error 21 ppm

NCBI **BLAST** search of SALSVAPSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.2	858.481064	0.001844	SALSVAPSK
15.7	858.481064	0.001844	KGSELTPK
13.1	858.481079	0.001829	GTVIIDNK
10.8	858.481094	0.001814	GTDQVLVK
10.2	858.481079	0.001829	SAVEQVVK
10.2	858.481094	0.001814	GTTGIPGLK
9.7	858.481094	0.001814	GITGIVGDK
9.1	858.481064	0.001844	KGGELLDK
7.6	858.481064	0.001844	SKPSIPSK
7.4	858.481064	0.001844	TGILQEAK

Mascot: http://www.matrixscience.com/

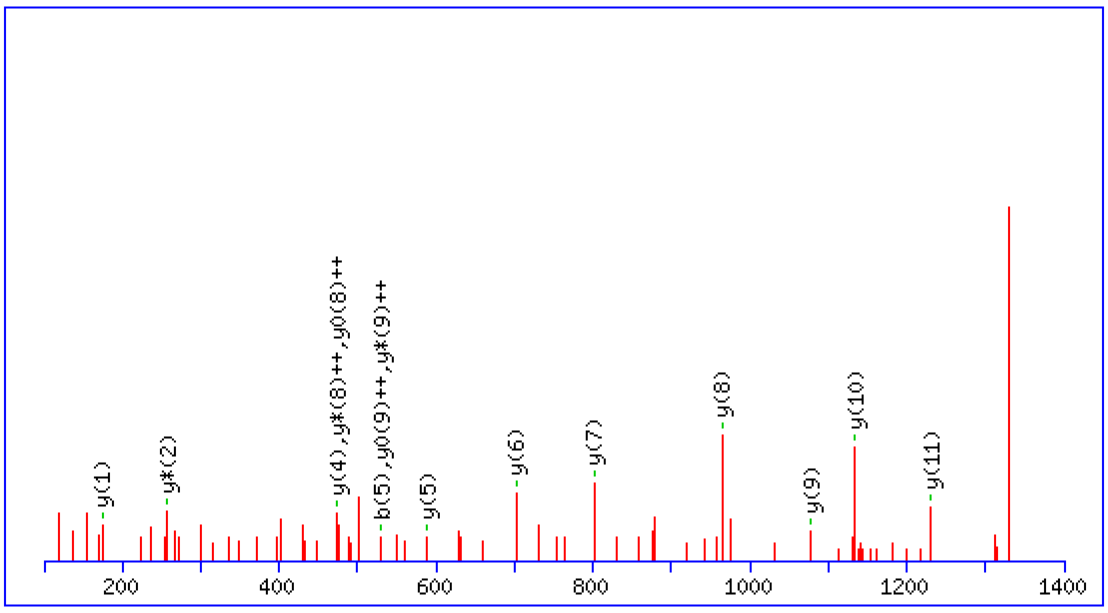
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VPGLYVIDSIVR**
Found in **SCAF8_HUMAN**, Protein SCAF8 OS=Homo sapiens GN=SCAF8 PE=1 SV=1

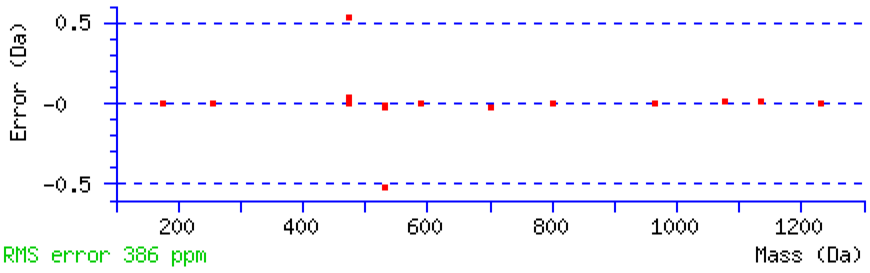
Match to Query 37728: 1329.765908 from(665.890230,2+) rtinseconds(3646) index(52836)
Title: Locus:1.1.1.2781.14
Data file 2011-11-14 - TFD - EP 8-1.mgf

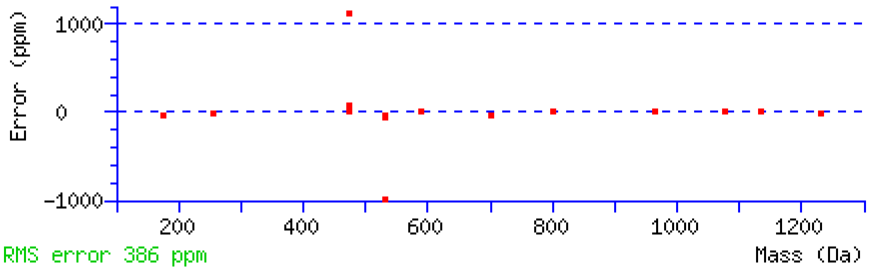
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1329.765640
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 44 **Expect:** 0.00019
Matches : 15/90 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483			V							12
2	197.128454	99.067865			P	***1231.704500***	616.355888	1214.677951	607.842613	1213.693935	607.350605	11
3	254.149918	127.578597			G	***1134.651736***	567.829506	1117.625187	559.316232	1116.641171	558.824224	10
4	367.233982	184.120629			L	***1077.630272***	539.318774	1060.603723	530.805500	1059.619707	530.313491	9
5	530.297311	265.652294			Y	***964.546208***	482.776742	947.519659	474.263467	946.535643	473.771459	8
6	629.365725	315.186501			V	***801.482879***	401.245077	784.456330	392.731803	783.472314	392.239795	7
7	742.449789	371.728533			I	***702.414465***	351.710871	685.387916	343.197596	684.403900	342.705588	6
8	857.476732	429.242004	839.466167	420.236721	D	***589.330401***	295.168838	572.303852	286.655564	571.319836	286.163556	5
9	944.508760	472.758018	926.498195	463.752735	S	***474.303458***	237.655367	457.276909	229.142092	456.292893	228.650084	4
10	1057.592824	529.300050	1039.582259	520.294767	I	387.271430	194.139353	370.244881	185.626078			3
11	1156.661238	578.834257	1138.650673	569.828974	V	274.187366	137.597321	257.160817	129.084047			2
12					R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of VPGLYVIDSIVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.1	1329.765640	0.000268	VPGLYVIDSIVR

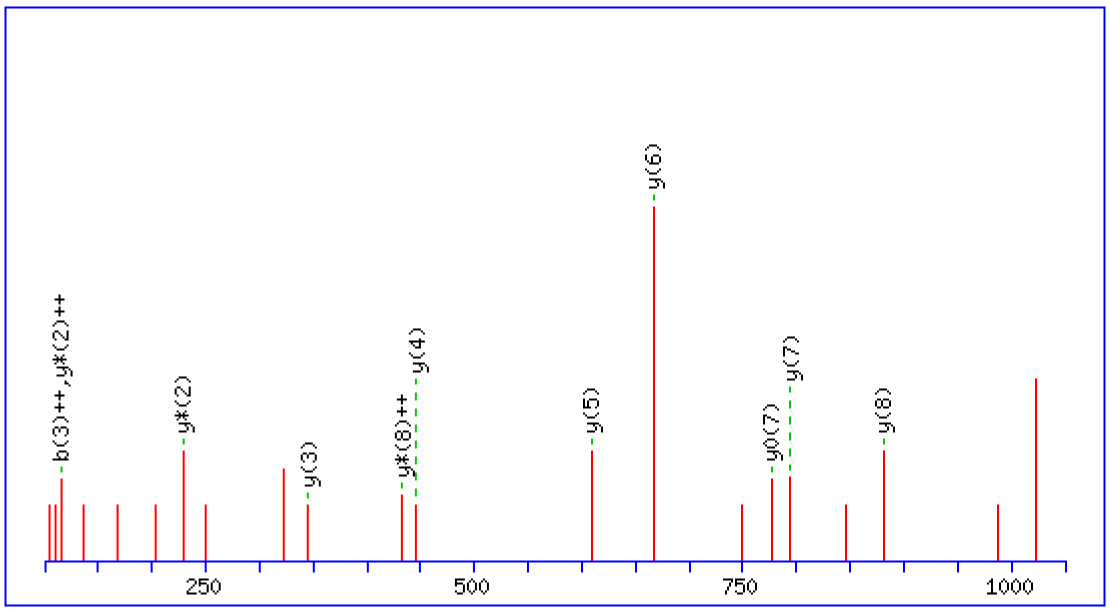
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AASQGYTVAR**
Found in **SE1L1_HUMAN**, Protein sel-1 homolog 1 OS=Homo sapiens GN=SEL1L PE=1 SV=3

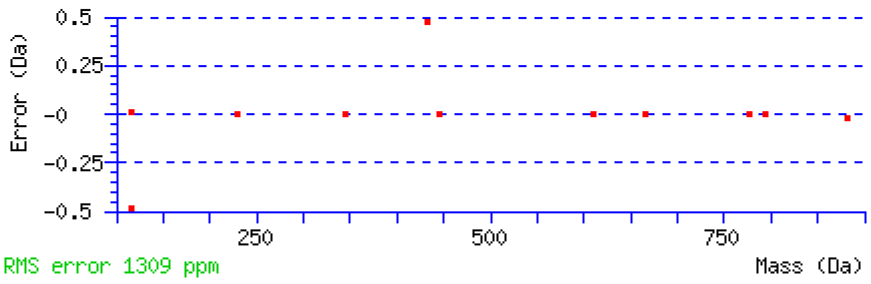
Match to Query 19383: 1022.512448 from(512.263500,2+) rtinseconds(1049) index(4227)
Title: Locus:1.1.1.1832.30
Data file 2011-11-14 - TFD - EP 8-2.mgf

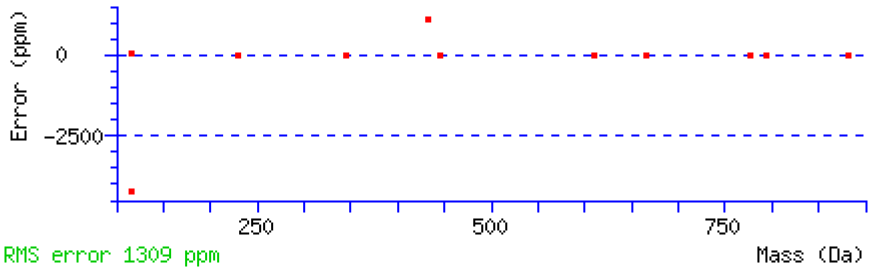
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1022.514496
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 47 **Expect:** 0.00027
Matches : 11/92 fragment ions using 15 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	72.044390	36.525833					A							10
2	143.081504	72.044390					A	952.484672	476.745974	935.458123	468.232700	934.474107	467.740692	9
3	230.113532	115.560404			212.102967	106.555121	S	***881.447558***	441.227417	864.421009	432.714143	863.436993	432.222135	8
4	358.172110	179.589693	341.145561	171.076419	340.161545	170.584411	Q	***794.415530***	397.711403	777.388981	389.198129	776.404965	388.706121	7
5	415.193574	208.100425	398.167025	199.587151	397.183009	199.095143	G	***666.356952***	333.682114	649.330403	325.168839	648.346387	324.676831	6
6	578.256903	289.632090	561.230354	281.118815	560.246338	280.626807	Y	***609.335488***	305.171382	592.308939	296.658107	591.324923	296.166099	5
7	679.304582	340.155929	662.278033	331.642655	661.294017	331.150647	T	***446.272159***	223.639717	429.245610	215.126443	428.261594	214.634435	4
8	778.372996	389.690136	761.346447	381.176862	760.362431	380.684854	V	***345.224480***	173.115878	328.197931	164.602603			3
9	849.410110	425.208693	832.383561	416.695419	831.399545	416.203411	A	246.156066	123.581671	229.129517	115.068396			2
10							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of AASQGYTVAR
(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	1022.514496	-0.002048	AASQGYTVAR

Mascot: http://www.matrixscience.com/

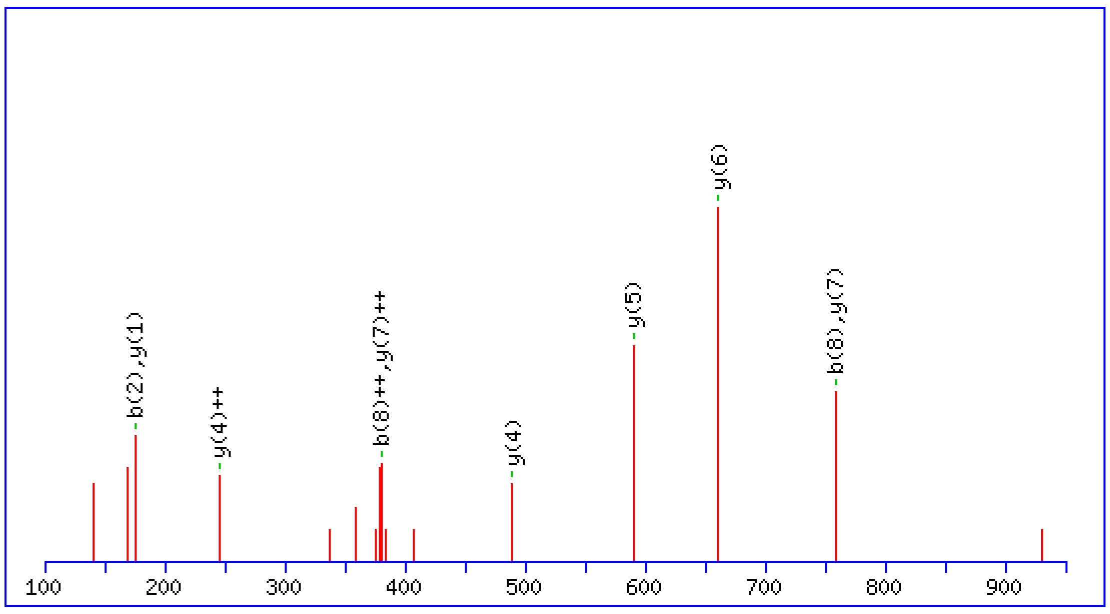
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SSPATADKR**
Found in **SHRM3_HUMAN**, Protein Shroom3 OS=Homo sapiens GN=SHROOM3 PE=1 SV=2

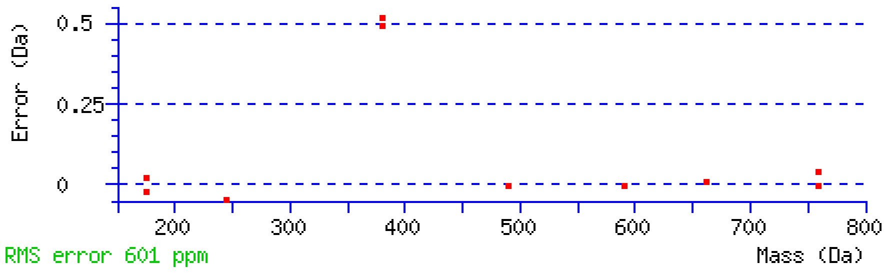
Match to Query 10996: 931.473528 from(466.744040,2+) rtinseconds(873) index(501)
Title: Locus:1.1.1.1601.5
Data file 2011-11-10 - TFD - EP 3-6.mgf

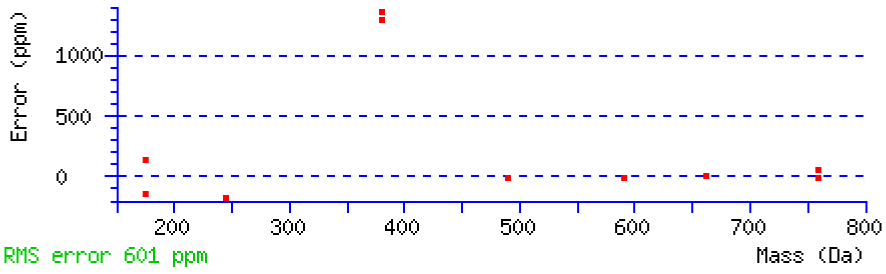
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 931.472290
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 48 **Expect:** 0.0002
Matches : 10/78 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							9
2	**175.071332**	88.039304			157.060767	79.034021	S	845.447557	423.227417	828.421008	414.714142	827.436992	414.222134	8
3	272.124096	136.565686			254.113531	127.560403	P	***758.415529***	379.711403	741.388980	371.198128	740.404964	370.706120	7
4	343.161210	172.084243			325.150645	163.078960	A	***661.362765***	331.185021	644.336216	322.671746	643.352200	322.179738	6
5	444.208889	222.608082			426.198324	213.602800	T	***590.325651***	295.666464	573.299102	287.153189	572.315086	286.661181	5
6	515.246003	258.126640			497.235438	249.121357	A	***489.277972***	245.142624	472.251423	236.629349	471.267407	236.137341	4
7	630.272946	315.640111			612.262381	306.634828	D	418.240858	209.624067	401.214309	201.110793	400.230293	200.618785	3
8	**758.367909**	379.687592	741.341360	371.174318	740.357344	370.682310	K	303.213915	152.110596	286.187366	143.597321			2
9							R	***175.118952***	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of SSPATADKR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.8	931.472290	0.001238	SSPATADKR
16.4	931.465759	0.007769	CRPNLSR
14.3	931.479675	-0.006147	SLIMEAPR
13.6	931.479706	-0.006178	IMTTVDPR
11.1	931.479691	-0.006163	SLMPSIPR
11.1	931.476349	-0.002821	SPFTVPPR
9.6	931.472290	0.001238	ASISPSSGAR
7.9	931.476990	-0.003462	ASRCRPR
7.9	931.465759	0.007769	GCEAGRLR
7.9	931.481033	-0.007505	HFGMLRR

Mascot: http://www.matrixscience.com/

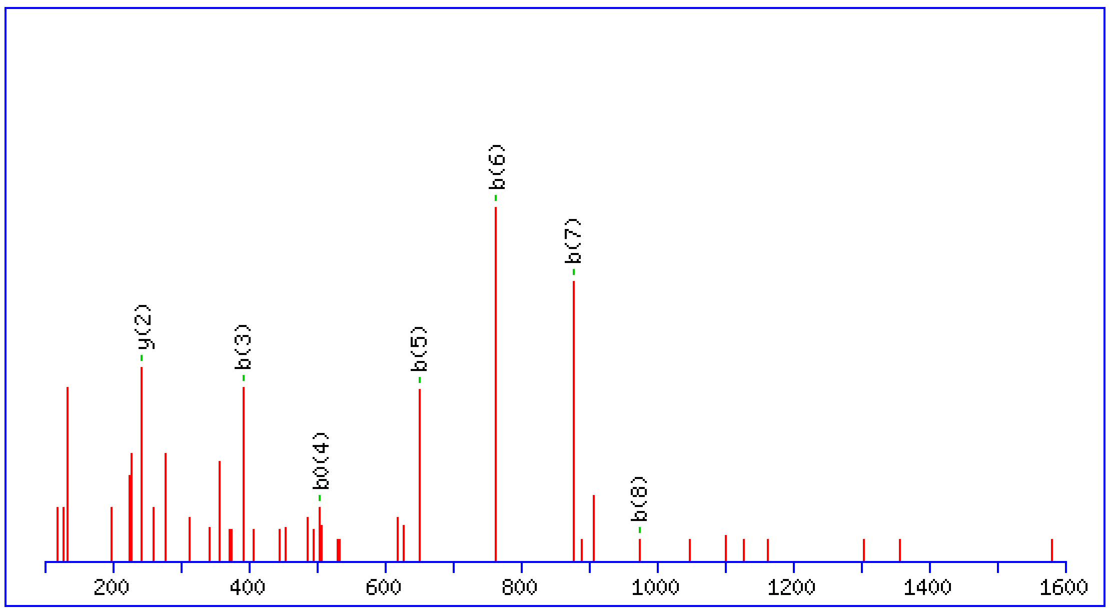
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VEYMKLLPK**
Found in **SMAG1_HUMAN**, Protein Smaug homolog 1 OS=Homo sapiens GN=SAMD4A PE=1 SV=3

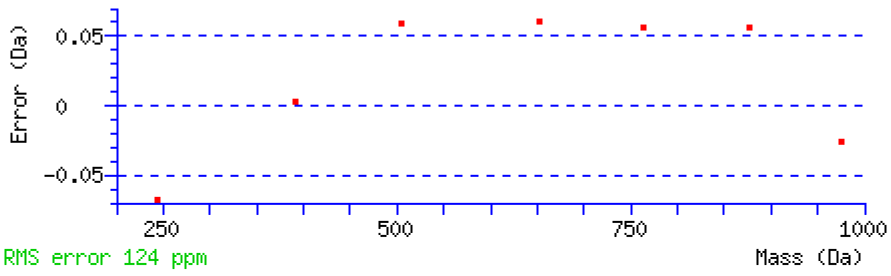
Match to Query 24795: 1119.626588 from(560.820570,2+) rtinseconds(3687) index(54379)
Title: Locus:1.1.1.2741.11
Data file 2011-11-10 - TFD - EP 3-4.mgf

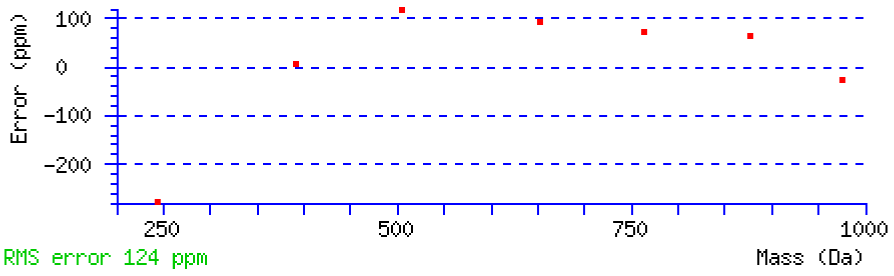
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1119.636169
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 37  Expect: 0.0013
Matches : 7/72 fragment ions using 10 most intense peaks   (help)
```

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	100.075690	50.541483					V							9
2	229.118283	115.062780			211.107718	106.057497	E	1021.575066	511.291171	1004.548517	502.777897	1003.564501	502.285889	8
3	***392.181612***	196.594444			374.171047	187.589162	Y	892.532473	446.769875	875.505924	438.256600			7
4	523.222097	262.114687			505.211532	253.109404	M	729.469144	365.238210	712.442595	356.724936			6
5	***651.317060***	326.162168	634.290511	317.648894	633.306495	317.156886	K	598.428659	299.717968	581.402110	291.204693			5
6	***764.401124***	382.704200	747.374575	374.190926	746.390559	373.698918	L	470.333696	235.670486	453.307147	227.157212			4
7	***877.485188***	439.246232	860.458639	430.732958	859.474623	430.240950	L	357.249632	179.128454	340.223083	170.615180			3
8	***974.537952***	487.772614	957.511403	479.259340	956.527387	478.767332	P	244.165568	122.586422	227.139019	114.073148			2
9							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of VEYMKLLPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.5	1119.636169	-0.009581	VEYMKLLPK
10.9	1119.617554	0.009034	DAGIYEVILK
9.6	1119.617554	0.009034	EKVLEDFLK
9.1	1119.632813	-0.006224	VYEKLFPPK
8.2	1119.617554	0.009034	LLEDYKVPK
3.3	1119.632828	-0.006240	QFPILLDFK

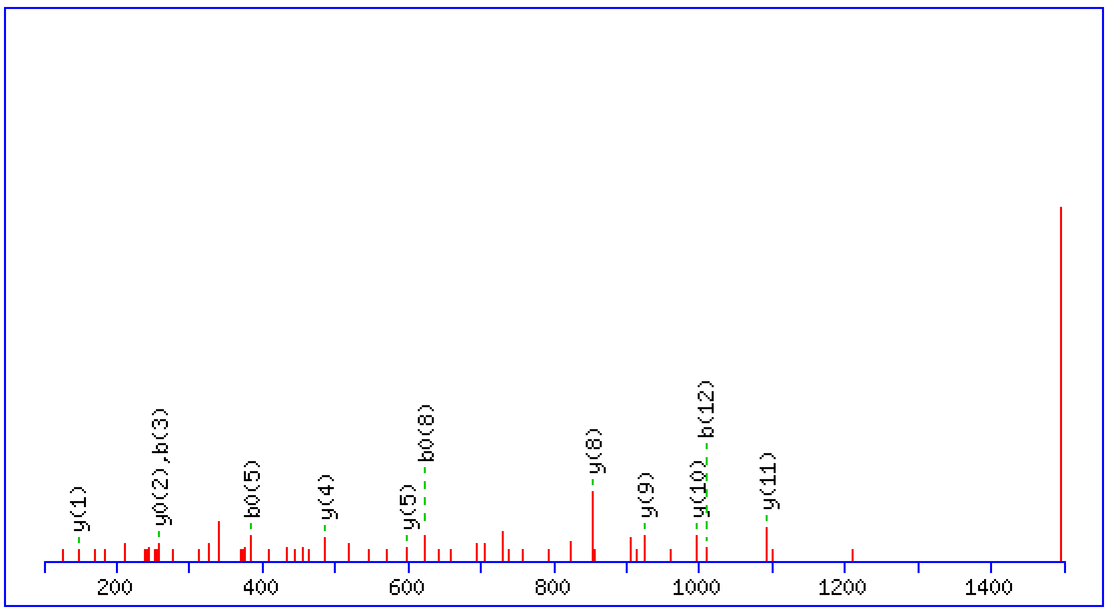
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EGAGSPAAPGTLPLEK**
Found in **SOX15_HUMAN**, Protein SOX-15 OS=Homo sapiens GN=SOX15 PE=2 SV=1

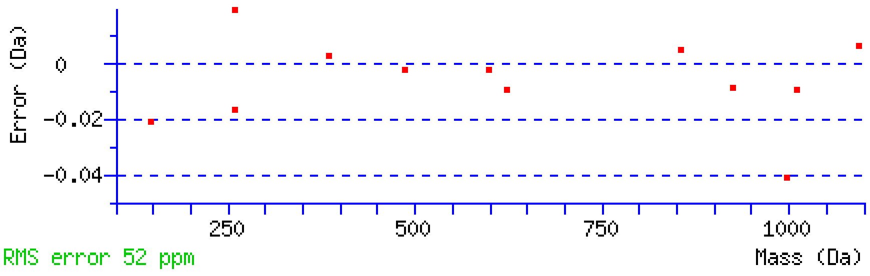
Match to Query 833358: 1493.778008 from(747.896280,2+) rtinseconds(2086) index(264200)
Title: Locus:1.1.1.1243.33
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

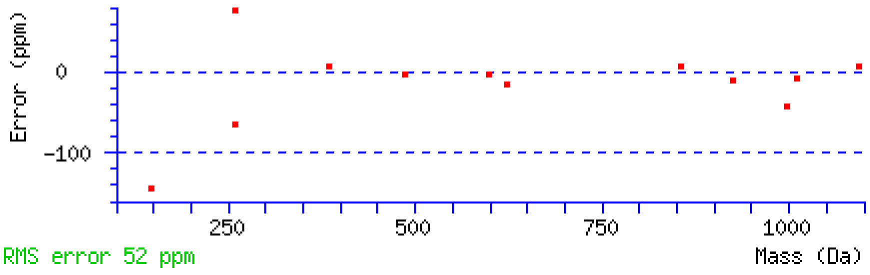
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1493.772552
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 40 **Expect:** 0.0012
Matches : 12/148 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572	112.039304	56.523290	E							16
2	187.071333	94.039305	169.060768	85.034022	G	1365.737258	683.372267	1348.710709	674.858993	1347.726693	674.366984	15
3	**258.108447**	129.557862	240.097882	120.552579	A	1308.715794	654.861535	1291.689245	646.348261	1290.705229	645.856252	14
4	315.129911	158.068593	297.119346	149.063311	G	1237.678680	619.342978	1220.652131	610.829704	1219.668115	610.337696	13
5	402.161939	201.584608	384.151374	192.579325	S	1180.657216	590.832246	1163.630667	582.318972	1162.646651	581.826964	12
6	499.214703	250.110990	481.204138	241.105707	P	***1093.625188***	547.316232	1076.598639	538.802958	1075.614623	538.310949	11
7	570.251817	285.629547	552.241252	276.624264	A	***996.572424***	498.789850	979.545875	490.276575	978.561859	489.784567	10
8	641.288931	321.148104	623.278366	312.142821	A	***925.535310***	463.271293	908.508761	454.758018	907.524745	454.266010	9
9	738.341695	369.674486	720.331130	360.669203	P	***854.498196***	427.752736	837.471647	419.239462	836.487631	418.747454	8
10	795.363159	398.185218	777.352594	389.179935	G	757.445432	379.226354	740.418883	370.713079	739.434867	370.221071	7
11	896.410838	448.709057	878.400273	439.703775	T	700.423968	350.715622	683.397419	342.202347	682.413403	341.710339	6
12	**1009.494902**	505.251089	991.484337	496.245807	L	***599.376289***	300.191782	582.349740	291.678508	581.365724	291.186500	5
13	1106.547666	553.777471	1088.537101	544.772189	P	***486.292225***	243.649750	469.265676	235.136476	468.281660	234.644468	4
14	1219.631730	610.319503	1201.621165	601.314221	L	389.239461	195.123368	372.212912	186.610094	371.228896	186.118086	3
15	1348.674323	674.840800	1330.663758	665.835517	E	276.155397	138.581336	259.128848	130.068062	258.144832	129.576054	2
16					K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of EGAGSPAAPGTLPLEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.7	1493.772552	0.005456	EGAGSPAAPGTLPLEK
11.2	1493.783768	-0.005760	LDPAALSPANPREK

Mascot: http://www.matrixscience.com/

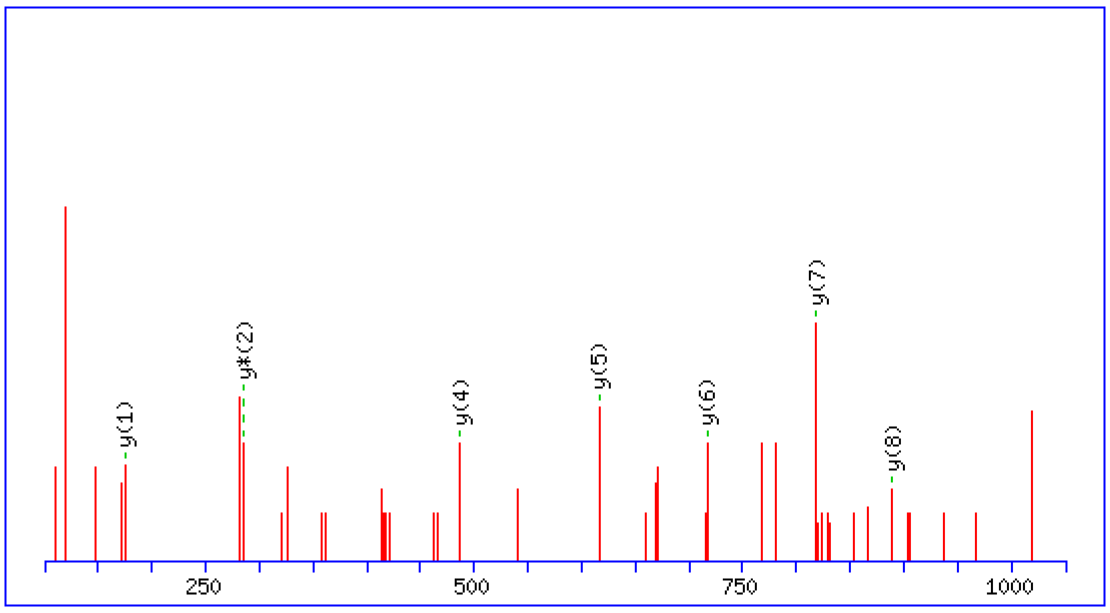
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FATTEAIQR**
Found in **SC16B_HUMAN**, Protein transport protein Sec16B OS=Homo sapiens GN=SEC16B PE=1 SV=2

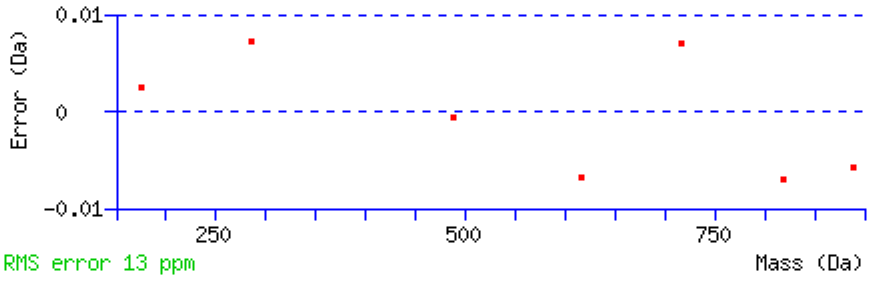
Match to Query 308284: 1035.528748 from(518.771650,2+) rtinseconds(1521) index(420695)
Title: Locus:1.1.1.919.20
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

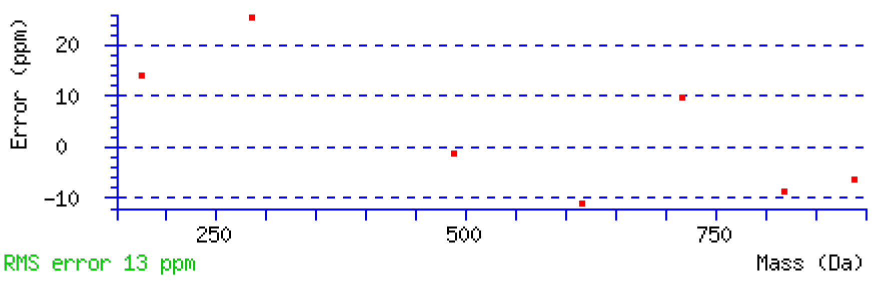
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1035.534897
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33  Expect: 0.0075
Matches : 7/70 fragment ions using 18 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.075690	74.541483					**F**							9
2	219.112804	110.060040					**A**	*889.473773*	445.240525	872.447224	436.727250	871.463208	436.235242	8
3	320.160483	160.583879			302.149918	151.578597	**T**	*818.436659*	409.721968	801.410110	401.208693	800.426094	400.716685	7
4	421.208162	211.107719			403.197597	202.102437	**T**	*717.388980*	359.198128	700.362431	350.684853	699.378415	350.192845	6
5	550.250755	275.629016			532.240190	266.623733	**E**	*616.341301*	308.674288	599.314752	300.161014	598.330736	299.669006	5
6	621.287869	311.147573			603.277304	302.142290	**A**	*487.298708*	244.152992	470.272159	235.639717			4
7	734.371933	367.689605			716.361368	358.684322	**I**	416.261594	208.634435	399.235045	200.121160			3
8	862.430511	431.718894	845.403962	423.205619	844.419946	422.713611	**Q**	303.177530	152.092403	286.150981	143.579128			2
9							**R**	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of FATTEAIQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.7	1035.534897	-0.006149	FATTEAIQR
16.2	1035.534912	-0.006164	VAVVQYSDR
11.2	1035.520493	0.008255	MASMLLAQR
4.9	1035.534882	-0.006134	VNYDEIKR
3.6	1035.528366	0.000382	MARSLTWR

Mascot: http://www.matrixscience.com/

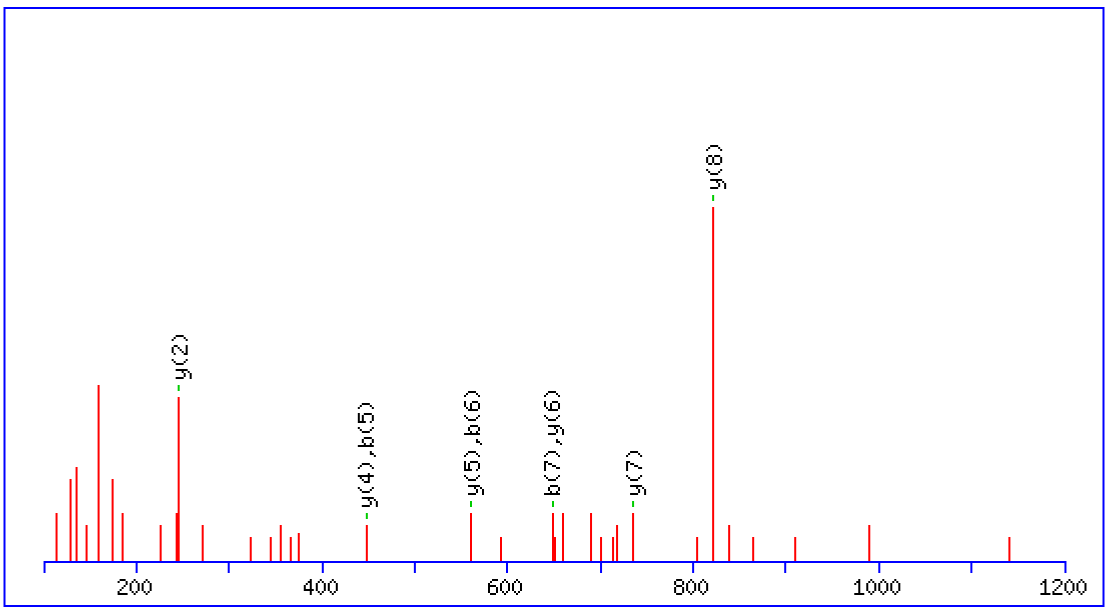
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SVSSSLSDAR**
Found in **SC24B_HUMAN**, Protein transport protein Sec24B OS=Homo sapiens GN=SEC24B PE=1 SV=2

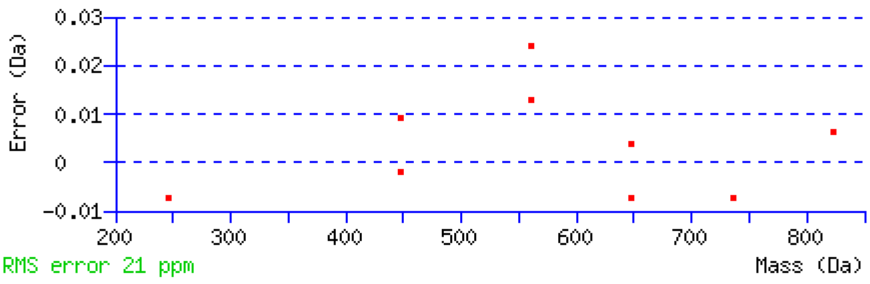
Match to Query 270505: 1007.488248 from(504.751400,2+) rtinseconds(1210) index(332530)
Title: Locus:1.1.1.795.16
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

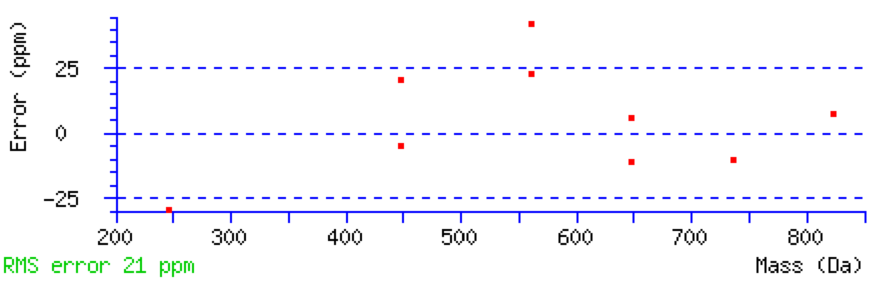
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1007.488342
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 52 **Expect:** 7e-005
Matches : 9/86 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	S							10
2	187.107718	94.057497	169.097153	85.052214	V	921.463599	461.235438	904.437050	452.722163	903.453034	452.230155	9
3	274.139746	137.573511	256.129181	128.568229	S	***822.395185***	411.701231	805.368636	403.187956	804.384620	402.695948	8
4	361.171774	181.089525	343.161209	172.084242	S	***735.363157***	368.185217	718.336608	359.671942	717.352592	359.179934	7
5	**448.203802**	224.605539	430.193237	215.600256	S	***648.331129***	324.669203	631.304580	316.155928	630.320564	315.663920	6
6	**561.287866**	281.147571	543.277301	272.142289	L	***561.299101***	281.153189	544.272552	272.639914	543.288536	272.147906	5
7	**648.319894**	324.663585	630.309329	315.658302	S	***448.215037***	224.611156	431.188488	216.097882	430.204472	215.605874	4
8	763.346837	382.177056	745.336272	373.171774	D	361.183009	181.095142	344.156460	172.581868	343.172444	172.089860	3
9	834.383951	417.695613	816.373386	408.690331	A	***246.156066***	123.581671	229.129517	115.068397			2
10					R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of SVSSSLSDAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.1	1007.488342	-0.000094	SVSSSLSDAR
15.4	1007.485825	0.002423	APQYTMAAR
5.0	1007.478455	0.009793	GTPGYRGER
2.0	1007.495743	-0.007495	SVSLAGNTIM
0.4	1007.478455	0.009793	QEPHPGTSR

Mascot: http://www.matrixscience.com/

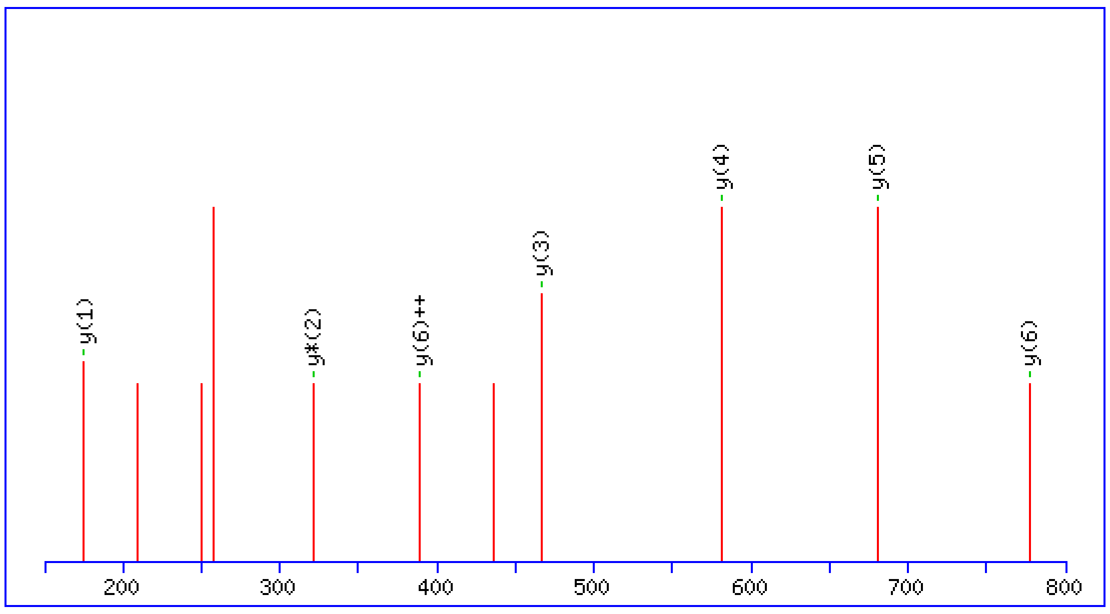
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LPVDQYR**
Found in **TRIQK_HUMAN**, Protein TRIQK OS=Homo sapiens GN=C8orf83 PE=2 SV=1

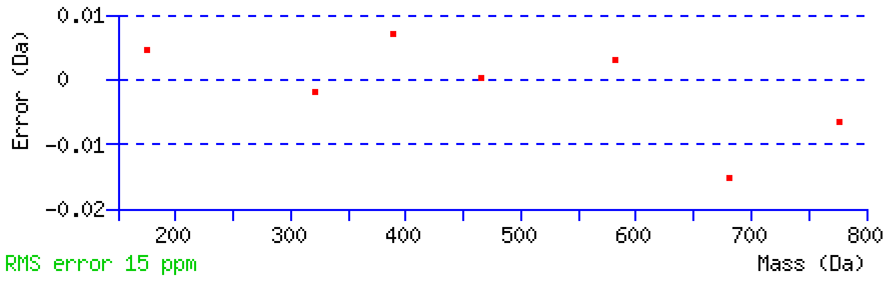
Match to Query 7389: 889.469868 from(445.742210,2+) rtinseconds(1580) index(9274)
Title: Locus:1.1.1.2008.7
Data file 2011-11-10 - TFD - EP 3-7.mgf

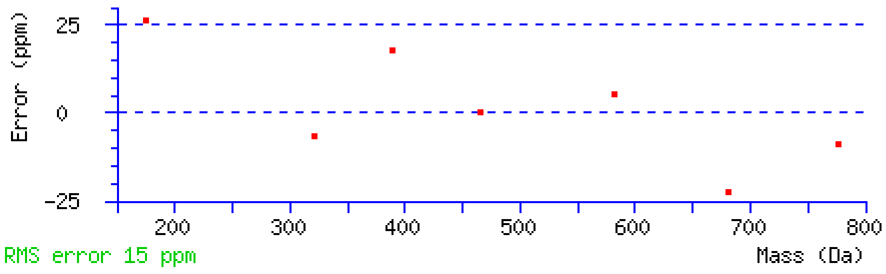
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 889.465759
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 43  Expect: 0.0012
Matches : 7/52 fragment ions using 8 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					**L**							7
2	211.144104	106.075690					**P**	*777.388980*	389.198128	760.362431	380.684854	759.378415	380.192846	6
3	310.212518	155.609897					**V**	*680.336216*	340.671746	663.309667	332.158472	662.325651	331.666464	5
4	425.239461	213.123369			407.228896	204.118086	**D**	*581.267802*	291.137539	564.241253	282.624265	563.257237	282.132257	4
5	553.298039	277.152658	536.271490	268.639383	535.287474	268.147375	**Q**	*466.240859*	233.624067	449.214310	225.110793			3
6	716.361368	358.684322	699.334819	350.171048	698.350803	349.679040	**Y**	338.182281	169.594778	321.155732	161.081504			2
7							**R**	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LPVDQYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
43.1	889.465759	0.004109	LPVDQYR
15.3	889.469116	0.000752	LPKTEMR
14.7	889.476974	-0.007106	IPADRYR
12.1	889.465759	0.004109	IPFDRDK
10.2	889.472961	-0.003093	LSGNTSRR
9.6	889.476990	-0.007122	LNFGLGNR
8.6	889.476517	-0.006649	IVIMPCK
8.3	889.476990	-0.007122	LPRADFR
6.9	889.476974	-0.007106	LDYPRAR
6.9	889.465744	0.004124	LNYLDPR

Mascot: http://www.matrixscience.com/

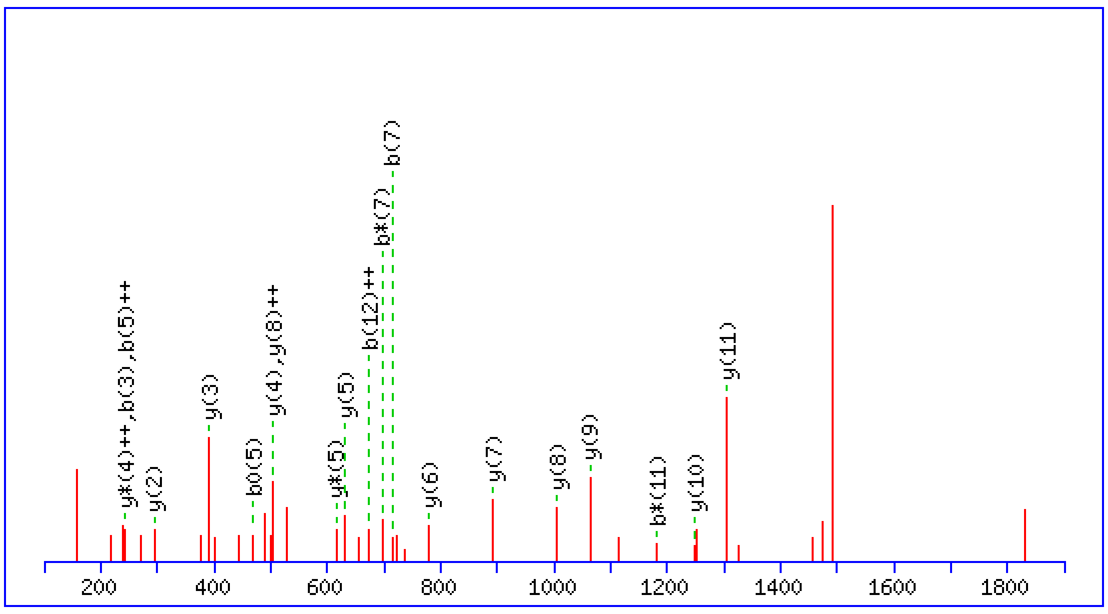
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SVGWGNIFQLPFK**
Found in **UN93B_HUMAN**, Protein unc-93 homolog B1 OS=Homo sapiens GN=UNC93B1 PE=1 SV=2

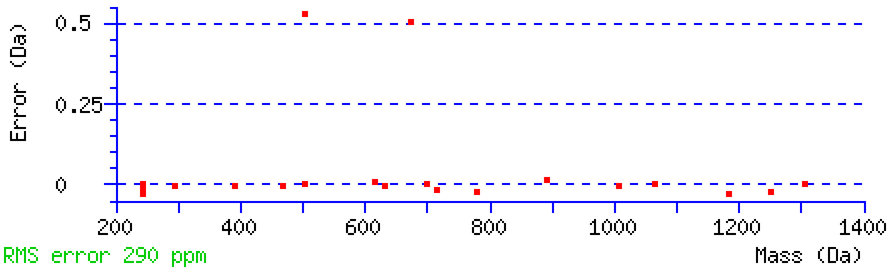
Match to Query 45760: 1491.790708 from(746.902630,2+) rtinseconds(4281) index(64332)
Title: Locus:1.1.1.3016.32
Data file 2011-11-14 - TFD - EP 8-1.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●

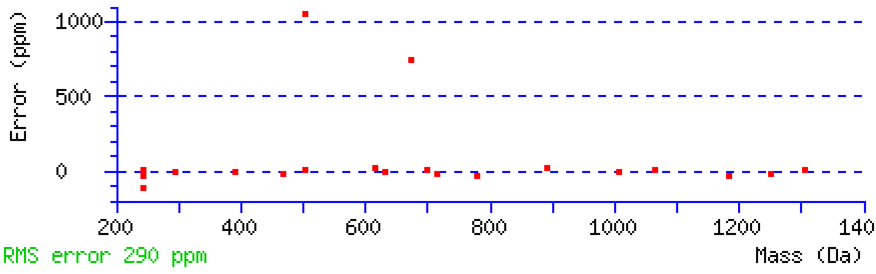


```
Monoisotopic mass of neutral peptide Mr(calc): 1491.787445
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 66  Expect: 2.9e-006
Matches : 20/110 fragment ions using 35 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	88.039304	44.523290			70.028739	35.518008	S					13
2	187.107718	94.057497			169.097153	85.052214	V	1405.762684	703.384980	1388.736135	694.871706	12
3	**244.129182**	122.568229			226.118617	113.562946	G	***1306.694270***	653.850773	1289.667721	645.337499	11
4	430.208495	215.607886			412.197930	206.602603	W	***1249.672806***	625.340041	1232.646257	616.826767	10
5	487.229959	**244.118618**			469.219394	235.113335	G	***1063.593493***	532.300385	1046.566944	523.787110	9
6	601.272886	301.140081	584.246337	292.626807	583.262321	292.134799	N	***1006.572029***	503.789653	989.545480	495.276378	8
7	**714.356950**	357.682113	697.330401	349.168839	696.346385	348.676831	I	***892.529102***	446.768189	875.502553	438.254915	7
8	861.425364	431.216320	844.398815	422.703046	843.414799	422.211038	F	***779.445038***	390.226157	762.418489	381.712883	6
9	989.483942	495.245609	972.457393	486.732335	971.473377	486.240327	Q	***632.376624***	316.691950	615.350075	308.178676	5
10	1102.568006	551.787641	1085.541457	543.274367	1084.557441	542.782358	L	***504.318046***	252.662661	487.291497	244.149386	4
11	1199.620770	600.314023	1182.594221	591.800749	1181.610205	591.308741	P	***391.233982***	196.120629	374.207433	187.607355	3
12	1346.689184	**673.848230**	1329.662635	665.334956	1328.678619	664.842948	F	***294.181218***	147.594247	277.154669	139.080973	2
13							K	147.112804	74.060040	130.086255	65.546765	1



RMS error 290 ppm



RMS error 290 ppm

NCBI **BLAST** search of SVGWGNIFQLPFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
65.8	1491.787445	0.003263	SVGWGNIFQLPFK
7.0	1491.804504	-0.013796	ELEDLIPKNHIR
1.8	1491.804535	-0.013827	QSTSQHIPKLPPK

Mascot: http://www.matrixscience.com/

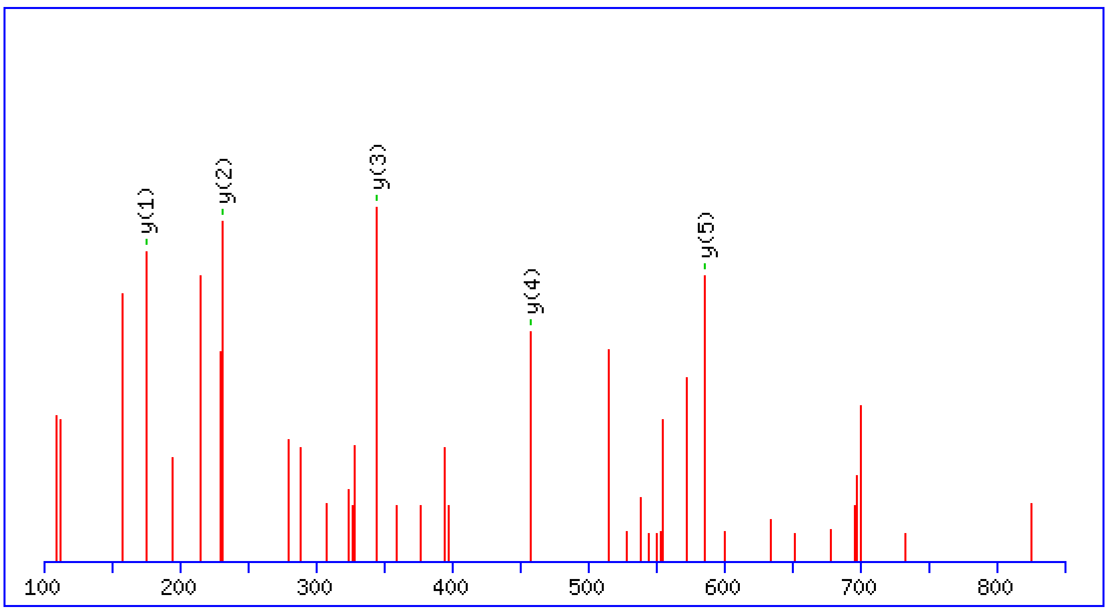
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLKPPGR**
Found in **WNT6_HUMAN**, Protein Wnt-6 OS=Homo sapiens GN=WNT6 PE=2 SV=2

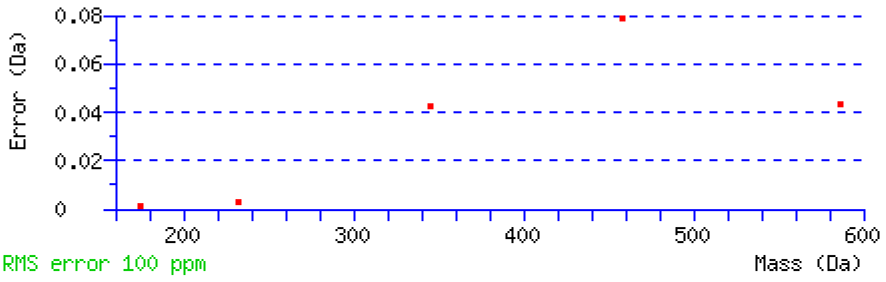
Match to Query 142: 799.458968 from(400.736760,2+) rtinseconds(1464) index(12319)
Title: Locus:1.1.1.2002.2
Data file 2011-11-10 - TFD - EP 3-2.mgf

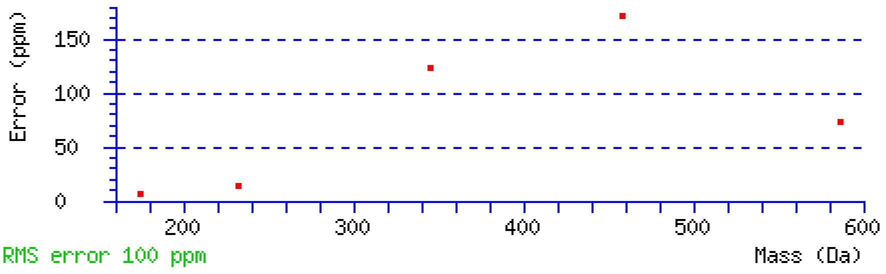
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 799.455200
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P4 : Oxidation (P)
P5 : Oxidation (P)
Ions Score: 41 **Expect:** 0.0016
Matches : 5/56 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	102.054955	51.531116			84.044390	42.525833	T					7
2	215.139019	108.073147			197.128454	99.067865	L	699.414801	350.211039	682.388252	341.697764	6
3	343.233982	172.120629	326.207433	163.607355	325.223417	163.115347	K	***586.330737***	293.669007	569.304188	285.155732	5
4	456.281661	228.644469	439.255112	220.131194	438.271096	219.639186	P	***458.235774***	229.621525	441.209225	221.108251	4
5	569.329340	285.168308	552.302791	276.655034	551.318775	276.163026	P	***345.188095***	173.097685	328.161546	164.584411	3
6	626.350804	313.679040	609.324255	305.165766	608.340239	304.673758	G	***232.140416***	116.573846	215.113867	108.060571	2
7							R	***175.118952***	88.063114	158.092403	79.549839	1





NCBI **BLAST** search of TLKPPGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.4	799.455200	0.003768	TLKPPGR
29.8	799.455185	0.003783	DLNILGR
25.2	799.455185	0.003783	AALSPLGR
24.9	799.466415	-0.007447	VARELGR
24.9	799.455200	0.003768	VLKDPGR
24.7	799.455200	0.003768	LGDLGLGR
21.7	799.455200	0.003768	VADLVAGR
19.3	799.455185	0.003783	VDAILNR
13.3	799.455200	0.003768	DQLVLGR
11.6	799.455200	0.003768	ITGLSPGR

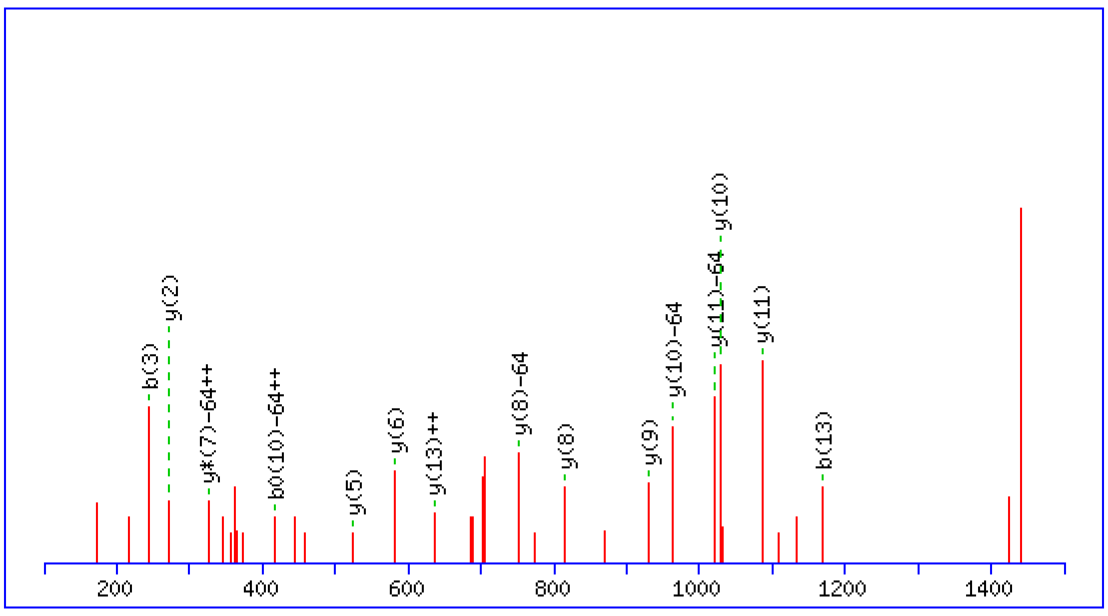
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TAALGPDSMGGPVPR**
Found in **YIF1A_HUMAN**, Protein YIF1A OS=Homo sapiens GN=YIF1A PE=1 SV=2

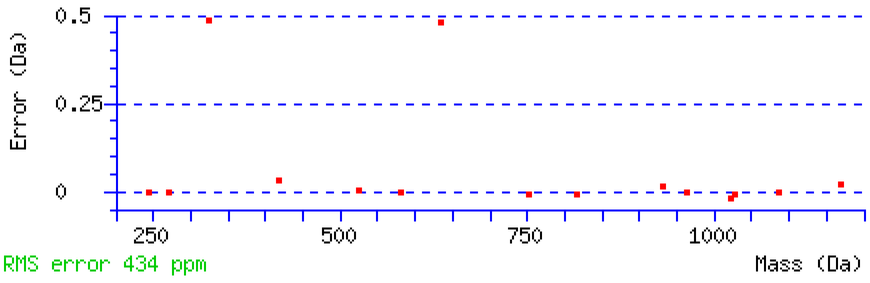
Match to Query 42755: 1440.699108 from(721.356830,2+) rtinseconds(1709) index(15492)
Title: Locus:1.1.1.1966.48
Data file 2011-11-10 - TFD - EP 4-5.mgf

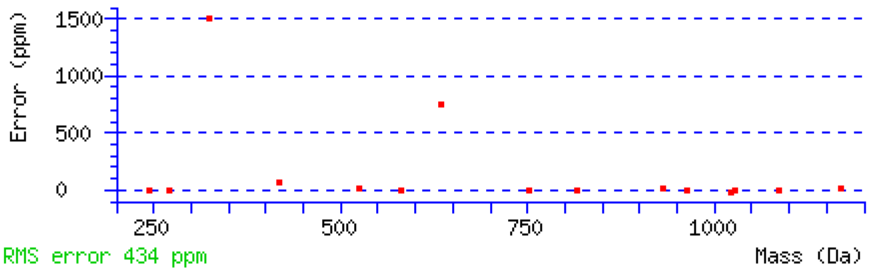
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1440.703125
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M9      : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 50  Expect: 2.4e-005
Matches : 15/196 fragment ions using 20 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116	84.044390	42.525833	T							15
2	173.092069	87.049672	155.081504	78.044390	A	1340.662713	670.834994	1323.636164	662.321720	1322.652148	661.829712	14
3	**244.129183**	122.568229	226.118618	113.562947	A	1269.625599	635.316438	1252.599050	626.803163	1251.615034	626.311155	13
4	357.213247	179.110261	339.202682	170.104979	L	1198.588485	599.797881	1181.561936	591.284606	1180.577920	590.792598	12
5	414.234711	207.620993	396.224146	198.615711	G	***1085.504421***	543.255848	1068.477872	534.742574	1067.493856	534.250566	11
6	511.287475	256.147375	493.276910	247.142093	P	***1028.482957***	514.745116	1011.456408	506.231842	1010.472392	505.739834	10
7	626.314418	313.660847	608.303853	304.655564	D	***931.430193***	466.218735	914.403644	457.705460	913.419628	457.213452	9
8	713.346446	357.176861	695.335881	348.171578	S	***816.403250***	408.705263	799.376701	400.191989	798.392685	399.699981	8
9	860.381846	430.694561	842.371281	421.689278	M	729.371222	365.189249	712.344673	356.675975			7
10	917.403310	459.205293	899.392745	450.200010	G	***582.335822***	291.671549	565.309273	283.158275			6
11	974.424774	487.716025	956.414209	478.710742	G	***525.314358***	263.160817	508.287809	254.647543			5
12	1071.477538	536.242407	1053.466973	527.237124	P	468.292894	234.650085	451.266345	226.136810			4
13	**1170.545952**	585.776614	1152.535387	576.771331	V	371.240130	186.123703	354.213581	177.610429			3
14	1267.598716	634.302996	1249.588151	625.297713	P	***272.171716***	136.589496	255.145167	128.076221			2
15					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of TAALGPDSMGGPVPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.8	1440.703125	-0.004017	TAALGPDSMGGPVPR
20.5	1440.703125	-0.004017	TAALGPDSMGGPVPR
20.4	1440.703125	-0.004017	TAALGPDSMGGPVPR
10.2	1440.703125	-0.004017	TAALGPDSMGGPVPR
0.5	1440.695724	0.003384	DSGPGAGAGVGELGAAR

Mascot: http://www.matrixscience.com/

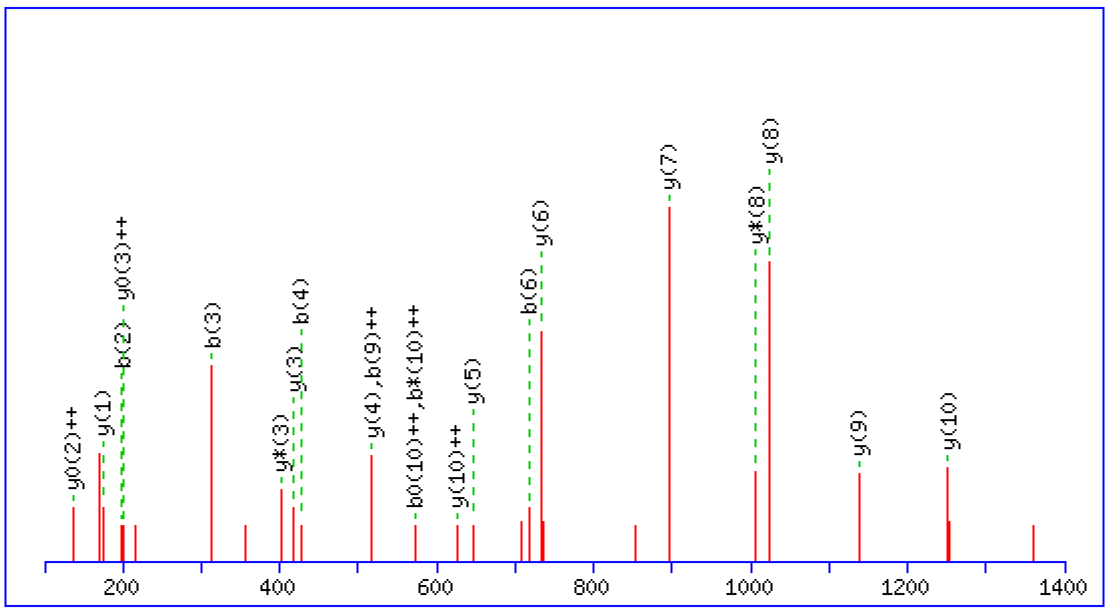
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVNLQYSEVQDR**
Found in **YPEL5_HUMAN**, Protein yippee-like 5 OS=Homo sapiens GN=YPEL5 PE=2 SV=1

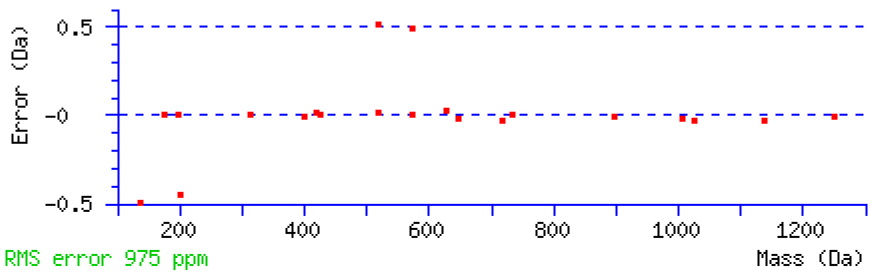
Match to Query 38024: 1448.727528 from(725.371040,2+) rtinseconds(2060) index(16255)
Title: Locus:1.1.1.2240.47
Data file 2011-11-10 - TFD - EP 4-7.mgf

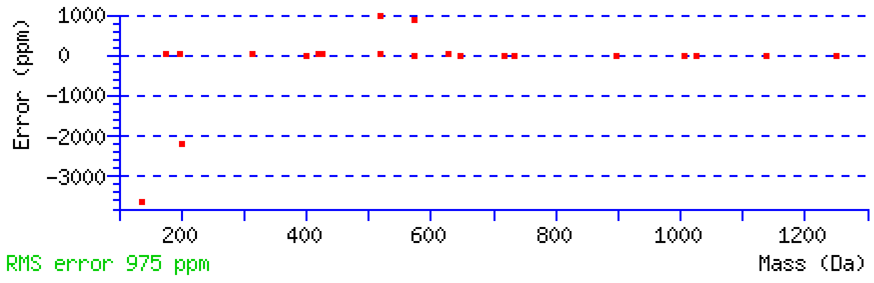
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1448.725952
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 74 **Expect:** 1.3e-006
Matches : 21/114 fragment ions using 26 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	100.075690	50.541483					V							12
2	**199.144104**	100.075690					V	1350.664820	675.836048	1333.638271	667.322774	1332.654255	666.830766	11
3	**313.187031**	157.097153	296.160482	148.583879			N	***1251.596406***	626.301841	1234.569857	617.788567	1233.585841	617.296559	10
4	**426.271095**	213.639186	409.244546	205.125911			L	***1137.553479***	569.280378	1120.526930	560.767103	1119.542914	560.275095	9
5	554.329673	277.668475	537.303124	269.155200			Q	***1024.469415***	512.738346	1007.442866	504.225071	1006.458850	503.733063	8
6	**717.393002**	359.200139	700.366453	350.686865			Y	***896.410837***	448.709057	879.384288	440.195782	878.400272	439.703774	7
7	804.425030	402.716153	787.398481	394.202879	786.414465	393.710871	S	***733.347508***	367.177392	716.320959	358.664118	715.336943	358.172110	6
8	933.467623	467.237450	916.441074	458.724175	915.457058	458.232167	E	***646.315480***	323.661378	629.288931	315.148104	628.304915	314.656096	5
9	1032.536037	516.771657	1015.509488	508.258382	1014.525472	507.766374	V	***517.272887***	259.140082	500.246338	250.626807	499.262322	250.134799	4
10	1160.594615	580.800946	1143.568066	572.287671	1142.584050	571.795663	Q	***418.204473***	209.605875	401.177924	201.092600	400.193908	200.600592	3
11	1275.621558	638.314417	1258.595009	629.801143	1257.610993	629.309135	D	290.145895	145.576585	273.119346	137.063311	272.135330	136.571303	2
12							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of VVNLQYSEVQDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
74.2	1448.725952	0.001576	VVNLQYSEVQDR
8.8	1448.716034	0.011494	GPSAELASRYWGR
5.5	1448.725967	0.001561	GPGLLEPTDAGGPPR
1.4	1448.729309	-0.001781	MAADTQVSETLKR
0.3	1448.714706	0.012822	GLSIPRADTLDEY

Mascot: http://www.matrixscience.com/

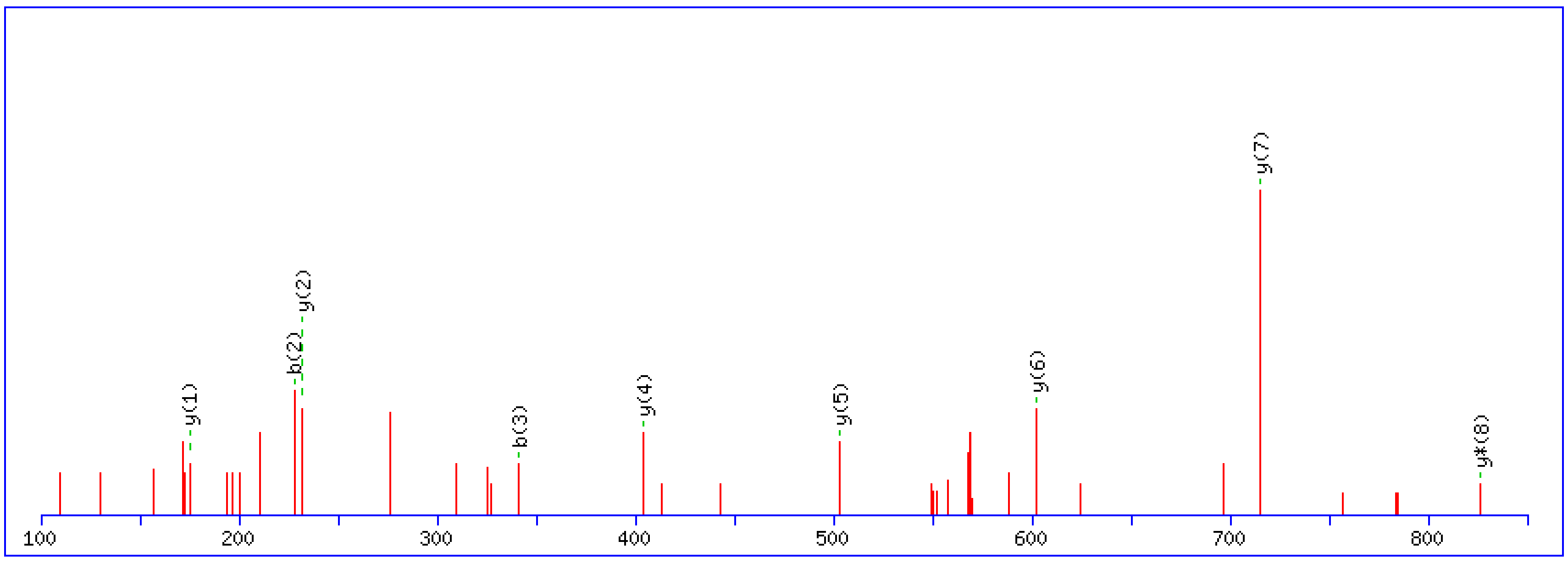
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VQLVVGDGR**
Found in **PIMT_HUMAN**, Protein-L-isoaspartate(D-aspartate) O-methyltransferase OS=Homo sapiens GN=PCMT1 PE=1 SV=4

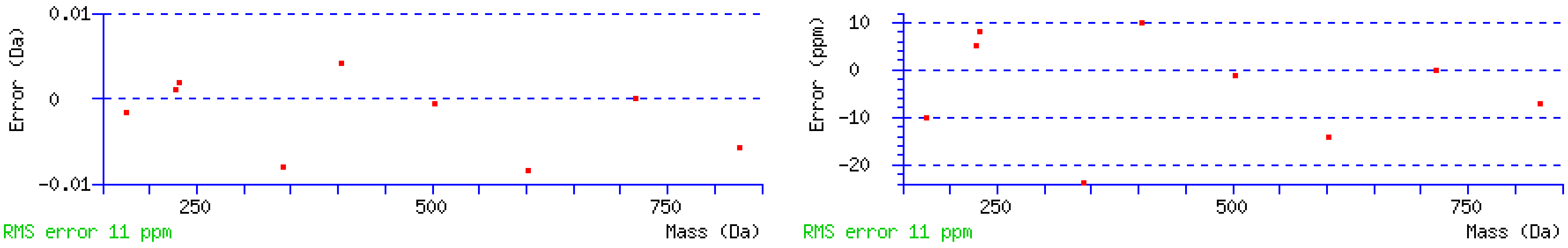
Match to Query 9381: 941.526548 from(471.770550,2+) rtinseconds(1600) index(15552)
Title: Locus:1.1.1.998.15
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 1.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 941.529449
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 44 **Expect:** 0.00046
Matches : 9/78 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							9
2	**228.134268**	114.570772	211.107719	106.057498			Q	843.468293	422.237785	826.441744	413.724510	825.457728	413.232502	8
3	**341.218332**	171.112804	324.191783	162.599530			L	***715.409715***	358.208496	698.383166	349.695221	697.399150	349.203213	7
4	440.286746	220.647011	423.260197	212.133737			V	***602.325651***	301.666464	585.299102	293.153189	584.315086	292.661181	6
5	539.355160	270.181218	522.328611	261.667944			V	***503.257237***	252.132257	486.230688	243.618982	485.246672	243.126974	5
6	596.376624	298.691950	579.350075	290.178676			G	***404.188823***	202.598050	387.162274	194.084775	386.178258	193.592767	4
7	711.403567	356.205422	694.377018	347.692147	693.393002	347.200139	D	347.167359	174.087318	330.140810	165.574043	329.156794	165.082035	3
8	768.425031	384.716154	751.398482	376.202879	750.414466	375.710871	G	***232.140416***	116.573846	215.113867	108.060572			2
9							R	***175.118952***	88.063114	158.092403	79.549840			1



NCBI **BLAST** search of VQLVVGDGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.1	941.529449	-0.002901	VQLVVGDGR
8.1	941.529404	-0.002856	ARPEVNLK
7.9	941.529404	-0.002856	LNIQGLER
7.9	941.529404	-0.002856	LNPADIKR
4.3	941.529434	-0.002886	AGVQSLVPR
3.0	941.529419	-0.002871	GPSIPAKTR
2.7	941.529434	-0.002886	VNLVLGDGR
2.1	941.529404	-0.002856	KEPALTAGR
2.0	941.533447	-0.006899	FILPAPPR
2.0	941.533447	-0.006899	FILPAPPR

Mascot: http://www.matrixscience.com/

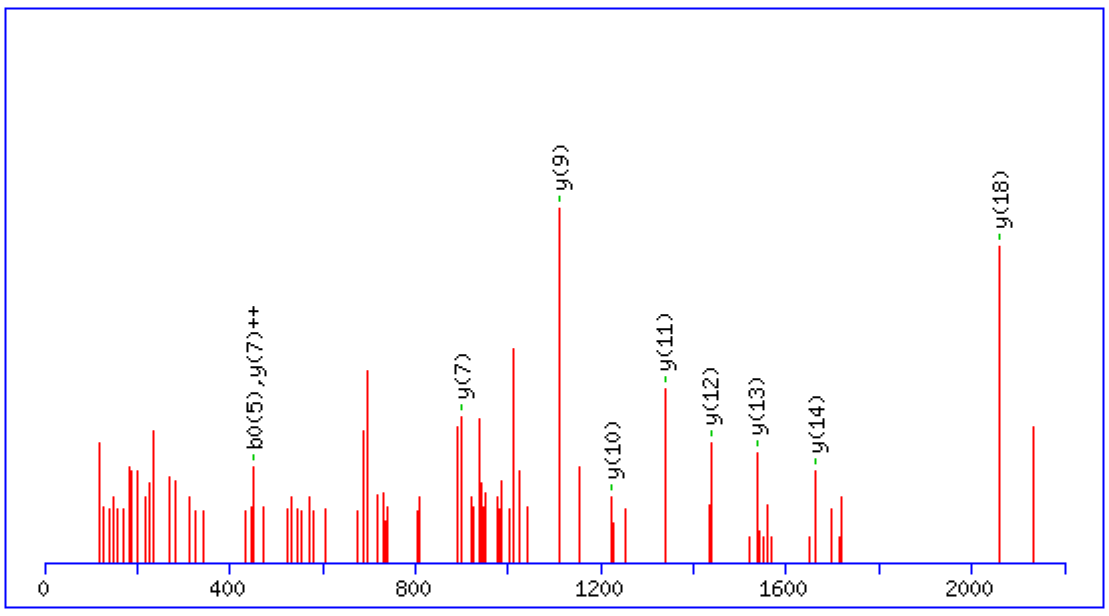
Mascot Search Results

Peptide View

MS/MS Fragmentation of GQPSVLQVVNLPIVERPVCK
Found in THRB_HUMAN, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

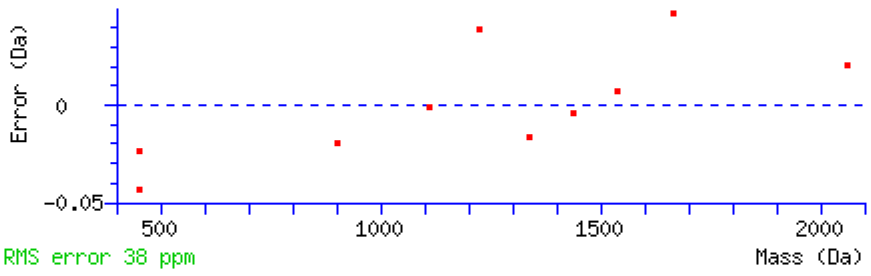
Match to Query 68142: 2245.265442 from(749.429090,3+) rtinseconds(3328) index(46687)
Title: Locus:1.1.1.2651.35
Data file 2011-11-12 - TFD - EP 6-2.mgf

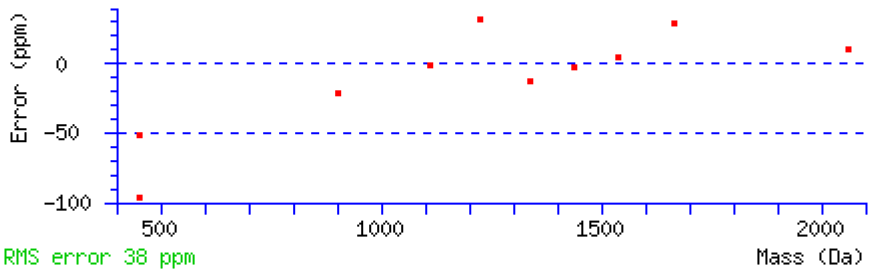
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2245.261658
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 38 **Expect:** 0.00034
Matches : 10/210 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	58.028740	29.518008					G							20
2	186.087318	93.547297	169.060769	85.034023			Q	2189.247472	1095.127374	2172.220923	1086.614099	2171.236907	1086.122091	19
3	283.140082	142.073679	266.113533	133.560405			P	***2061.188894***	1031.098085	2044.162345	1022.584810	2043.178329	1022.092802	18
4	370.172110	185.589693	353.145561	177.076419	352.161545	176.584411	S	1964.136130	982.571703	1947.109581	974.058428	1946.125565	973.566420	17
5	469.240524	235.123900	452.213975	226.610626	451.229959	226.118618	V	1877.104102	939.055689	1860.077553	930.542414	1859.093537	930.050406	16
6	582.324588	291.665932	565.298039	283.152658	564.314023	282.660650	L	1778.035688	889.521482	1761.009139	881.008207	1760.025123	880.516199	15
7	710.383166	355.695221	693.356617	347.181947	692.372601	346.689939	Q	***1664.951624***	832.979450	1647.925075	824.466175	1646.941059	823.974167	14
8	809.451580	405.229428	792.425031	396.716154	791.441015	396.224146	V	***1536.893046***	768.950161	1519.866497	760.436886	1518.882481	759.944878	13
9	908.519994	454.763635	891.493445	446.250361	890.509429	445.758353	V	***1437.824632***	719.415954	1420.798083	710.902679	1419.814067	710.410671	12
10	1022.562921	511.785099	1005.536372	503.271824	1004.552356	502.779816	N	***1338.756218***	669.881747	1321.729669	661.368472	1320.745653	660.876464	11
11	1135.646985	568.327130	1118.620436	559.813856	1117.636420	559.321848	L	***1224.713291***	612.860283	1207.686742	604.347009	1206.702726	603.855001	10
12	1232.699749	616.853512	1215.673200	608.340238	1214.689184	607.848230	P	***1111.629227***	556.318251	1094.602678	547.804977	1093.618662	547.312969	9
13	1345.783813	673.395544	1328.757264	664.882270	1327.773248	664.390262	I	1014.576463	507.791869	997.549914	499.278595	996.565898	498.786587	8
14	1444.852227	722.929751	1427.825678	714.416477	1426.841662	713.924469	V	***901.492399***	451.249838	884.465850	442.736563	883.481834	442.244555	7
15	1573.894820	787.451048	1556.868271	778.937773	1555.884255	778.445765	E	802.423985	401.715630	785.397436	393.202356	784.413420	392.710348	6
16	1729.995931	865.501603	1712.969382	856.988329	1711.985366	856.496321	R	673.381392	337.194334	656.354843	328.681060			5
17	1827.048695	914.027985	1810.022146	905.514711	1809.038130	905.022703	P	517.280281	259.143779	500.253732	250.630504			4
18	1926.117109	963.562192	1909.090560	955.048918	1908.106544	954.556910	V	420.227517	210.617396	403.200968	202.104122			3
19	2100.163408	1050.585342	2083.136859	1042.072067	2082.152843	1041.580059	C	321.159103	161.083189	304.132554	152.569915			2
20							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of GQPSVLQVVNLPIVERPVCK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.6	2245.261658	0.003784	GQPSVLQVVNLPIVERPVCK

Mascot: http://www.matrixscience.com/

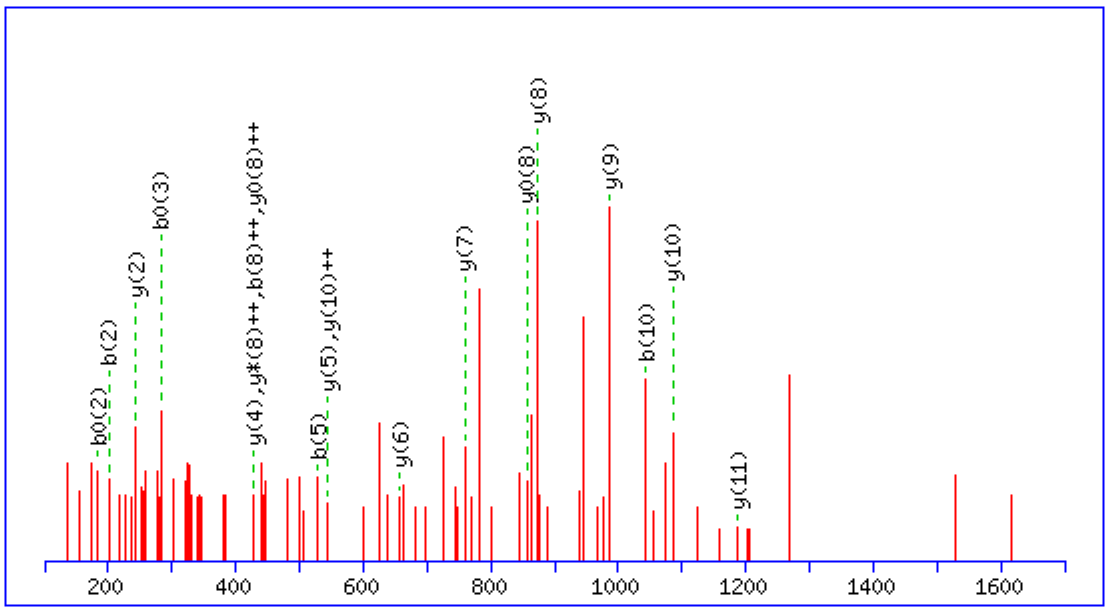
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VTVLDTNDNAPK**
Found in **PCDH1_HUMAN**, Protocadherin-1 OS=Homo sapiens GN=PCDH1 PE=1 SV=2

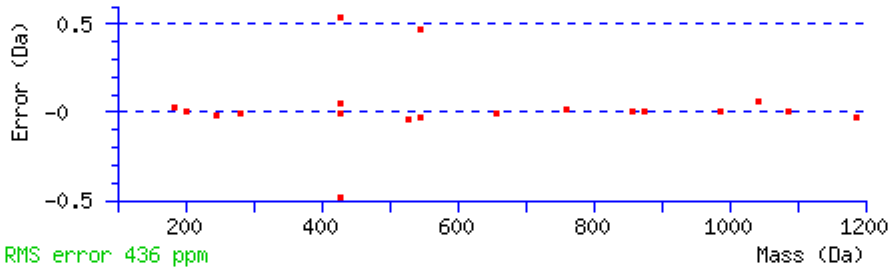
Match to Query 31499: 1285.650728 from(643.832640,2+) rtinseconds(1555) index(11268)
Title: Locus:1.1.1.2154.45
Data file 2011-11-12 - TFD - EP 5-1.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●

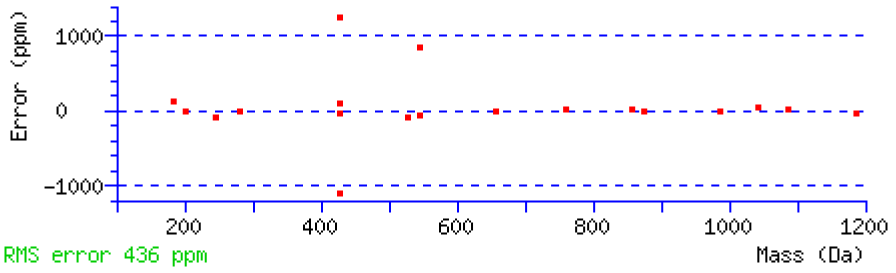


Monoisotopic mass of neutral peptide Mr(calc): 1285.651398
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 46 **Expect:** 0.00031
Matches : 19/110 fragment ions using 45 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	100.075690	50.541483					V							12
2	**201.123369**	101.065322			183.112804	92.060040	T	***1187.590258***	594.298767	1170.563709	585.785493	1169.579693	585.293484	11
3	300.191783	150.599529			282.181218	141.594247	V	***1086.542579***	543.774927	1069.516030	535.261653	1068.532014	534.769645	10
4	413.275847	207.141561			395.265282	198.136279	L	***987.474165***	494.240721	970.447616	485.727446	969.463600	485.235438	9
5	**528.302790**	264.655033			510.292225	255.649751	D	***874.390101***	437.698689	857.363552	429.185414	856.379536	428.693406	8
6	629.350469	315.178873			611.339904	306.173590	T	***759.363158***	380.185217	742.336609	371.671943	741.352593	371.179935	7
7	743.393396	372.200336	726.366847	363.687062	725.382831	363.195054	N	***658.315479***	329.661378	641.288930	321.148103	640.304914	320.656095	6
8	858.420339	429.713808	841.393790	421.200533	840.409774	420.708525	D	***544.272552***	272.639914	527.246003	264.126640	526.261987	263.634632	5
9	972.463266	486.735271	955.436717	478.221996	954.452701	477.729988	N	***429.245609***	215.126442	412.219060	206.613168			4
10	**1043.500380**	522.253828	1026.473831	513.740554	1025.489815	513.248545	A	315.202682	158.104979	298.176133	149.591704			3
11	1140.553144	570.780210	1123.526595	562.266936	1122.542579	561.774927	P	***244.165568***	122.586422	227.139019	114.073148			2
12							K	147.112804	74.060040	130.086255	65.546765			1



RMS error 436 ppm



RMS error 436 ppm

NCBI **BLAST** search of VTVLDTNDNAPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.4	1285.651398	-0.000670	VTVLDTNDNAPK
15.2	1285.641510	0.009218	QDVYGPQPQVR

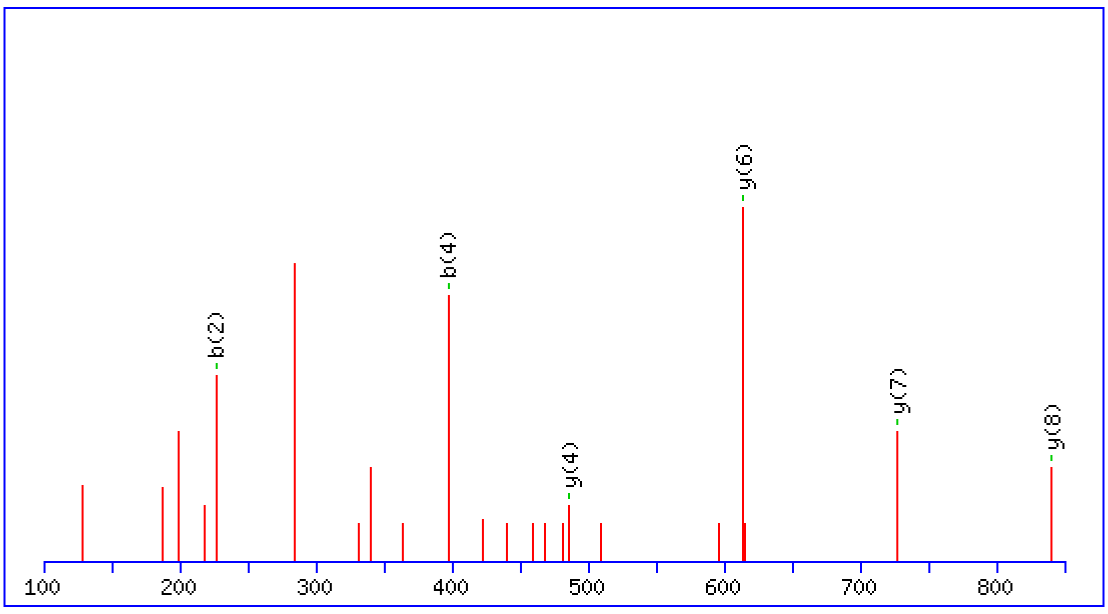
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLLGATLPR**
Found in **MOS_HUMAN**, Proto-oncogene serine/threonine-protein kinase mos OS=Homo sapiens GN=MOS PE=2 SV=1

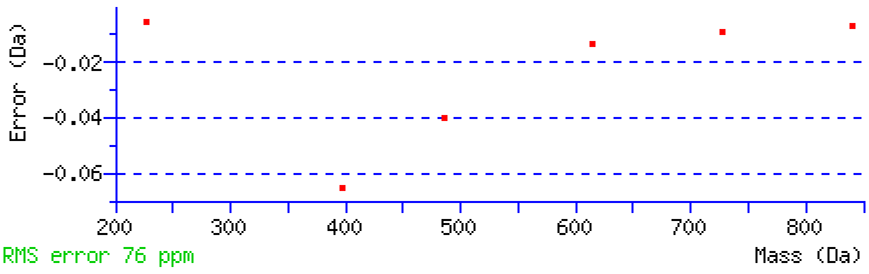
Match to Query 13140: 952.599748 from(477.307150,2+) rtinseconds(3129) index(40370)
Title: Locus:1.1.1.2465.7
Data file 2011-11-14 - TFD - EP 8-6.mgf

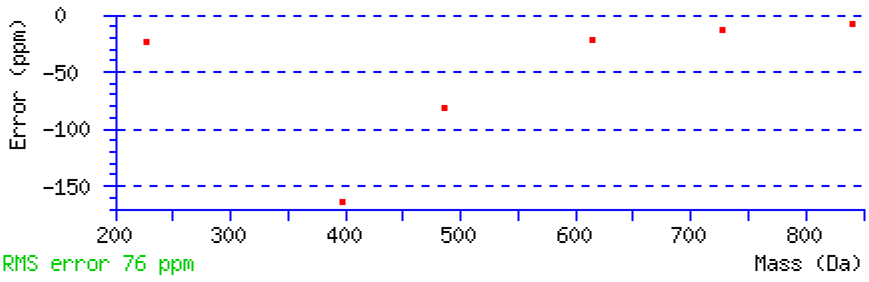
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 952.606934
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 34 Expect: 0.00096
Matches : 6/64 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308			L							9
2	**227.175404**	114.091340			L	***840.530165***	420.768721	823.503616	412.255446	822.519600	411.763438	8
3	340.259468	170.633372			L	***727.446101***	364.226689	710.419552	355.713414	709.435536	355.221406	7
4	**397.280932**	199.144104			G	***614.362037***	307.684657	597.335488	299.171382	596.351472	298.679374	6
5	468.318046	234.662661			A	557.340573	279.173925	540.314024	270.660650	539.330008	270.168642	5
6	569.365725	285.186501	551.355160	276.181218	T	***486.303459***	243.655367	469.276910	235.142093	468.292894	234.650085	4
7	682.449789	341.728533	664.439224	332.723250	L	385.255780	193.131528	368.229231	184.618253			3
8	779.502553	390.254915	761.491988	381.249632	P	272.171716	136.589496	255.145167	128.076221			2
9					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LLLGATLPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.5	952.595688	0.004060	LLLPGELAK
34.0	952.606934	-0.007186	LLLGATLPR
29.1	952.595688	0.004060	LLIKEPPK
25.7	952.595688	0.004060	LLIKEPPK
22.2	952.595688	0.004060	IIIPEIQK
21.6	952.595703	0.004045	ILGILPPSK
21.2	952.595703	0.004045	ILGILPPSK
20.0	952.595688	0.004060	ILLLEAGPK
15.5	952.606934	-0.007186	EPLKVVLR
14.4	952.606918	-0.007170	LLIPNKQK

Mascot: http://www.matrixscience.com/

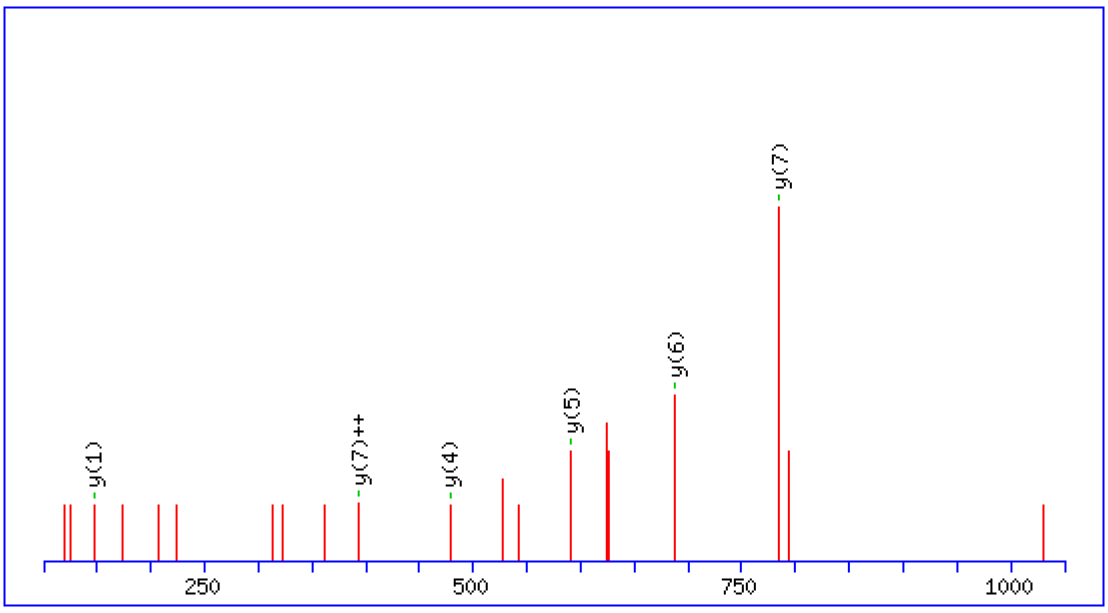
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FSPPPAMEK**
Found in **HDHD1_HUMAN**, Pseudouridine-5'-monophosphatase OS=Homo sapiens GN=HDHD1 PE=1 SV=3

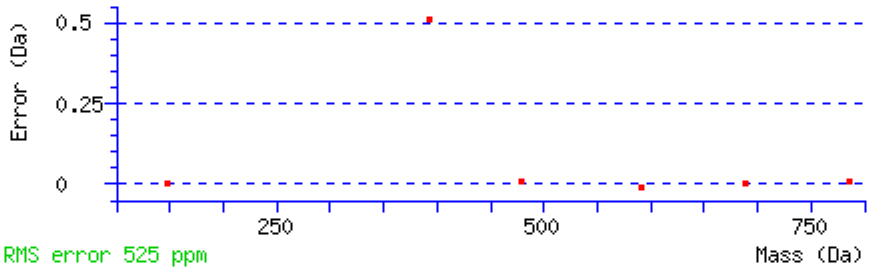
Match to Query 17744: 1018.487268 from(510.250910,2+) rtinseconds(1210) index(5938)
Title: Locus:1.1.1.1775.28
Data file 2011-11-10 - TFD - EP 4-5.mgf

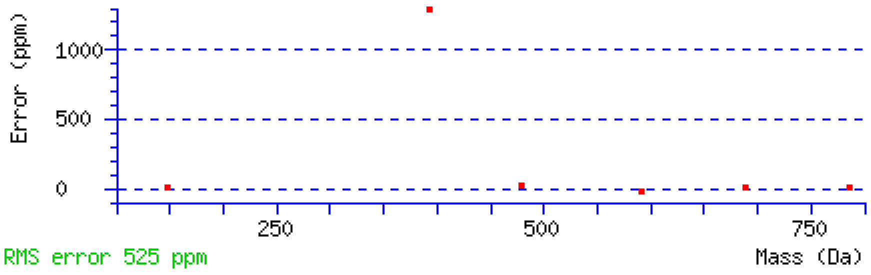
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1018.479355
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P5 : Oxidation (P)
Ions Score: 40 **Expect:** 0.0011
Matches : 6/76 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.075690	74.541483			F							9
2	235.107718	118.057497	217.097153	109.052214	S	872.418231	436.712754	855.391682	428.199479	854.407666	427.707471	8
3	332.160482	166.583879	314.149917	157.578596	P	***785.386203***	393.196740	768.359654	384.683465	767.375638	384.191457	7
4	429.213246	215.110261	411.202681	206.104978	P	***688.333439***	344.670358	671.306890	336.157083	670.322874	335.665075	6
5	542.260925	271.634101	524.250360	262.628818	P	***591.280675***	296.143976	574.254126	287.630701	573.270110	287.138693	5
6	613.298039	307.152658	595.287474	298.147375	A	***478.232996***	239.620136	461.206447	231.106861	460.222431	230.614853	4
7	744.338524	372.672900	726.327959	363.667618	M	407.195882	204.101579	390.169333	195.588304	389.185317	195.096296	3
8	873.381117	437.194197	855.370552	428.188914	E	276.155397	138.581336	259.128848	130.068062	258.144832	129.576054	2
9					K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of FSPPPAMEK
(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	1018.479355	0.007913	FSPPPAMEK
28.9	1018.479355	0.007913	FSPPPAMEK
24.8	1018.479355	0.007913	FSPPPAMEK
12.1	1018.479355	0.007913	FSPPPAMEK

Mascot: http://www.matrixscience.com/

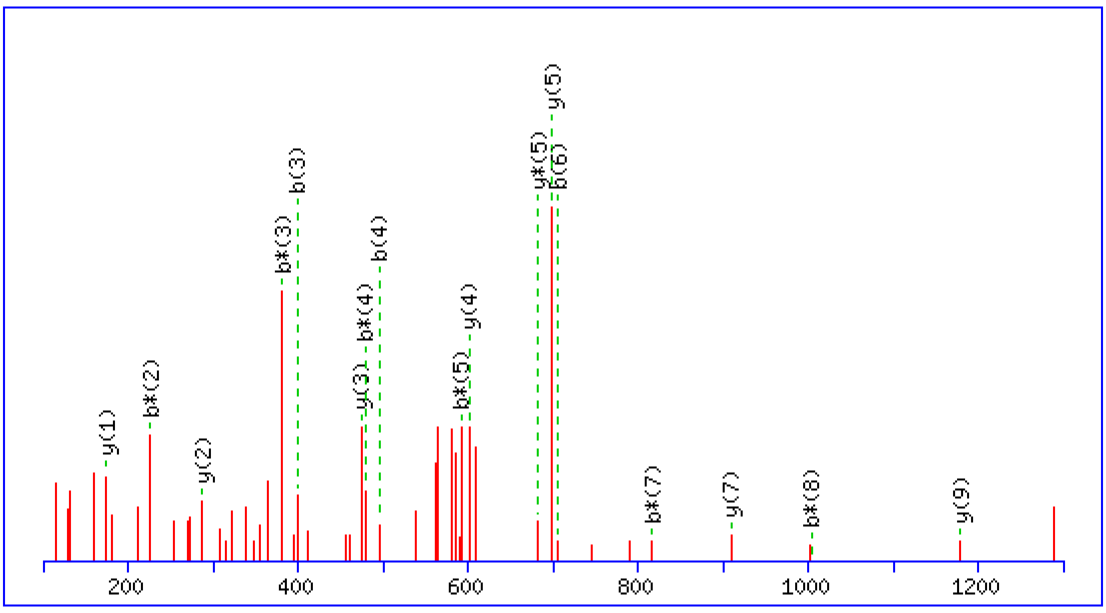
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of QNRPIPQWIR
Found in R39L5_HUMAN, Putative 60S ribosomal protein L39-like 5 OS=Homo sapiens GN=RPL39P5 PE=5 SV=2

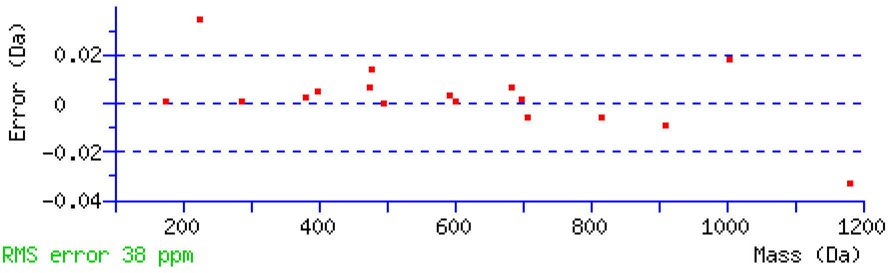
Match to Query 31350: 1306.726572 from(436.582800,3+) rtinseconds(2221) index(20599)
Title: Locus:1.1.1.2297.8
Data file 2011-11-13 - TFD - EP 7-7.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●

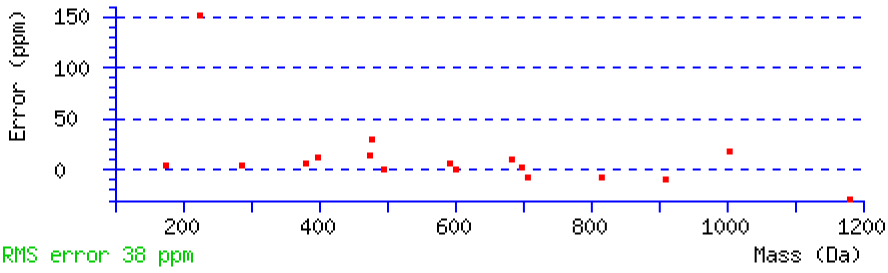


Monoisotopic mass of neutral peptide Mr(calc): 1306.725815
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 52 **Expect:** 1.7e-005
Matches : 17/72 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	129.065854	65.036565	112.039305	56.523291	Q					10
2	243.108781	122.058029	226.082232	113.544754	N	***1179.674537***	590.340907	1162.647988	581.827632	9
3	**399.209892**	200.108584	382.183343	191.595310	R	1065.631610	533.319443	1048.605061	524.806169	8
4	**496.262656**	248.634966	479.236107	240.121692	P	***909.530499***	455.268888	892.503950	446.755613	7
5	609.346720	305.176998	592.320171	296.663724	I	812.477735	406.742505	795.451186	398.229231	6
6	**706.399484**	353.703380	689.372935	345.190106	P	***699.393671***	350.200473	682.367122	341.687199	5
7	834.458062	417.732669	817.431513	409.219395	Q	***602.340907***	301.674091	585.314358	293.160817	4
8	1020.537375	510.772326	1003.510826	502.259051	W	***474.282329***	237.644802	457.255780	229.131528	3
9	1133.621439	567.314358	1116.594890	558.801083	I	***288.203016***	144.605146	271.176467	136.091871	2
10					R	***175.118952***	88.063114	158.092403	79.549839	1



RMS error 38 ppm



RMS error 38 ppm

NCBI **BLAST** search of QNRPIPQWIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.9	1306.725815	0.000757	QNRPIPQWIR
0.9	1306.724487	0.002085	TVSFESKIQLR

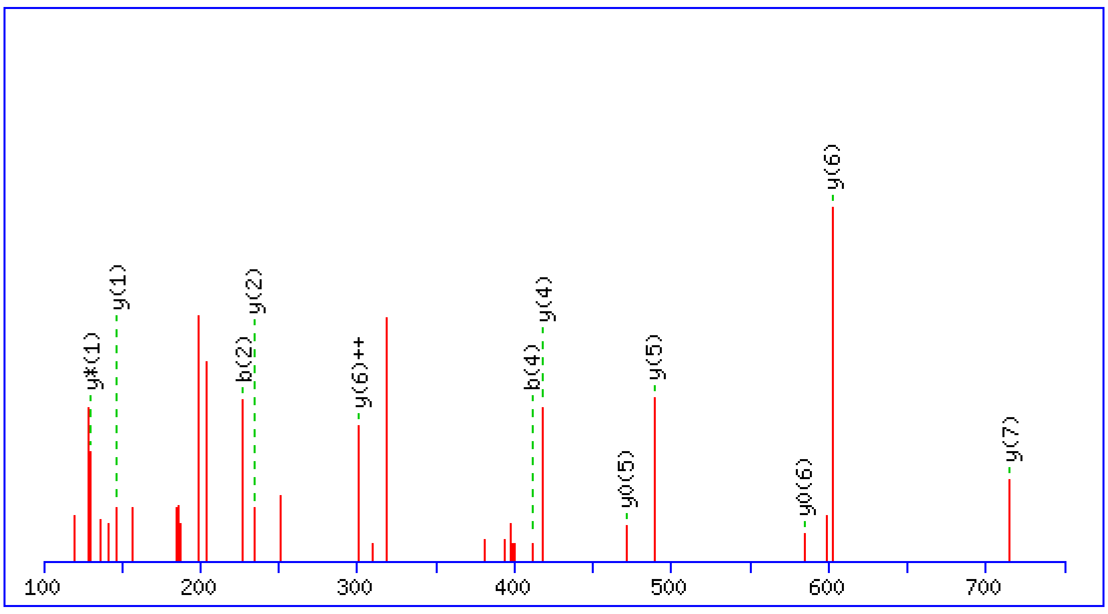
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLLAPSSK**
Found in **MOV10_HUMAN**, Putative helicase MOV-10 OS=Homo sapiens GN=MOV10 PE=1 SV=2

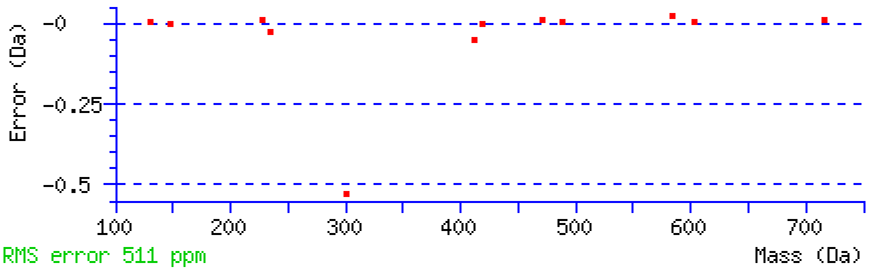
Match to Query 2187: 827.512428 from(414.763490,2+) rtinseconds(1996) index(18369)
Title: Locus:1.1.1.2346.4
Data file 2011-11-12 - TFD - EP 5-5.mgf

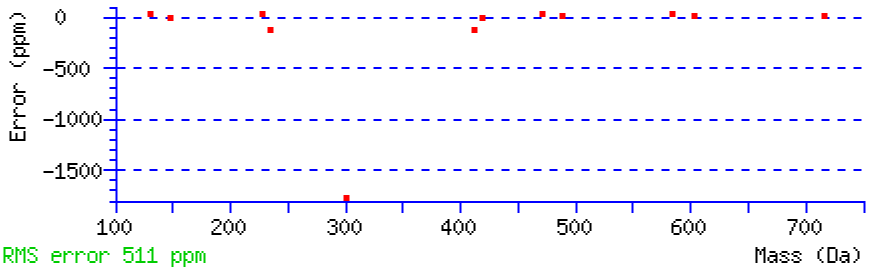
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 827.511627
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 37  Expect: 0.0007
Matches : 12/58 fragment ions using 24 most intense peaks   (help)
```

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308			L							8
2	**227.175404**	114.091340			L	***715.434866***	358.221071	698.408317	349.707797	697.424301	349.215789	7
3	340.259468	170.633372			L	***602.350802***	301.679039	585.324253	293.165765	584.340237	292.673757	6
4	**411.296582**	206.151929			A	***489.266738***	245.137007	472.240189	236.623732	471.256173	236.131724	5
5	508.349346	254.678311			P	***418.229624***	209.618450	401.203075	201.105175	400.219059	200.613167	4
6	595.381374	298.194325	577.370809	289.189043	S	321.176860	161.092068	304.150311	152.578793	303.166295	152.086785	3
7	682.413402	341.710339	664.402837	332.705057	S	***234.144832***	117.576054	217.118283	109.062779	216.134267	108.570771	2
8					K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of LLLAPSSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.9	827.511627	0.000801	LLLAPSSK
14.0	827.511627	0.000801	LLLLNDK
10.7	827.511627	0.000801	LLPLASSK
7.1	827.511642	0.000786	PIVDKLK
6.9	827.511627	0.000801	EPTKLLK
5.9	827.511627	0.000801	IIPTKEK
5.9	827.511642	0.000786	ILDLVQK
5.3	827.511642	0.000786	LLVKDPK
4.7	827.511642	0.000786	IPQILTK
4.4	827.511627	0.000801	IIENLVK

Mascot: http://www.matrixscience.com/

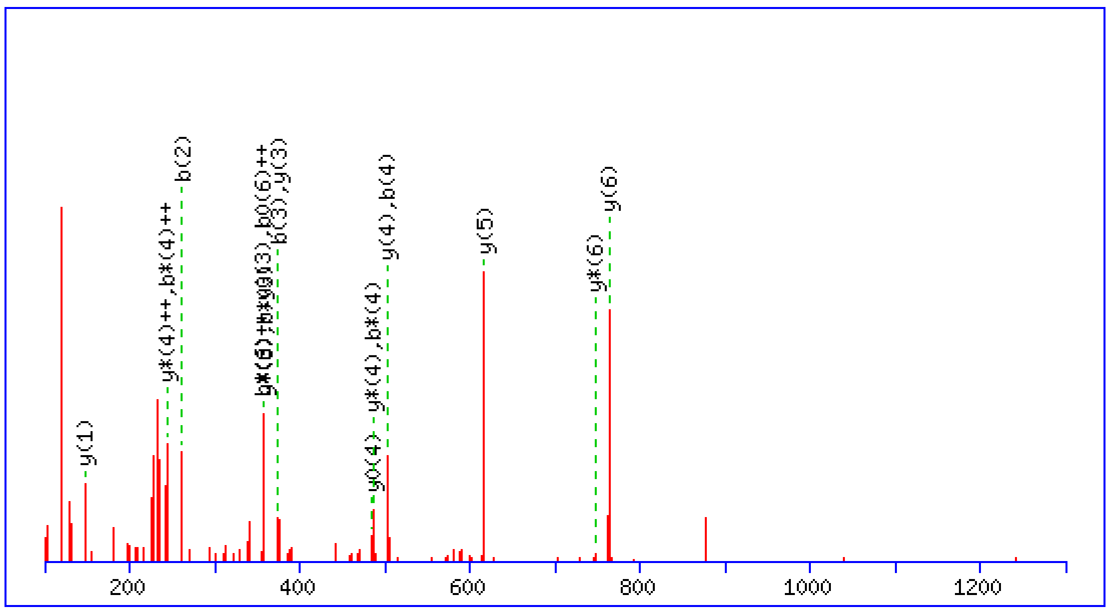
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IFNKVEK**
Found in **NSUN6_HUMAN**, Putative methyltransferase NSUN6 OS=Homo sapiens GN=NSUN6 PE=1 SV=1

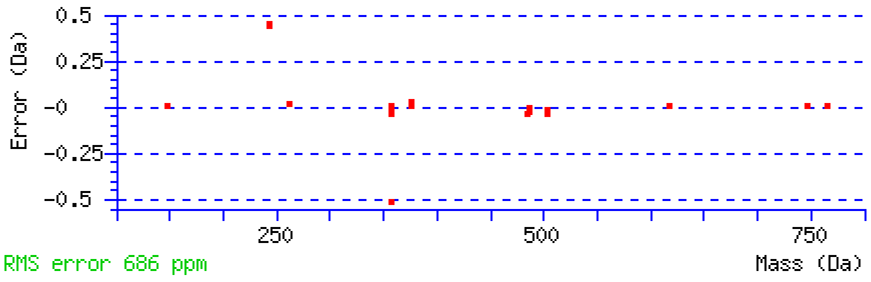
Match to Query 7422: 876.513628 from(439.264090,2+) rtinseconds(2486) index(30191)
Title: Locus:1.1.1.2166.7
Data file 2011-11-12 - TFD - EP 5-6.mgf

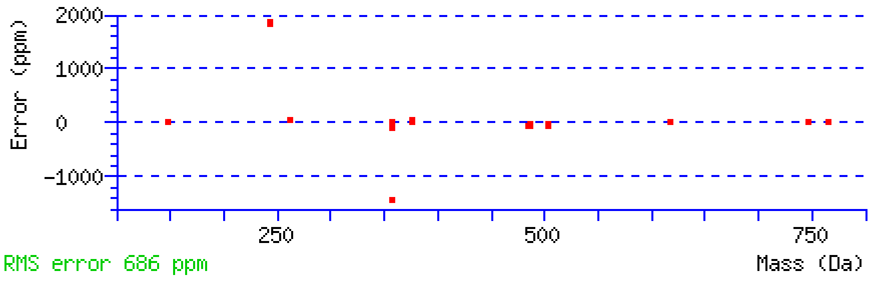
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 876.506882
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 31  Expect: 0.0048
Matches : 19/56 fragment ions using 21 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					**I**							7
2	**261.159754**	131.083515					**F**	***764.430115***	382.718696	747.403566	374.205421	746.419550	373.713413	6
3	**375.202681**	188.104978	358.176132	179.591704			**N**	***617.361701***	309.184489	600.335152	300.671214	599.351136	300.179206	5
4	**503.297644**	252.152460	486.271095	243.639186			**K**	***503.318774***	252.163025	486.292225	243.649751	485.308209	243.157743	4
5	602.366058	301.686667	585.339509	293.173393			**V**	***375.223811***	188.115544	358.197262	179.602269	357.213246	179.110261	3
6	731.408651	366.207964	714.382102	357.694689	713.398086	357.202681	**E**	276.155397	138.581336	259.128848	130.068062	258.144832	129.576054	2
7							**K**	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of IFNKVEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.7	876.506882	0.006746	IFNKVEK
16.2	876.506882	0.006746	LFILESR
15.6	876.506882	0.006746	LVYQLNK
13.8	876.506882	0.006746	LDFKNIK
9.4	876.506882	0.006746	NLFLKDK
9.1	876.506882	0.006746	VEFKLNK
8.3	876.510239	0.003389	LLSKMASK
4.9	876.506882	0.006746	YPLLISR
3.6	876.506882	0.006746	KFINDIK
3.4	876.506882	0.006746	LFSKPASK

Mascot: http://www.matrixscience.com/

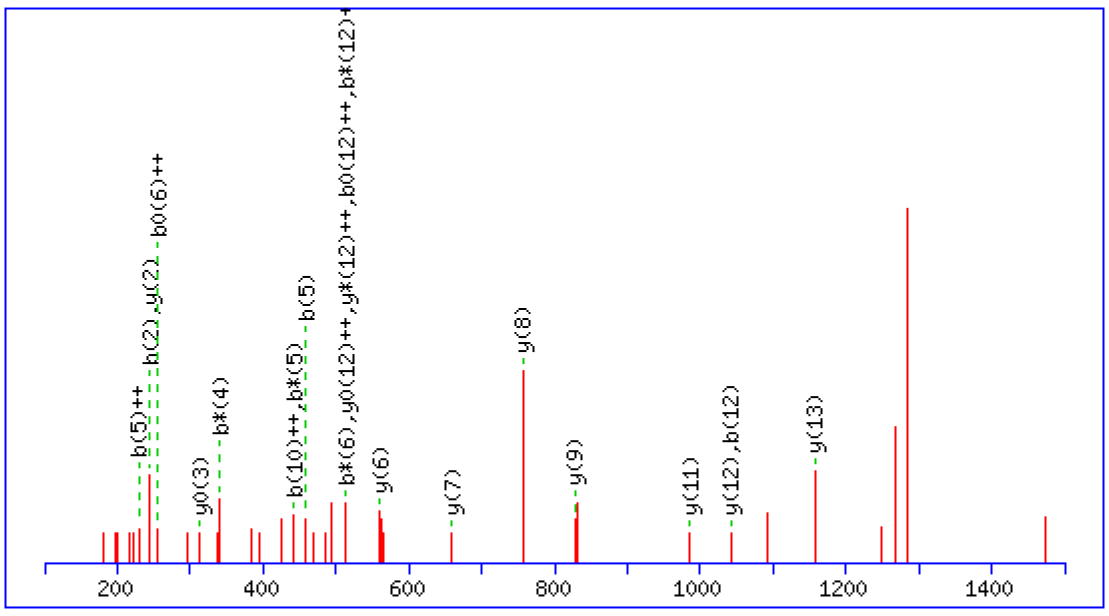
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QDGGTAPVASASPK**
Found in **RBM15_HUMAN**, Putative RNA-binding protein 15 OS=Homo sapiens GN=RBM15 PE=1 SV=2

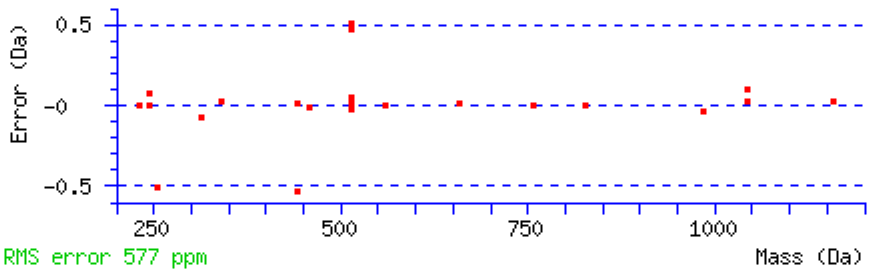
Match to Query 623486: 1284.634988 from(643.324770,2+) rtinseconds(1010) index(158460)
Title: Locus:1.1.1.1069.11
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

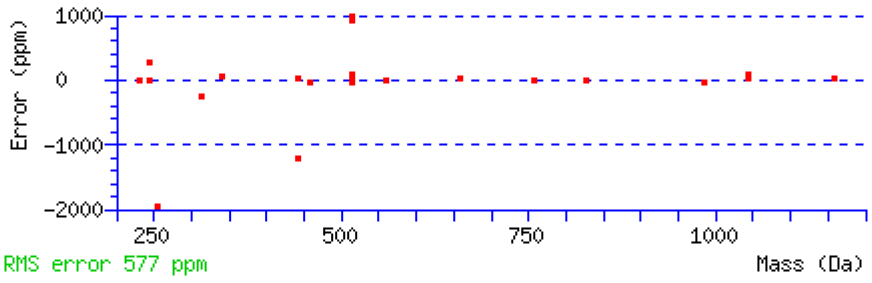
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1284.630997
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 63 **Expect:** 3.8e-006
Matches : 22/150 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	129.065854	65.036565	112.039305	56.523291			Q							14
2	**244.092797**	122.550037	227.066248	114.036762	226.082232	113.544754	D	***1157.579694***	579.293485	1140.553145	570.780211	1139.569129	570.288203	13
3	301.114261	151.060768	284.087712	142.547494	283.103696	142.055486	G	***1042.552751***	521.780014	1025.526202	513.266739	1024.542186	512.774731	12
4	358.135725	179.571500	341.109176	171.058226	340.125160	170.566218	G	***985.531287***	493.269282	968.504738	484.756007	967.520722	484.263999	11
5	**459.183404**	**230.095340**	442.156855	221.582066	441.172839	221.090058	T	928.509823	464.758550	911.483274	456.245275	910.499258	455.753267	10
6	530.220518	265.613897	513.193969	257.100623	512.209953	256.608615	A	***827.462144***	414.234710	810.435595	405.721436	809.451579	405.229428	9
7	627.273282	314.140279	610.246733	305.627005	609.262717	305.134997	P	***756.425030***	378.716153	739.398481	370.202879	738.414465	369.710871	8
8	726.341696	363.674486	709.315147	355.161212	708.331131	354.669204	V	***659.372266***	330.189771	642.345717	321.676497	641.361701	321.184489	7
9	797.378810	399.193043	780.352261	390.679769	779.368245	390.187761	A	***560.303852***	280.655564	543.277303	272.142290	542.293287	271.650282	6
10	884.410838	**442.709057**	867.384289	434.195783	866.400273	433.703775	S	489.266738	245.137007	472.240189	236.623733	471.256173	236.131725	5
11	955.447952	478.227614	938.421403	469.714339	937.437387	469.222332	A	402.234710	201.620993	385.208161	193.107719	384.224145	192.615711	4
12	**1042.479980**	521.743628	1025.453431	513.230354	1024.469415	512.738346	S	331.197596	166.102436	314.171047	157.589162	313.187031	157.097154	3
13	1139.532744	570.270010	1122.506195	561.756736	1121.522179	561.264728	P	***244.165568***	122.586422	227.139019	114.073148			2
14							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of QDGGTAPVASASPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
62.6	1284.630997	0.003991	QDGGTAPVASASPK
4.5	1284.642197	-0.007209	ENRNLDNVSPK
3.0	1284.628494	0.006494	FRGPAPPPNAVM
3.0	1284.628494	0.006494	FRGPAPPPNAVM
2.8	1284.642212	-0.007224	QSPSRSSSPQPK
1.7	1284.638397	-0.003409	GAVLTTTQYGKM
0.7	1284.630997	0.003991	QNSPVAPTAQPK
0.6	1284.635696	-0.000708	SRAPACLGSGGPR
0.1	1284.635681	-0.000693	MERPPPRAAGR

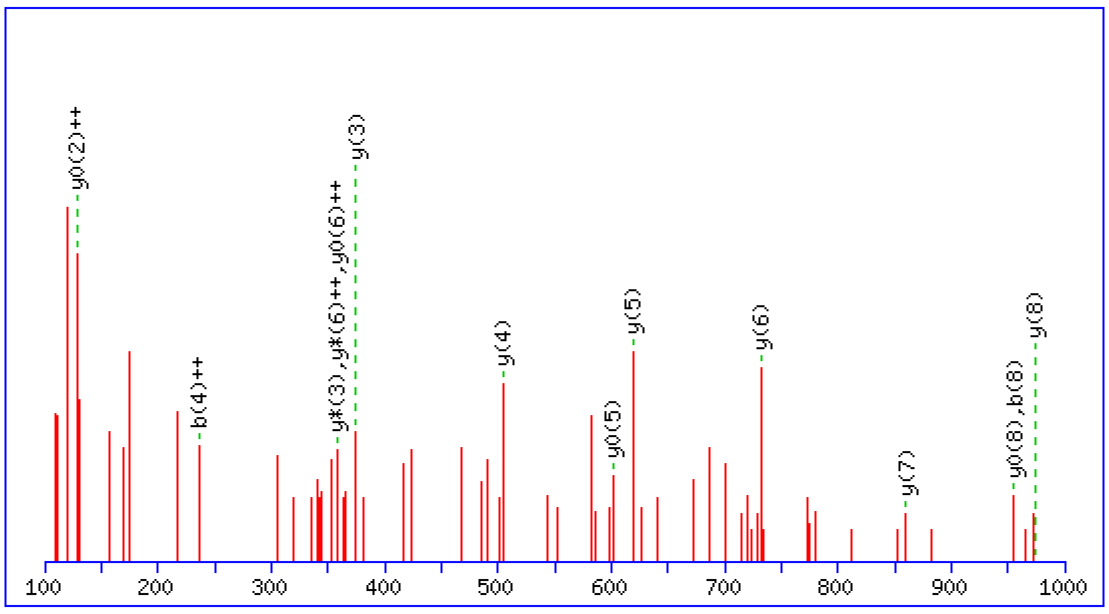
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LDQPKLDEVTR**
Found in **RB15B_HUMAN**, Putative RNA-binding protein 15B OS=Homo sapiens GN=RBM15B PE=1 SV=3

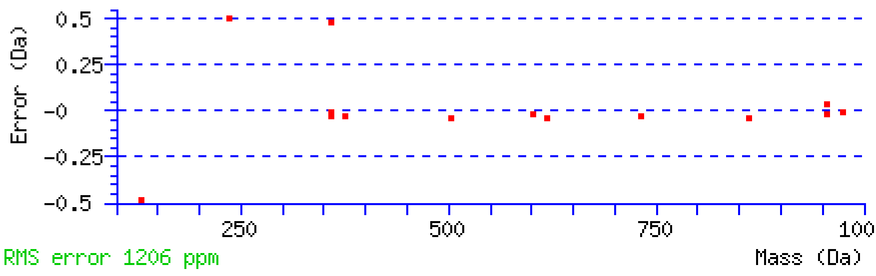
Match to Query 30836: 1328.692482 from(443.904770,3+) rtinseconds(2091) index(24525)
Title: Locus:1.1.1.2285.9
Data file 2011-11-10 - TFD - EP 4-3.mgf

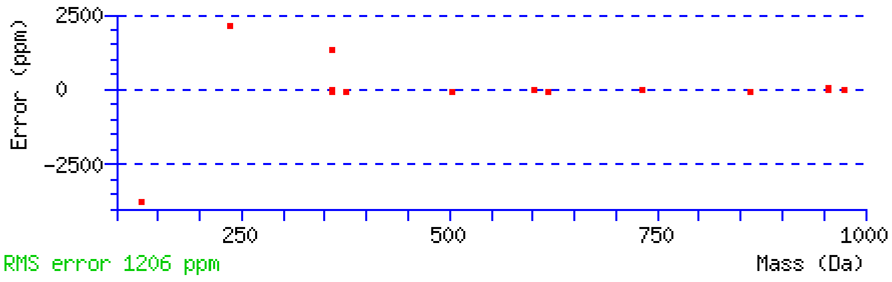
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1328.693588
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P4      : Oxidation (P)
Ions Score: 34  Expect: 0.0059
Matches : 14/112 fragment ions using 18 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							11
2	229.118283	115.062779			211.107718	106.057497	D	1216.616808	608.812042	1199.590259	600.298768	1198.606243	599.806760	10
3	357.176861	179.092068	340.150312	170.578794	339.166296	170.086786	Q	1101.589865	551.298571	1084.563316	542.785296	1083.579300	542.293288	9
4	470.224540	235.615908	453.197991	227.102634	452.213975	226.610626	P	***973.531287***	487.269282	956.504738	478.756007	955.520722	478.263999	8
5	598.319503	299.663390	581.292954	291.150115	580.308938	290.658107	K	***860.483608***	430.745442	843.457059	422.232168	842.473043	421.740160	7
6	711.403567	356.205422	694.377018	347.692147	693.393002	347.200139	L	***732.388645***	366.697961	715.362096	358.184686	714.378080	357.692678	6
7	826.430510	413.718893	809.403961	405.205619	808.419945	404.713611	D	***619.304581***	310.155929	602.278032	301.642654	601.294016	301.150646	5
8	955.473103	478.240190	938.446554	469.726915	937.462538	469.234907	E	***504.277638***	252.642457	487.251089	244.129183	486.267073	243.637175	4
9	1054.541517	527.774397	1037.514968	519.261122	1036.530952	518.769114	V	***375.235045***	188.121161	358.208496	179.607886	357.224480	179.115878	3
10	1155.589196	578.298236	1138.562647	569.784962	1137.578631	569.292954	T	276.166631	138.586953	259.140082	130.073679	258.156066	129.581671	2
11							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LDQPKLDEVTR
(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	1328.693588	-0.001106	LDQPKLDEVTR
12.0	1328.691757	0.000725	KLWGPGPPFFPS
5.5	1328.700958	-0.008476	EIPQNLMEVLK
4.6	1328.700958	-0.008476	EIPQNLMEVLK
3.1	1328.694427	-0.001945	KMNALHMLDIK
1.9	1328.693558	-0.001076	QKAELQQEVEK

Mascot: http://www.matrixscience.com/

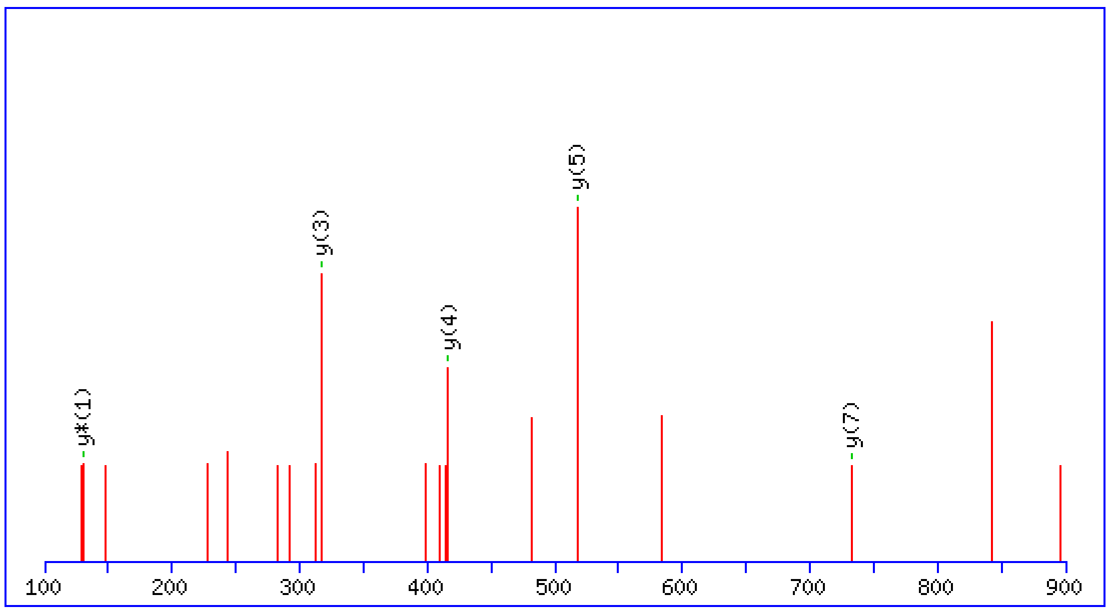
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KNTTVPGK**
Found in **CB052_HUMAN**, Putative uncharacterized protein LINC00471 OS=Homo sapiens GN=LINC00471 PE=5 SV=1

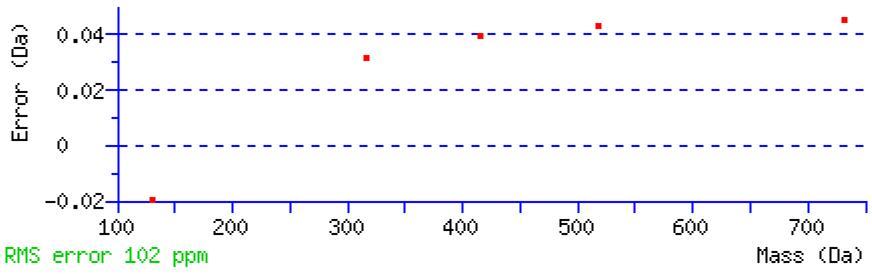
Match to Query 4874: 859.469608 from(430.742080,2+) rtinseconds(958) index(2249)
Title: Locus:1.1.1.1783.13
Data file 2011-11-12 - TFD - EP 5-4.mgf

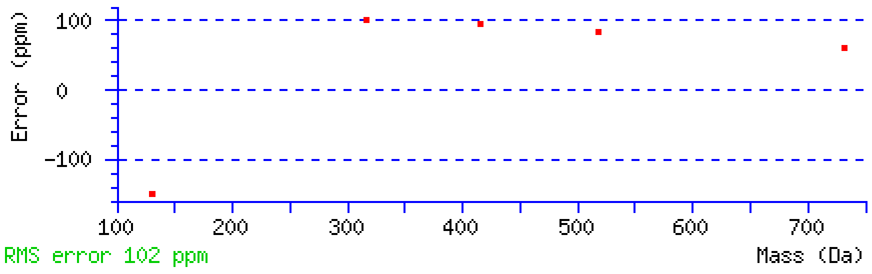
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 859.476334
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P6      : Oxidation (P)
Ions Score: 35  Expect: 0.0056
Matches : 5/72 fragment ions using 7 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	129.102239	65.054757	112.075690	56.541483			**K**							8
2	243.145166	122.076221	226.118617	113.562947			**N**	***732.388646***	366.697961	715.362097	358.184687	714.378081	357.692679	7
3	344.192845	172.600061	327.166296	164.086786	326.182280	163.594778	**T**	618.345719	309.676498	601.319170	301.163223	600.335154	300.671215	6
4	445.240524	223.123900	428.213975	214.610626	427.229959	214.118618	**T**	***517.298040***	259.152658	500.271491	250.639384	499.287475	250.147376	5
5	544.308938	272.658107	527.282389	264.144833	526.298373	263.652825	**V**	***416.250361***	208.628819	399.223812	200.115544			4
6	657.356617	329.181947	640.330068	320.668672	639.346052	320.176664	**P**	***317.181947***	159.094612	300.155398	150.581337			3
7	714.378081	357.692679	697.351532	349.179404	696.367516	348.687396	**G**	204.134268	102.570772	187.107719	94.057498			2
8							**K**	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of KNTTVPGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.1	859.476334	-0.006726	KNTTVPGK
33.9	859.476334	-0.006726	QGSATVGLK
13.3	859.465073	0.004535	KVEEDLK
11.0	859.465073	0.004535	ELTEKPK
9.1	859.476303	-0.006695	QGSAKLEK
9.1	859.476303	-0.006695	QQSELKK
8.9	859.476318	-0.006710	KPATAAGTK
8.3	859.465073	0.004535	KEVVEEK
8.1	859.476334	-0.006726	TGGQLSLGK
7.4	859.465088	0.004520	ELAVTSPK

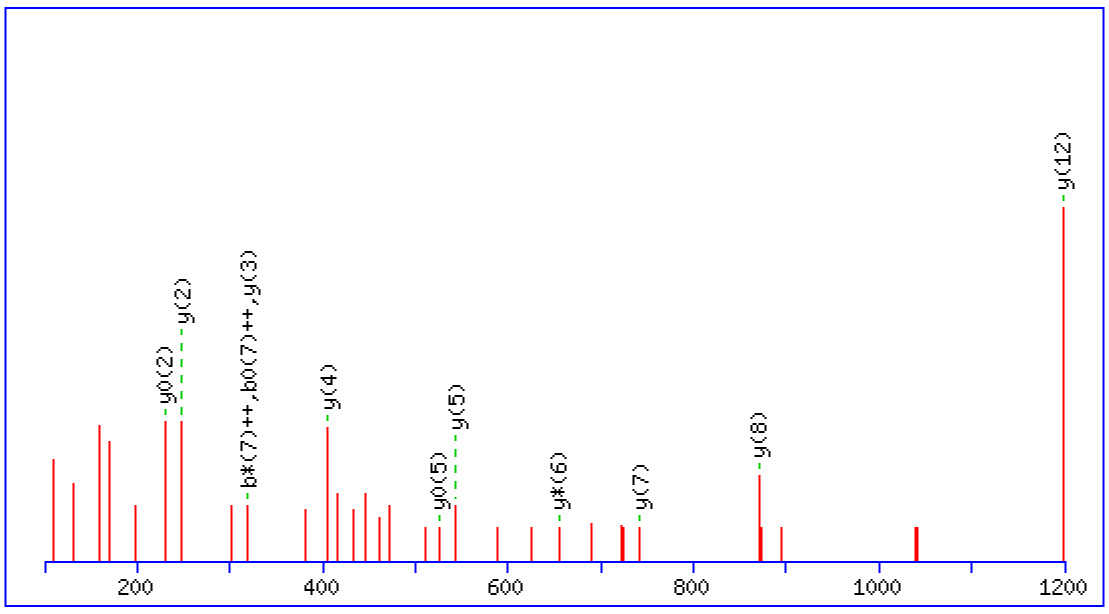
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVSAAVQAQHSATK**
Found in **RBGPR_HUMAN**, Rab3 GTPase-activating protein non-catalytic subunit OS=Homo sapiens GN=RAB3GAP2 PE=1 SV=1

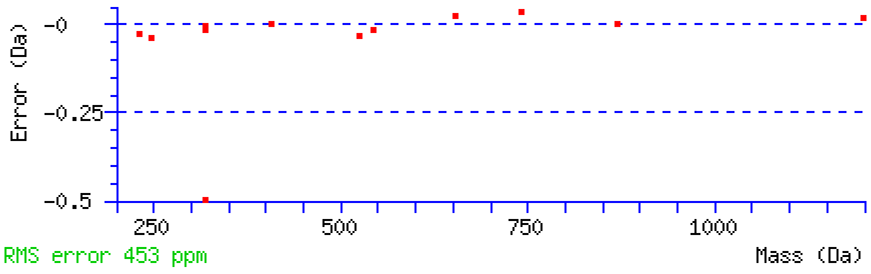
Match to Query 742784: 1395.744582 from(466.255470,3+) rtinseconds(936) index(327594)
Title: Locus:1.1.1.688.14
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

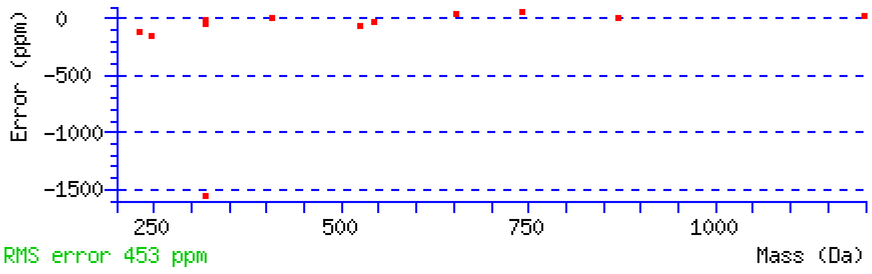
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1395.747025
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 45 **Expect:** 0.00025
Matches : 12/138 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							14
2	199.144104	100.075690					V	1297.685891	649.346583	1280.659342	640.833309	1279.675326	640.341301	13
3	286.176132	143.591704			268.165567	134.586422	S	***1198.617477***	599.812377	1181.590928	591.299102	1180.606912	590.807094	12
4	357.213246	179.110261			339.202681	170.104978	A	1111.585449	556.296362	1094.558900	547.783088	1093.574884	547.291080	11
5	428.250360	214.628818			410.239795	205.623535	A	1040.548335	520.777806	1023.521786	512.264531	1022.537770	511.772523	10
6	527.318774	264.163025			509.308209	255.157742	V	969.511221	485.259249	952.484672	476.745974	951.500656	476.253966	9
7	655.377352	328.192314	638.350803	319.679039	637.366787	319.187031	Q	***870.442807***	435.725042	853.416258	427.211767	852.432242	426.719759	8
8	726.414466	363.710871	709.387917	355.197596	708.403901	354.705588	A	***742.384229***	371.695753	725.357680	363.182478	724.373664	362.690470	7
9	854.473044	427.740160	837.446495	419.226885	836.462479	418.734877	Q	671.347115	336.177196	654.320566	327.663921	653.336550	327.171913	6
10	991.531956	496.269616	974.505407	487.756341	973.521391	487.264333	H	***543.288537***	272.147907	526.261988	263.634632	525.277972	263.142624	5
11	1078.563984	539.785630	1061.537435	531.272356	1060.553419	530.780347	S	***406.229625***	203.618450	389.203076	195.105176	388.219060	194.613168	4
12	1149.601098	575.304187	1132.574549	566.790912	1131.590533	566.298904	A	***319.197597***	160.102436	302.171048	151.589162	301.187032	151.097154	3
13	1250.648777	625.828026	1233.622228	617.314752	1232.638212	616.822744	T	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.578597	2
14							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of VVSAAVQAQHSATK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.5	1395.747025	-0.002443	VVSAAVQAQHSATK
6.0	1395.750595	-0.006013	IFMLLVVGITSGM
4.7	1395.735794	0.008788	DLPPVKDPGALSR

Mascot: http://www.matrixscience.com/

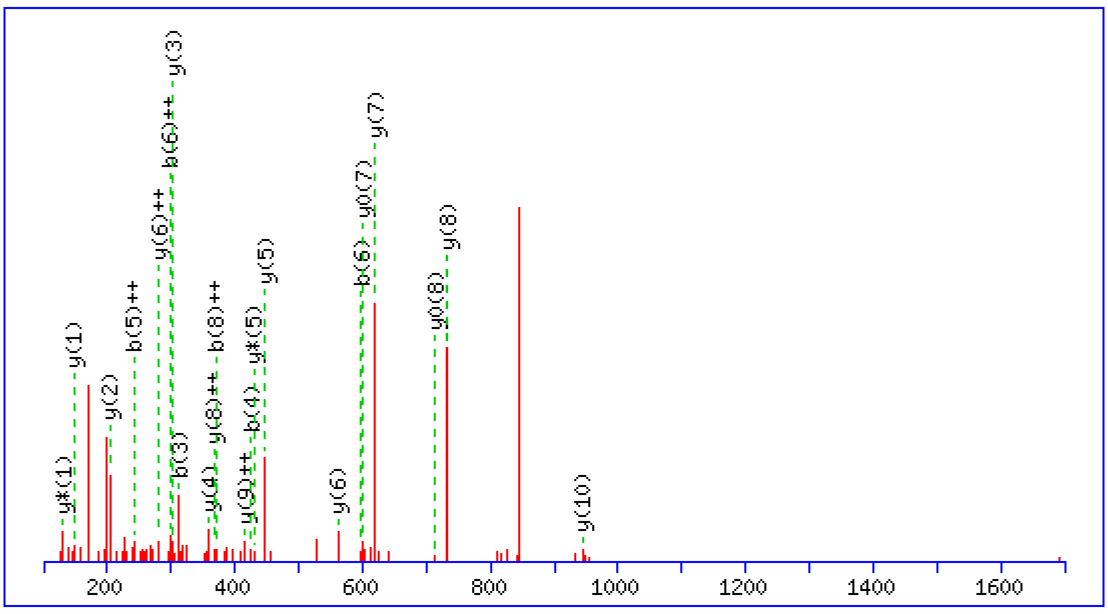
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLVLGDSGVGK**
Found in **RABL3_HUMAN**, Rab-like protein 3 OS=Homo sapiens GN=RABL3 PE=1 SV=1

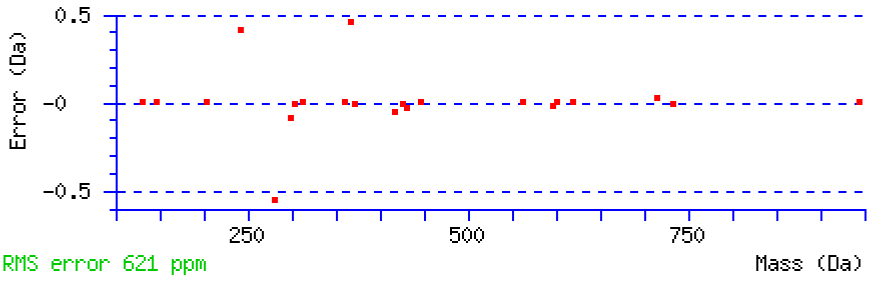
Match to Query 18289: 1042.603548 from(522.309050,2+) rtinseconds(1989) index(20262)
Title: Locus:1.1.1.2176.25
Data file 2011-11-13 - TFD - EP 7-5.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●

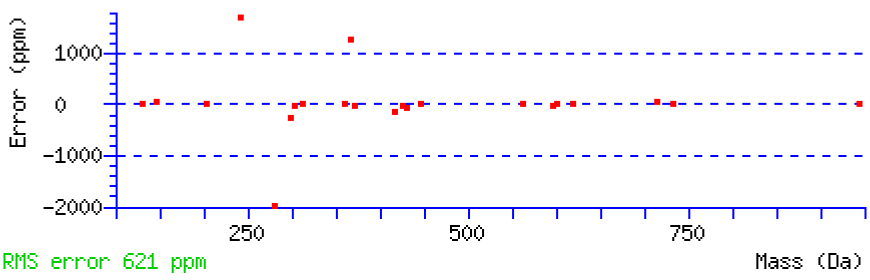


```
Monoisotopic mass of neutral peptide Mr(calc): 1042.602280
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 57  Expect: 1.9e-005
Matches : 22/82 fragment ions using 44 most intense peaks   (help)
```

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	100.075690	50.541483			V							11
2	213.159754	107.083515			L	***944.541123***	472.774200	927.514574	464.260925	926.530558	463.768917	10
3	**312.228168**	156.617722			V	831.457059	416.232168	814.430510	407.718893	813.446494	407.226885	9
4	**425.312232**	213.159754			L	***732.388645***	366.697961	715.362096	358.184686	714.378080	357.692678	8
5	482.333696	**241.670486**			G	***619.304581***	310.155929	602.278032	301.642654	601.294016	301.150646	7
6	**597.360639**	**299.183958**	579.350074	290.178675	D	***562.283117***	281.645197	545.256568	273.131922	544.272552	272.639914	6
7	684.392667	342.699972	666.382102	333.694689	S	***447.256174***	224.131725	430.229625	215.618450	429.245609	215.126443	5
8	741.414131	**371.210704**	723.403566	362.205421	G	***360.224146***	180.615711	343.197597	172.102437			4
9	840.482545	420.744911	822.471980	411.739628	V	***303.202682***	152.104979	286.176133	143.591704			3
10	897.504009	449.255643	879.493444	440.250360	G	***204.134268***	102.570772	187.107719	94.057498			2
11					K	***147.112804***	74.060040	130.086255	65.546765			1



RMS error 621 ppm



RMS error 621 ppm

NCBI **BLAST** search of VLVLGDSGVGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
71.3	1042.602280	0.001268	VVLIGDSGVGK
57.4	1042.602280	0.001268	VLVLGDSGVGK
4.8	1042.613495	-0.009947	KKPVSGGSVGK
3.6	1042.613495	-0.009947	VVTPGASRLK
2.3	1042.595718	0.007830	VAMTPALRGK

Mascot: http://www.matrixscience.com/

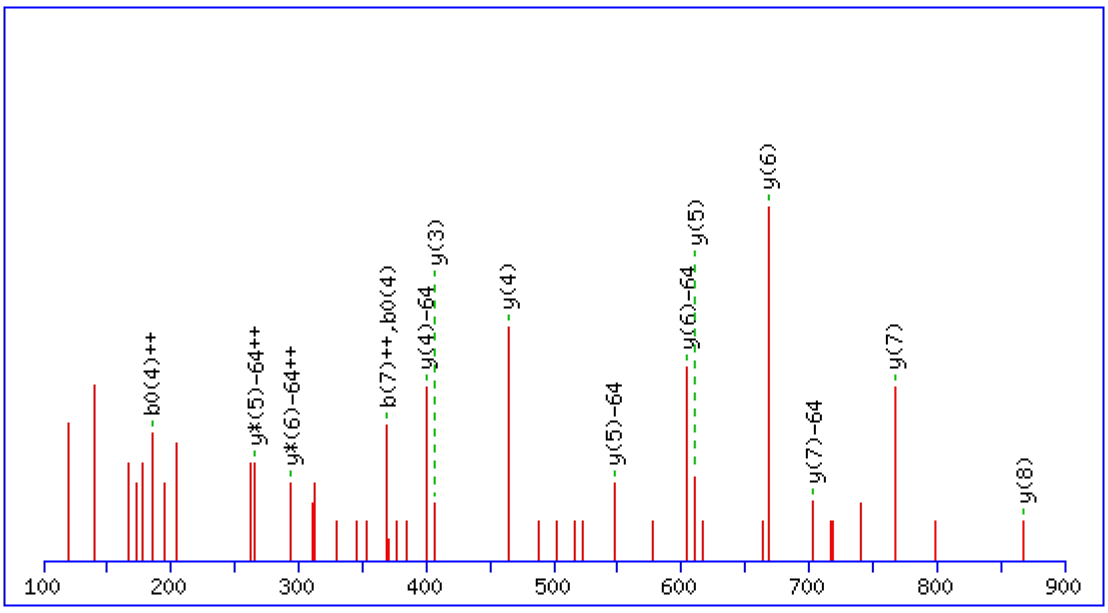
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ETVGFGMLK**
Found in **LTOR2_HUMAN**, Ragulator complex protein LAMTOR2 OS=Homo sapiens GN=LAMTOR2 PE=1 SV=1

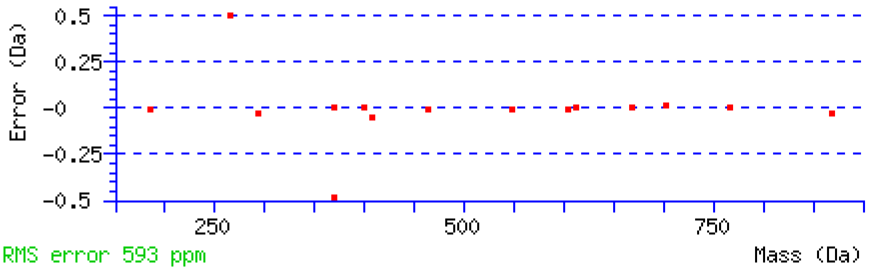
Match to Query 15367: 996.497828 from(499.256190,2+) rtinseconds(2130) index(18864)
Title: Locus:1.1.1.2262.23
Data file 2011-11-13 - TFD - EP 7-7.mgf

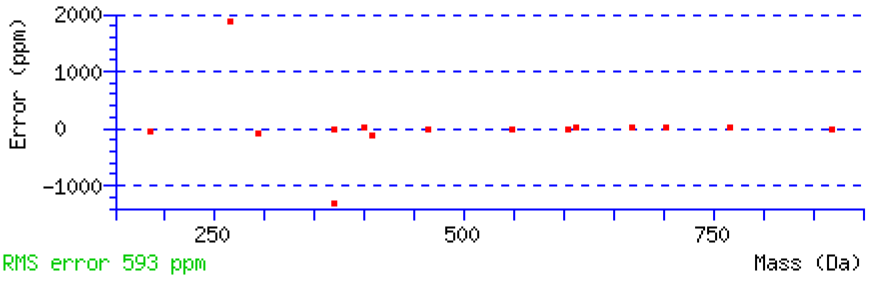
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 996.495026
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M7 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 35 **Expect:** 0.0029
Matches : 15/100 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	130.049869	65.528572	112.039304	56.523290	E							9
2	231.097548	116.052412	213.086983	107.047130	T	*868.459703*	434.733490	851.433154	426.220215	850.449138	425.728207	8
3	330.165962	165.586619	312.155397	156.581337	V	*767.412024*	384.209650	750.385475	375.696376			7
4	387.187426	194.097351	369.176861	185.092069	G	*668.343610*	334.675443	651.317061	326.162169			6
5	534.255840	267.631558	516.245275	258.626276	F	*611.322146*	306.164711	594.295597	297.651437			5
6	591.277304	296.142290	573.266739	287.137008	G	*464.253732*	232.630504	447.227183	224.117230			4
7	738.312704	369.659990	720.302139	360.654708	M	*407.232268*	204.119772	390.205719	195.606497			3
8	851.396768	426.202022	833.386203	417.196740	L	260.196868	130.602072	243.170319	122.088798			2
9					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of ETVGFGMLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.8	996.495026	0.002802	ETVGFGMLK
7.9	996.502853	-0.005025	AKFENFNK

Mascot: http://www.matrixscience.com/

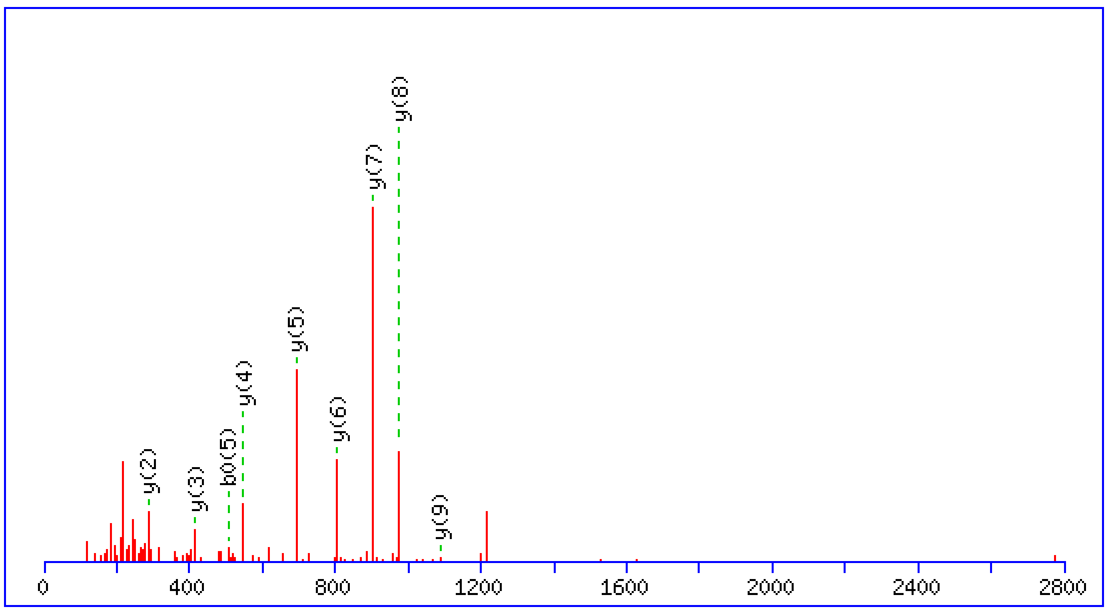
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELAPLFEELR**
Found in **LTOR3_HUMAN**, Ragulator complex protein LAMTOR3 OS=Homo sapiens GN=LAMTOR3 PE=1 SV=1

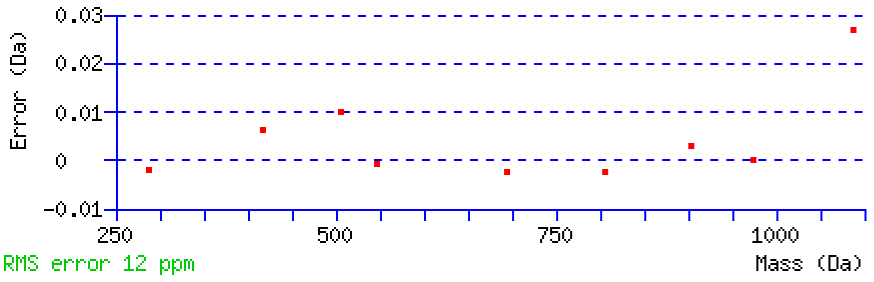
Match to Query 26879: 1215.649788 from(608.832170,2+) rtinseconds(3507) index(37948)
Title: Locus:1.1.1.2789.8
Data file 2011-11-13 - TFD - EP 7-7.mgf

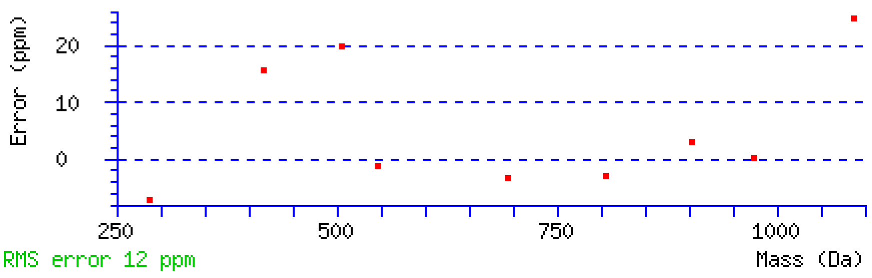
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1215.649902
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 79 **Expect:** 1.9e-007
Matches : 9/86 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	130.049869	65.528572	112.039304	56.523290	E							10
2	243.133933	122.070605	225.123368	113.065322	L	***1087.614622***	544.310949	1070.588073	535.797674	1069.604057	535.305666	9
3	314.171047	157.589161	296.160482	148.583879	A	***974.530558***	487.768917	957.504009	479.255642	956.519993	478.763634	8
4	411.223811	206.115544	393.213246	197.110261	P	***903.493444***	452.250360	886.466895	443.737085	885.482879	443.245077	7
5	524.307875	262.657576	506.297310	253.652293	L	***806.440680***	403.723978	789.414131	395.210703	788.430115	394.718695	6
6	671.376289	336.191783	653.365724	327.186500	F	***693.356616***	347.181946	676.330067	338.668671	675.346051	338.176663	5
7	800.418882	400.713079	782.408317	391.707797	E	***546.288202***	273.647739	529.261653	265.134464	528.277637	264.642456	4
8	929.461475	465.234376	911.450910	456.229093	E	***417.245609***	209.126442	400.219060	200.613168	399.235044	200.121160	3
9	1042.545539	521.776408	1024.534974	512.771125	L	***288.203016***	144.605146	271.176467	136.091871			2
10					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of ELAPLFEELR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
79.0	1215.649902	-0.000114	ELAPLFEELR
12.7	1215.657120	-0.007332	ELSGSGLERLR
6.7	1215.639374	0.010414	LESSVCPVRR
6.5	1215.661148	-0.011360	VPNASLEAFLR
5.5	1215.657120	-0.007332	KNQETISQLR
5.4	1215.647247	0.002541	QAGGLSRFPGAR
0.8	1215.649918	-0.000130	ELPDPLLTYR
0.1	1215.658478	-0.008690	HRQASPLVHR
0.0	1215.645905	0.003883	LTVSPEPSSKR

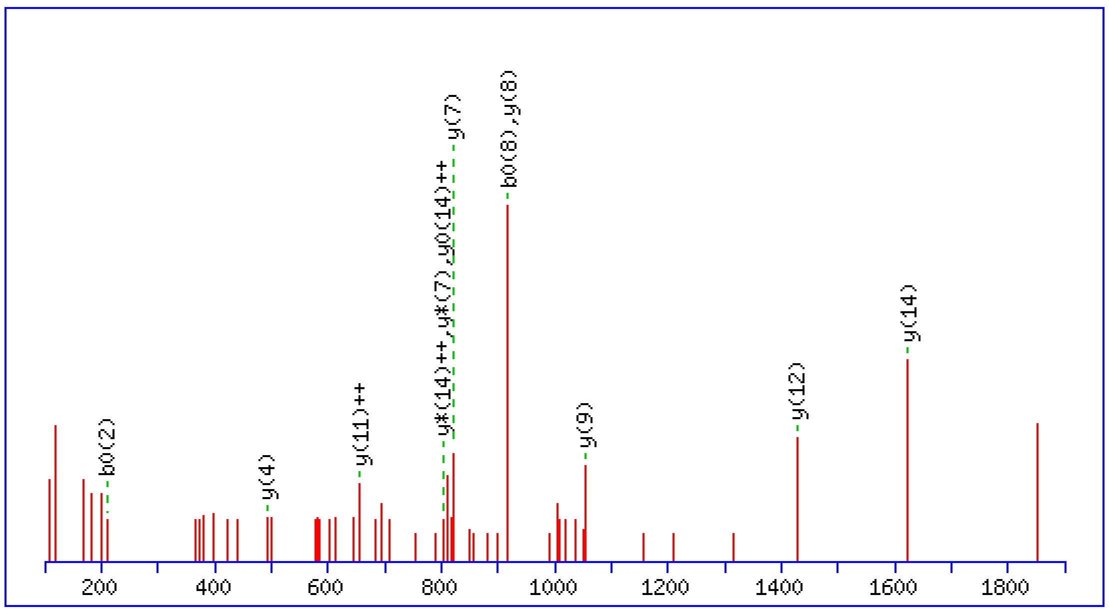
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EVPVIFIHPLNTGLFR**
Found in **RLGPB_HUMAN**, Ral GTPase-activating protein subunit beta OS=Homo sapiens GN=RALGAPB PE=1 SV=1

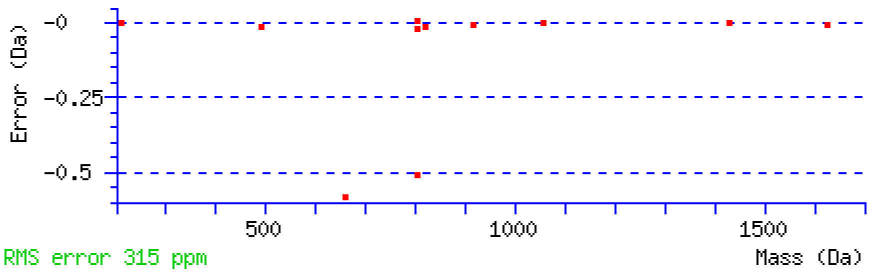
Match to Query 58437: 1851.034482 from(618.018770,3+) rtinseconds(3789) index(55485)
Title: Locus:1.1.1.2834.13
Data file 2011-11-14 - TFD - EP 8-1.mgf

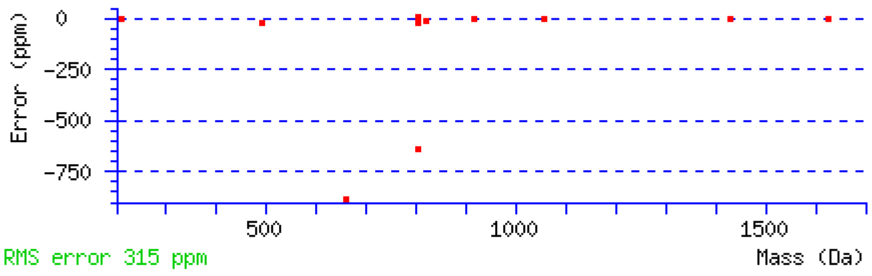
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1851.040695
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 31  Expect: 0.0022
Matches : 12/152 fragment ions using 14 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	**E**							**16**
2	229.118283	115.062780			211.107718	106.057497	**V**	1723.005374	862.006325	1705.978825	853.493050	1704.994809	853.001042	**15**
3	326.171047	163.589161			308.160482	154.583879	**P**	***1623.936960***	812.472118	1606.910411	803.958843	1605.926395	803.466835	**14**
4	425.239461	213.123369			407.228896	204.118086	**V**	1526.884196	763.945736	1509.857647	755.432461	1508.873631	754.940453	**13**
5	538.323525	269.665401			520.312960	260.660118	**I**	***1427.815782***	714.411529	1410.789233	705.898254	1409.805217	705.406246	**12**
6	685.391939	343.199608			667.381374	334.194325	**F**	1314.731718	657.869497	1297.705169	649.356222	1296.721153	648.864214	**11**
7	798.476003	399.741640			780.465438	390.736357	**I**	1167.663304	584.335290	1150.636755	575.822016	1149.652739	575.330007	**10**
8	935.534915	468.271096			917.524350	459.265813	**H**	***1054.579240***	527.793258	1037.552691	519.279983	1036.568675	518.787975	**9**
9	1032.587679	516.797478			1014.577114	507.792195	**P**	***917.520328***	459.263802	900.493779	450.750527	899.509763	450.258519	**8**
10	1145.671743	573.339509			1127.661178	564.334227	**L**	***820.467564***	410.737420	803.441015	402.224145	802.456999	401.732137	**7**
11	1259.714670	630.360973	1242.688121	621.847698	1241.704105	621.355690	**N**	707.383500	354.195388	690.356951	345.682113	689.372935	345.190105	**6**
12	1360.762349	680.884812	1343.735800	672.371538	1342.751784	671.879530	**T**	593.340573	297.173925	576.314024	288.660650	575.330008	288.168642	**5**
13	1417.783813	709.395544	1400.757264	700.882270	1399.773248	700.390262	**G**	***492.292894***	246.650085	475.266345	238.136810			**4**
14	1530.867877	765.937576	1513.841328	757.424302	1512.857312	756.932294	**L**	435.271430	218.139353	418.244881	209.626078			**3**
15	1677.936291	839.471783	1660.909742	830.958509	1659.925726	830.466501	**F**	322.187366	161.597321	305.160817	153.084047			**2**
16							**R**	175.118952	88.063114	158.092403	79.549839			**1**





NCBI **BLAST** search of EVPVIFIHPLNTGLFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.7	1851.040695	-0.006213	EVPVIFIHPLNTGLFR

Mascot: http://www.matrixscience.com/

{MATRIX SCIENCE}

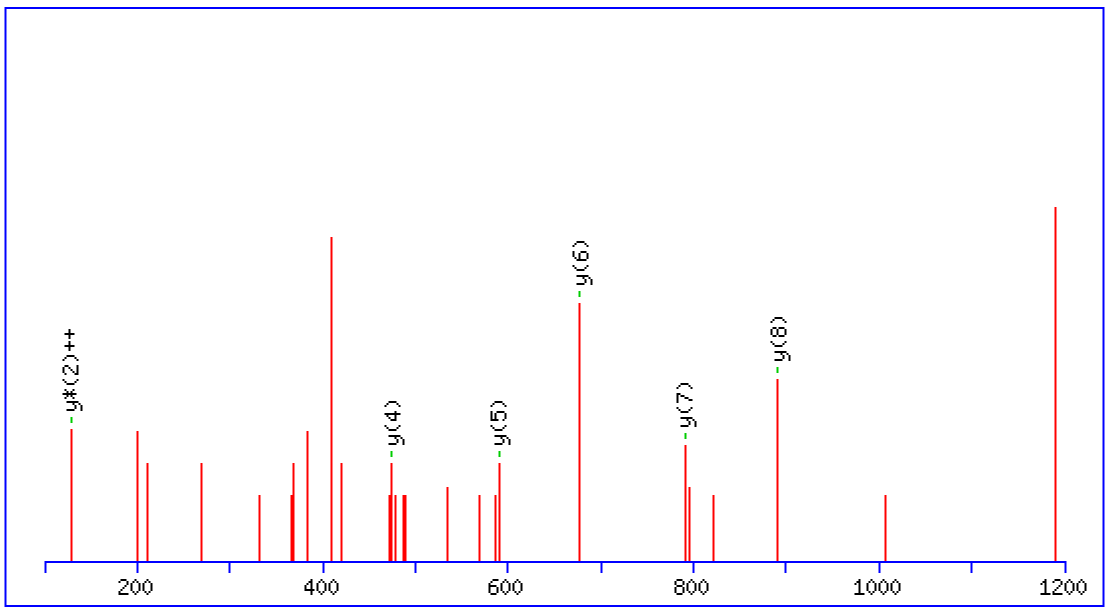
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EGLTLSDAEQK**
Found in **REPS1_HUMAN**, RalBP1-associated Eps domain-containing protein 1 OS=Homo sapiens GN=REPS1 PE=1 SV=3

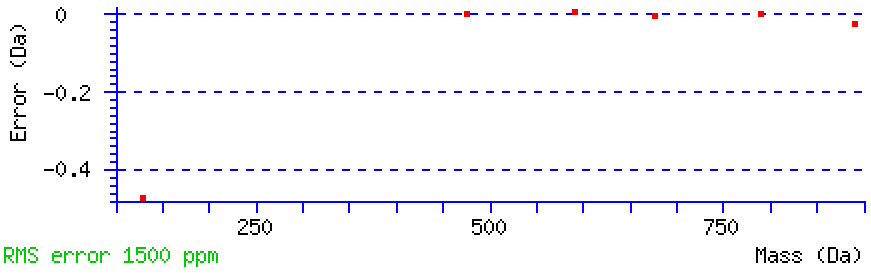
Match to Query 508181: 1189.588268 from(595.801410,2+) rtinseconds(1854) index(344508)
Title: Locus:1.1.1.1046.19
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

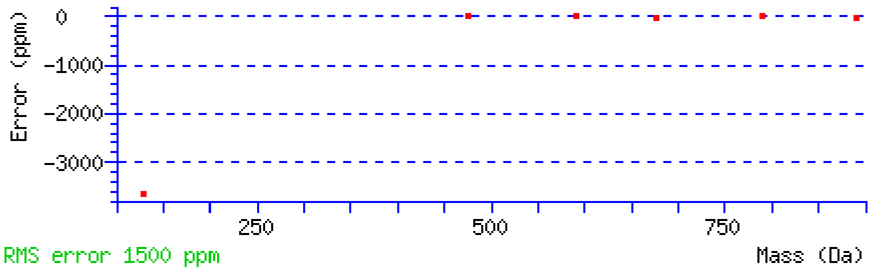
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1189.582626
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 35 **Expect:** 0.0047
Matches : 6/98 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	E							11
2	187.071333	94.039305			169.060768	85.034022	G	1061.547331	531.277304	1044.520782	522.764029	1043.536766	522.272021	10
3	300.155397	150.581336			282.144832	141.576054	L	1004.525867	502.766572	987.499318	494.253297	986.515302	493.761289	9
4	401.203076	201.105176			383.192511	192.099894	T	***891.441803***	446.224540	874.415254	437.711265	873.431238	437.219257	8
5	514.287140	257.647208			496.276575	248.641926	L	***790.394124***	395.700700	773.367575	387.187426	772.383559	386.695418	7
6	601.319168	301.163222			583.308603	292.157940	S	***677.310060***	339.158668	660.283511	330.645394	659.299495	330.153386	6
7	716.346111	358.676694			698.335546	349.671411	D	***590.278032***	295.642654	573.251483	287.129380	572.267467	286.637372	5
8	787.383225	394.195250			769.372660	385.189968	A	***475.251089***	238.129183	458.224540	229.615908	457.240524	229.123900	4
9	916.425818	458.716547			898.415253	449.711264	E	404.213975	202.610626	387.187426	194.097351	386.203410	193.605343	3
10	1044.484396	522.745836	1027.457847	514.232562	1026.473831	513.740554	Q	275.171382	138.089329	258.144833	129.576055			2
11							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of EGLTLSDAEQK
(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	1189.582626	0.005642	EGLTLSDAEQK
10.5	1189.590042	-0.001774	GEITPELLGVM
1.5	1189.593872	-0.005604	QPSSSPSSIIR
0.6	1189.597885	-0.009617	AEEVFTLPER

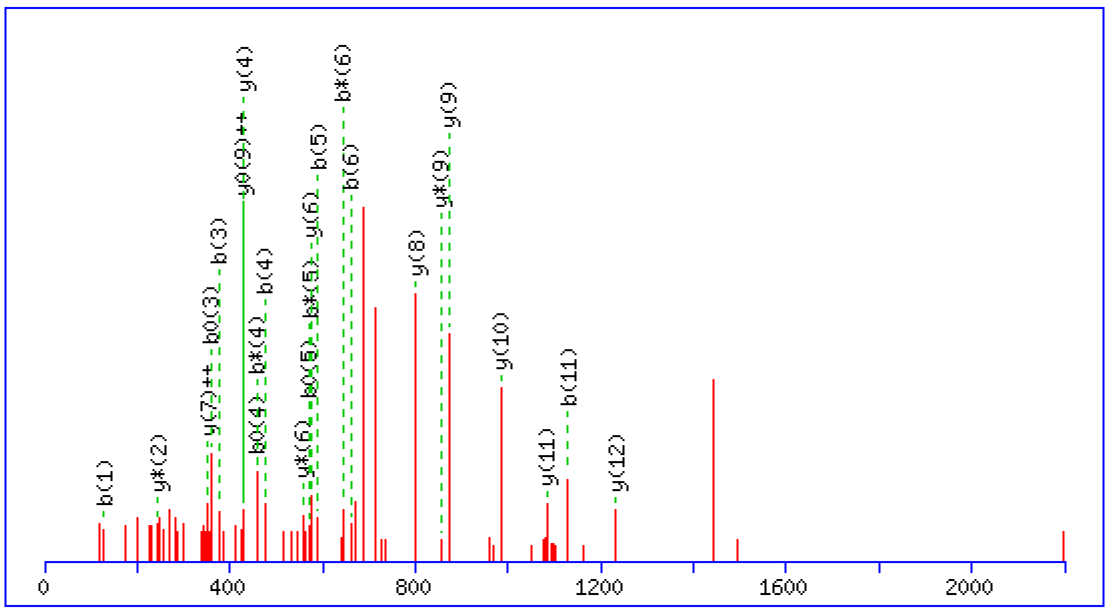
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QTFVLAPEGSVANK**
Found in **G3BP1_HUMAN**, Ras GTPase-activating protein-binding protein 1 OS=Homo sapiens GN=G3BP1 PE=1 SV=1

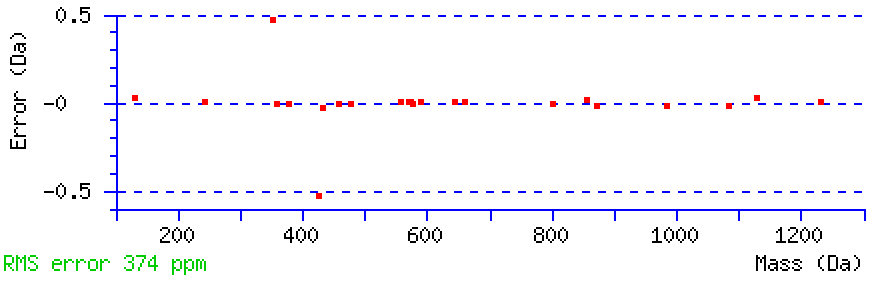
Match to Query 803236: 1459.765708 from(730.890130,2+) rtinseconds(2352) index(518680)
Title: Locus:1.1.1.1230.43
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

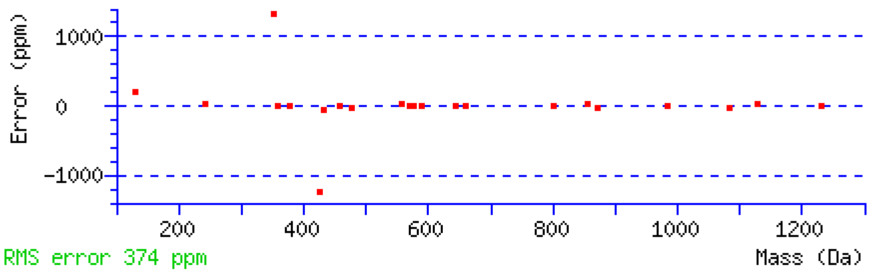
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1459.767090
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 37 **Expect:** 0.0019
Matches : 24/146 fragment ions using 46 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	***129.065854***	65.036565	112.039305	56.523291			Q							14
2	230.113533	115.560405	213.086984	107.047130	212.102968	106.555122	T	1332.715793	666.861535	1315.689244	658.348260	1314.705228	657.856252	13
3	***377.181947***	189.094611	360.155398	180.581337	359.171382	180.089329	F	***1231.668114***	616.337695	1214.641565	607.824421	1213.657549	607.332413	12
4	***476.250361***	238.628818	459.223812	230.115544	458.239796	229.623536	V	***1084.599700***	542.803488	1067.573151	534.290214	1066.589135	533.798206	11
5	***589.334425***	295.170851	572.307876	286.657576	571.323860	286.165568	L	***985.531286***	493.269281	968.504737	484.756007	967.520721	484.263999	10
6	***660.371539***	330.689408	643.344990	322.176133	642.360974	321.684125	A	***872.447222***	436.727249	855.420673	428.213975	854.436657	427.721967	9
7	757.424303	379.215790	740.397754	370.702515	739.413738	370.210507	P	***801.410108***	401.208692	784.383559	392.695418	783.399543	392.203410	8
8	886.466896	443.737086	869.440347	435.223812	868.456331	434.731804	E	704.357344	352.682310	687.330795	344.169036	686.346779	343.677028	7
9	943.488360	472.247818	926.461811	463.734544	925.477795	463.242536	G	***575.314751***	288.161014	558.288202	279.647739	557.304186	279.155731	6
10	1030.520388	515.763832	1013.493839	507.250558	1012.509823	506.758550	S	518.293287	259.650282	501.266738	251.137007	500.282722	250.644999	5
11	***1129.588802***	565.298039	1112.562253	556.784765	1111.578237	556.292757	V	***431.261259***	216.134267	414.234710	207.620993			4
12	1200.625916	600.816596	1183.599367	592.303322	1182.615351	591.811314	A	332.192845	166.600060	315.166296	158.086786			3
13	1314.668843	657.838060	1297.642294	649.324785	1296.658278	648.832777	N	261.155731	131.081503	244.129182	122.568229			2
14							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of QTFVLAPEGSVANK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.2	1459.767090	-0.001382	QTFVLAPEGSVANK
7.7	1459.763077	0.002631	SRDVVDEVSVSLR
2.7	1459.767075	-0.001367	GVVIKYSEPPEAR
2.6	1459.767075	-0.001367	GVVIKYSEPPEAR
1.7	1459.778320	-0.012612	TQWKTQIQNVSK

Mascot: http://www.matrixscience.com/

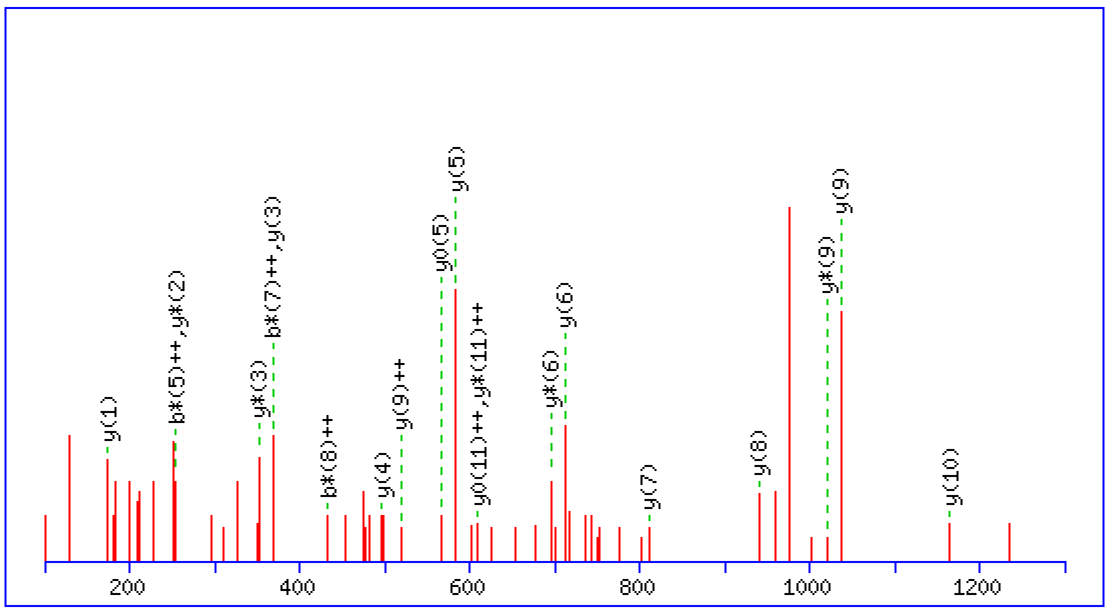
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VEAKPEVQSQPPR**
Found in **G3BP2_HUMAN**, Ras GTPase-activating protein-binding protein 2 OS=Homo sapiens GN=G3BP2 PE=1 SV=2

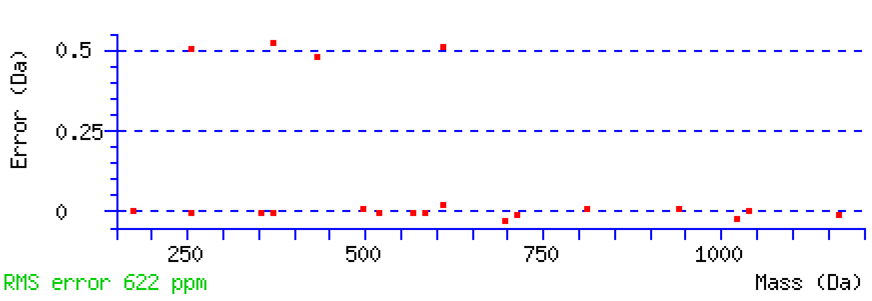
Match to Query 38586: 1463.769912 from(488.930580,3+) rtinseconds(978) index(2622)
Title: Locus:1.1.1.1883.26
Data file 2011-11-12 - TFD - EP 5-3.mgf

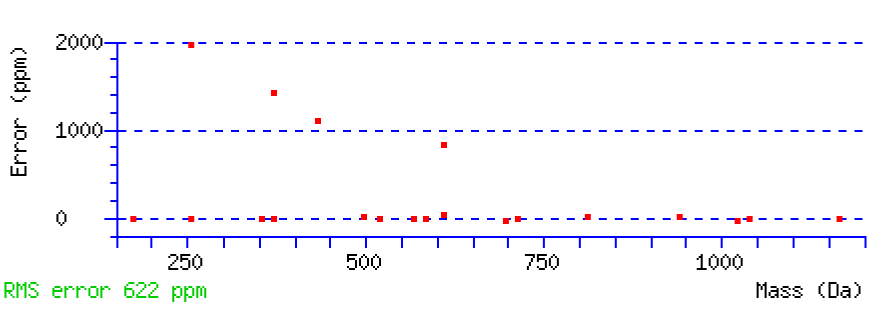
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1463.773224
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 53  Expect: 1.1e-005
Matches : 20/128 fragment ions using 31 most intense peaks   (help)
```

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	100.075690	50.541483					V							13
2	229.118283	115.062780			211.107718	106.057497	E	1365.712105	683.359691	1348.685556	674.846416	1347.701540	674.354408	12
3	300.155397	150.581337			282.144832	141.576054	A	1236.669512	618.838394	1219.642963	610.325120	1218.658947	609.833112	11
4	428.250360	214.628818	411.223811	206.115544	410.239795	205.623536	K	***1165.632398***	583.319837	1148.605849	574.806563	1147.621833	574.314554	10
5	525.303124	263.155200	508.276575	254.641926	507.292559	254.149918	P	***1037.537435***	519.272356	1020.510886	510.759081	1019.526870	510.267073	9
6	654.345717	327.676497	637.319168	319.163222	636.335152	318.671214	E	***940.484671***	470.745974	923.458122	462.232699	922.474106	461.740691	8
7	753.414131	377.210704	736.387582	368.697429	735.403566	368.205421	V	***811.442078***	406.224677	794.415529	397.711403	793.431513	397.219395	7
8	881.472709	441.239993	864.446160	432.726718	863.462144	432.234710	Q	***712.373664***	356.690470	695.347115	348.177196	694.363099	347.685188	6
9	968.504737	484.756007	951.478188	476.242732	950.494172	475.750724	S	***584.315086***	292.661181	567.288537	284.147907	566.304521	283.655899	5
10	1096.563315	548.785296	1079.536766	540.272021	1078.552750	539.780013	Q	***497.283058***	249.145167	480.256509	240.631892			4
11	1193.616079	597.311678	1176.589530	588.798403	1175.605514	588.306395	P	***369.224480***	185.115878	352.197931	176.602603			3
12	1290.668843	645.838060	1273.642294	637.324785	1272.658278	636.832777	P	272.171716	136.589496	255.145167	128.076221			2
13							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of VEAKPEVQSQPPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
53.0	1463.773224	-0.003312	VEAKPEVQSQPPR
0.2	1463.784454	-0.014542	QRVLIQQHEDAK

Mascot: http://www.matrixscience.com/

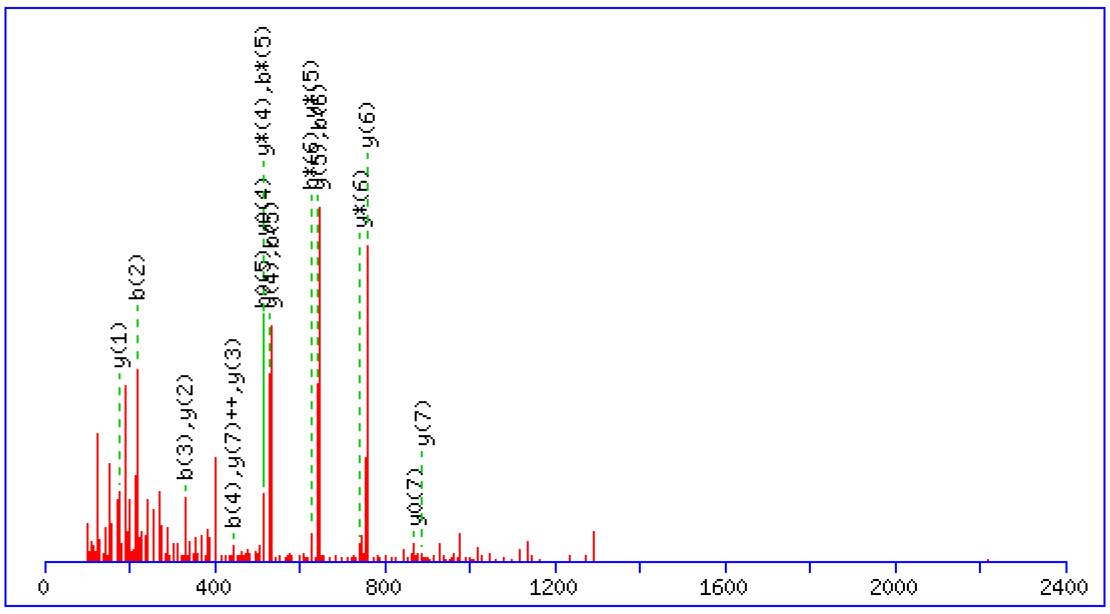
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SENLSLRR**
Found in **RAIN_HUMAN**, Ras-interacting protein 1 OS=Homo sapiens GN=RASIP1 PE=1 SV=1

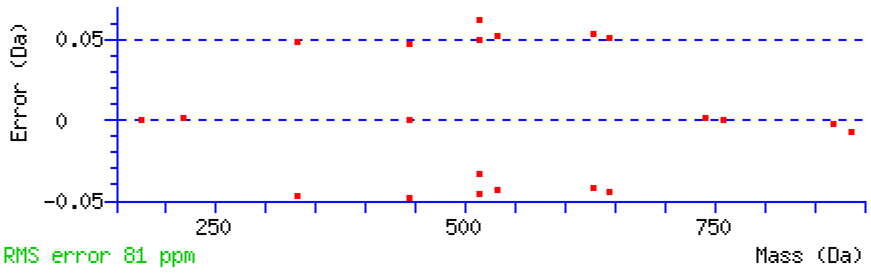
Match to Query 11570: 973.530068 from(487.772310,2+) rtinseconds(1913) index(21171)
Title: Locus:1.1.1.2097.21
Data file 2011-11-12 - TFD - EP 6-3.mgf

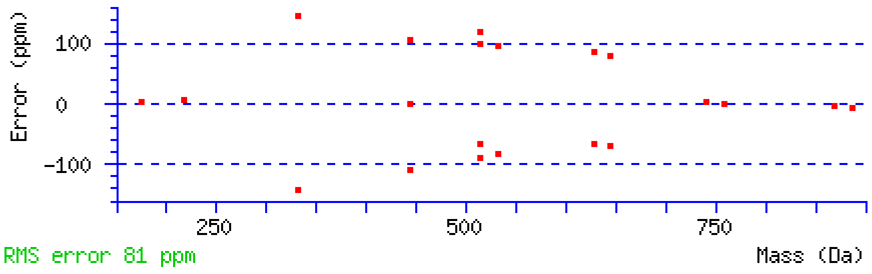
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 973.530457
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 35  Expect: 0.0033
Matches : 21/74 fragment ions using 36 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							8
2	**217.081897**	109.044586			199.071332	100.039304	E	*887.505739*	444.256508	870.479190	435.743233	869.495174	435.251225	7
3	**331.124824**	166.066050	314.098275	157.552776	313.114259	157.060768	N	*758.463146*	379.735211	741.436597	371.221937	740.452581	370.729929	6
4	**444.208888**	222.608082	427.182339	214.094808	426.198323	213.602800	L	*644.420219*	322.713748	627.393670	314.200473	626.409654	313.708465	5
5	**531.240916**	266.124096	514.214367	257.610822	513.230351	257.118814	S	*531.336155*	266.171716	514.309606	257.658441	513.325590	257.166433	4
6	**644.324980**	322.666128	627.298431	314.152854	626.314415	313.660846	L	*444.304127*	222.655701	427.277578	214.142427			3
7	800.426091	400.716684	783.399542	392.203409	782.415526	391.711401	R	*331.220063*	166.113669	314.193514	157.600395			2
8							R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of SENLSLRR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.3	973.530457	-0.000389	SENLSLRR
14.2	973.523285	0.006783	DTLLPPFR
14.2	973.523285	0.006783	DTLLPPFR
9.6	973.530487	-0.000419	LTSTQPRR
7.3	973.530472	-0.000404	SAPTALSRR
7.0	973.523270	0.006798	AFAGPLSPAK
6.1	973.530472	-0.000404	STVREINR
5.6	973.530472	-0.000404	LSSDQIRR
5.0	973.530457	-0.000389	SENSRIIR
3.7	973.534485	-0.004417	AKPFQNAAK

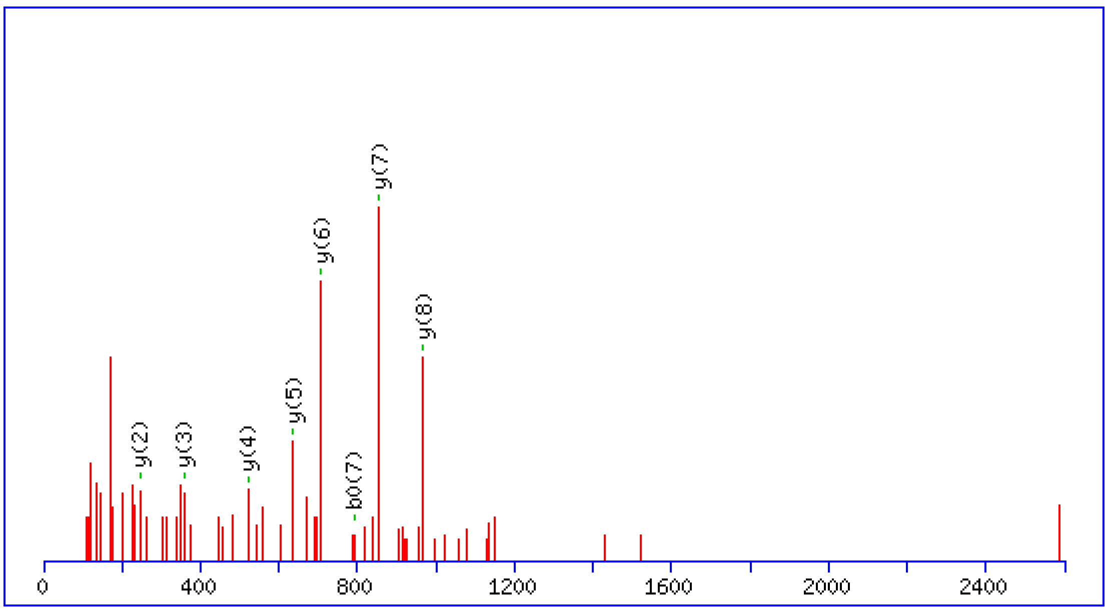
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **SIIFANYIAR**
Found in **RRAGA_HUMAN**, Ras-related GTP-binding protein A OS=Homo sapiens GN=RRAGA PE=1 SV=1

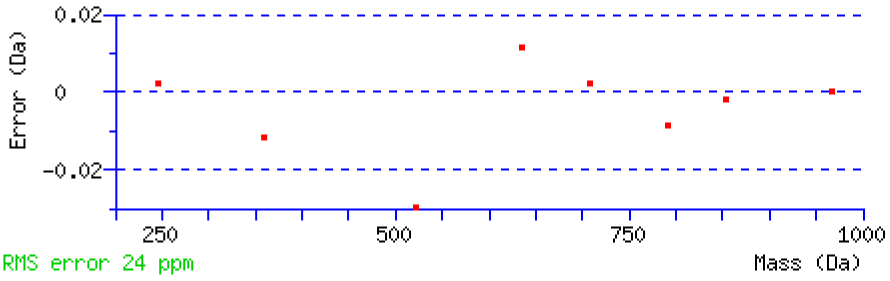
Match to Query 28865: 1166.644908 from(584.329730,2+) rtinseconds(3087) index(43217)
Title: Locus:1.1.1.2558.12
Data file 2011-11-14 - TFD - EP 8-4.mgf

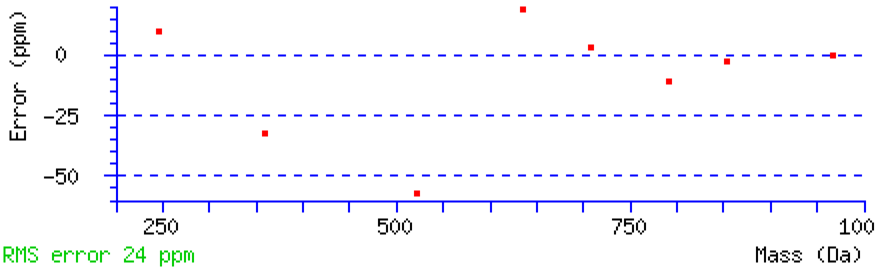
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1166.644760
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 36  Expect: 0.0023
Matches : 8/80 fragment ions using 22 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	#
1	88.039304	44.523290			70.028739	35.518008	S					10
2	201.123368	101.065322			183.112803	92.060039	I	1080.620042	540.813659	1063.593493	532.300385	9
3	314.207432	157.607354			296.196867	148.602071	I	***967.535978***	484.271627	950.509429	475.758353	8
4	461.275846	231.141561			443.265281	222.136278	F	***854.451914***	427.729595	837.425365	419.216321	7
5	532.312960	266.660118			514.302395	257.654835	A	***707.383500***	354.195388	690.356951	345.682114	6
6	646.355887	323.681581	629.329338	315.168307	628.345322	314.676299	N	***636.346386***	318.676831	619.319837	310.163557	5
7	809.419216	405.213246	792.392667	396.699972	791.408651	396.207964	Y	***522.303459***	261.655368	505.276910	253.142093	4
8	922.503280	461.755278	905.476731	453.242004	904.492715	452.749996	I	***359.240130***	180.123703	342.213581	171.610429	3
9	993.540394	497.273835	976.513845	488.760561	975.529829	488.268553	A	***246.156066***	123.581671	229.129517	115.068397	2
10							R	175.118952	88.063114	158.092403	79.549840	1





NCBI **BLAST** search of SIIFANYIAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.8	1166.644760	0.000148	SIIFANYIAR
12.4	1166.648148	-0.003240	VTRIAYSMVK

Mascot: http://www.matrixscience.com/

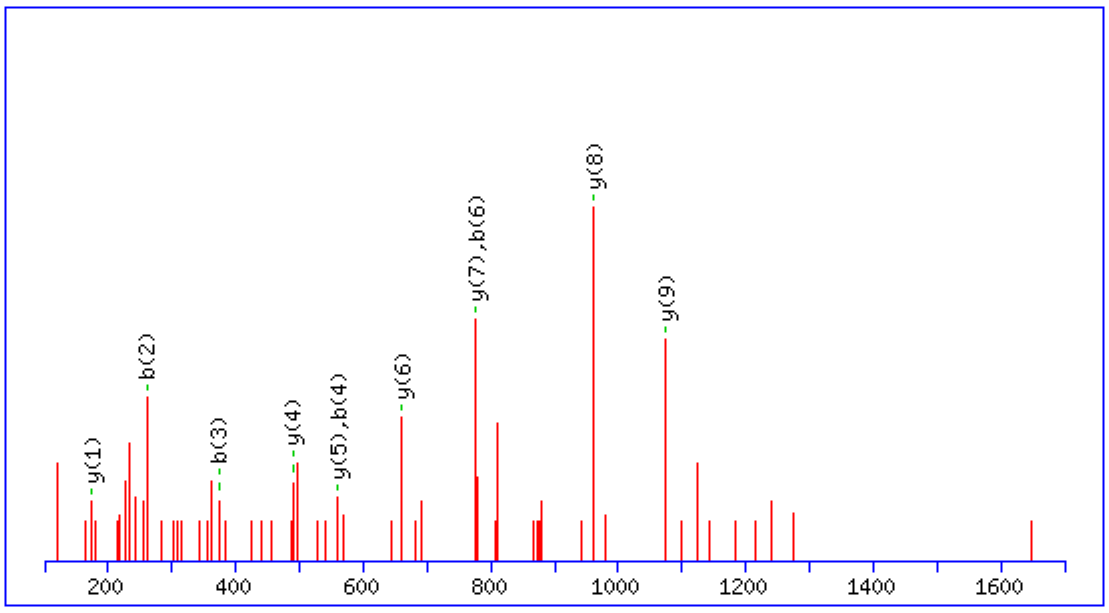
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FLIWDTAGQER**
Found in **RAB31_HUMAN**, Ras-related protein Rab-31 OS=Homo sapiens GN=RAB31 PE=1 SV=1

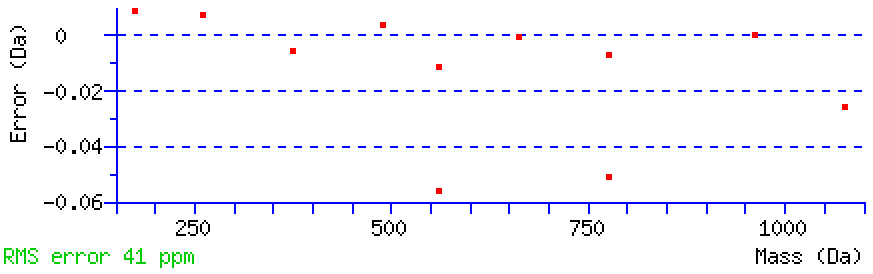
Match to Query 43496: 1334.662928 from(668.338740,2+) rtinseconds(3172) index(42705)
Title: Locus:1.1.1.2464.35
Data file 2011-11-10 - TFD - EP 4-6.mgf

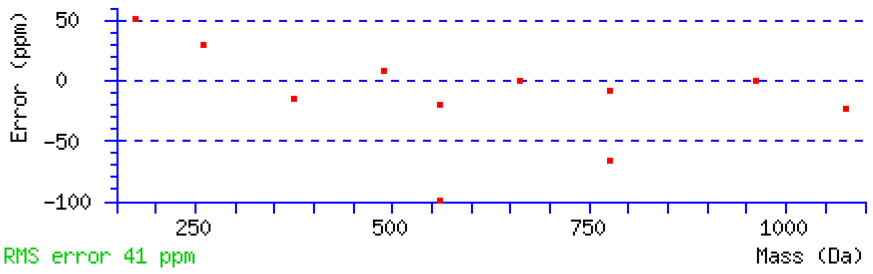
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1334.661896
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 32  Expect: 0.0079
Matches : 11/94 fragment ions using 24 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.075690	74.541483					F							11
2	**261.159754**	131.083515					L	1188.600764	594.804020	1171.574215	586.290746	1170.590199	585.798738	10
3	**374.243818**	187.625547					I	***1075.516700***	538.261988	1058.490151	529.748714	1057.506135	529.256706	9
4	**560.323131**	280.665204					W	***962.432636***	481.719956	945.406087	473.206682	944.422071	472.714674	8
5	675.350074	338.178675			657.339509	329.173393	D	***776.353323***	388.680300	759.326774	380.167025	758.342758	379.675017	7
6	**776.397753**	388.702515			758.387188	379.697232	T	***661.326380***	331.166828	644.299831	322.653554	643.315815	322.161546	6
7	847.434867	424.221072			829.424302	415.215789	A	***560.278701***	280.642989	543.252152	272.129714	542.268136	271.637706	5
8	904.456331	452.731804			886.445766	443.726521	G	***489.241587***	245.124432	472.215038	236.611157	471.231022	236.119149	4
9	1032.514909	516.761093	1015.488360	508.247818	1014.504344	507.755810	Q	432.220123	216.613700	415.193574	208.100425	414.209558	207.608417	3
10	1161.557502	581.282389	1144.530953	572.769115	1143.546937	572.277107	E	304.161545	152.584411	287.134996	144.071136	286.150980	143.579128	2
11							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of FLIWDTAGQER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.4	1334.661896	0.001032	FLIWDTAGQER

Mascot: http://www.matrixscience.com/

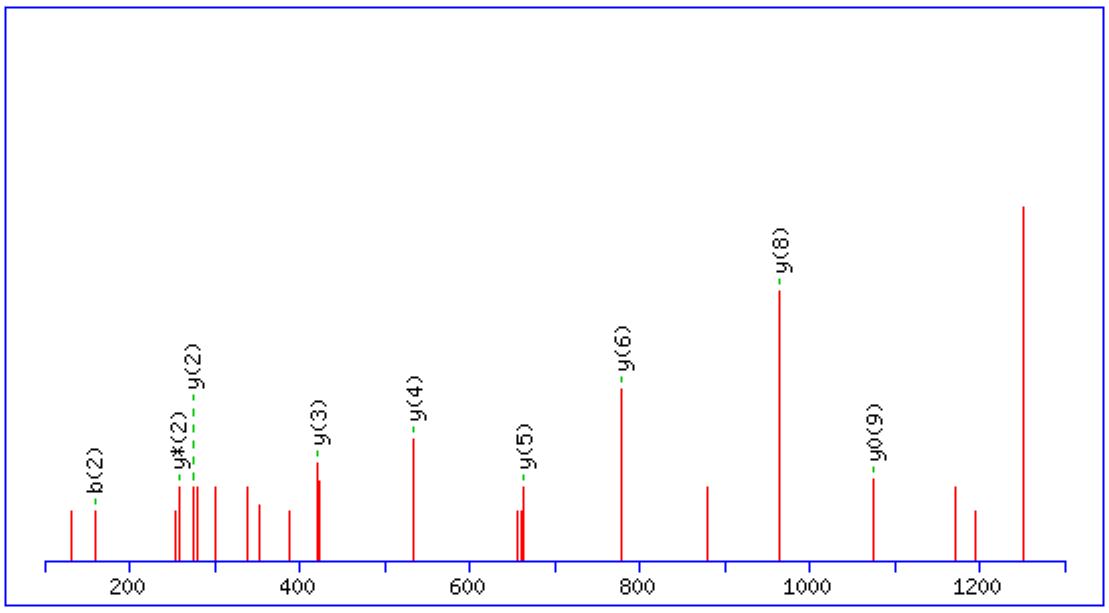
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TGQSVDELFQK**
Found in **RAB24_HUMAN**, Ras-related protein Rab-24 OS=Homo sapiens GN=RAB24 PE=1 SV=1

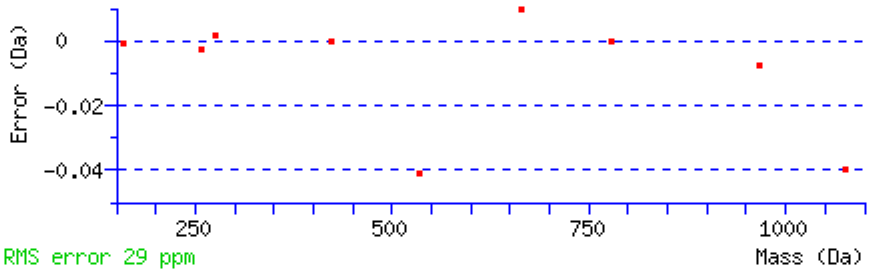
Match to Query 32296: 1250.616068 from(626.315310,2+) rtinseconds(2368) index(26621)
Title: Locus:1.1.1.2169.37
Data file 2011-11-10 - TFD - EP 3-6.mgf

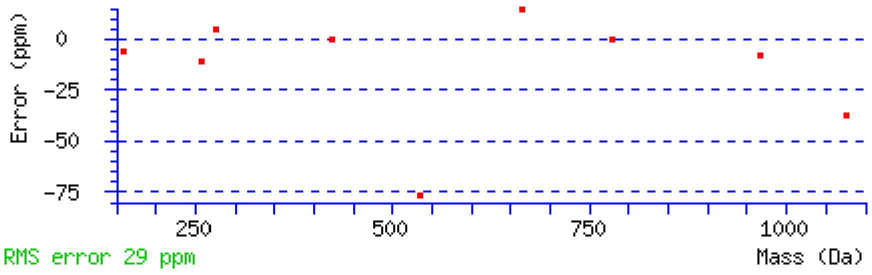
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1250.614288
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 38 **Expect:** 0.00098
Matches : 9/108 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							11
2	159.076419	80.041847			141.065854	71.036565	G	1150.573880	575.790578	1133.547331	567.277304	1132.563315	566.785296	10
3	287.134997	144.071136	270.108448	135.557862	269.124432	135.065854	Q	1093.552416	547.279846	1076.525867	538.766572	1075.541851	538.274564	9
4	374.167025	187.587151	357.140476	179.073876	356.156460	178.581868	S	***965.493838***	483.250557	948.467289	474.737283	947.483273	474.245275	8
5	473.235439	237.121358	456.208890	228.608083	455.224874	228.116075	V	878.461810	439.734543	861.435261	431.221269	860.451245	430.729261	7
6	588.262382	294.634829	571.235833	286.121555	570.251817	285.629547	D	***779.393396***	390.200336	762.366847	381.687062	761.382831	381.195054	6
7	717.304975	359.156126	700.278426	350.642851	699.294410	350.150843	E	***664.366453***	332.686865	647.339904	324.173590	646.355888	323.681582	5
8	830.389039	415.698158	813.362490	407.184883	812.378474	406.692875	L	***535.323860***	268.165568	518.297311	259.652294			4
9	977.457453	489.232365	960.430904	480.719090	959.446888	480.227082	F	***422.239796***	211.623536	405.213247	203.110261			3
10	1105.516031	553.261654	1088.489482	544.748379	1087.505466	544.256371	Q	***275.171382***	138.089329	258.144833	129.576055			2
11							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of TGQSVDELFQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.8	1250.614288	0.001780	TGQSVDELFQK
5.7	1250.617630	-0.001562	DEQSAVSMLKK

Mascot: http://www.matrixscience.com/

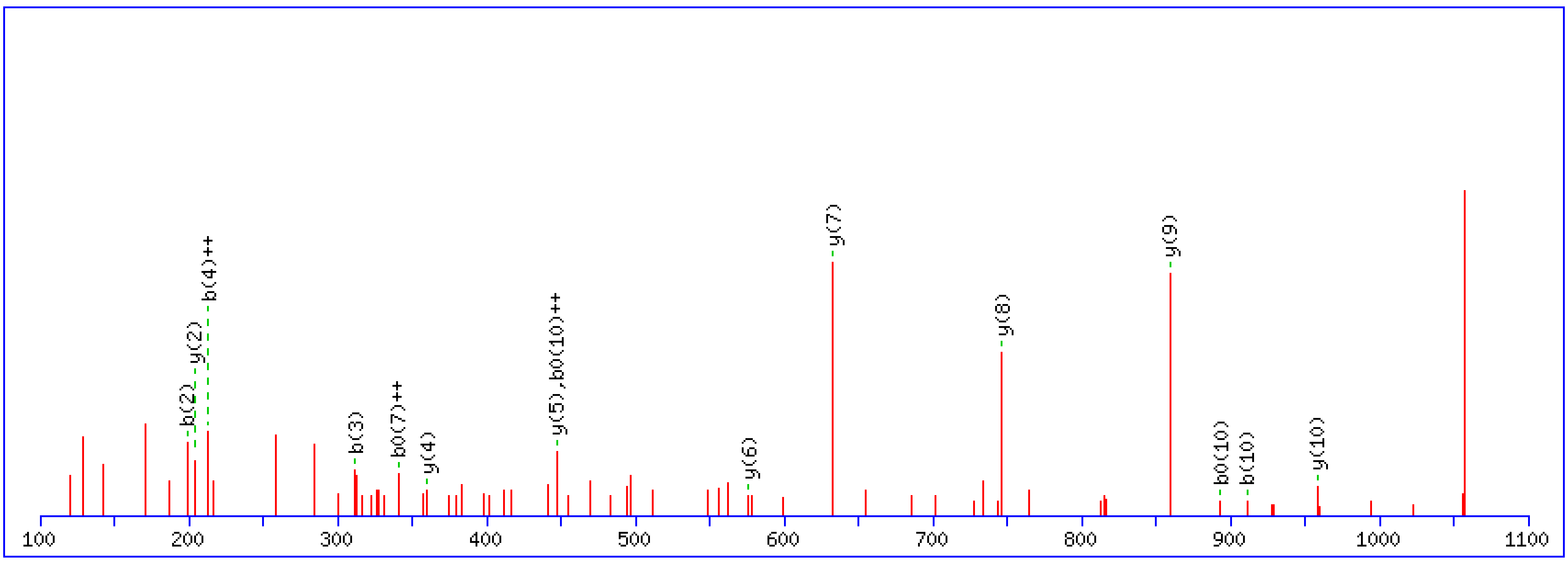
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVLIGESGVGK**
Found in **RAB25_HUMAN**, Ras-related protein Rab-25 OS=Homo sapiens GN=RAB25 PE=1 SV=2

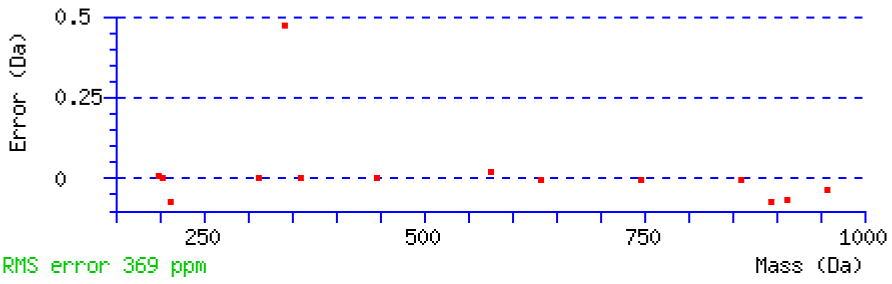
Match to Query 12319: 1056.615888 from(529.315220,2+) rtinseconds(1832) index(19532)
Title: Locus:1.1.1.1080.23
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 2.mgf

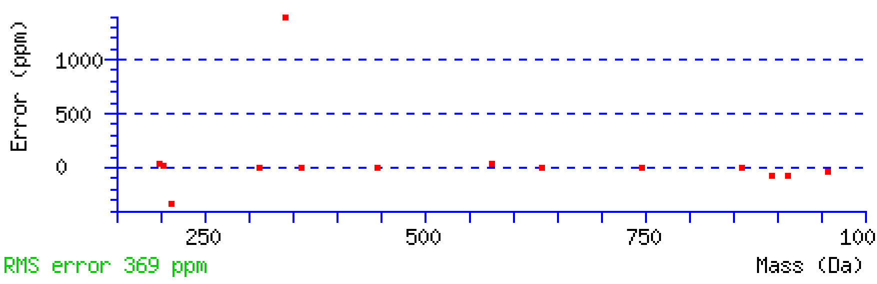
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1056.617920
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 35 **Expect:** 0.0015
Matches : 15/82 fragment ions using 44 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483			V							11
2	**199.144104**	100.075690			V	***958.556773***	479.782025	941.530224	471.268750	940.546208	470.776742	10
3	**312.228168**	156.617722			L	***859.488359***	430.247818	842.461810	421.734543	841.477794	421.242535	9
4	425.312232	213.159754			I	***746.404295***	373.705786	729.377746	365.192511	728.393730	364.700503	8
5	482.333696	241.670486			G	***633.320231***	317.163754	616.293682	308.650479	615.309666	308.158471	7
6	611.376289	306.191783	593.365724	297.186500	E	***576.298767***	288.653022	559.272218	280.139747	558.288202	279.647739	6
7	698.408317	349.707797	680.397752	340.702514	S	***447.256174***	224.131725	430.229625	215.618450	429.245609	215.126443	5
8	755.429781	378.218529	737.419216	369.213246	G	***360.224146***	180.615711	343.197597	172.102437			4
9	854.498195	427.752736	836.487630	418.747453	V	303.202682	152.104979	286.176133	143.591704			3
10	**911.519659**	456.263468	893.509094	447.258185	G	***204.134268***	102.570772	187.107719	94.057498			2
11					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of VVLIGESGVGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.0	1056.617920	-0.002032	VVLIGESGVGK
4.8	1056.608017	0.007871	KHTGVKPFK
2.6	1056.617920	-0.002032	VIILGDSGVGK
1.1	1056.608002	0.007886	KIVQWDIR
1.1	1056.617874	-0.001986	KINSLPEIK

Mascot: http://www.matrixscience.com/

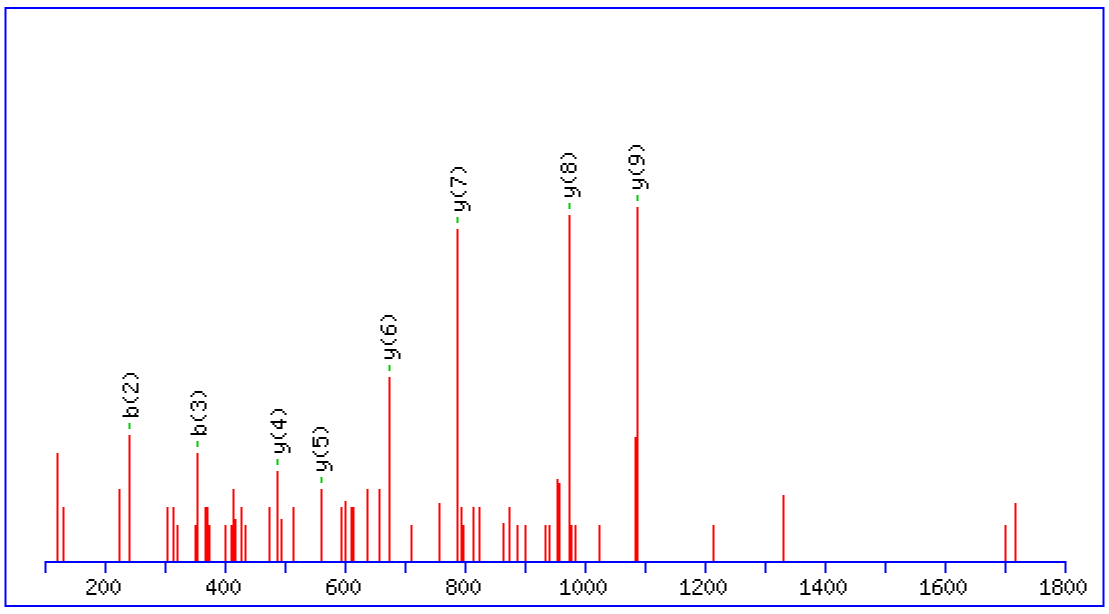
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LQLWDIAGQER**
Found in **RAB32_HUMAN**, Ras-related protein Rab-32 OS=Homo sapiens GN=RAB32 PE=1 SV=3

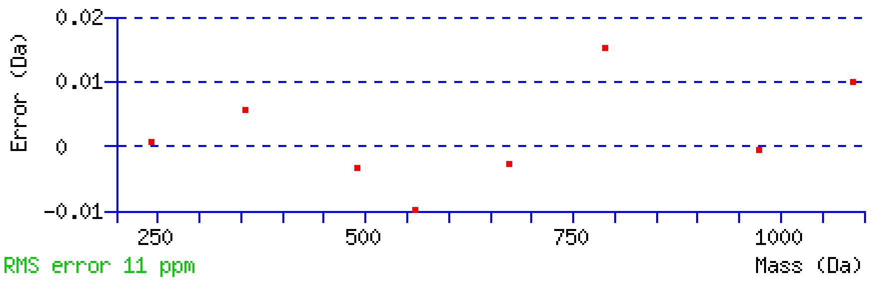
Match to Query 38170: 1327.698768 from(664.856660,2+) rtinseconds(3115) index(42019)
Title: Locus:1.1.1.2507.30
Data file 2011-11-14 - TFD - EP 8-5.mgf

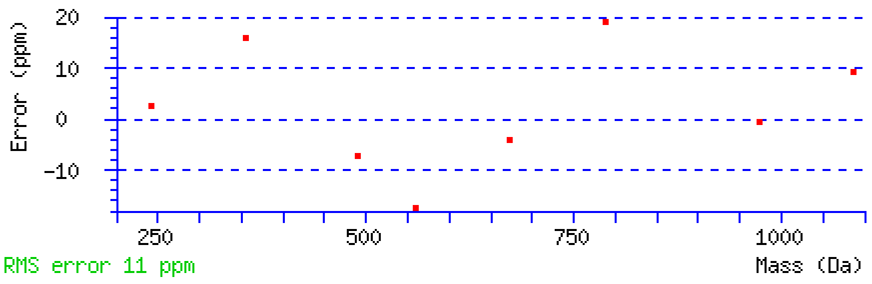
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1327.688431
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 46 **Expect:** 8.3e-005
Matches : 8/108 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							11
2	**242.149918**	121.578597	225.123369	113.065323			Q	1215.611663	608.309470	1198.585114	599.796195	1197.601098	599.304187	10
3	**355.233982**	178.120629	338.207433	169.607355			L	***1087.553085***	544.280181	1070.526536	535.766906	1069.542520	535.274898	9
4	541.313295	271.160286	524.286746	262.647011			W	***974.469021***	487.738149	957.442472	479.224874	956.458456	478.732866	8
5	656.340238	328.673757	639.313689	320.160483	638.329673	319.668475	D	***788.389708***	394.698492	771.363159	386.185217	770.379143	385.693209	7
6	769.424302	385.215789	752.397753	376.702515	751.413737	376.210507	I	***673.362765***	337.185021	656.336216	328.671746	655.352200	328.179738	6
7	840.461416	420.734346	823.434867	412.221072	822.450851	411.729064	A	***560.278701***	280.642989	543.252152	272.129714	542.268136	271.637706	5
8	897.482880	449.245078	880.456331	440.731804	879.472315	440.239796	G	***489.241587***	245.124431	472.215038	236.611157	471.231022	236.119149	4
9	1025.541458	513.274367	1008.514909	504.761093	1007.530893	504.269085	Q	432.220123	216.613699	415.193574	208.100425	414.209558	207.608417	3
10	1154.584051	577.795664	1137.557502	569.282389	1136.573486	568.790381	E	304.161545	152.584410	287.134996	144.071136	286.150980	143.579128	2
11							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LQLWDIAGQER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.0	1327.688431	0.010337	LQLWDIAGQER
2.3	1327.695663	0.003105	LGAPVGRSGGGASAR
1.4	1327.688431	0.010337	QLPSLVNAWER
0.3	1327.709564	-0.010796	LQQEILDVQSR

Mascot Search Results

Peptide View

MS/MS Fragmentation of **VIIPVKR**
Found in **PTPRA_HUMAN**, Receptor-type tyrosine-protein phosphatase alpha OS=Homo sapiens GN=PTPRA PE=1 SV=2

Match to Query 50109: 839.560108 from(420.787330,2+) rtinseconds(2491) index(764718)
Title: Locus:1.1.1.1296.5
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.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
Label all possible matches ○ Label matches used for scoring ●

```
Monoisotopic mass of neutral peptide Mr(calc): 839.559265
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
P4      : Oxidation (P)
Ions Score: 38  Expect: 0.00021
Matches : 8/38 fragment ions using 12 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	100.075690	50.541483			V					7
2	213.159754	107.083515			I	741.498136	371.252706	724.471587	362.739432	6
3	326.243818	163.625547			I	***628.414072***	314.710674	611.387523	306.197400	5
4	439.291497	220.149386			P	***515.330008***	258.168642	498.303459	249.655368	4
5	538.359911	269.683594			V	***402.282329***	201.644802	385.255780	193.131528	3
6	666.454874	333.731075	649.428325	325.217801	K	***303.213915***	152.110595	286.187366	143.597321	2
7					R	***175.118952***	88.063114	158.092403	79.549839	1

NCBI **BLAST** search of VIIPVKR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.7	839.559265	0.000843	VIIPVKR
24.1	839.559265	0.000843	VLPVIKR
22.2	839.559265	0.000843	VLLLGAVR
13.2	839.559265	0.000843	IVVLLQR
9.8	839.559265	0.000843	LPVLKVR
2.7	839.559265	0.000843	LVQLLVR
2.4	839.559265	0.000843	VIVGALLR
2.1	839.559265	0.000843	IVGLGLLR

Mascot: http://www.matrixscience.com/

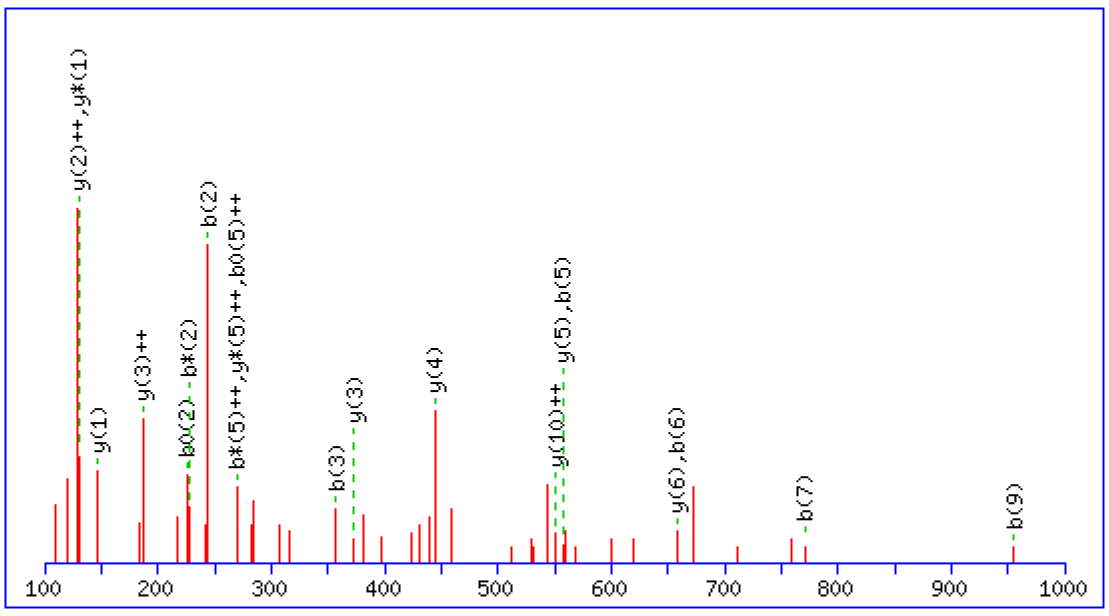
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NELAETLALLK**
Found in **RSF1_HUMAN**, Remodeling and spacing factor 1 OS=Homo sapiens GN=RSF1 PE=1 SV=2

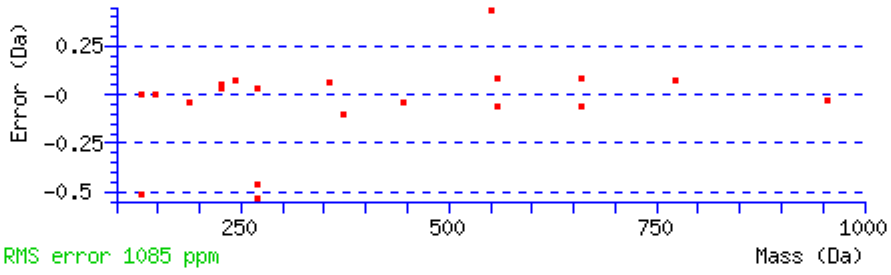
Match to Query 29461: 1213.694142 from(405.571990,3+) rtinseconds(1985) index(21664)
Title: Locus:1.1.1.2185.5
Data file 2011-11-10 - TFD - EP 3-1.mgf

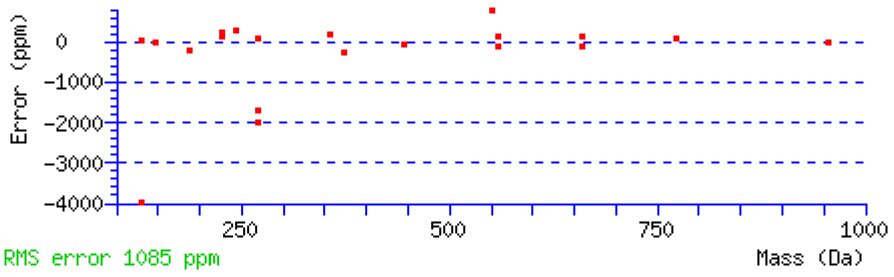
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1213.691757
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 30  Expect: 0.0068
Matches : 20/108 fragment ions using 36 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			N							11
2	***244.092796***	122.550036	227.066247	114.036762	226.082231	113.544754	E	1100.656153	550.831715	1083.629604	542.318440	1082.645588	541.826432	10
3	***357.176860***	179.092068	340.150311	170.578794	339.166295	170.086786	L	971.613560	486.310418	954.587011	477.797144	953.602995	477.305136	9
4	428.213974	214.610625	411.187425	206.097351	410.203409	205.605343	A	858.529496	429.768386	841.502947	421.255112	840.518931	420.763104	8
5	***557.256567***	279.131922	540.230018	270.618647	539.246002	270.126639	E	787.492382	394.249829	770.465833	385.736555	769.481817	385.244547	7
6	***658.304246***	329.655761	641.277697	321.142487	640.293681	320.650479	T	***658.449789***	329.728533	641.423240	321.215258	640.439224	320.723250	6
7	***771.388310***	386.197793	754.361761	377.684519	753.377745	377.192511	L	***557.402110***	279.204693	540.375561	270.691419			5
8	842.425424	421.716350	825.398875	413.203076	824.414859	412.711068	A	***444.318046***	222.662661	427.291497	214.149386			4
9	***955.509488***	478.258382	938.482939	469.745108	937.498923	469.253100	L	***373.280932***	187.144104	356.254383	178.630829			3
10	1068.593552	534.800414	1051.567003	526.287140	1050.582987	525.795132	L	260.196868	130.602072	243.170319	122.088797			2
11							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of NELAETLALLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.4	1213.691757	0.002385	NELAETLALLK
29.8	1213.691803	0.002339	LKTDVDVSLPK
14.9	1213.691772	0.002370	QLDELEKVIK
13.7	1213.691772	0.002370	KLQEEVDLLK
10.1	1213.691772	0.002370	DLAGEVEKLLK
9.9	1213.691772	0.002370	ETAEALLQVLK
9.7	1213.703018	-0.008876	KVSSQKPPALK
9.5	1213.691788	0.002354	TLIKSEPVSPK
6.6	1213.691788	0.002354	TLIKSEPVSPK
4.8	1213.703003	-0.008861	RTLLIDELNK

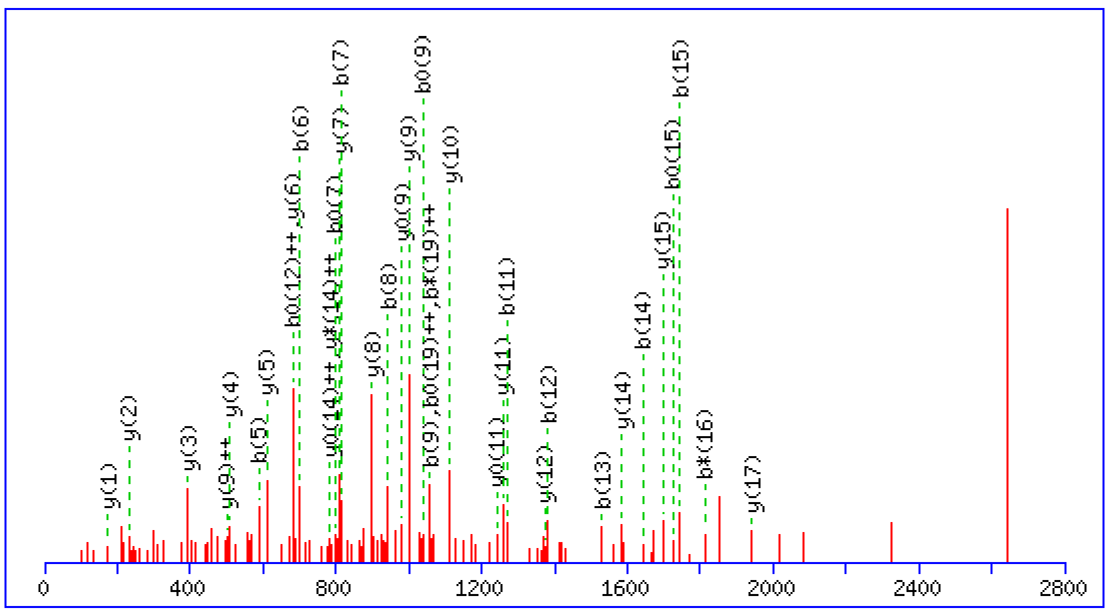
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSEEEILENPDLFLTSEATDYGR**
Found in **RCN2_HUMAN**, Reticulocalbin-2 OS=Homo sapiens GN=RCN2 PE=1 SV=1

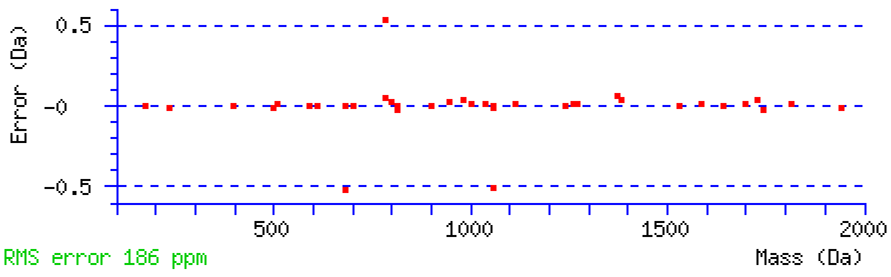
Match to Query 51760: 2640.227862 from(881.083230,3+) rtinseconds(4009) index(60368)
Title: Locus:1.1.1.3040.31
Data file 2011-11-12 - TFD - EP 5-3.mgf

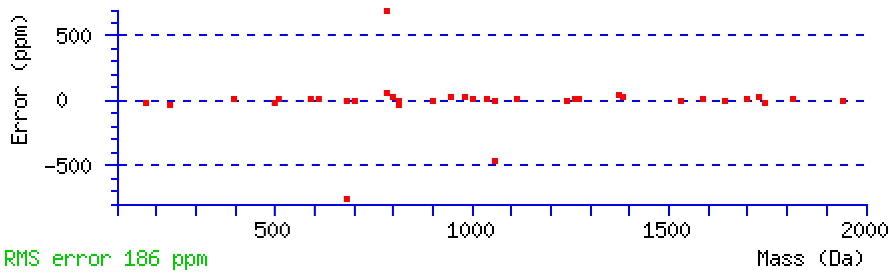
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2640.244232
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 93 **Expect:** 3.8e-009
Matches : 37/240 fragment ions using 57 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					L							23
2	201.123368	101.065322			183.112803	92.060039	S	2528.167485	1264.587380	2511.140936	1256.074106	2510.156920	1255.582098	22
3	330.165961	165.586618			312.155396	156.581336	E	2441.135457	1221.071366	2424.108908	1212.558092	2423.124892	1212.066084	21
4	459.208554	230.107915			441.197989	221.102633	E	2312.092864	1156.550070	2295.066315	1148.036795	2294.082299	1147.544787	20
5	**588.251147**	294.629212			570.240582	285.623929	E	2183.050271	1092.028773	2166.023722	1083.515499	2165.039706	1083.023491	19
6	**701.335211**	351.171244			683.324646	342.165961	I	2054.007678	1027.507477	2036.981129	1018.994202	2035.997113	1018.502194	18
7	**814.419275**	407.713276			796.408710	398.707993	L	***1940.923614***	970.965445	1923.897065	962.452170	1922.913049	961.960162	17
8	**943.461868**	472.234572			925.451303	463.229290	E	1827.839550	914.423413	1810.813001	905.910139	1809.828985	905.418130	16
9	**1057.504795**	529.256036	1040.478246	520.742761	1039.494230	520.250753	N	***1698.796957***	849.902116	1681.770408	841.388842	1680.786392	840.896834	15
10	1154.557559	577.782418	1137.531010	569.269143	1136.546994	568.777135	P	***1584.754030***	792.880653	1567.727481	784.367378	1566.743465	783.875370	14
11	**1269.584502**	635.295889	1252.557953	626.782615	1251.573937	626.290607	D	1487.701266	744.354271	1470.674717	735.840996	1469.690701	735.348988	13
12	**1382.668566**	691.837921	1365.642017	683.324647	1364.658001	682.832639	L	***1372.674323***	686.840799	1355.647774	678.327525	1354.663758	677.835517	12
13	**1529.736980**	765.372128	1512.710431	756.858854	1511.726415	756.366846	F	***1259.590259***	630.298767	1242.563710	621.785493	1241.579694	621.293485	11
14	**1642.821044**	821.914160	1625.794495	813.400886	1624.810479	812.908878	L	***1112.521845***	556.764560	1095.495296	548.251286	1094.511280	547.759278	10
15	**1743.868723**	872.438000	1726.842174	863.924725	1725.858158	863.432717	T	***999.437781***	500.222528	982.411232	491.709254	981.427216	491.217246	9
16	1830.900751	915.954014	1813.874202	907.440739	1812.890186	906.948731	S	***898.390102***	449.698689	881.363553	441.185414	880.379537	440.693406	8
17	1959.943344	980.475310	1942.916795	971.962036	1941.932779	971.470028	E	***811.358074***	406.182675	794.331525	397.669400	793.347509	397.177392	7
18	2030.980458	1015.993867	2013.953909	1007.480593	2012.969893	1006.988585	A	***682.315481***	341.661378	665.288932	333.148104	664.304916	332.656096	6
19	2132.028137	1066.517706	2115.001588	1058.004432	2114.017572	1057.512424	T	***611.278367***	306.142821	594.251818	297.629547	593.267802	297.137539	5
20	2247.055080	1124.031178	2230.028531	1115.517903	2229.044515	1115.025895	D	***510.230688***	255.618982	493.204139	247.105707	492.220123	246.613699	4
21	2410.118409	1205.562842	2393.091860	1197.049568	2392.107844	1196.557560	Y	***395.203745***	198.105510	378.177196	189.592236			3
22	2467.139873	1234.073574	2450.113324	1225.560300	2449.129308	1225.068292	G	***232.140416***	116.573846	215.113867	108.060571			2
23							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LSEEEILENPDLFLTSEATDYGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
93.1	2640.244232	-0.016370	LSEEEILENPDLFLTSEATDYGR
3.1	2640.227859	0.000003	ELCPPDPAFAPLSSWPGSGPAGGSTR
3.1	2640.227859	0.000003	ELCPPDPAFAPLSSWPGSGPAGGSTR
3.1	2640.227859	0.000003	ELCPPDPAFAPLSSWPGSGPAGGSTR
0.8	2640.252884	-0.025022	GEGGPPGVAGPPGGSGPAGPPGPQGVKGER
0.2	2640.209244	0.018618	TFGPPPSLSPGAFSYSSSSRFSSSR

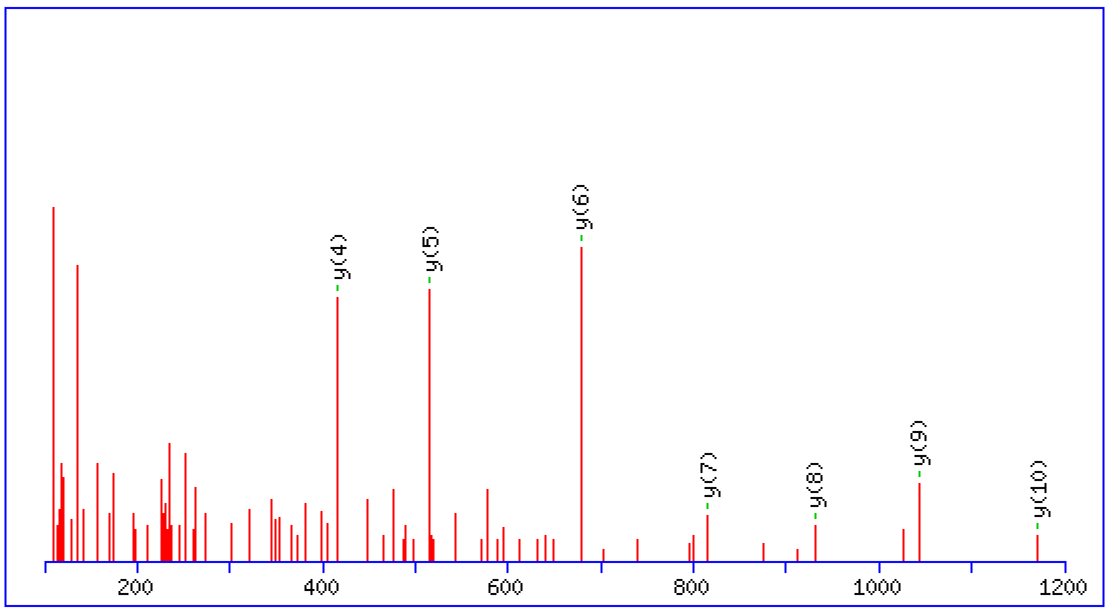
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TQIDHYVGIAR**
Found in **RTN3_HUMAN**, Reticulon-3 OS=Homo sapiens GN=RTN3 PE=1 SV=2

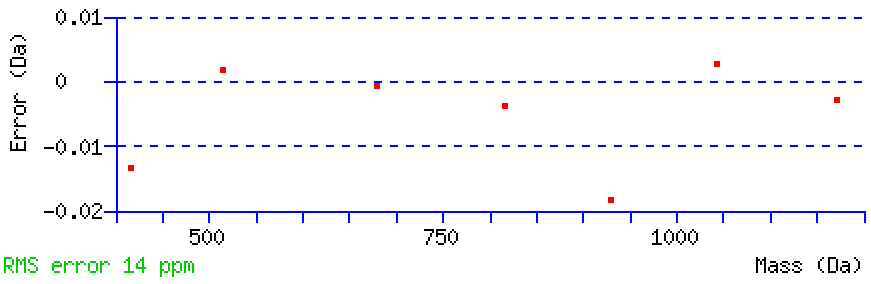
Match to Query 35188: 1271.665272 from(424.895700,3+) rtinseconds(1883) index(19068)
Title: Locus:1.1.1.2039.5
Data file 2011-11-14 - TFD - EP 8-5.mgf

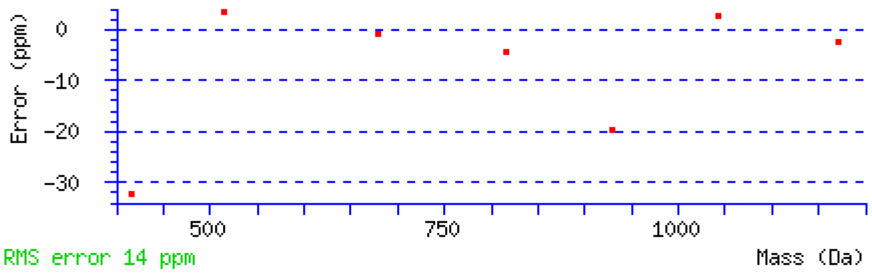
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1271.662231
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 52 **Expect:** 4.1e-005
Matches : 7/104 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							11
2	230.113533	115.560405	213.086984	107.047130	212.102968	106.555122	Q	***1171.621834***	586.314555	1154.595285	577.801281	1153.611269	577.309273	10
3	343.197597	172.102437	326.171048	163.589162	325.187032	163.097154	I	***1043.563256***	522.285266	1026.536707	513.771992	1025.552691	513.279984	9
4	458.224540	229.615908	441.197991	221.102634	440.213975	220.610626	D	***930.479192***	465.743234	913.452643	457.229960	912.468627	456.737952	8
5	595.283452	298.145364	578.256903	289.632090	577.272887	289.140082	H	***815.452249***	408.229762	798.425700	399.716488			7
6	758.346781	379.677029	741.320232	371.163754	740.336216	370.671746	Y	***678.393337***	339.700307	661.366788	331.187032			6
7	857.415195	429.211236	840.388646	420.697961	839.404630	420.205953	V	***515.330008***	258.168642	498.303459	249.655367			5
8	914.436659	457.721968	897.410110	449.208693	896.426094	448.716685	G	***416.261594***	208.634435	399.235045	200.121160			4
9	1027.520723	514.264000	1010.494174	505.750725	1009.510158	505.258717	I	359.240130	180.123703	342.213581	171.610428			3
10	1098.557837	549.782557	1081.531288	541.269282	1080.547272	540.777274	A	246.156066	123.581671	229.129517	115.068396			2
11							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of TQIDHYVGIAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.7	1271.662231	0.003041	TQIDHYVGIAR
4.8	1271.672119	-0.006847	TQEQSDVKLPK
4.4	1271.672119	-0.006847	QTSPLGSSLPAAK
4.0	1271.673462	-0.008190	IEVQPKPHHR
1.9	1271.665604	-0.000332	TEVQVMGGARPK

Mascot: http://www.matrixscience.com/

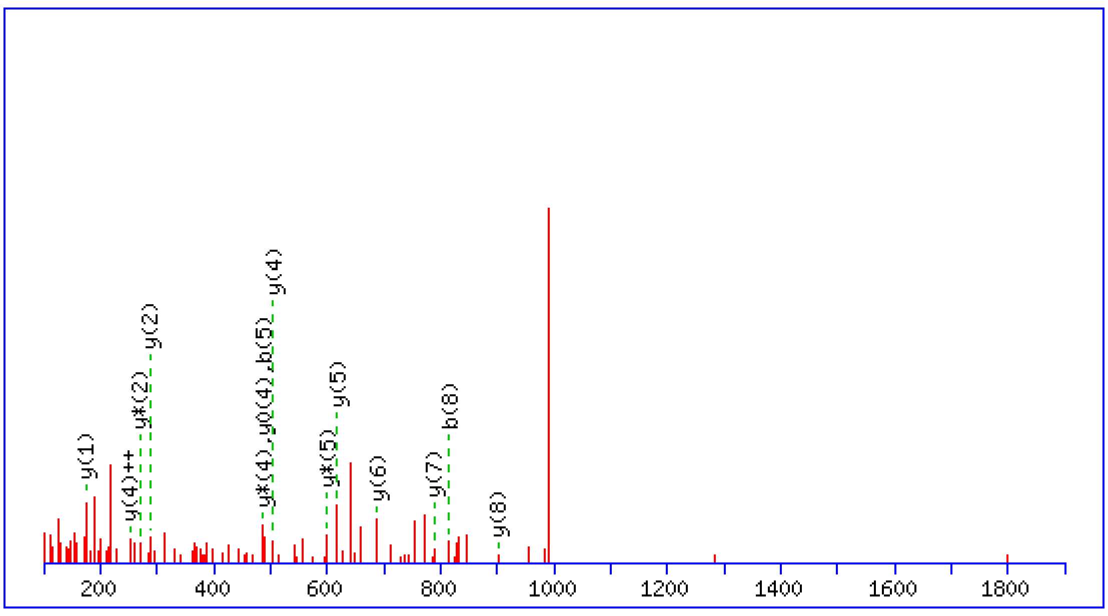
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SLTALSEPR**
Found in **RAI1_HUMAN**, Retinoic acid-induced protein 1 OS=Homo sapiens GN=RAI1 PE=1 SV=2

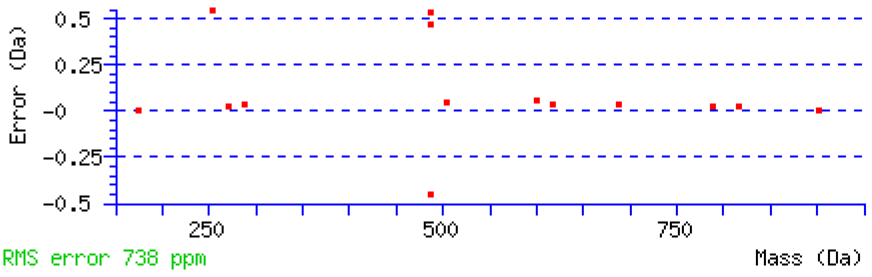
Match to Query 12189: 988.524548 from(495.269550,2+) rtinseconds(1185) index(7476)
Title: Locus:1.1.1.1864.21
Data file 2011-11-10 - TFD - EP 3-3.mgf

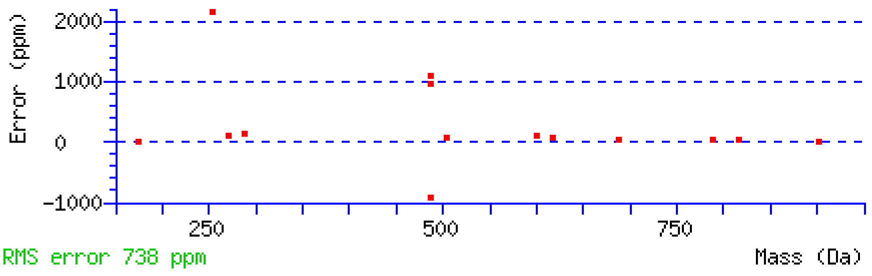
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1900] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 988.518906
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P8 : Oxidation (P)
Ions Score: 34 **Expect:** 0.0065
Matches : 14/76 fragment ions using 35 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	**S**							9
2	201.123368	101.065322	183.112803	92.060039	**L**	***902.494173***	451.750725	885.467624	443.237450	884.483608	442.745442	8
3	302.171047	151.589161	284.160482	142.583879	**T**	***789.410109***	395.208693	772.383560	386.695418	771.399544	386.203410	7
4	373.208161	187.107718	355.197596	178.102436	**A**	***688.362430***	344.684853	671.335881	336.171579	670.351865	335.679571	6
5	**486.292225**	243.649750	468.281660	234.644468	**L**	***617.325316***	309.166296	600.298767	300.653022	599.314751	300.161014	5
6	573.324253	287.165765	555.313688	278.160482	**S**	***504.241252***	252.624264	487.214703	244.110990	486.230687	243.618982	4
7	702.366846	351.687061	684.356281	342.681779	**E**	417.209224	209.108250	400.182675	200.594976	399.198659	200.102968	3
8	**815.414525**	408.210901	797.403960	399.205618	**P**	***288.166631***	144.586954	271.140082	136.073679			2
9					**R**	***175.118952***	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of SLTALSEPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.6	988.518906	0.005642	SLTALSEPR
25.5	988.530121	-0.005573	SEISELRR
17.2	988.518936	0.005612	SPSTIDVVR
15.0	988.530136	-0.005588	SEVTELRR
10.2	988.523605	0.000943	RAGAACTLR
9.3	988.518936	0.005612	TSTVPPSLR
9.0	988.530136	-0.005588	DRTLESLR
4.8	988.534180	-0.009632	SPFLPGSIR
4.8	988.534149	-0.009601	YREPPALK
4.2	988.518921	0.005627	TSITQQPSK

Mascot: http://www.matrixscience.com/

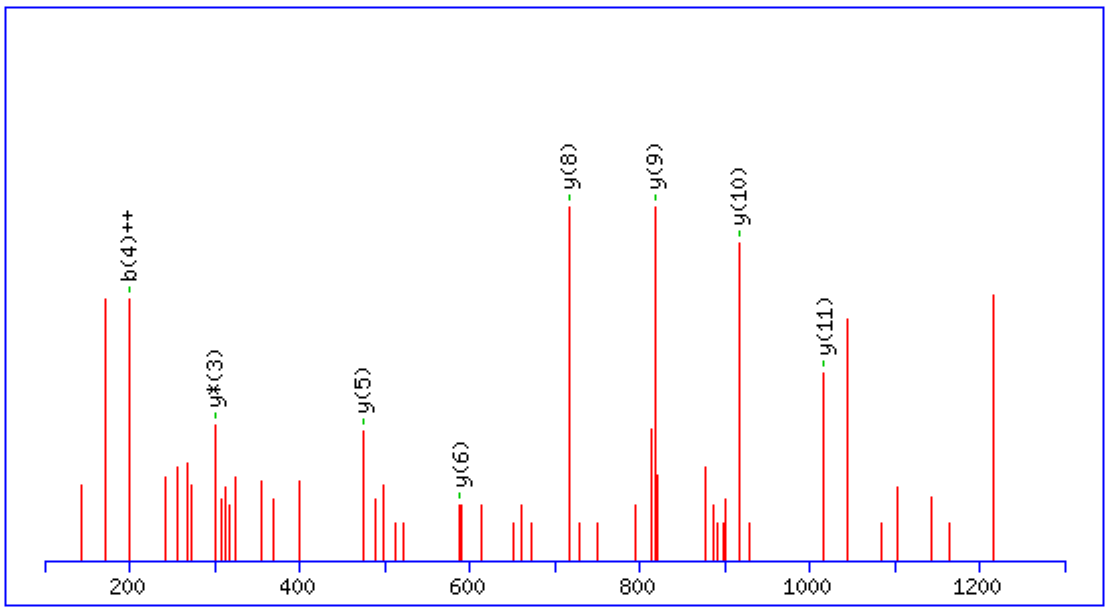
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVVVTGANTGIGK**
Found in **RDH11_HUMAN**, Retinol dehydrogenase 11 OS=Homo sapiens GN=RDH11 PE=1 SV=2

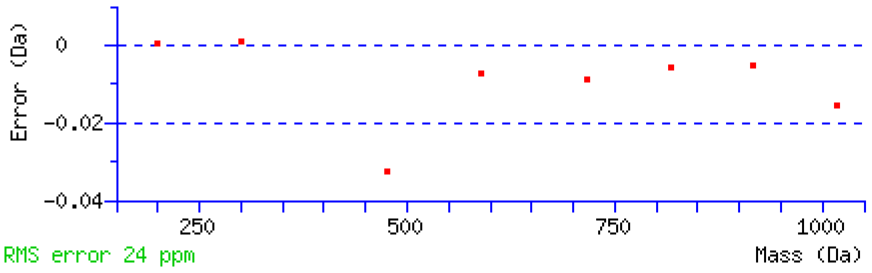
Match to Query 31272: 1213.705068 from(607.859810,2+) rtinseconds(1758) index(16436)
Title: Locus:1.1.1.1985.42
Data file 2011-11-10 - TFD - EP 4-5.mgf

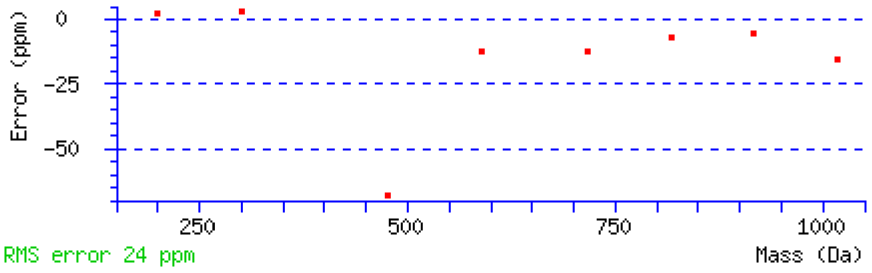
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1300] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1213.703064
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.00042
Matches : 9/114 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							13
2	199.144104	100.075690					V	1115.641901	558.324589	1098.615352	549.811314	1097.631336	549.319306	12
3	298.212518	149.609897					V	***1016.573487***	508.790382	999.546938	500.277107	998.562922	499.785099	11
4	397.280932	199.144104					V	***917.505073***	459.256175	900.478524	450.742900	899.494508	450.250892	10
5	498.328611	249.667944			480.318046	240.662661	T	***818.436659***	409.721968	801.410110	401.208693	800.426094	400.716685	9
6	555.350075	278.178676			537.339510	269.173393	G	***717.388980***	359.198128	700.362431	350.684853	699.378415	350.192845	8
7	626.387189	313.697233			608.376624	304.691950	A	660.367516	330.687396	643.340967	322.174122	642.356951	321.682114	7
8	740.430116	370.718696	723.403567	362.205422	722.419551	361.713414	N	***589.330402***	295.168839	572.303853	286.655565	571.319837	286.163557	6
9	841.477795	421.242536	824.451246	412.729261	823.467230	412.237253	T	***475.287475***	238.147375	458.260926	229.634101	457.276910	229.142093	5
10	898.499259	449.753268	881.472710	441.239993	880.488694	440.747985	G	374.239796	187.623536	357.213247	179.110261			4
11	1011.583323	506.295300	994.556774	497.782025	993.572758	497.290017	I	317.218332	159.112804	300.191783	150.599529			3
12	1068.604787	534.806032	1051.578238	526.292757	1050.594222	525.800749	G	204.134268	102.570772	187.107719	94.057497			2
13							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of VVVVTGANTGIGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.3	1213.703064	0.002004	VVVVTGANTGIGK

Mascot: http://www.matrixscience.com/

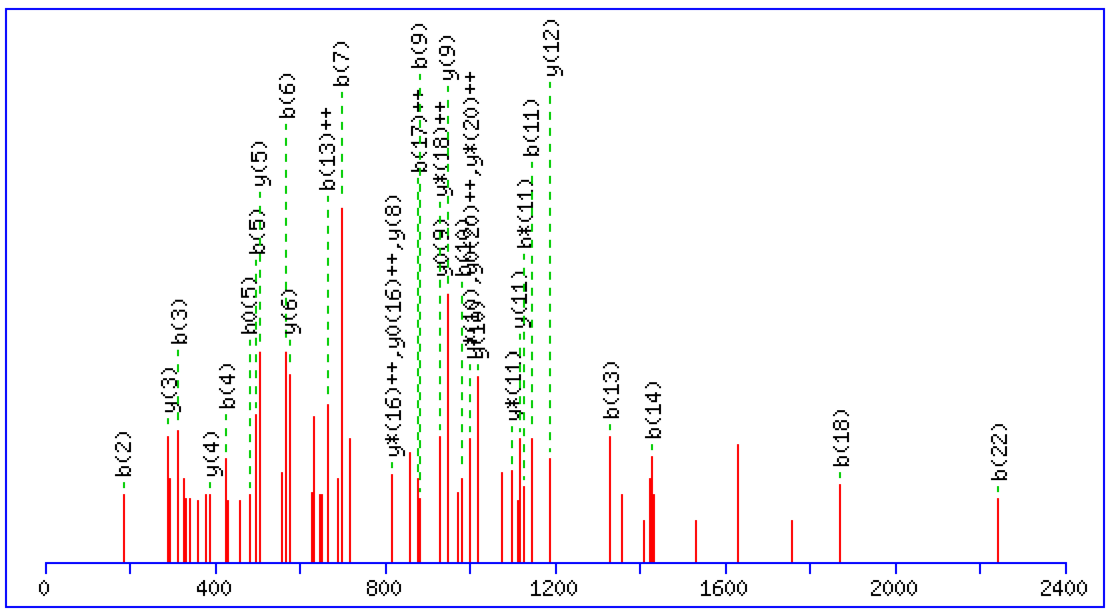
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SPELAAQPSTYLAVAEELADVSGK**
Found in **RDH13_HUMAN**, Retinol dehydrogenase 13 OS=Homo sapiens GN=RDH13 PE=1 SV=2

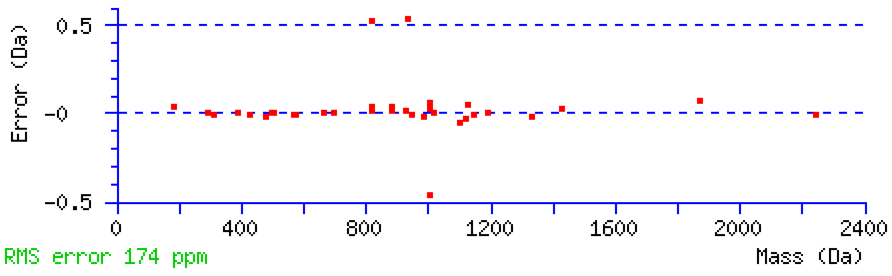
Match to Query 72209: 2445.239922 from(816.087250,3+) rtinseconds(4346) index(66797)
Title: Locus:1.1.1.2941.45
Data file 2011-11-12 - TFD - EP 6-4.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●

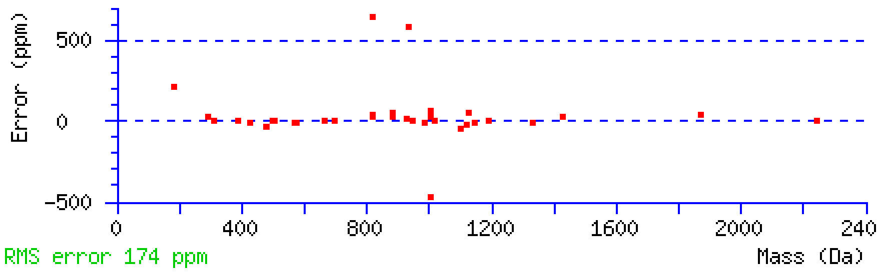


```
Monoisotopic mass of neutral peptide Mr(calc): 2445.227463
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 97  Expect: 1.9e-009
Matches : 34/260 fragment ions using 47 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	88.039304	44.523290			70.028739	35.518008	S							24
2	***185.092068***	93.049672			167.081503	84.044389	P	2359.202750	1180.105013	2342.176201	1171.591738	2341.192185	1171.099730	23
3	***314.134661***	157.570968			296.124096	148.565686	E	2262.149986	1131.578631	2245.123437	1123.065356	2244.139421	1122.573348	22
4	***427.218725***	214.113001			409.208160	205.107718	L	2133.107393	1067.057334	2116.080844	1058.544060	2115.096828	1058.052052	21
5	***498.255839***	249.631557			480.245274	240.626275	A	2020.023329	1010.515303	2002.996780	1002.002028	2002.012764	1001.510020	20
6	***569.292953***	285.150115			551.282388	276.144832	A	1948.986215	974.996745	1931.959666	966.483471	1930.975650	965.991463	19
7	***697.351531***	349.179404	680.324982	340.666129	679.340966	340.174121	Q	1877.949101	939.478188	1860.922552	930.964914	1859.938536	930.472906	18
8	794.404295	397.705786	777.377746	389.192511	776.393730	388.700503	P	1749.890523	875.448899	1732.863974	866.935625	1731.879958	866.443617	17
9	***881.436323***	441.221800	864.409774	432.708525	863.425758	432.216517	S	1652.837759	826.922517	1635.811210	818.409243	1634.827194	817.917235	16
10	***982.484002***	491.745639	965.457453	483.232365	964.473437	482.740357	T	1565.805731	783.406503	1548.779182	774.893229	1547.795166	774.401221	15
11	***1145.547331***	573.277304	1128.520782	564.764029	1127.536766	564.272021	Y	1464.758052	732.882664	1447.731503	724.369390	1446.747487	723.877381	14
12	1258.631395	629.819335	1241.604846	621.306061	1240.620830	620.814053	L	1301.694723	651.350999	1284.668174	642.837725	1283.684158	642.345717	13
13	***1329.668509***	665.337892	1312.641960	656.824618	1311.657944	656.332610	A	***1188.610659***	594.808967	1171.584110	586.295693	1170.600094	585.803685	12
14	***1428.736923***	714.872099	1411.710374	706.358825	1410.726358	705.866817	V	***1117.573545***	559.290411	1100.546996	550.777136	1099.562980	550.285128	11
15	1499.774037	750.390656	1482.747488	741.877382	1481.763472	741.385374	A	***1018.505131***	509.756203	1001.478582	501.242929	1000.494566	500.750921	10
16	1628.816630	814.911953	1611.790081	806.398679	1610.806065	805.906671	E	***947.468017***	474.237646	930.441468	465.724372	929.457452	465.232364	9
17	1757.859223	879.433250	1740.832674	870.919975	1739.848658	870.427967	E	***818.425424***	409.716350	801.398875	401.203075	800.414859	400.711067	8
18	***1870.943287***	935.975282	1853.916738	927.462007	1852.932722	926.969999	L	689.382831	345.195053	672.356282	336.681779	671.372266	336.189771	7
19	1941.980401	971.493839	1924.953852	962.980564	1923.969836	962.488556	A	***576.298767***	288.653021	559.272218	280.139747	558.288202	279.647739	6
20	2057.007344	1029.007310	2039.980795	1020.494035	2038.996779	1020.002027	D	***505.261653***	253.134464	488.235104	244.621190	487.251088	244.129182	5
21	2156.075758	1078.541517	2139.049209	1070.028242	2138.065193	1069.536234	V	***390.234710***	195.620993	373.208161	187.107718	372.224145	186.615710	4
22	***2243.107786***	1122.057531	2226.081237	1113.544256	2225.097221	1113.052248	S	***291.166296***	146.086786	274.139747	137.573512	273.155731	137.081504	3
23	2300.129250	1150.568263	2283.102701	1142.054988	2282.118685	1141.562980	G	204.134268	102.570772	187.107719	94.057497			2
24							K	147.112804	74.060040	130.086255	65.546765			1



RMS error 174 ppm



RMS error 174 ppm

NCBI **BLAST** search of SPELAAQPSTYLAVAEELADVSGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
96.9	2445.227463	0.012459	SPELAAQPSTYLAVAEELADVSGK
3.8	2445.260742	-0.020820	MATRVEVGSITPLTAVPGLGEMGK
1.9	2445.260742	-0.020820	MATRVEVGSITPLTAVPGLGEMGK

Mascot: http://www.matrixscience.com/

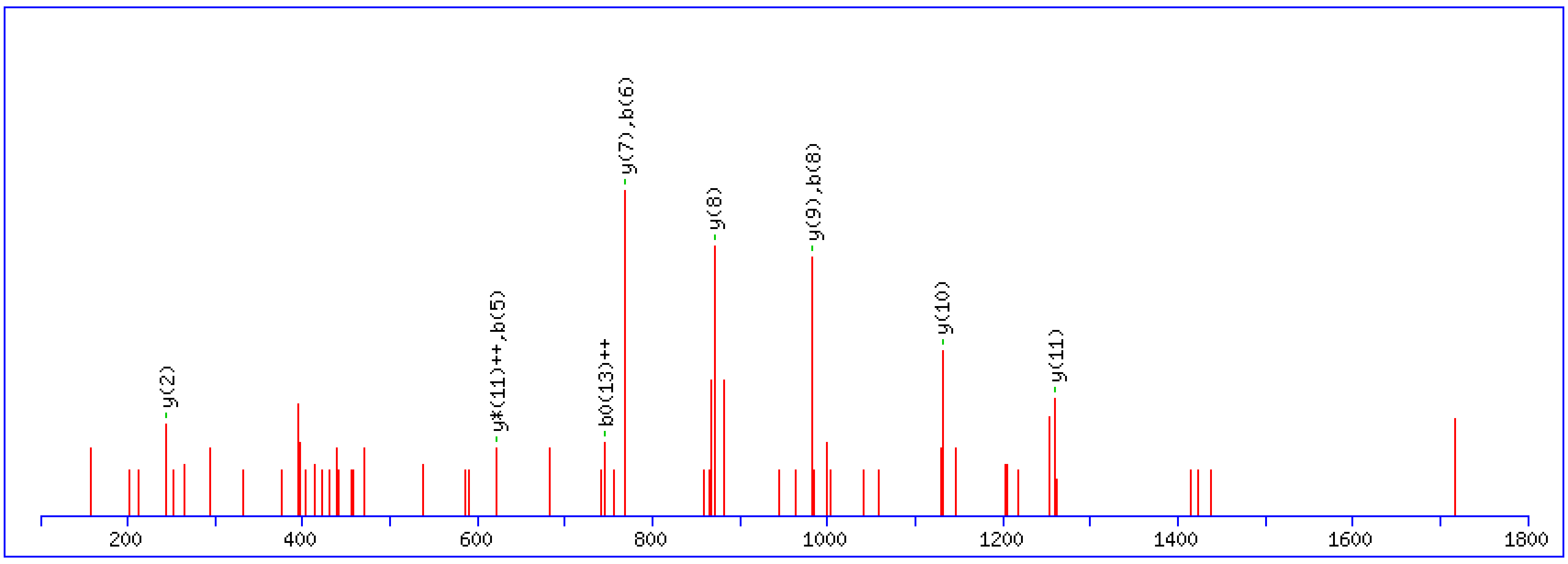
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AEEYEFLTPVEEAPK**
Found in **GDIR1_HUMAN**, Rho GDP-dissociation inhibitor 1 OS=Homo sapiens GN=ARHGDIA PE=1 SV=3

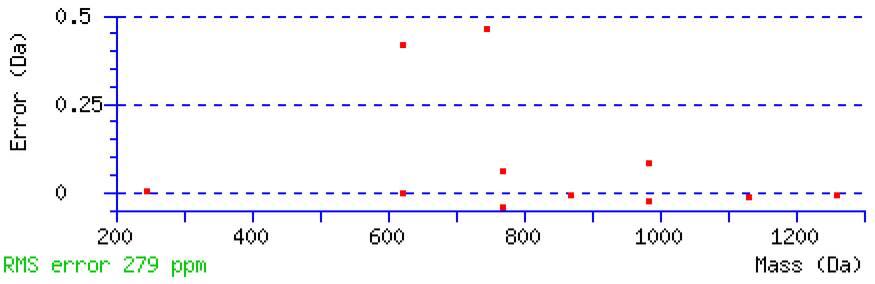
Match to Query 65581: 1750.826168 from(876.420360,2+) rtinseconds(2976) index(41734)
Title: Locus:1.1.1.1521.47
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 1.mgf

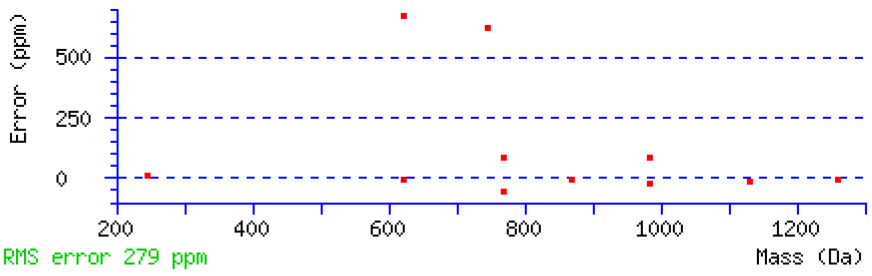
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1750.830109
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 37  Expect: 0.00036
Matches : 11/132 fragment ions using 14 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			A							15
2	201.086983	101.047130	183.076418	92.041847	E	1680.800311	840.903794	1663.773762	832.390519	1662.789746	831.898511	14
3	330.129576	165.568426	312.119011	156.563144	E	1551.757718	776.382497	1534.731169	767.869223	1533.747153	767.377215	13
4	493.192905	247.100090	475.182340	238.094808	Y	1422.715125	711.861201	1405.688576	703.347926	1404.704560	702.855918	12
5	**622.235498**	311.621387	604.224933	302.616105	E	***1259.651796***	630.329536	1242.625247	621.816262	1241.641231	621.324254	11
6	**769.303912**	385.155594	751.293347	376.150311	F	***1130.609203***	565.808240	1113.582654	557.294965	1112.598638	556.802957	10
7	882.387976	441.697626	864.377411	432.692343	L	***983.540789***	492.274033	966.514240	483.760758	965.530224	483.268750	9
8	**983.435655**	492.221466	965.425090	483.216183	T	***870.456725***	435.732001	853.430176	427.218726	852.446160	426.726718	8
9	1080.488419	540.747848	1062.477854	531.742565	P	***769.409046***	385.208161	752.382497	376.694887	751.398481	376.202879	7
10	1179.556833	590.282055	1161.546268	581.276772	V	672.356282	336.681779	655.329733	328.168505	654.345717	327.676497	6
11	1308.599426	654.803351	1290.588861	645.798069	E	573.287868	287.147572	556.261319	278.634298	555.277303	278.142290	5
12	1437.642019	719.324648	1419.631454	710.319365	E	444.245275	222.626276	427.218726	214.113001	426.234710	213.620993	4
13	1508.679133	754.843205	1490.668568	745.837922	A	315.202682	158.104979	298.176133	149.591704			3
14	1605.731897	803.369587	1587.721332	794.364304	P	***244.165568***	122.586422	227.139019	114.073148			2
15					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of AEEYEFLTPVEEAPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.8	1750.830109	-0.003941	AEEYEFLTPVEEAPK
0.0	1750.834854	-0.008686	HANALFDYAVTGDVKM

Mascot: http://www.matrixscience.com/

MATRIX SCIENCE

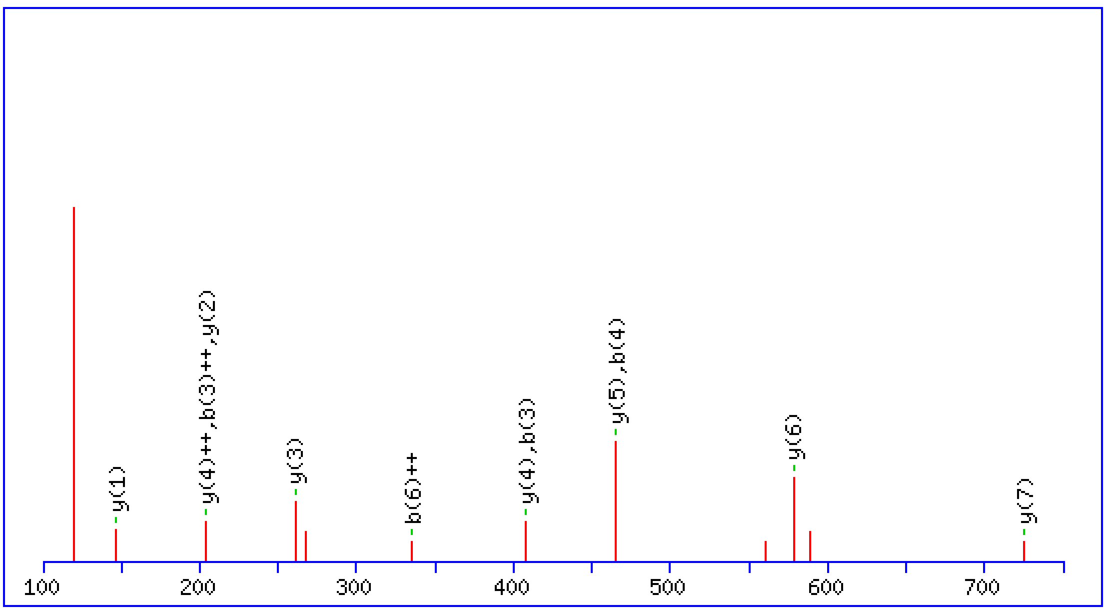
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FFIGFGGK**
Found in **RBSK_HUMAN**, Ribokinase OS=Homo sapiens GN=RBKS PE=1 SV=1

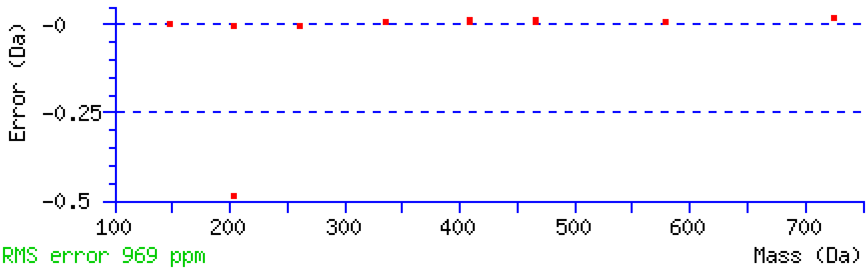
Match to Query 5577: 871.458768 from(436.736660,2+) rtinseconds(2973) index(40748)
Title: Locus:1.1.1.2560.2
Data file 2011-11-13 - TFD - EP 7-4.mgf

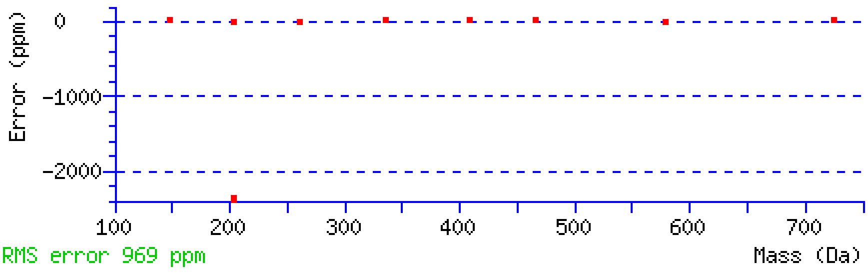
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 871.459244
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 65 **Expect:** 4.9e-006
Matches : 12/42 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	148.075690	74.541483	F					8
2	295.144104	148.075690	F	725.398088	363.202682	708.371539	354.689408	7
3	408.228168	204.617722	I	578.329674	289.668475	561.303125	281.155201	6
4	465.249632	233.128454	G	465.245610	233.126443	448.219061	224.613169	5
5	612.318046	306.662661	F	408.224146	204.615711	391.197597	196.102437	4
6	669.339510	335.173393	G	261.155732	131.081504	244.129183	122.568230	3
7	726.360974	363.684125	G	204.134268	102.570772	187.107719	94.057498	2
8			K	147.112804	74.060040	130.086255	65.546765	1





NCBI **BLAST** search of FFIGFGGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
64.6	871.459244	-0.000476	FFIGFGGK
23.9	871.459229	-0.000461	FGFIFNK
8.1	871.466415	-0.007647	AQKHFNK
5.2	871.458557	0.000211	NLCLPGGK
4.8	871.451187	0.007581	RGPSTPGGK
4.8	871.451187	0.007581	RGPSTPGGK
3.9	871.462402	-0.003634	RRPQDGK
2.1	871.458572	0.000196	HTVLMQK

Mascot: http://www.matrixscience.com/

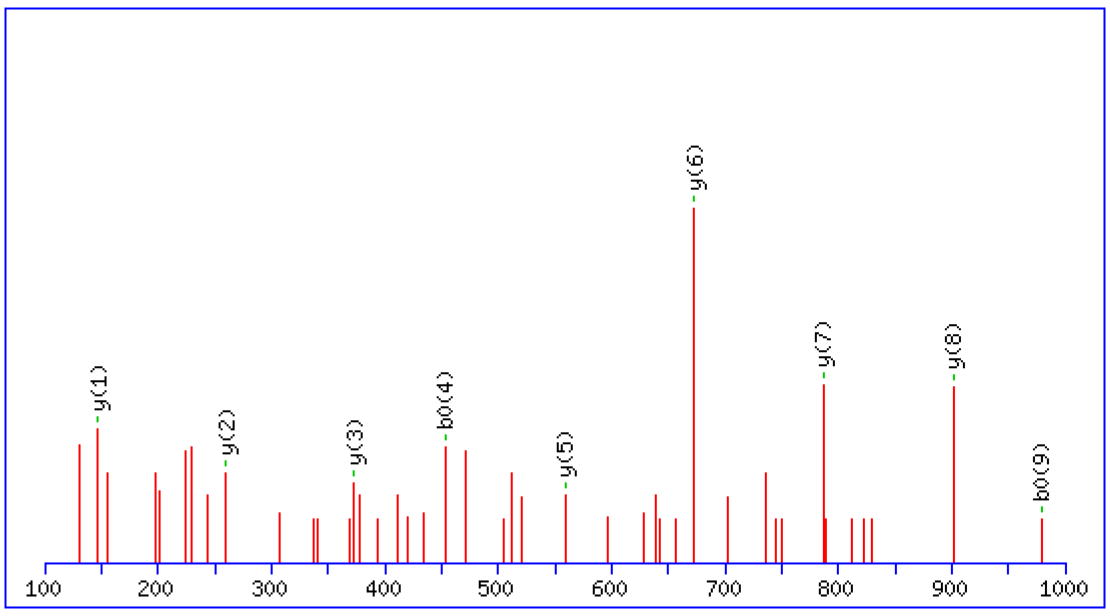
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELDLNSVLLK**
Found in **RNT2_HUMAN**, Ribonuclease T2 OS=Homo sapiens GN=RNASET2 PE=1 SV=2

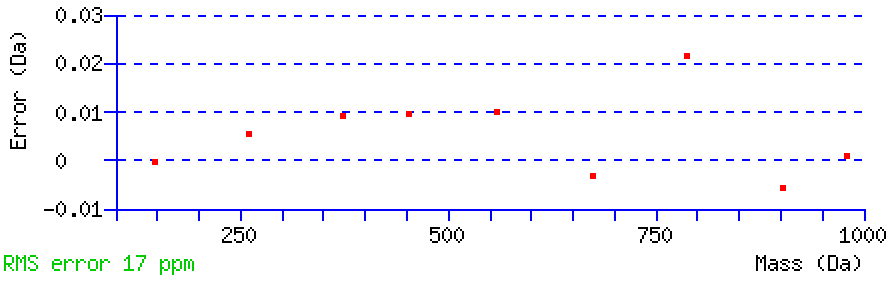
Match to Query 25427: 1142.657428 from(572.335990,2+) rtinseconds(3216) index(42130)
Title: Locus:1.1.1.2515.19
Data file 2011-11-13 - TFD - EP 7-6.mgf

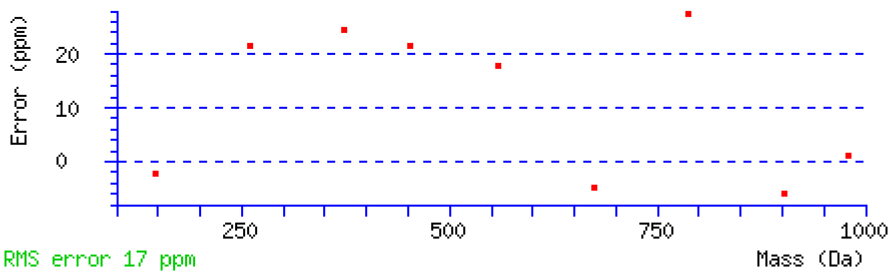
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1142.654663
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 62  Expect: 4.7e-006
Matches : 9/92 fragment ions using 9 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	E							10
2	243.133933	122.070605			225.123368	113.065322	L	1014.619372	507.813324	997.592823	499.300050	996.608807	498.808042	9
3	358.160876	179.584076			340.150311	170.578794	D	***901.535308***	451.271292	884.508759	442.758017	883.524743	442.266010	8
4	471.244940	236.126108			453.234375	227.120826	L	***786.508365***	393.757820	769.481816	385.244546	768.497800	384.752538	7
5	585.287867	293.147572	568.261318	284.634297	567.277302	284.142289	N	***673.424301***	337.215789	656.397752	328.702514	655.413736	328.210506	6
6	672.319895	336.663586	655.293346	328.150311	654.309330	327.658303	S	***559.381374***	280.194325	542.354825	271.681050	541.370809	271.189042	5
7	771.388309	386.197793	754.361760	377.684518	753.377744	377.192510	V	472.349346	236.678311	455.322797	228.165036			4
8	884.472373	442.739825	867.445824	434.226550	866.461808	433.734542	L	***373.280932***	187.144104	356.254383	178.630829			3
9	997.556437	499.281857	980.529888	490.768582	979.545872	490.276574	L	***260.196868***	130.602072	243.170319	122.088797			2
10							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of ELDLNSVLLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
62.0	1142.654663	0.002765	ELDLNSVLLK
17.9	1142.654663	0.002765	LEDLATLIQK
17.4	1142.665909	-0.008481	TKQIQEGVIK
17.4	1142.665894	-0.008466	NQEVTIKALK
15.5	1142.665894	-0.008466	LEGEVRSLLK
9.6	1142.665894	-0.008466	ATAEVLNIGKK
7.8	1142.648148	0.009280	ERVCPLVIK
6.3	1142.654678	0.002750	VDLDSGALLIK
5.7	1142.654694	0.002734	GTTLVVELAPK
5.2	1142.665878	-0.008450	ELANTIKNIK

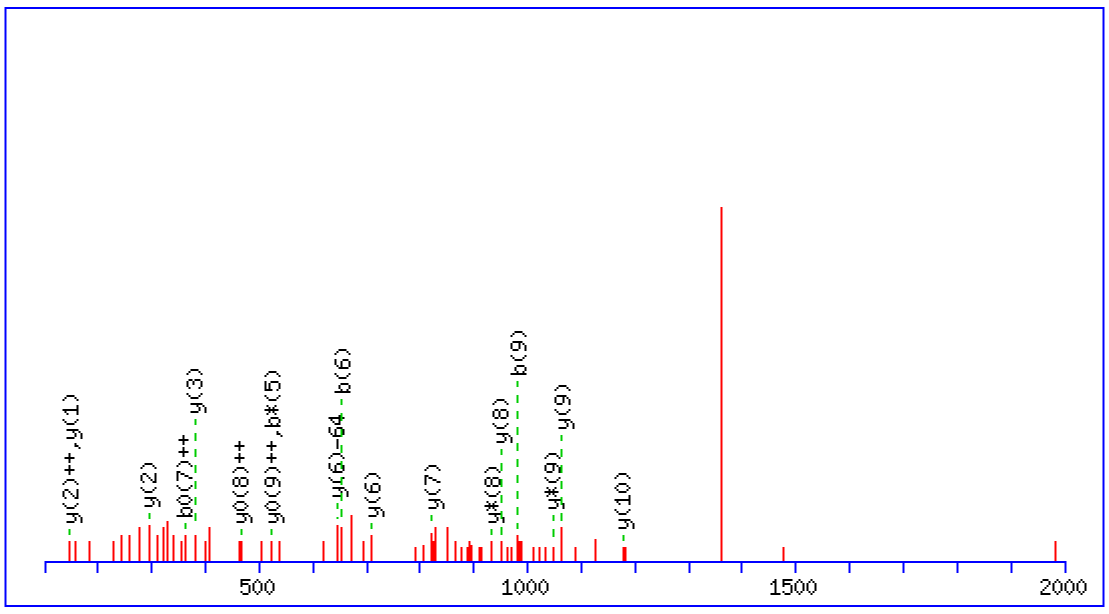
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LALNQISQISMK**
Found in **RRFM_HUMAN**, Ribosome-recycling factor, mitochondrial OS=Homo sapiens GN=MRRF PE=1 SV=1

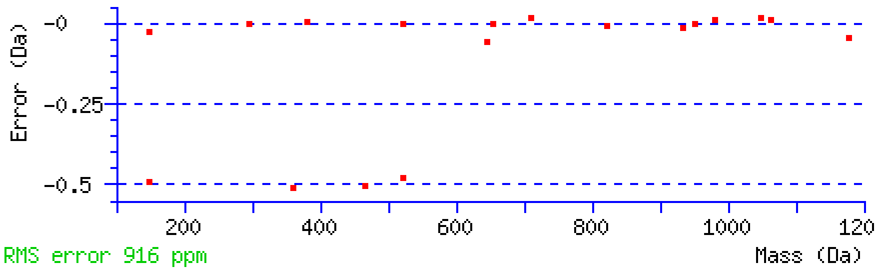
Match to Query 38880: 1360.740668 from(681.377610,2+) rtinseconds(2498) index(30791)
Title: Locus:1.1.1.2242.42
Data file 2011-11-12 - TFD - EP 6-5.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●

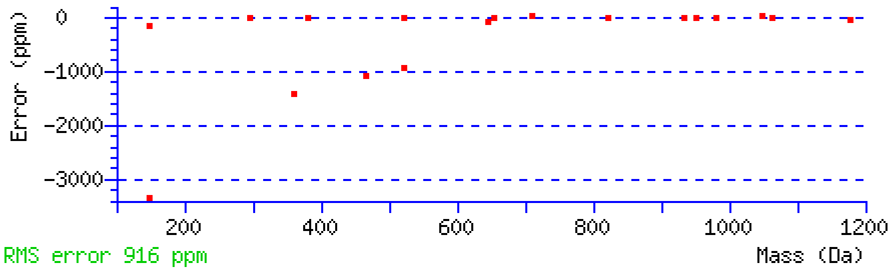


```
Monoisotopic mass of neutral peptide Mr(calc): 1360.738403
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M11     : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 46  Expect: 0.00045
Matches : 18/174 fragment ions using 32 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							12
2	185.128454	93.067865					A	1248.661649	624.834463	1231.635100	616.321188	1230.651084	615.829180	11
3	298.212518	149.609897					L	***1177.624535***	589.315906	1160.597986	580.802631	1159.613970	580.310623	10
4	412.255445	206.631361	395.228896	198.118086			N	***1064.540471***	532.773874	1047.513922	524.260599	1046.529906	523.768591	9
5	540.314023	270.660650	523.287474	262.147375			Q	***950.497544***	475.752410	933.470995	467.239136	932.486979	466.747128	8
6	**653.398087**	327.202682	636.371538	318.689407			I	***822.438966***	411.723121	805.412417	403.209847	804.428401	402.717839	7
7	740.430115	370.718696	723.403566	362.205421	722.419550	361.713413	S	***709.354902***	355.181089	692.328353	346.667815	691.344337	346.175807	6
8	868.488693	434.747985	851.462144	426.234710	850.478128	425.742702	Q	622.322874	311.665075	605.296325	303.151801	604.312309	302.659793	5
9	**981.572757**	491.290017	964.546208	482.776742	963.562192	482.284734	I	494.264296	247.635786	477.237747	239.122512	476.253731	238.630504	4
10	1068.604785	534.806031	1051.578236	526.292756	1050.594220	525.800748	S	***381.180232***	191.093754	364.153683	182.580480	363.169667	182.088472	3
11	1215.640185	608.323731	1198.613636	599.810456	1197.629620	599.318448	M	***294.148204***	147.577740	277.121655	139.064465			2
12							K	***147.112804***	74.060040	130.086255	65.546765			1



RMS error 916 ppm



RMS error 916 ppm

NCBI **BLAST** search of LALNQISQISMK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.3	1360.738403	0.002265	LALNQISQISMK
10.1	1360.738403	0.002265	ANKILIADTQMK
8.2	1360.735062	0.005606	KPVAGALDVSFNK

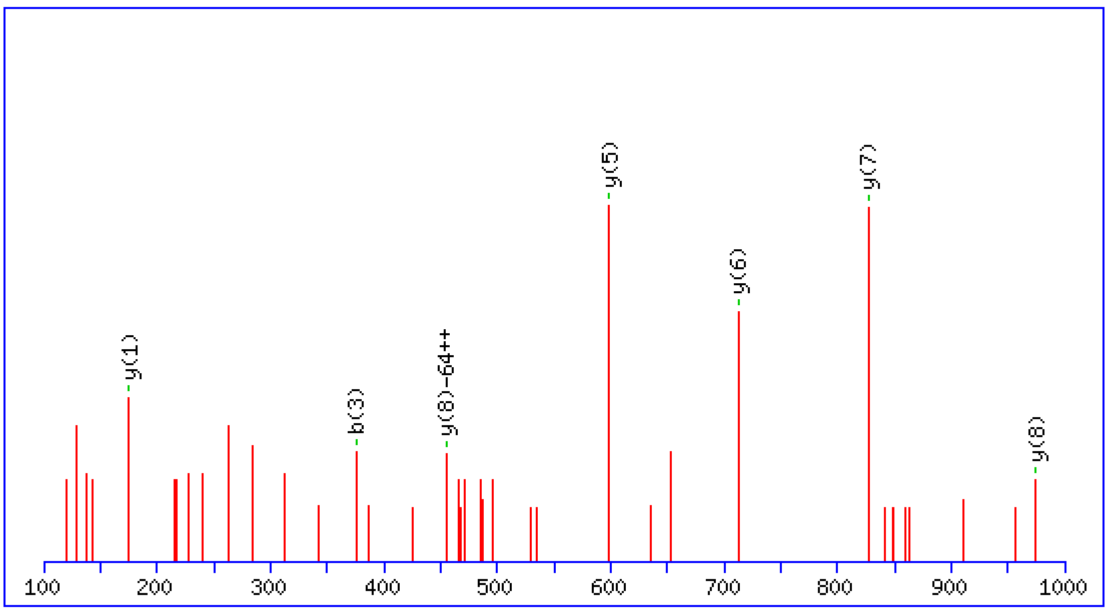
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IMDLPTLLR**
Found in **RN170_HUMAN**, RING finger protein 170 OS=Homo sapiens GN=RNF170 PE=2 SV=2

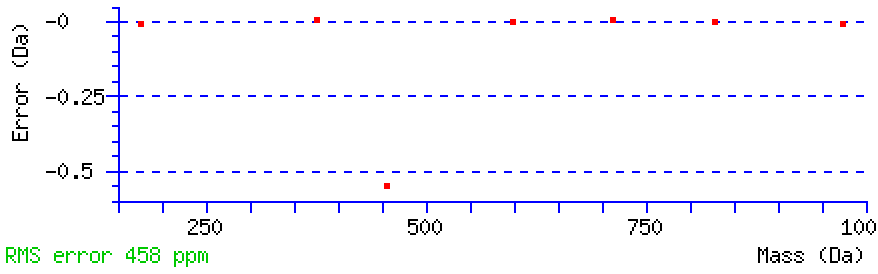
Match to Query 22039: 1086.612508 from(544.313530,2+) rtinseconds(2845) index(37316)
Title: Locus:1.1.1.2373.17
Data file 2011-11-12 - TFD - EP 6-5.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●

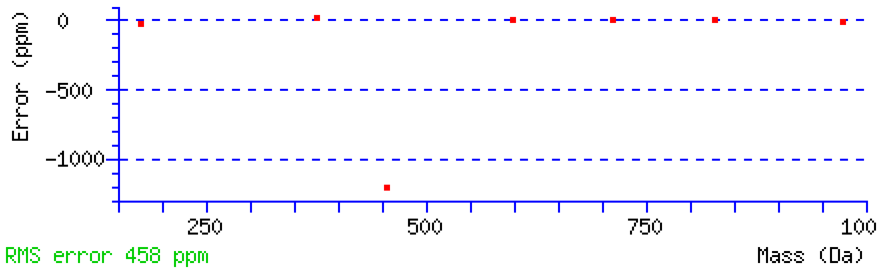


```
Monoisotopic mass of neutral peptide Mr(calc): 1086.610703
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M2      : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 40  Expect: 0.0011
Matches : 7/102 fragment ions using 8 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							9
2	261.126740	131.067008			M	***974.533930***	487.770603	957.507381	479.257329	956.523365	478.765321	8
3	376.153683	188.580480	358.143118	179.575197	D	***827.498530***	414.252903	810.471981	405.739629	809.487965	405.247621	7
4	489.237747	245.122512	471.227182	236.117229	L	***712.471587***	356.739432	695.445038	348.226157	694.461022	347.734149	6
5	586.290511	293.648894	568.279946	284.643611	P	***599.387523***	300.197400	582.360974	291.684125	581.376958	291.192117	5
6	687.338190	344.172733	669.327625	335.167451	T	502.334759	251.671018	485.308210	243.157743	484.324194	242.665735	4
7	800.422254	400.714765	782.411689	391.709483	L	401.287080	201.147178	384.260531	192.633904			3
8	913.506318	457.256797	895.495753	448.251515	L	288.203016	144.605146	271.176467	136.091872			2
9					R	***175.118952***	88.063114	158.092403	79.549840			1



RMS error 458 ppm



RMS error 458 ppm

NCBI **BLAST** search of IMDLPTLLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.7	1086.610703	0.001805	IMDLPTLLR
7.8	1086.603287	0.009221	DIEKLLSNR
4.1	1086.621918	-0.009410	ITPAMAARIK
3.3	1086.621918	-0.009410	ILAKVQEMR
3.0	1086.618561	-0.006053	LGLPLQQYR
1.4	1086.603302	0.009206	LLGEALSTAGR
0.3	1086.607315	0.005193	LEPLYSPIR
0.3	1086.603302	0.009206	LEQGTSALIR

Mascot: http://www.matrixscience.com/

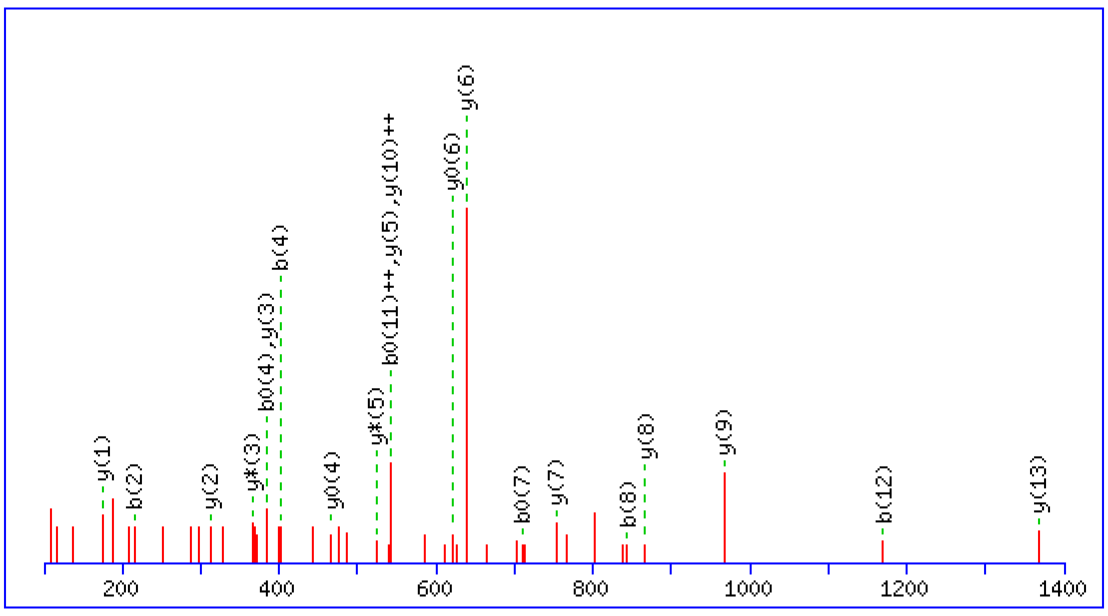
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LTADLTLDPGTAHR**
Found in **RNF39_HUMAN**, RING finger protein 39 OS=Homo sapiens GN=RNF39 PE=1 SV=2

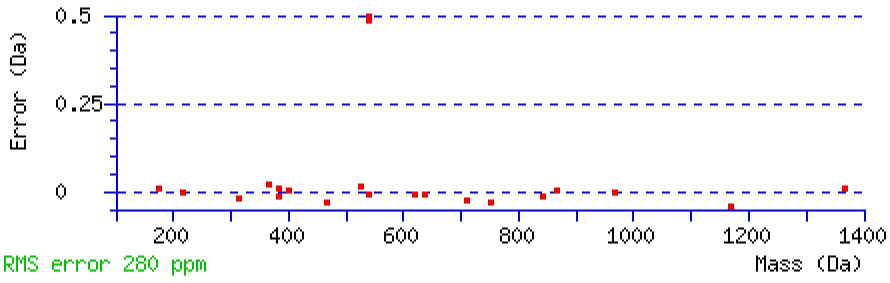
Match to Query 44661: 1479.769062 from(494.263630,3+) rtinseconds(2105) index(24412)
Title: Locus:1.1.1.2233.16
Data file 2011-11-13 - TFD - EP 7-4.mgf

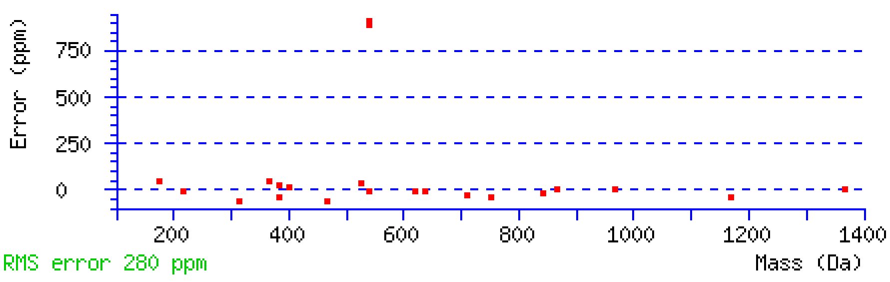
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1479.768158
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 58  Expect: 1.8e-005
Matches : 21/122 fragment ions using 34 most intense peaks    (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							14
2	**215.139019**	108.073147	197.128454	99.067865	T	***1367.691371***	684.349324	1350.664822	675.836049	1349.680806	675.344041	13
3	286.176133	143.591704	268.165568	134.586422	A	1266.643692	633.825484	1249.617143	625.312210	1248.633127	624.820202	12
4	**401.203076**	201.105176	383.192511	192.099894	D	1195.606578	598.306927	1178.580029	589.793653	1177.596013	589.301645	11
5	514.287140	257.647208	496.276575	248.641926	L	1080.579635	540.793456	1063.553086	532.280181	1062.569070	531.788173	10
6	615.334819	308.171048	597.324254	299.165765	T	***967.495571***	484.251424	950.469022	475.738149	949.485006	475.246141	9
7	728.418883	364.713080	710.408318	355.707797	L	***866.447892***	433.727584	849.421343	425.214310	848.437327	424.722302	8
8	**843.445826**	422.226551	825.435261	413.221269	D	***753.363828***	377.185552	736.337279	368.672278	735.353263	368.180270	7
9	940.498590	470.752933	922.488025	461.747651	P	***638.336885***	319.672081	621.310336	311.158806	620.326320	310.666798	6
10	997.520054	499.263665	979.509489	490.258383	G	***541.284121***	271.145699	524.257572	262.632424	523.273556	262.140416	5
11	1098.567733	549.787505	1080.557168	540.782222	T	484.262657	242.634966	467.236108	234.121692	466.252092	233.629684	4
12	**1169.604847**	585.306062	1151.594282	576.300779	A	***383.214978***	192.111127	366.188429	183.597852			3
13	1306.663759	653.835518	1288.653194	644.830235	H	***312.177864***	156.592570	295.151315	148.079295			2
14					R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LTADLTLDPGTAHR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.0	1479.768158	0.000904	LTADLTLDPGTAHR
9.3	1479.765488	0.003574	GGGGRPRQQVSPPR
5.7	1479.779373	-0.010311	LLRAESPAGGAPGPR
5.6	1479.775528	-0.006466	LKNPNAPMLPPPK
5.6	1479.775528	-0.006466	LKNPNAPMLPPPK
3.2	1479.783401	-0.014339	WSGALPLQALGSHK
2.1	1479.775543	-0.006481	LNGTKDSMFGIAVK
1.6	1479.772156	-0.003094	TILPAAAQDVYYR
1.2	1479.779373	-0.010311	LSINHPSQGVREK

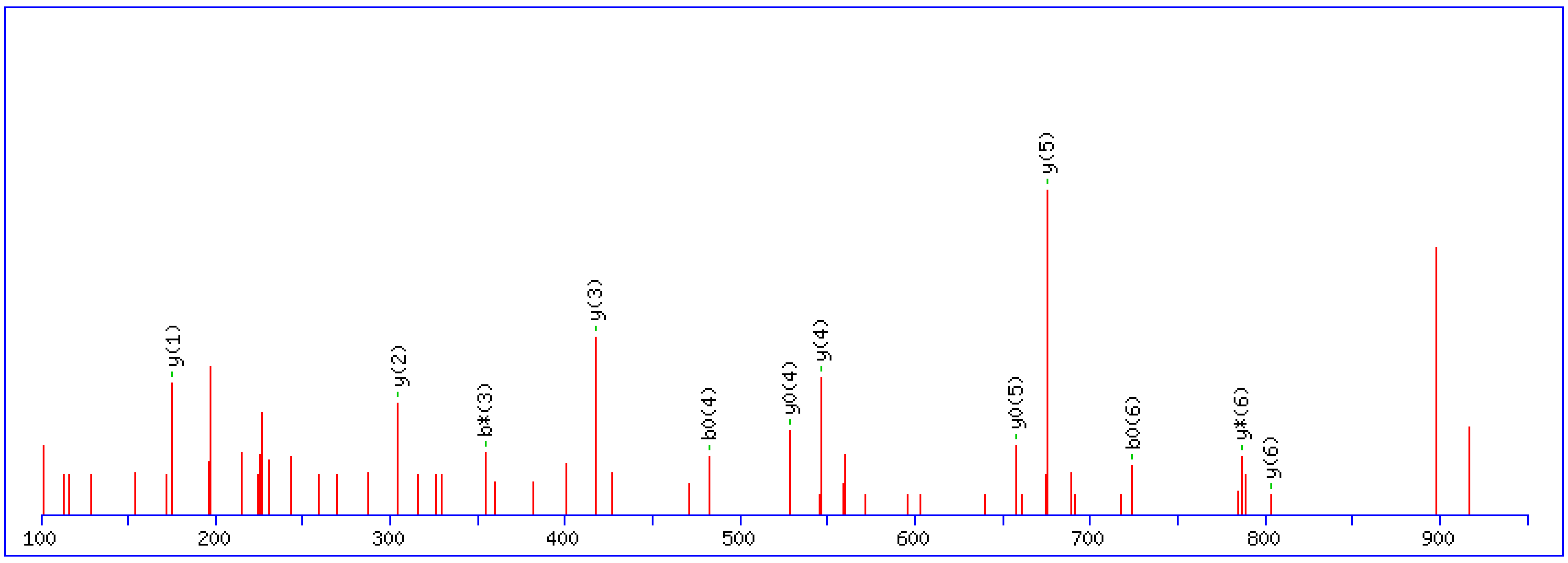
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LQEELER**
Found in **BSN_HUMAN**, Protein bassoon OS=Homo sapiens GN=BSN PE=1 SV=4

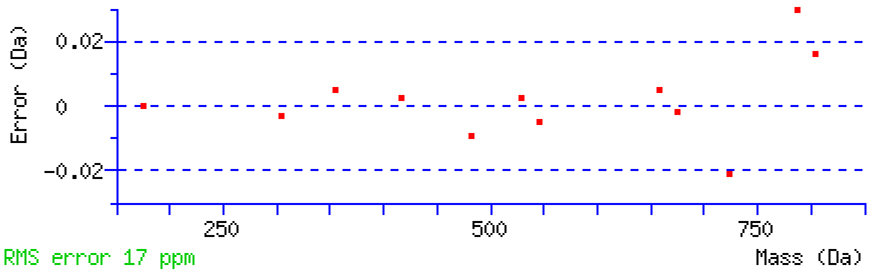
Match to Query 7582: 915.469948 from(458.742250,2+) rtinseconds(1341) index(10596)
Title: Locus:1.1.1.899.9
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 1.mgf

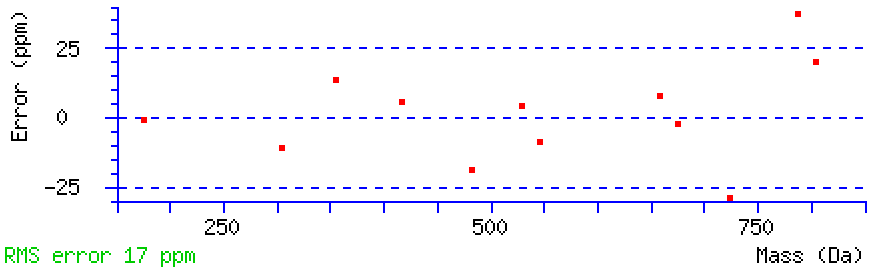
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 915.466125
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 44  Expect: 0.0007
Matches : 12/64 fragment ions using 16 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							7
2	242.149918	121.578597	225.123369	113.065323			Q	***803.389373***	402.198325	786.362824	393.685050	785.378808	393.193042	6
3	371.192511	186.099894	354.165962	177.586619	353.181946	177.094611	E	***675.330795***	338.169036	658.304246	329.655761	657.320230	329.163753	5
4	500.235104	250.621190	483.208555	242.107916	482.224539	241.615908	E	***546.288202***	273.647739	529.261653	265.134465	528.277637	264.642457	4
5	613.319168	307.163222	596.292619	298.649948	595.308603	298.157940	L	***417.245609***	209.126442	400.219060	200.613168	399.235044	200.121160	3
6	742.361761	371.684519	725.335212	363.171244	724.351196	362.679236	E	***304.161545***	152.584410	287.134996	144.071136	286.150980	143.579128	2
7							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LQEELER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.5	915.466125	0.003823	LQEELER
33.5	915.466125	0.003823	QLEELER
30.7	915.466125	0.003823	IQELEER
19.2	915.477356	-0.007408	LQEENRK
19.1	915.477371	-0.007423	LQEQKDR
18.4	915.477356	-0.007408	LEKENQR
16.9	915.466125	0.003823	LQLEEER
16.9	915.466125	0.003823	ELQELER
12.8	915.477371	-0.007423	QLEQKDR
11.4	915.477356	-0.007408	QLENEKR

Mascot Search Results

Peptide View

MS/MS Fragmentation of **AQPSVSLGAPYR**
Found in **RBM14_HUMAN**, RNA-binding protein 14 OS=Homo sapiens GN=RBM14 PE=1 SV=2

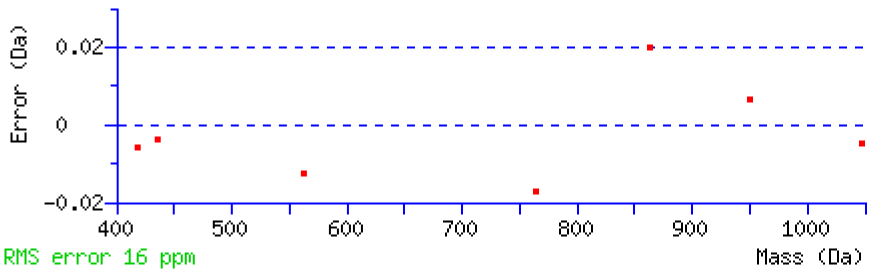
Match to Query 32393: 1244.656968 from(623.335760,2+) rtinseconds(2014) index(22051)
Title: Locus:1.1.1.2260.41
Data file 2011-11-10 - TFD - EP 4-2.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●

MS/MS spectrum of AQPSVSLGAPYR

Monoisotopic mass of neutral peptide Mr(calc): 1244.651321
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 43 **Expect:** 0.00024
Matches : 7/112 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							12
2	200.102968	100.555122	183.076419	92.041848			Q	1174.621499	587.814388	1157.594950	579.301113	1156.610934	578.809105	11
3	297.155732	149.081504	280.129183	140.568230			P	***1046.562921***	523.785099	1029.536372	515.271824	1028.552356	514.779816	10
4	384.187760	192.597518	367.161211	184.084243	366.177195	183.592235	S	***949.510157***	475.258717	932.483608	466.745442	931.499592	466.253434	9
5	483.256174	242.131725	466.229625	233.618450	465.245609	233.126443	V	***862.478129***	431.742703	845.451580	423.229428	844.467564	422.737420	8
6	570.288202	285.647739	553.261653	277.134465	552.277637	276.642457	S	***763.409715***	382.208496	746.383166	373.695221	745.399150	373.203213	7
7	683.372266	342.189771	666.345717	333.676497	665.361701	333.184489	L	676.377687	338.692482	659.351138	330.179207			6
8	740.393730	370.700503	723.367181	362.187229	722.383165	361.695221	G	***563.293623***	282.150450	546.267074	273.637175			5
9	811.430844	406.219060	794.404295	397.705786	793.420279	397.213778	A	506.272159	253.639717	489.245610	245.126443			4
10	908.483608	454.745442	891.457059	446.232168	890.473043	445.740160	P	***435.235045***	218.121160	418.208496	209.607886			3
11	1071.546937	536.277107	1054.520388	527.763832	1053.536372	527.271824	Y	338.182281	169.594778	321.155732	161.081504			2
12							R	175.118952	88.063114	158.092403	79.549839			1



Error Distribution (ppm)

NCBI **BLAST** search of AQPSVSLGAPYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.7	1244.651321	0.005647	AQPSVSLGAPYR
4.0	1244.651306	0.005662	AQPEGKNNLFK

Mascot: http://www.matrixscience.com/

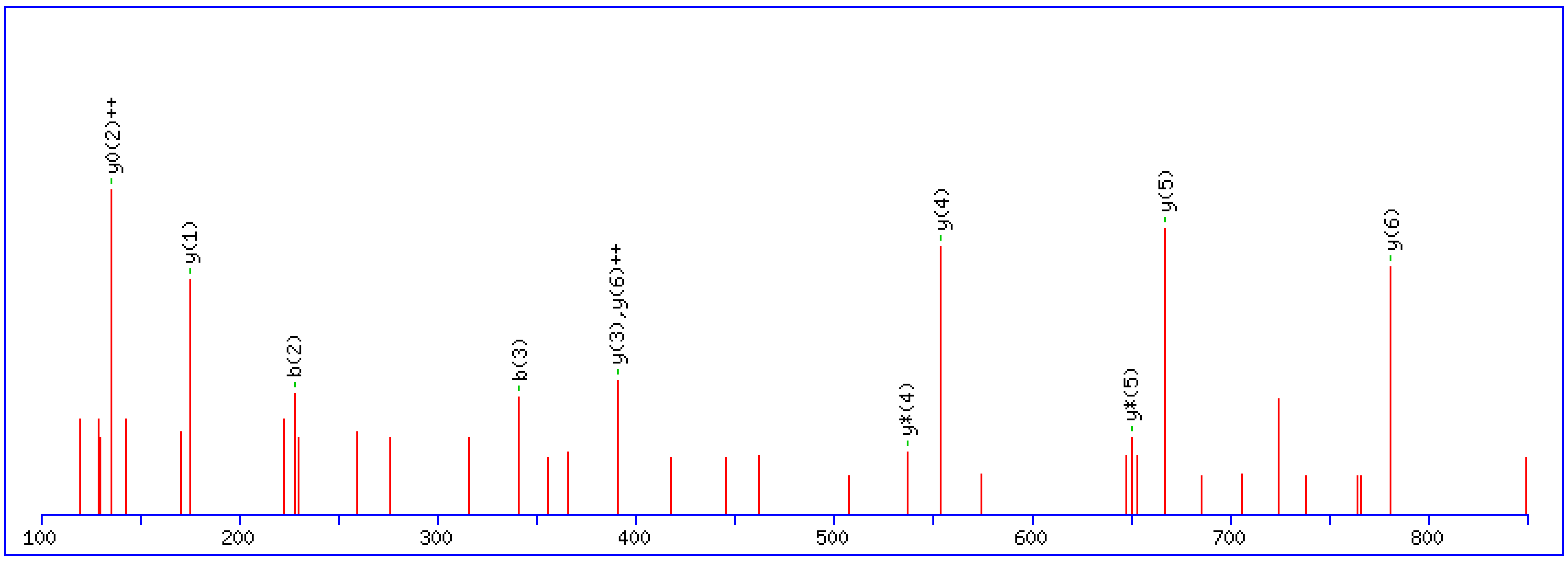
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **INLYTDR**
Found in **FUS_HUMAN**, RNA-binding protein FUS OS=Homo sapiens GN=FUS PE=1 SV=1

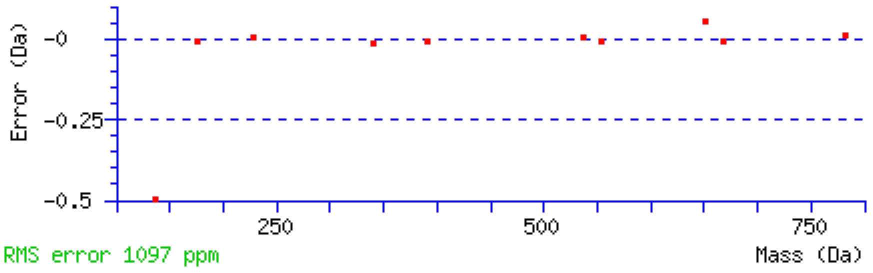
Match to Query 6137: 893.457448 from(447.736000,2+) rtinseconds(1626) index(16046)
Title: Locus:1.1.1.1008.9
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 1.mgf

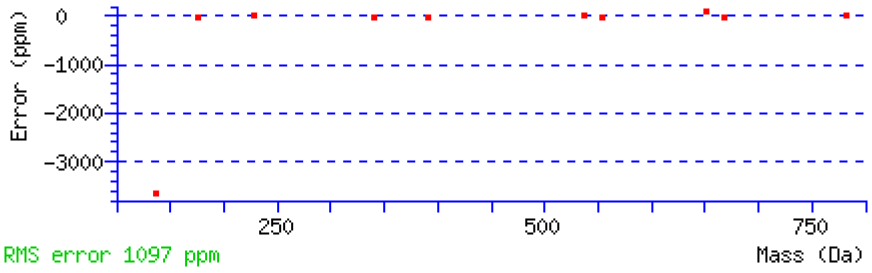
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 893.460663
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.003
Matches : 11/60 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					**I**							7
2	**228.134267**	114.570771	211.107718	106.057497			**N**	***781.383894***	391.195585	764.357345	382.682310	763.373329	382.190302	6
3	**341.218331**	171.112803	324.191782	162.599529			**L**	***667.340967***	334.174122	650.314418	325.660847	649.330402	325.168839	5
4	504.281660	252.644468	487.255111	244.131193			**Y**	***554.256903***	277.632090	537.230354	269.118815	536.246338	268.626807	4
5	605.329339	303.168308	588.302790	294.655033	587.318774	294.163025	**T**	***391.193574***	196.100425	374.167025	187.587150	373.183009	187.095142	3
6	720.356282	360.681779	703.329733	352.168504	702.345717	351.676496	**D**	290.145895	145.576585	273.119346	137.063311	272.135330	136.571303	2
7							**R**	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of INLYTDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.1	893.460663	-0.003215	INLYTDR
8.7	893.460648	-0.003200	NPYAASKK
5.6	893.452805	0.004643	LTSMAVEK
3.1	893.454147	0.003301	IHPGMAPR
2.3	893.449432	0.008016	KPVDEYK
0.5	893.454147	0.003301	IHPGMAPR

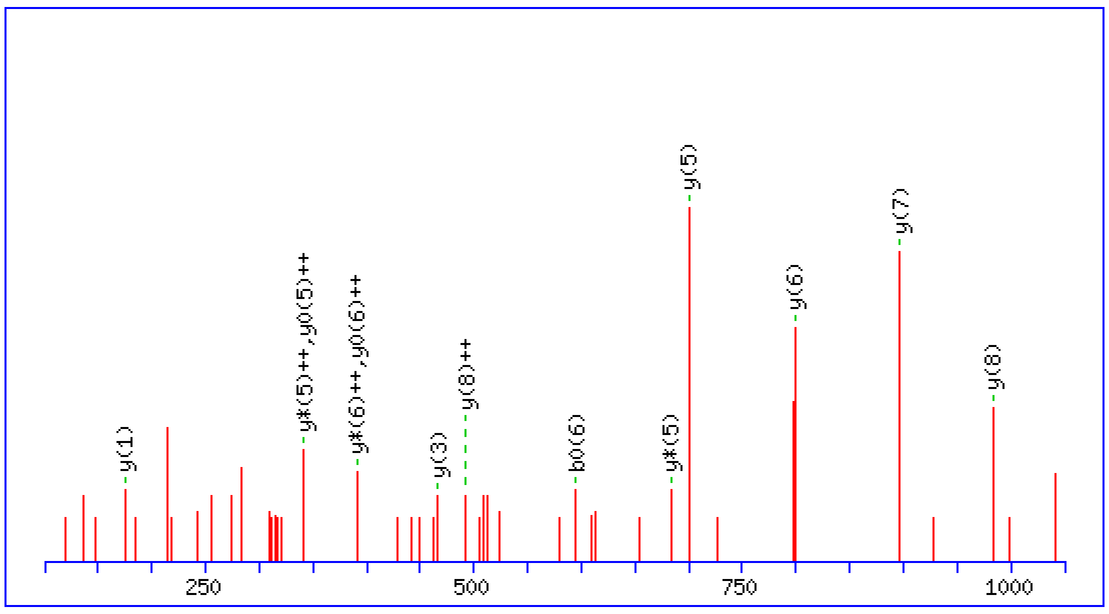
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELSPVSFQYR**
Found in **RWDD4_HUMAN**, RWD domain-containing protein 4 OS=Homo sapiens GN=RWDD4 PE=1 SV=3

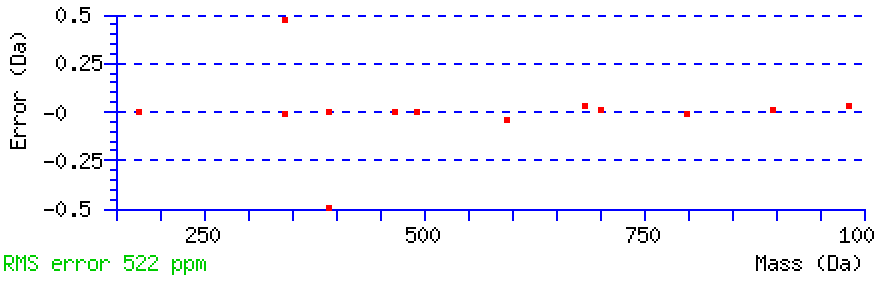
Match to Query 30783: 1224.609968 from(613.312260,2+) rtinseconds(2576) index(30510)
Title: Locus:1.1.1.2249.31
Data file 2011-11-10 - TFD - EP 3-6.mgf

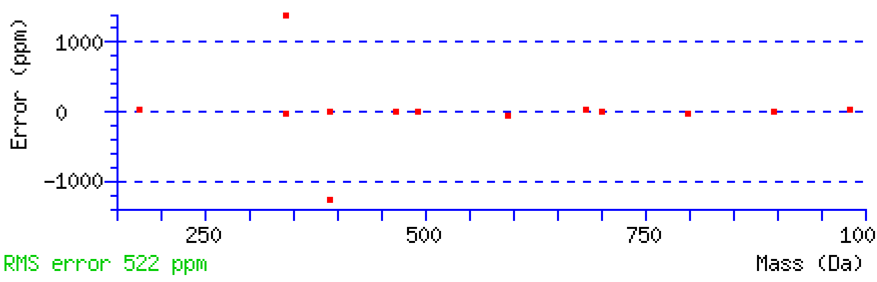
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1224.613876
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 34 **Expect:** 0.0043
Matches : 13/86 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	E							10
2	243.133933	122.070605			225.123368	113.065322	L	1096.578571	548.792923	1079.552022	540.279649	1078.568006	539.787641	9
3	330.165961	165.586618			312.155396	156.581336	S	***983.494507***	492.250891	966.467958	483.737617	965.483942	483.245609	8
4	427.218725	214.113001			409.208160	205.107718	P	***896.462479***	448.734877	879.435930	440.221603	878.451914	439.729595	7
5	526.287139	263.647208			508.276574	254.641925	V	***799.409715***	400.208495	782.383166	391.695221	781.399150	391.203213	6
6	613.319167	307.163222			595.308602	298.157939	S	***700.341301***	350.674288	683.314752	342.161014	682.330736	341.669006	5
7	760.387581	380.697429			742.377016	371.692146	F	613.309273	307.158275	596.282724	298.645000			4
8	888.446159	444.726718	871.419610	436.213443	870.435594	435.721435	Q	***466.240859***	233.624067	449.214310	225.110793			3
9	1051.509488	526.258382	1034.482939	517.745108	1033.498923	517.253099	Y	338.182281	169.594778	321.155732	161.081504			2
10							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of ELSPVSFQYR
(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	1224.613876	-0.003908	ELSPVSFQYR
8.8	1224.617264	-0.007296	LVVDVSGSMYR
5.9	1224.602005	0.007963	MVSNTKSVDTK
4.5	1224.613861	-0.003893	ELYPSLGAGYR
4.0	1224.617233	-0.007265	MPDPAKSAPAPK

Mascot: http://www.matrixscience.com/

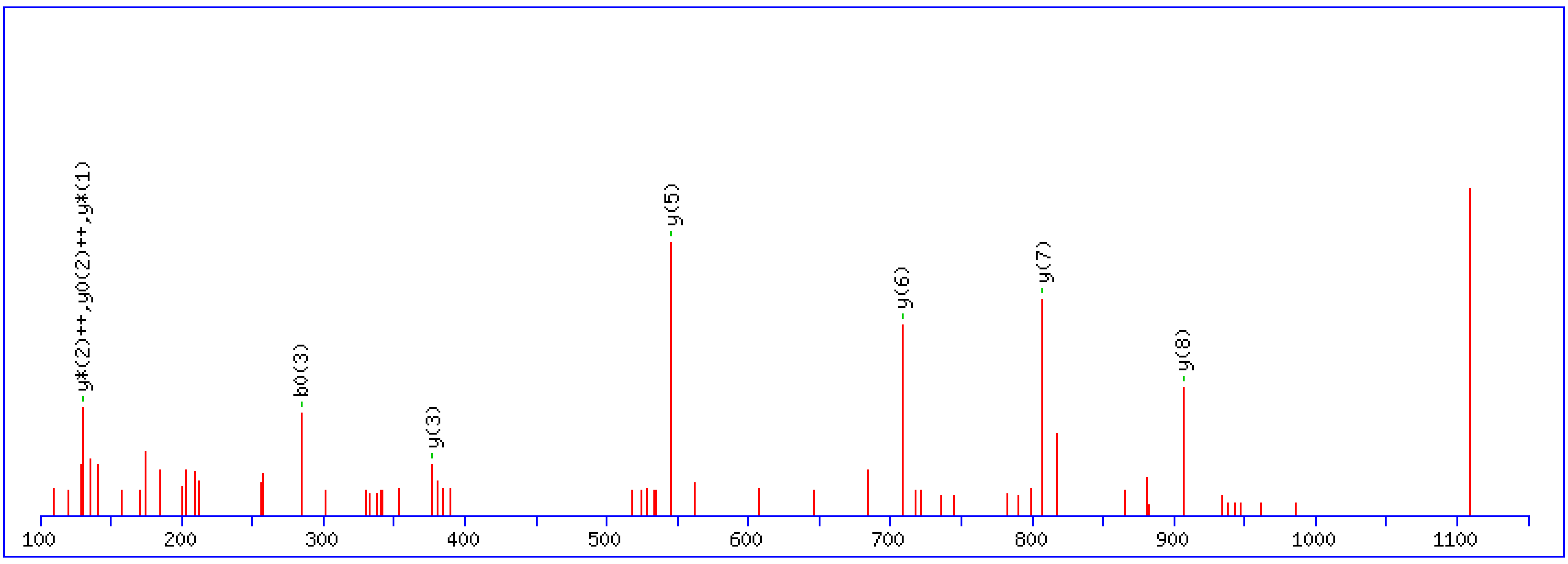
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TTVVYPATEK**
Found in **DCPS_HUMAN**, Scavenger mRNA-decapping enzyme DcpS OS=Homo sapiens GN=DCPS PE=1 SV=2

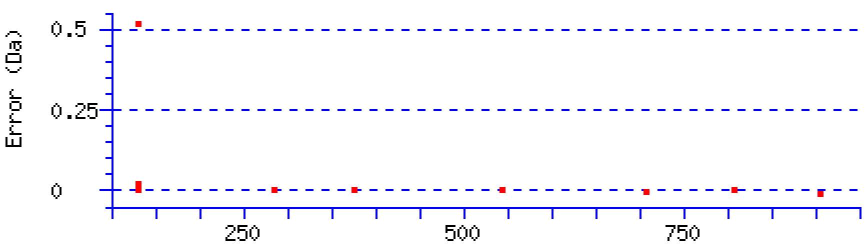
Match to Query 16983: 1107.572328 from(554.793440,2+) rtinseconds(1163) index(6694)
Title: Locus:1.1.1.889.24
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 3.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●

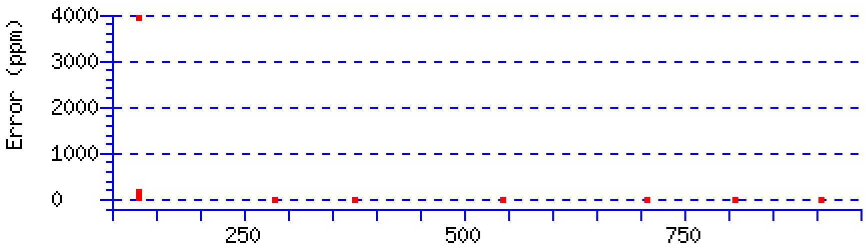


Monoisotopic mass of neutral peptide Mr(calc): 1107.581192
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 40 **Expect:** 0.0014
Matches : 9/88 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116	84.044390	42.525833	T							10
2	203.102634	102.054955	185.092069	93.049672	T	1007.540790	504.274033	990.514241	495.760759	989.530225	495.268751	9
3	302.171048	151.589162	284.160483	142.583879	V	***906.493111***	453.750194	889.466562	445.236919	888.482546	444.744911	8
4	401.239462	201.123369	383.228897	192.118087	V	***807.424697***	404.215987	790.398148	395.702712	789.414132	395.210704	7
5	564.302791	282.655034	546.292226	273.649751	Y	***708.356283***	354.681780	691.329734	346.168505	690.345718	345.676497	6
6	661.355555	331.181416	643.344990	322.176133	P	***545.292954***	273.150115	528.266405	264.636841	527.282389	264.144833	5
7	732.392669	366.699973	714.382104	357.694690	A	448.240190	224.623733	431.213641	216.110458	430.229625	215.618450	4
8	833.440348	417.223812	815.429783	408.218530	T	***377.203076***	189.105176	360.176527	180.591901	359.192511	180.099893	3
9	962.482941	481.745109	944.472376	472.739826	E	276.155397	138.581336	259.128848	130.068062	258.144832	129.576054	2
10					K	147.112804	74.060040	130.086255	65.546765			1



RMS error 1319 ppm
Mass (Da)



RMS error 1319 ppm
Mass (Da)

NCBI **BLAST** search of TTVVYPATEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.7	1107.581192	-0.008864	TTVVYPATEK
9.8	1107.578506	-0.006178	EGPPGPVRQR
9.1	1107.578506	-0.006178	EGPPGPVRQR
5.9	1107.567261	0.005067	EPHVEQITR
2.8	1107.567261	0.005067	AEHIPSGPLR
0.7	1107.567276	0.005052	AGQQPPPPLR
0.7	1107.567276	0.005052	AGQQPPPPLR
0.4	1107.567276	0.005052	AGQQPPPPLR

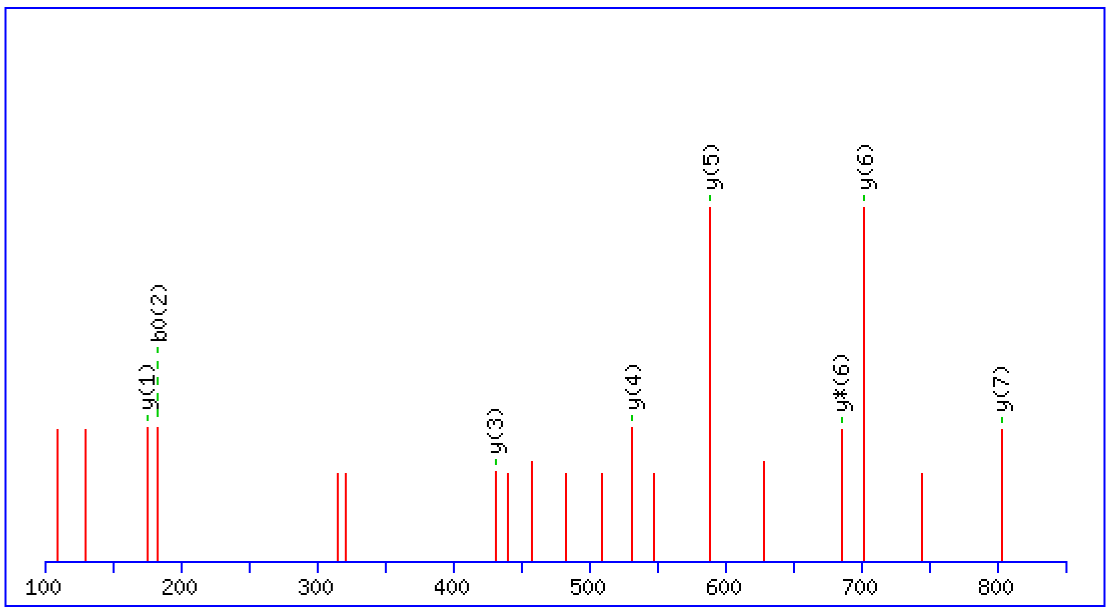
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VTLGTQQR**
Found in **SLFN5_HUMAN**, Schlafen family member 5 OS=Homo sapiens GN=SLFN5 PE=1 SV=1

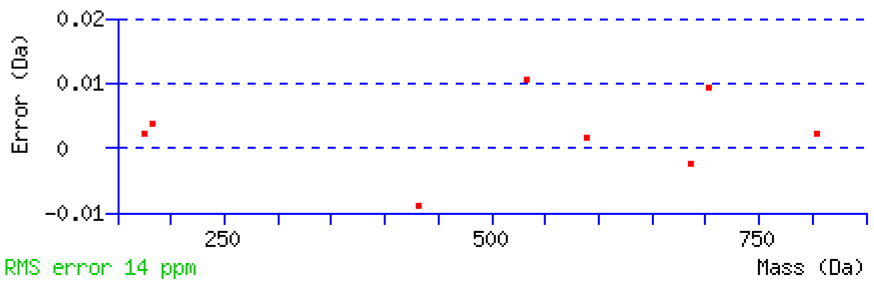
Match to Query 8427: 901.497508 from(451.756030,2+) rtinseconds(1028) index(4133)
Title: Locus:1.1.1.1838.16
Data file 2011-11-10 - TFD - EP 3-2.mgf

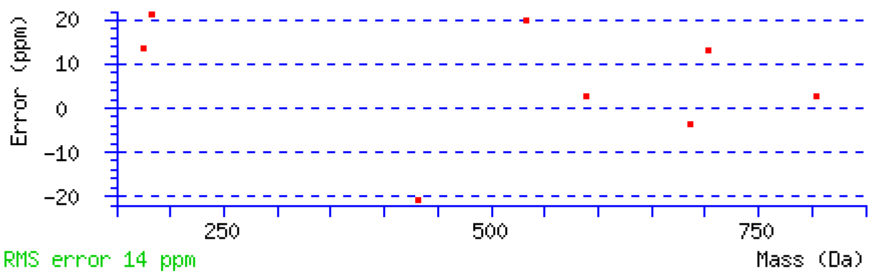
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 901.498138
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 46  Expect: 0.00031
Matches : 8/66 fragment ions using 12 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							8
2	201.123369	101.065322			183.112804	92.060040	T	***803.436994***	402.222135	786.410445	393.708861	785.426429	393.216853	7
3	314.207433	157.607354			296.196868	148.602072	L	***702.389315***	351.698296	685.362766	343.185021	684.378750	342.693013	6
4	371.228897	186.118086			353.218332	177.112804	G	***589.305251***	295.156264	572.278702	286.642989	571.294686	286.150981	5
5	472.276576	236.641926			454.266011	227.636643	T	***532.283787***	266.645532	515.257238	258.132257	514.273222	257.640249	4
6	600.335154	300.671215	583.308605	292.157941	582.324589	291.665933	Q	***431.236108***	216.121692	414.209559	207.608418			3
7	728.393732	364.700504	711.367183	356.187230	710.383167	355.695222	Q	303.177530	152.092403	286.150981	143.579129			2
8							R	***175.118952***	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of VTLGTQQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.9	901.498138	-0.000630	VTLGTQQR
15.1	901.502136	-0.004628	SLLDWLR
15.1	901.498093	-0.000585	SLLEERR
13.7	901.498123	-0.000615	VTATANLGR
13.7	901.498108	-0.000600	VTRIEER
13.7	901.502151	-0.004643	VTVEWLR
8.7	901.498123	-0.000615	TVAVASAQR
8.1	901.498093	-0.000585	IEAASQKR
6.8	901.505524	-0.008016	VVGDLMLR
6.4	901.498108	-0.000600	ELKTQQR

Mascot: http://www.matrixscience.com/

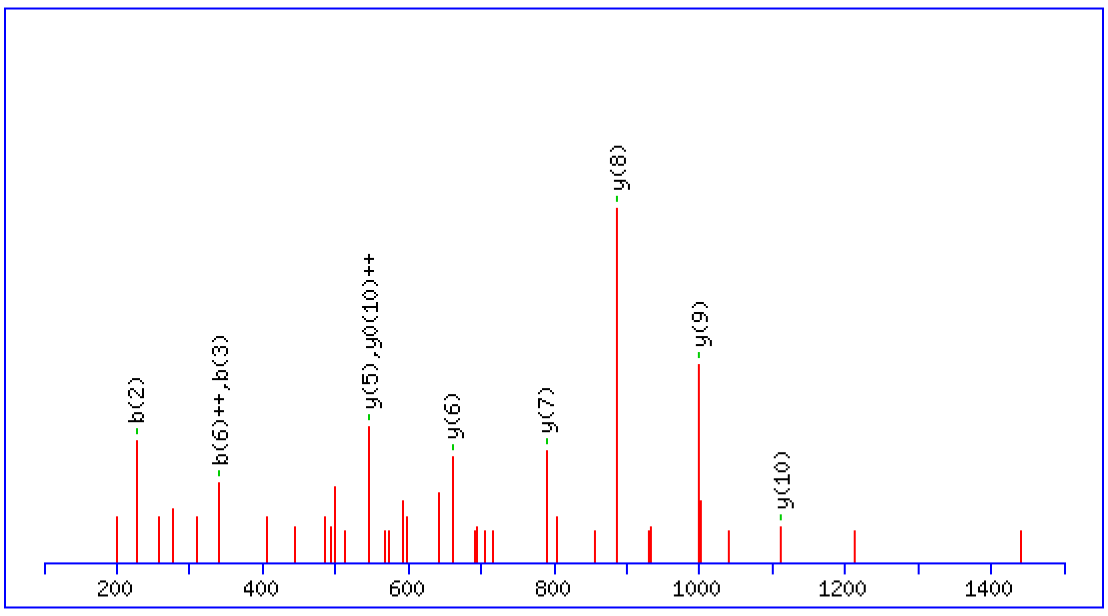
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LILPELGPVFK**
Found in **SCYL2_HUMAN**, SCY1-like protein 2 OS=Homo sapiens GN=SCYL2 PE=1 SV=1

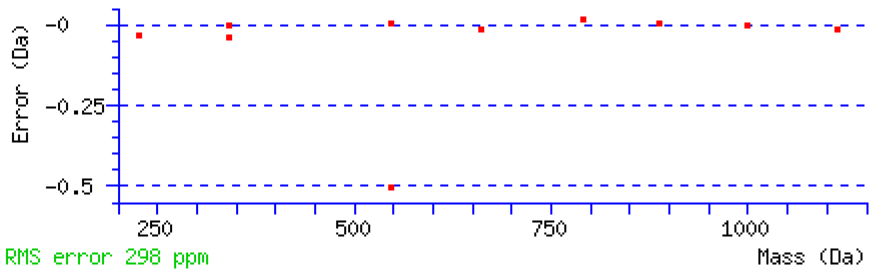
Match to Query 32962: 1224.751888 from(613.383220,2+) rtinseconds(3721) index(54211)
Title: Locus:1.1.1.2832.17
Data file 2011-11-14 - TFD - EP 8-2.mgf

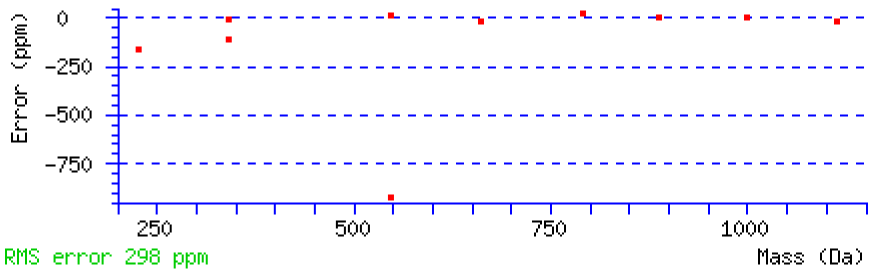
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1224.748184
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 47  Expect: 4e-005
Matches : 10/80 fragment ions using 11 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							11
2	**227.175404**	114.091340			I	***1112.671409***	556.839343	1095.644860	548.326068	1094.660844	547.834060	10
3	**340.259468**	170.633372			L	***999.587345***	500.297311	982.560796	491.784036	981.576780	491.292028	9
4	437.312232	219.159754			P	***886.503281***	443.755279	869.476732	435.242004	868.492716	434.749996	8
5	566.354825	283.681051	548.344260	274.675768	E	***789.450517***	395.228897	772.423968	386.715622	771.439952	386.223614	7
6	679.438889	340.223083	661.428324	331.217800	L	***660.407924***	330.707600	643.381375	322.194326			6
7	736.460353	368.733815	718.449788	359.728532	G	***547.323860***	274.165568	530.297311	265.652294			5
8	833.513117	417.260197	815.502552	408.254914	P	490.302396	245.654836	473.275847	237.141562			4
9	932.581531	466.794404	914.570966	457.789121	V	393.249632	197.128454	376.223083	188.615180			3
10	1079.649945	540.328611	1061.639380	531.323328	F	294.181218	147.594247	277.154669	139.080973			2
11					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of LILPELGPVFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.1	1224.748184	0.003704	LILPELGPVFK
14.7	1224.744171	0.007717	LIPGATVGLLQK
12.9	1224.755386	-0.003498	LLLNLISQVGR
12.9	1224.744141	0.007747	LPLALNPLKSK
12.9	1224.755386	-0.003498	LPLLTRLDLR
10.7	1224.745499	0.006389	LLPKHPHLVR
7.3	1224.744141	0.007747	IPELVKQLSAK
6.0	1224.744171	0.007717	ILPVLGSQTGKI
0.2	1224.744141	0.007747	LLELQELVLR

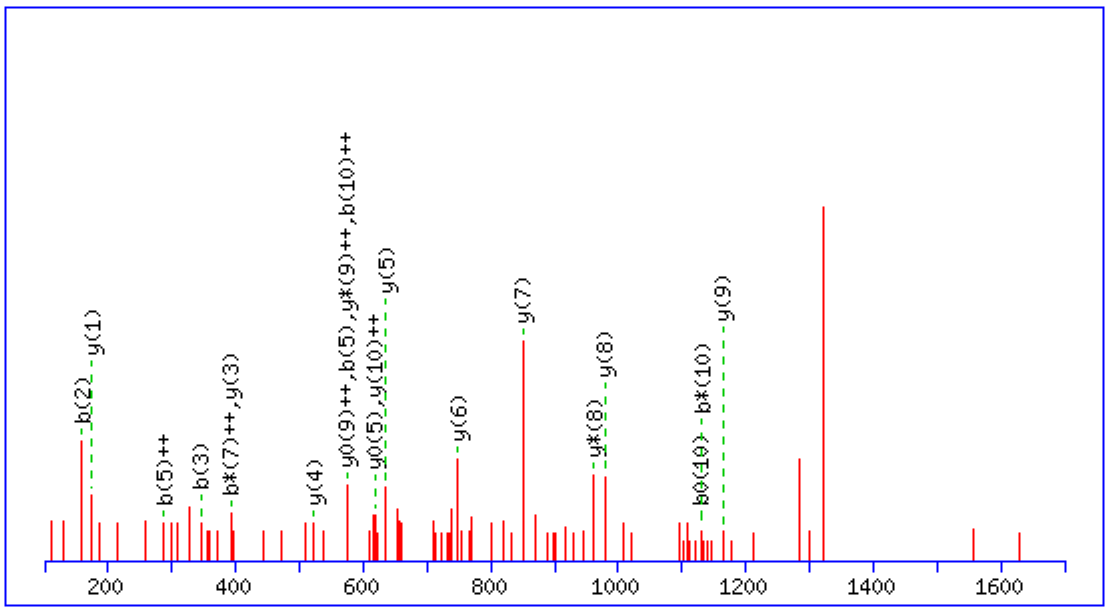
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SAWQTLNEFAR**
Found in **S23IP_HUMAN**, SEC23-interacting protein OS=Homo sapiens GN=SEC23IP PE=1 SV=1

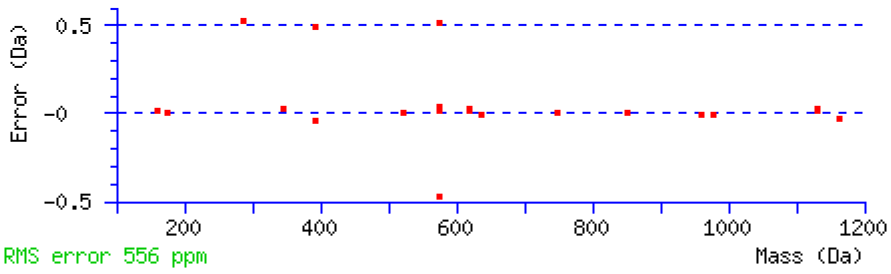
Match to Query 35666: 1321.643448 from(661.829000,2+) rtinseconds(3075) index(41590)
Title: Locus:1.1.1.2602.31
Data file 2011-11-14 - TFD - EP 7-1.mgf

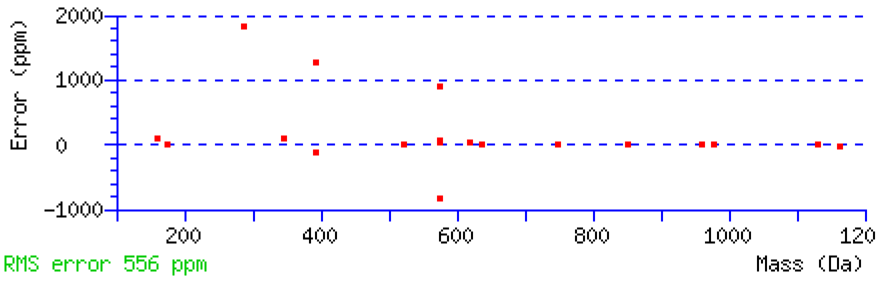
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1321.641479
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 45 **Expect:** 0.00038
Matches : 21/108 fragment ions using 35 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	88.039304	44.523290			70.028739	35.518008	S							11
2	**159.076418**	80.041847			141.065853	71.036564	A	1235.616748	618.312012	1218.590199	609.798738	1217.606183	609.306729	10
3	**345.155731**	173.081504			327.145166	164.076221	W	***1164.579634***	582.793455	1147.553085	574.280181	1146.569069	573.788172	9
4	473.214309	237.110793	456.187760	228.597518	455.203744	228.105510	Q	***978.500321***	489.753799	961.473772	481.240524	960.489756	480.748516	8
5	**574.261988**	**287.634632**	557.235439	279.121358	556.251423	278.629350	T	***850.441743***	425.724510	833.415194	417.211235	832.431178	416.719227	7
6	687.346052	344.176664	670.319503	335.663390	669.335487	335.171382	L	***749.394064***	375.200670	732.367515	366.687395	731.383499	366.195387	6
7	801.388979	401.198128	784.362430	392.684853	783.378414	392.192845	N	***636.310000***	318.658638	619.283451	310.145363	618.299435	309.653355	5
8	930.431572	465.719424	913.405023	457.206150	912.421007	456.714142	E	***522.267073***	261.637175	505.240524	253.123900	504.256508	252.631892	4
9	1077.499986	539.253631	1060.473437	530.740357	1059.489421	530.248349	F	***393.224480***	197.115878	376.197931	188.602603			3
10	1148.537100	**574.772188**	1131.510551	566.258914	1130.526535	565.766906	A	246.156066	123.581671	229.129517	115.068396			2
11							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of SAWQTLNEFAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.2	1321.641479	0.001969	SAWQTLNEFAR
9.4	1321.648682	-0.005234	SNNQNVEPHKR

Mascot: http://www.matrixscience.com/

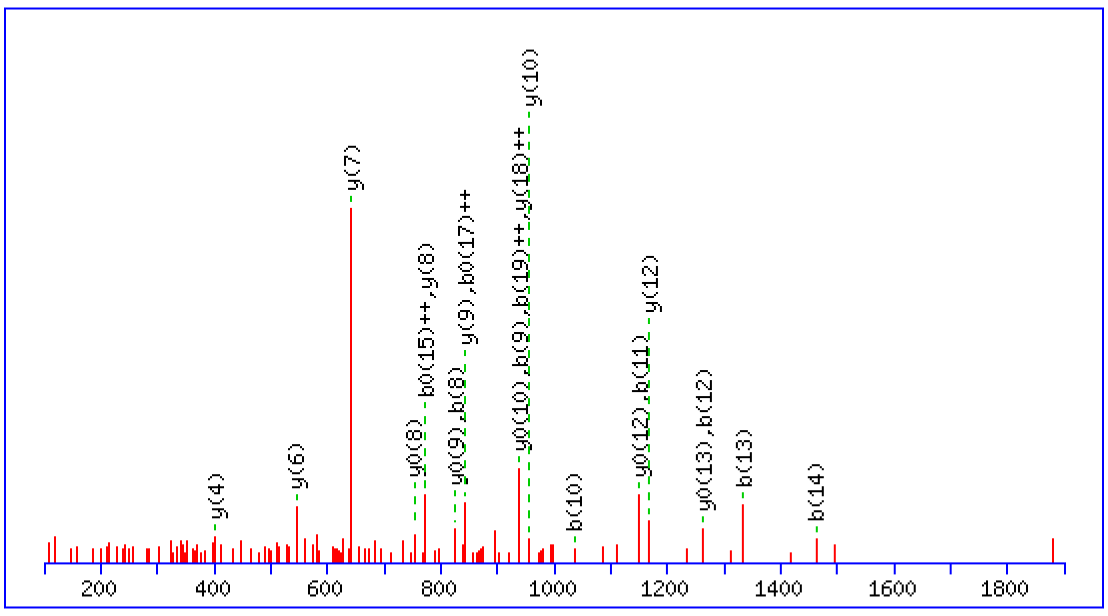
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SSGFPVHLLPDIAEPGSVAGR**
Found in **SHPK_HUMAN**, Sedoheptulokinase OS=Homo sapiens GN=SHPK PE=1 SV=3

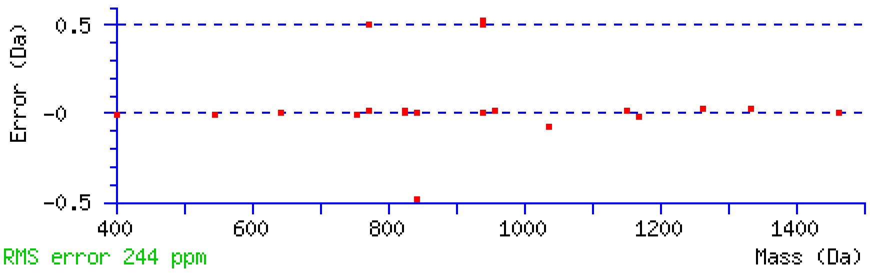
Match to Query 67937: 2105.092572 from(702.704800,3+) rtinseconds(3269) index(47074)
Title: Locus:1.1.1.2615.24
Data file 2011-11-12 - TFD - EP 6-3.mgf

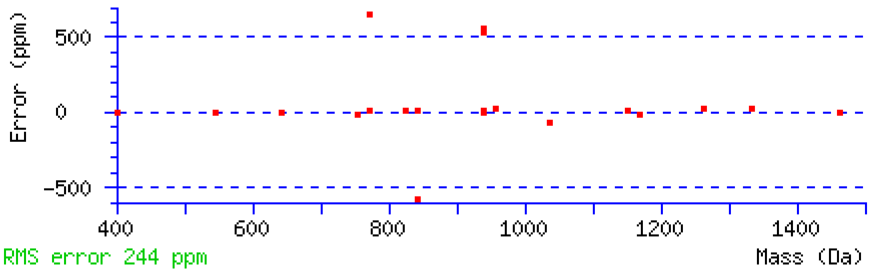
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2105.090561
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 39  Expect: 0.0014
Matches : 23/192 fragment ions using 29 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	S							21
2	175.071332	88.039304	157.060767	79.034021	S	2019.065802	1010.036539	2002.039253	1001.523265	2001.055237	1001.031256	20
3	232.092796	116.550036	214.082231	107.544753	G	1932.033774	966.520525	1915.007225	958.007251	1914.023209	957.515243	19
4	379.161210	190.084243	361.150645	181.078960	F	1875.012310	938.009793	1857.985761	929.496518	1857.001745	929.004510	18
5	476.213974	238.610625	458.203409	229.605342	P	1727.943896	864.475586	1710.917347	855.962312	1709.933331	855.470304	17
6	575.282388	288.144832	557.271823	279.139549	V	1630.891132	815.949204	1613.864583	807.435930	1612.880567	806.943921	16
7	712.341300	356.674288	694.330735	347.669005	H	1531.822718	766.414997	1514.796169	757.901723	1513.812153	757.409715	15
8	***825.425364***	413.216320	807.414799	404.211037	L	1394.763806	697.885541	1377.737257	689.372267	1376.753241	688.880259	14
9	***938.509428***	469.758352	920.498863	460.753069	L	1281.679742	641.343509	1264.653193	632.830235	1263.669177	632.338227	13
10	***1035.562192***	518.284734	1017.551627	509.279451	P	***1168.595678***	584.801477	1151.569129	576.288203	1150.585113	575.796194	12
11	***1150.589135***	575.798205	1132.578570	566.792923	D	1071.542914	536.275095	1054.516365	527.761821	1053.532349	527.269813	11
12	***1263.673199***	632.340237	1245.662634	623.334955	I	***956.515971***	478.761624	939.489422	470.248349	938.505406	469.756341	10
13	***1334.710313***	667.858794	1316.699748	658.853512	A	***843.431907***	422.219592	826.405358	413.706317	825.421342	413.214309	9
14	***1463.752906***	732.380091	1445.742341	723.374808	E	***772.394793***	386.701035	755.368244	378.187760	754.384228	377.695752	8
15	1560.805670	780.906473	1542.795105	771.901190	P	***643.352200***	322.179738	626.325651	313.666464	625.341635	313.174456	7
16	1617.827134	809.417205	1599.816569	800.411922	G	***546.299436***	273.653356	529.272887	265.140082	528.288871	264.648074	6
17	1704.859162	852.933219	1686.848597	843.927936	S	489.277972	245.142624	472.251423	236.629349	471.267407	236.137341	5
18	1803.927576	902.467426	1785.917011	893.462144	V	***402.245944***	201.626610	385.219395	193.113335			4
19	1874.964690	937.985983	1856.954125	928.980701	A	303.177530	152.092403	286.150981	143.579128			3
20	1931.986154	966.496715	1913.975589	957.491432	G	232.140416	116.573846	215.113867	108.060571			2
21					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of SSGFPVHLLPDIAEPGSVAGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.8	2105.090561	0.002011	SSGFPVHLLPDIAEPGSVAGR

Mascot: http://www.matrixscience.com/

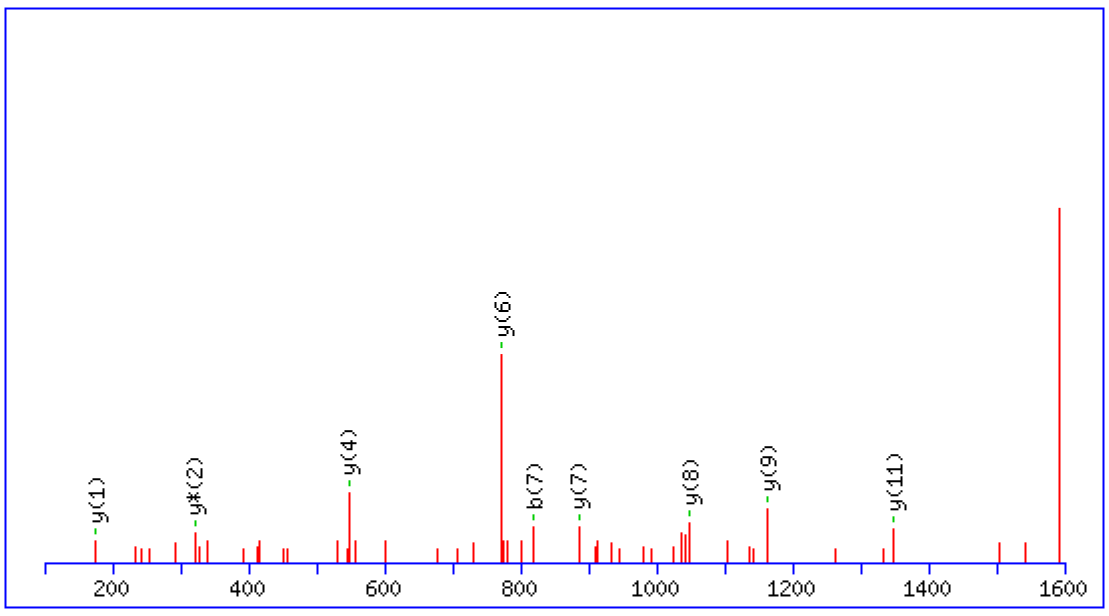
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IEGENYLPQPIYR**
Found in **SELT_HUMAN**, Selenoprotein T OS=Homo sapiens GN=SELT PE=2 SV=2

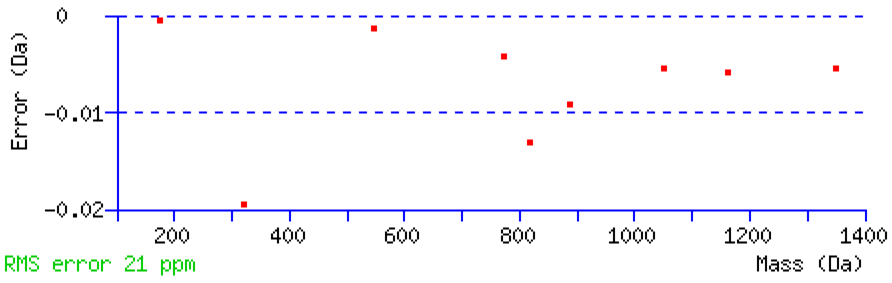
Match to Query 50511: 1590.806528 from(796.410540,2+) rtinseconds(2761) index(35091)
Title: Locus:1.1.1.2271.47
Data file 2011-11-12 - TFD - EP 5-6.mgf

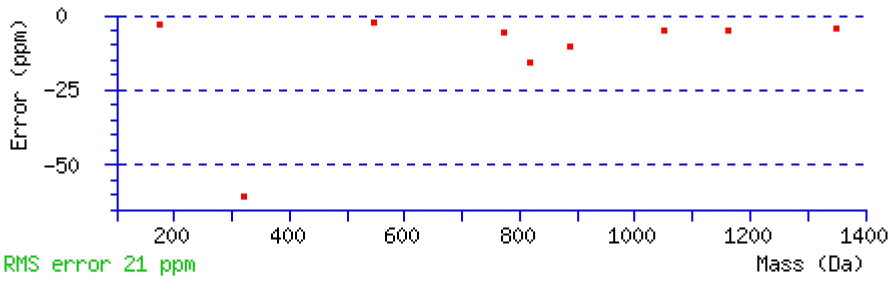
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1590.804169
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 48  Expect: 0.00019
Matches : 9/116 fragment ions using 13 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					I							13
2	243.133933	122.070605			225.123368	113.065322	E	1478.727421	739.867349	1461.700872	731.354074	1460.716856	730.862066	12
3	300.155397	150.581336			282.144832	141.576054	G	***1349.684828***	675.346052	1332.658279	666.832778	1331.674263	666.340770	11
4	429.197990	215.102633			411.187425	206.097351	E	1292.663364	646.835320	1275.636815	638.322046	1274.652799	637.830038	10
5	543.240917	272.124097	526.214368	263.610822	525.230352	263.118814	N	***1163.620771***	582.314024	1146.594222	573.800749			9
6	706.304246	353.655761	689.277697	345.142487	688.293681	344.650479	Y	***1049.577844***	525.292560	1032.551295	516.779286			8
7	819.388310	410.197793	802.361761	401.684519	801.377745	401.192511	L	***886.514515***	443.760896	869.487966	435.247621			7
8	916.441074	458.724175	899.414525	450.210901	898.430509	449.718893	P	***773.430451***	387.218864	756.403902	378.705589			6
9	1044.499652	522.753464	1027.473103	514.240190	1026.489087	513.748182	Q	676.377687	338.692482	659.351138	330.179207			5
10	1141.552416	571.279846	1124.525867	562.766572	1123.541851	562.274564	P	***548.319109***	274.663193	531.292560	266.149918			4
11	1254.636480	627.821878	1237.609931	619.308604	1236.625915	618.816596	I	451.266345	226.136810	434.239796	217.623536			3
12	1417.699809	709.353543	1400.673260	700.840268	1399.689244	700.348260	Y	338.182281	169.594778	321.155732	161.081504			2
13							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of IEGENYLPQPIYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.0	1590.804169	0.002359	IEGENYLPQPIYR
9.3	1590.792313	0.014215	VVETMQSTLDAEIR
7.0	1590.807587	-0.001059	KTGFPEIIMPGDVR
6.0	1590.797501	0.009027	AQARLPHSGGPAAGGGR
4.6	1590.807587	-0.001059	KEDMPSVWVVTIR
2.2	1590.810928	-0.004400	LTIQMMSPLQIER
2.2	1590.810928	-0.004400	LTIQMMSPLQIER
2.2	1590.804184	0.002344	ETPLHQLYSAAFSK

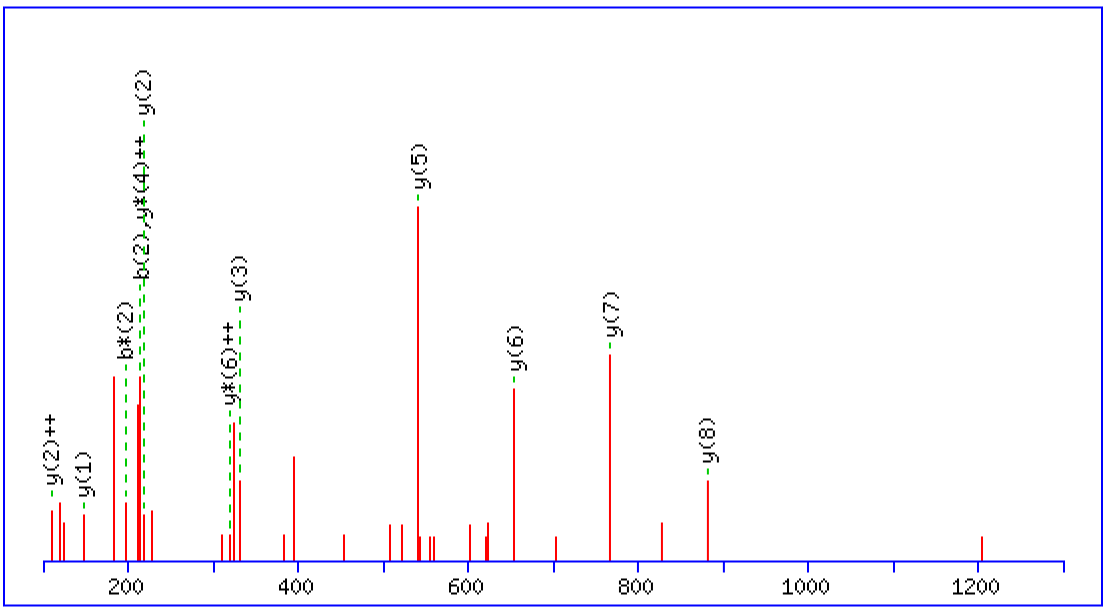
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VNIIPIIAK**
Found in **SEP11_HUMAN**, Septin-11 OS=Homo sapiens GN=SEPT11 PE=1 SV=3

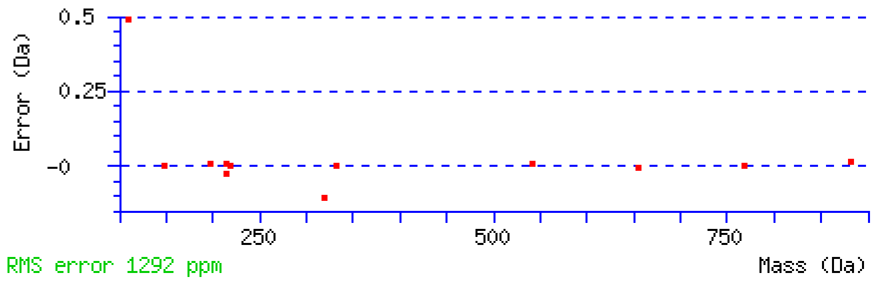
Match to Query 12810: 979.640968 from(490.827760,2+) rtinseconds(2837) index(38561)
Title: Locus:1.1.1.2502.7
Data file 2011-11-14 - TFD - EP 8-3.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●

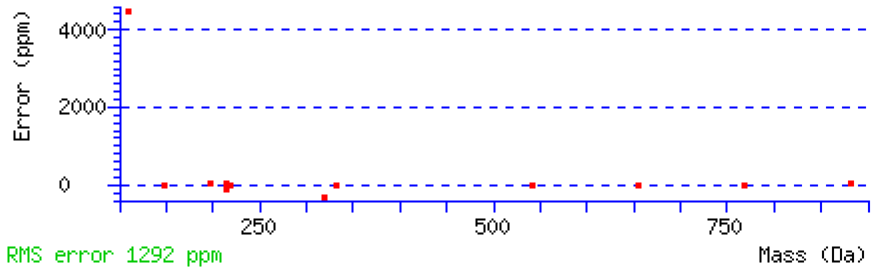


Monoisotopic mass of neutral peptide Mr(calc): 979.642975
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 35 **Expect:** 0.0003
Matches : 12/62 fragment ions using 29 most intense peaks (help)

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	100.075690	50.541483			V					9
2	214.118617	107.562947	197.092068	99.049672	N	***881.581865***	441.294571	864.555316	432.781296	8
3	327.202681	164.104978	310.176132	155.591704	I	***767.538938***	384.273107	750.512389	375.759833	7
4	440.286745	220.647010	423.260196	212.133736	I	***654.454874***	327.731075	637.428325	319.217801	6
5	537.339509	269.173393	520.312960	260.660118	P	***541.370810***	271.189043	524.344261	262.675769	5
6	650.423573	325.715425	633.397024	317.202150	I	444.318046	222.662661	427.291497	214.149386	4
7	763.507637	382.257457	746.481088	373.744182	I	***331.233982***	166.120629	314.207433	157.607354	3
8	834.544751	417.776014	817.518202	409.262739	A	***218.149918***	109.578597	201.123369	101.065322	2
9					K	***147.112804***	74.060040	130.086255	65.546765	1



RMS error 1292 ppm



RMS error 1292 ppm

NCBI **BLAST** search of VNIIPIIAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.3	979.642975	-0.002007	VNIIPIIAK
35.3	979.642975	-0.002007	VNIIPLIAK

Mascot: http://www.matrixscience.com/

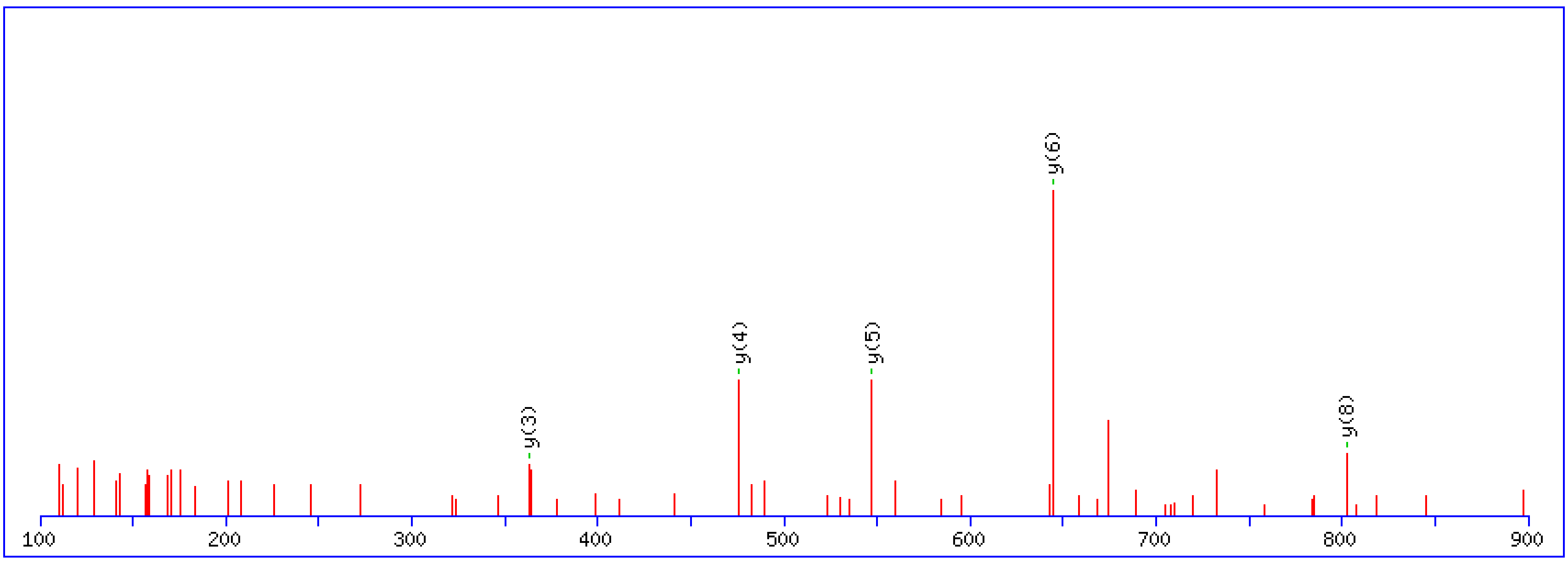
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGTPALTSR**
Found in **GLYC_HUMAN**, Serine hydroxymethyltransferase, cytosolic OS=Homo sapiens GN=SHMT1 PE=1 SV=1

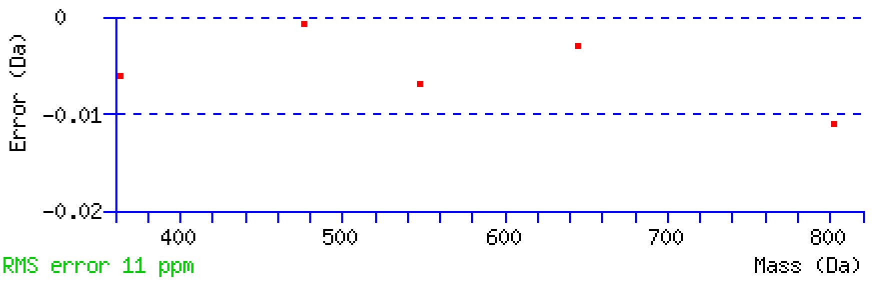
Match to Query 4628: 914.511268 from(458.262910,2+) rtinseconds(1328) index(9972)
Title: Locus:1.1.1.889.13
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 2.mgf

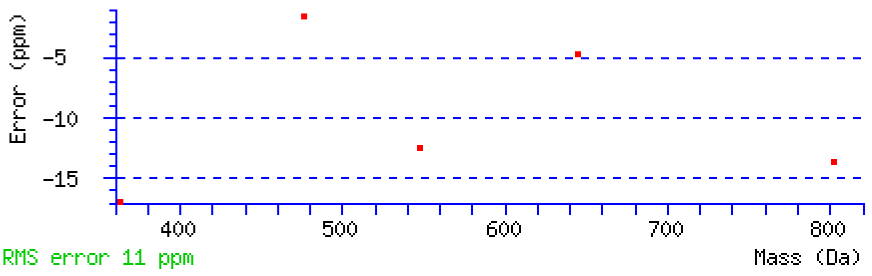
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [900] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 914.518524
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.0018
Matches : 5/74 fragment ions using 8 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.091340	57.549308			L							9
2	171.112804	86.060040			G	*802.441744*	401.724510	785.415195	393.211236	784.431179	392.719228	8
3	272.160483	136.583879	254.149918	127.578597	T	745.420280	373.213778	728.393731	364.700504	727.409715	364.208496	7
4	369.213247	185.110261	351.202682	176.104979	P	*644.372601*	322.689939	627.346052	314.176664	626.362036	313.684656	6
5	440.250361	220.628818	422.239796	211.623536	A	*547.319837*	274.163557	530.293288	265.650282	529.309272	265.158274	5
6	553.334425	277.170851	535.323860	268.165568	L	*476.282723*	238.645000	459.256174	230.131725	458.272158	229.639717	4
7	654.382104	327.694690	636.371539	318.689408	T	*363.198659*	182.102968	346.172110	173.589693	345.188094	173.097685	3
8	741.414132	371.210704	723.403567	362.205422	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
9					R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of LGTPALTSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.8	914.518524	-0.007256	LGTPALTSR
13.1	914.518509	-0.007241	LRPGLSEK
5.5	914.508621	0.002647	HPALQPPR
5.5	914.508606	0.002662	RNIYPPR
5.5	914.519836	-0.008568	YRARPPR
4.8	914.518524	-0.007256	LEGGTVLAR
4.6	914.507309	0.003959	ATVTPSPVK
4.6	914.507309	0.003959	ATVTPSPVK
4.0	914.508621	0.002647	IPFNRPR
2.0	914.508621	0.002647	IKFQSHR

Mascot: http://www.matrixscience.com/

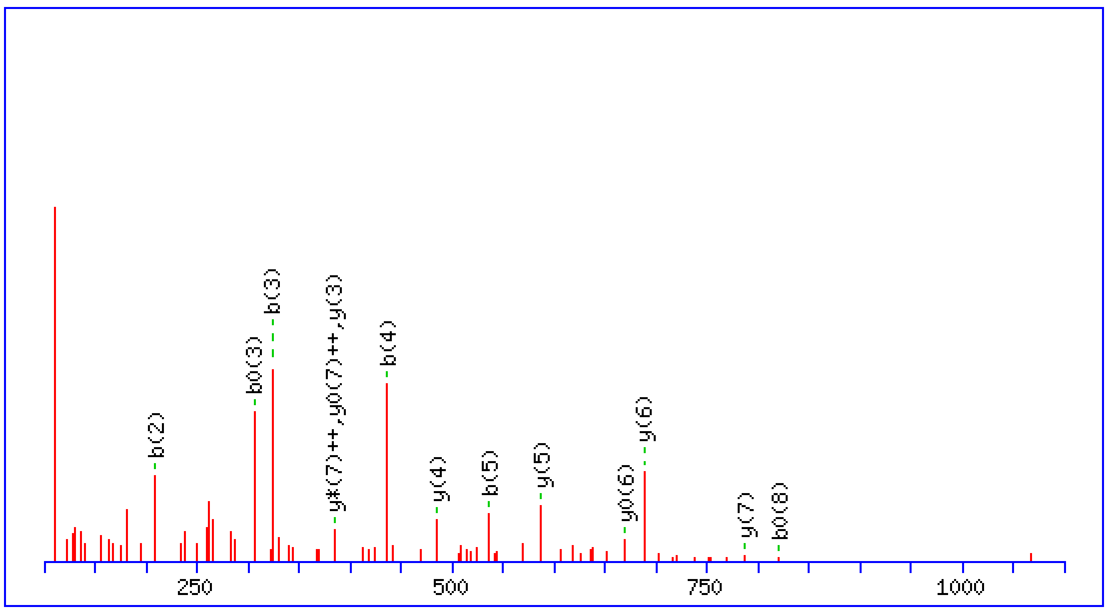
Mascot Search Results

Peptide View

MS/MS Fragmentation of **HADIVTTTTHK**
Found in **GLYM_HUMAN**, Serine hydroxymethyltransferase, mitochondrial OS=Homo sapiens GN=SHMT2 PE=1 SV=3

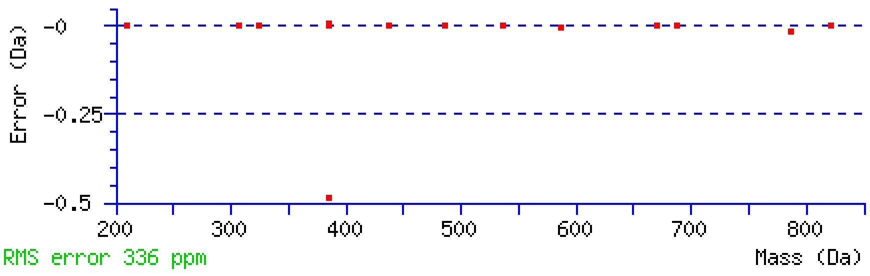
Match to Query 548318: 1222.633842 from(408.551890,3+) rtinseconds(811) index(656767)
Title: Locus:1.1.1.972.2
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

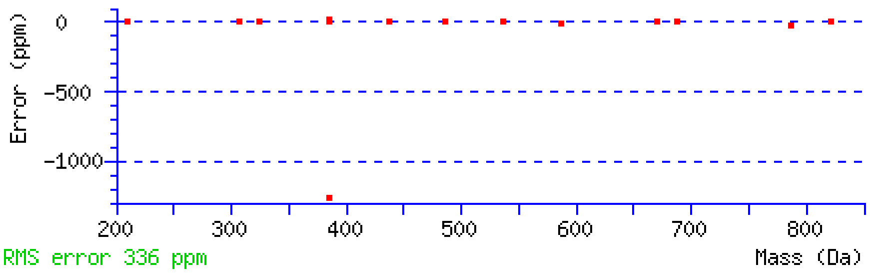
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1222.630615
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.00067
Matches : 14/92 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	138.066188	69.536732			H							11
2	***209.103302***	105.055289			A	1086.578967	543.793122	1069.552418	535.279847	1068.568402	534.787839	10
3	***324.130245***	162.568761	306.119680	153.563478	D	1015.541853	508.274565	998.515304	499.761290	997.531288	499.269282	9
4	***437.214309***	219.110793	419.203744	210.105510	I	900.514910	450.761093	883.488361	442.247819	882.504345	441.755811	8
5	***536.282723***	268.645000	518.272158	259.639717	V	***787.430846***	394.219061	770.404297	385.705787	769.420281	385.213779	7
6	637.330402	319.168839	619.319837	310.163557	T	***688.362432***	344.684854	671.335883	336.171580	670.351867	335.679572	6
7	738.378081	369.692679	720.367516	360.687396	T	***587.314753***	294.161015	570.288204	285.647740	569.304188	285.155732	5
8	839.425760	420.216518	821.415195	411.211236	T	***486.267074***	243.637175	469.240525	235.123900	468.256509	234.631892	4
9	940.473439	470.740358	922.462874	461.735075	T	***385.219395***	193.113335	368.192846	184.600061	367.208830	184.108053	3
10	1077.532351	539.269814	1059.521786	530.264531	H	284.171716	142.589496	267.145167	134.076221			2
11					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of HADIVTTTTHK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.6	1222.630615	0.003227	HADIVTTTTHK
6.3	1222.630585	0.003257	STKPGAAPTEHK
3.1	1222.626755	0.007087	NIFISPVSISM
1.3	1222.630600	0.003242	AGPGPGAVLESPR
0.7	1222.637970	-0.004128	IPEPVKNQAPM
0.3	1222.624054	0.009788	AATIHHRLASM
0.3	1222.645844	-0.012002	DAHPKLHVYK

Mascot: http://www.matrixscience.com/

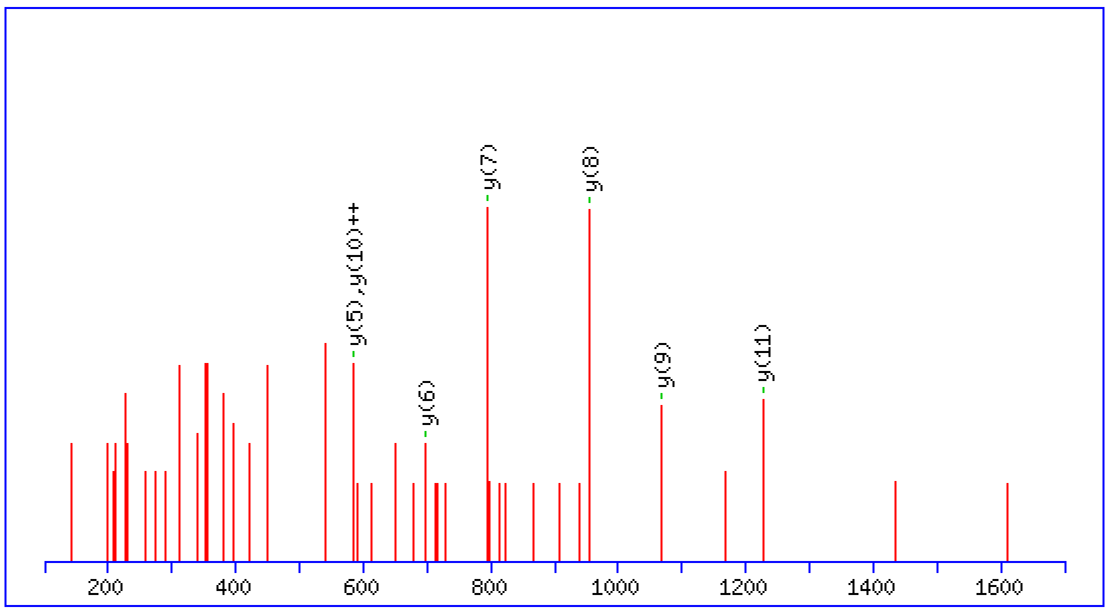
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NTGTICPLPELVK**
Found in **SPTC1_HUMAN**, Serine palmitoyltransferase 1 OS=Homo sapiens GN=SPTLC1 PE=1 SV=1

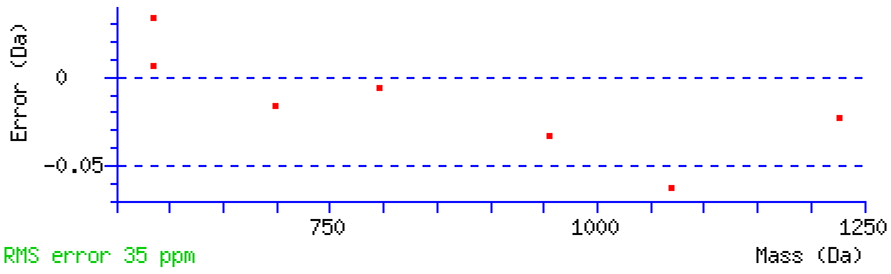
Match to Query 786598: 1440.763308 from(721.388930,2+) rtinseconds(2834) index(691587)
Title: Locus:1.1.1.1749.35
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

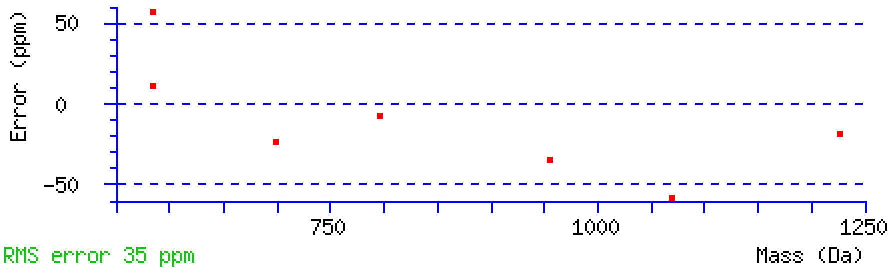
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1440.764648
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 34  Expect: 0.00068
Matches : 7/136 fragment ions using 12 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			N							13
2	216.097882	108.552579	199.071333	100.039305	198.087317	99.547296	T	1327.729002	664.368139	1310.702453	655.854865	1309.718437	655.362857	12
3	273.119346	137.063311	256.092797	128.550037	255.108781	128.058029	G	***1226.681323***	613.844300	1209.654774	605.331025	1208.670758	604.839017	11
4	374.167025	187.587151	357.140476	179.073876	356.156460	178.581868	T	1169.659859	585.333568	1152.633310	576.820293	1151.649294	576.328285	10
5	487.251089	244.129183	470.224540	235.615908	469.240524	235.123900	I	***1068.612180***	534.809728	1051.585631	526.296454	1050.601615	525.804446	9
6	647.281738	324.144507	630.255189	315.631233	629.271173	315.139225	C	***955.528116***	478.267696	938.501567	469.754422	937.517551	469.262414	8
7	744.334502	372.670889	727.307953	364.157615	726.323937	363.665607	P	***795.497467***	398.252372	778.470918	389.739097	777.486902	389.247089	7
8	857.418566	429.212921	840.392017	420.699647	839.408001	420.207639	L	***698.444703***	349.725990	681.418154	341.212715	680.434138	340.720707	6
9	954.471330	477.739303	937.444781	469.226029	936.460765	468.734021	P	***585.360639***	293.183958	568.334090	284.670683	567.350074	284.178675	5
10	1083.513923	542.260600	1066.487374	533.747325	1065.503358	533.255317	E	488.307875	244.657575	471.281326	236.144301	470.297310	235.652293	4
11	1196.597987	598.802632	1179.571438	590.289357	1178.587422	589.797349	L	359.265282	180.136279	342.238733	171.623004			3
12	1295.666401	648.336839	1278.639852	639.823564	1277.655836	639.331556	V	246.181218	123.594247	229.154669	115.080973			2
13							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of NTGTICPLPELVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.9	1440.764648	-0.001340	NTGTICPLPELVK
0.2	1440.764648	-0.001340	ELGVKPSQQPVLM

Mascot: http://www.matrixscience.com/

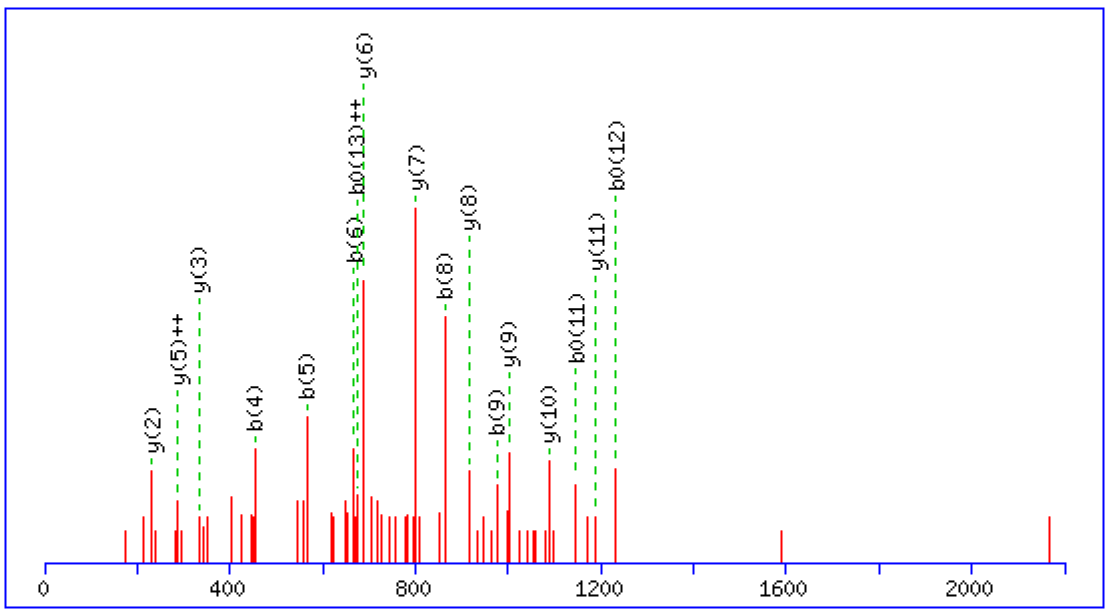
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DSIHLTPVLTSSILNQLTGR**
Found in **SRR_HUMAN**, Serine racemase OS=Homo sapiens GN=SRR PE=1 SV=1

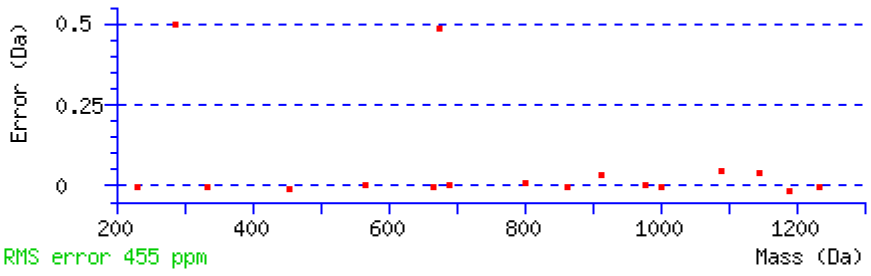
Match to Query 68232: 2164.185282 from(722.402370,3+) rtinseconds(4063) index(61569)
Title: Locus:1.1.1.2836.22
Data file 2011-11-12 - TFD - EP 6-4.mgf

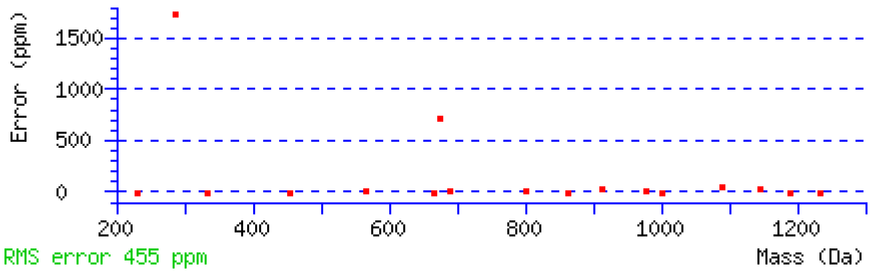
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2164.185181
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 61 **Expect:** 3.5e-006
Matches : 17/196 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.034219	58.520748			98.023654	49.515465	D							20
2	203.066247	102.036761			185.055682	93.031479	S	2050.165516	1025.586396	2033.138967	1017.073121	2032.154951	1016.581113	19
3	316.150311	158.578793			298.139746	149.573511	I	1963.133488	982.070382	1946.106939	973.557107	1945.122923	973.065099	18
4	***453.209223***	227.108250			435.198658	218.102967	H	1850.049424	925.528350	1833.022875	917.015075	1832.038859	916.523067	17
5	***566.293287***	283.650282			548.282722	274.644999	L	1712.990512	856.998894	1695.963963	848.485619	1694.979947	847.993611	16
6	***667.340966***	334.174121			649.330401	325.168839	T	1599.906448	800.456862	1582.879899	791.943587	1581.895883	791.451579	15
7	764.393730	382.700503			746.383165	373.695221	P	1498.858769	749.933022	1481.832220	741.419748	1480.848204	740.927740	14
8	***863.462144***	432.234710			845.451579	423.229428	V	1401.806005	701.406640	1384.779456	692.893366	1383.795440	692.401358	13
9	***976.546208***	488.776742			958.535643	479.771460	L	1302.737591	651.872433	1285.711042	643.359159	1284.727026	642.867151	12
10	1077.593887	539.300582			1059.583322	530.295299	T	***1189.653527***	595.330401	1172.626978	586.817127	1171.642962	586.325119	11
11	1164.625915	582.816596			1146.615350	573.811313	S	***1088.605848***	544.806562	1071.579299	536.293287	1070.595283	535.801279	10
12	1251.657943	626.332610			1233.647378	617.327327	S	***1001.573820***	501.290548	984.547271	492.777273	983.563255	492.285265	9
13	1364.742007	682.874642			1346.731442	673.869359	I	***914.541792***	457.774534	897.515243	449.261259	896.531227	448.769251	8
14	1477.826071	739.416674			1459.815506	730.411391	L	***801.457728***	401.232502	784.431179	392.719227	783.447163	392.227219	7
15	1591.868998	796.438137	1574.842449	787.924863	1573.858433	787.432854	N	***688.373664***	344.690470	671.347115	336.177195	670.363099	335.685187	6
16	1719.927576	860.467426	1702.901027	851.954151	1701.917011	851.462143	Q	574.330737	287.669006	557.304188	279.155732	556.320172	278.663724	5
17	1833.011640	917.009458	1815.985091	908.496183	1815.001075	908.004175	L	446.272159	223.639717	429.245610	215.126443	428.261594	214.634435	4
18	1934.059319	967.533297	1917.032770	959.020023	1916.048754	958.528015	T	***333.188095***	167.097685	316.161546	158.584411	315.177530	158.092403	3
19	1991.080783	996.044029	1974.054234	987.530755	1973.070218	987.038747	G	***232.140416***	116.573846	215.113867	108.060571			2
20							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of DSIHLTPVLTSSILNQLTGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
61.0	2164.185181	0.000101	DSIHLTPVLTSSILNQLTGR

Mascot: http://www.matrixscience.com/

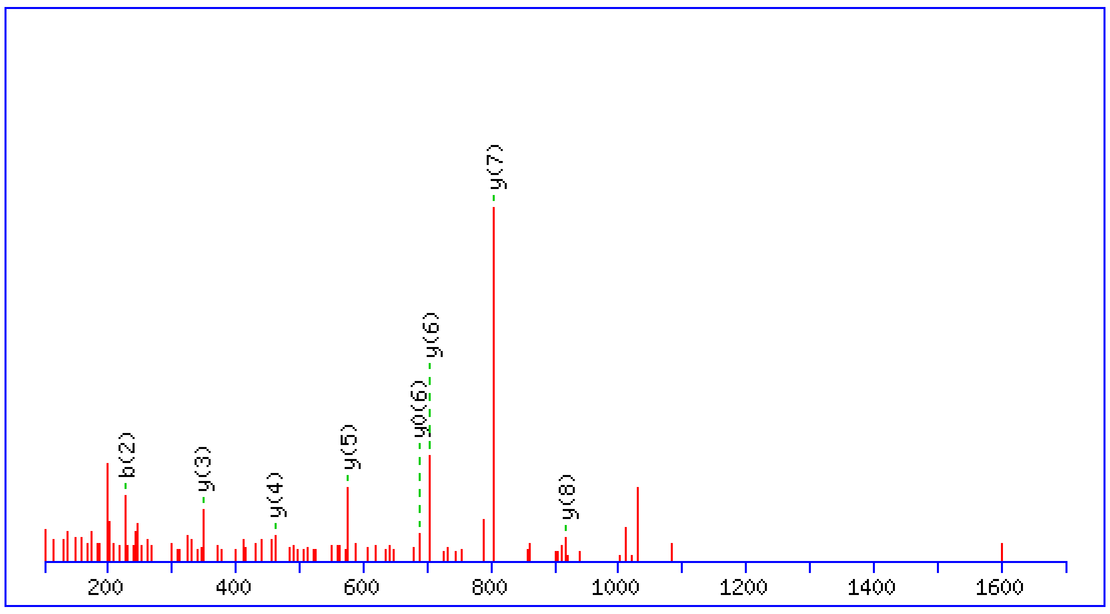
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LIVENLSSR**
Found in **SRSF4_HUMAN**, Serine/arginine-rich splicing factor 4 OS=Homo sapiens GN=SRSF4 PE=1 SV=2

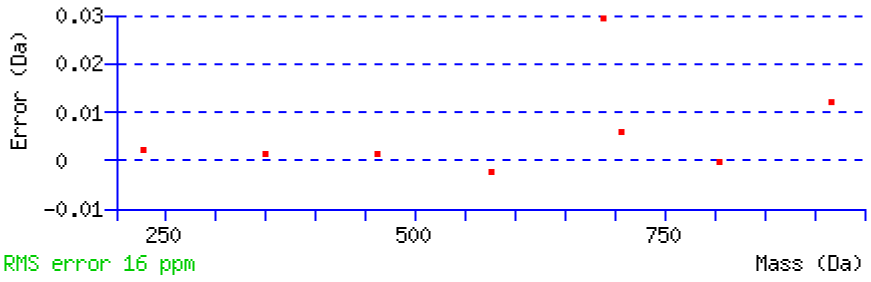
Match to Query 17281: 1029.585108 from(515.799830,2+) rtinseconds(1988) index(21730)
Title: Locus:1.1.1.2186.21
Data file 2011-11-10 - TFD - EP 3-1.mgf

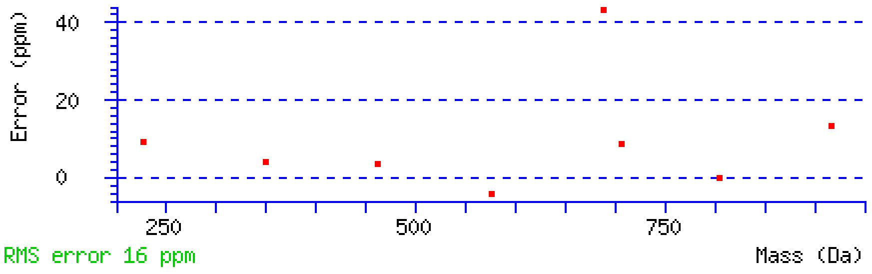
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1029.581833
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 52  Expect: 5.3e-005
Matches : 8/80 fragment ions using 10 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							9
2	227.175404	114.091340					I	***917.505070***	459.256173	900.478521	450.742899	899.494505	450.250891	8
3	326.243818	163.625547					V	***804.421006***	402.714141	787.394457	394.200867	786.410441	393.708859	7
4	455.286411	228.146843			437.275846	219.141561	E	***705.352592***	353.179934	688.326043	344.666660	687.342027	344.174652	6
5	569.329338	285.168307	552.302789	276.655033	551.318773	276.163025	N	***576.309999***	288.658638	559.283450	280.145363	558.299434	279.653355	5
6	682.413402	341.710339	665.386853	333.197065	664.402837	332.705057	L	***462.267072***	231.637174	445.240523	223.123899	444.256507	222.631891	4
7	769.445430	385.226353	752.418881	376.713078	751.434865	376.221071	S	***349.183008***	175.095142	332.156459	166.581867	331.172443	166.089859	3
8	856.477458	428.742367	839.450909	420.229092	838.466893	419.737084	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
9							R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of LIVENLSSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.3	1029.581833	0.003275	LIVENLSSR
17.4	1029.590561	-0.005453	LLWRICR
9.7	1029.593063	-0.007955	LLIRDASSR
0.5	1029.589249	-0.004141	IIGIPTCVK
0.1	1029.585876	-0.000768	LIPGFIPNK
0.1	1029.585892	-0.000784	LPTFVNVPK

Mascot: http://www.matrixscience.com/

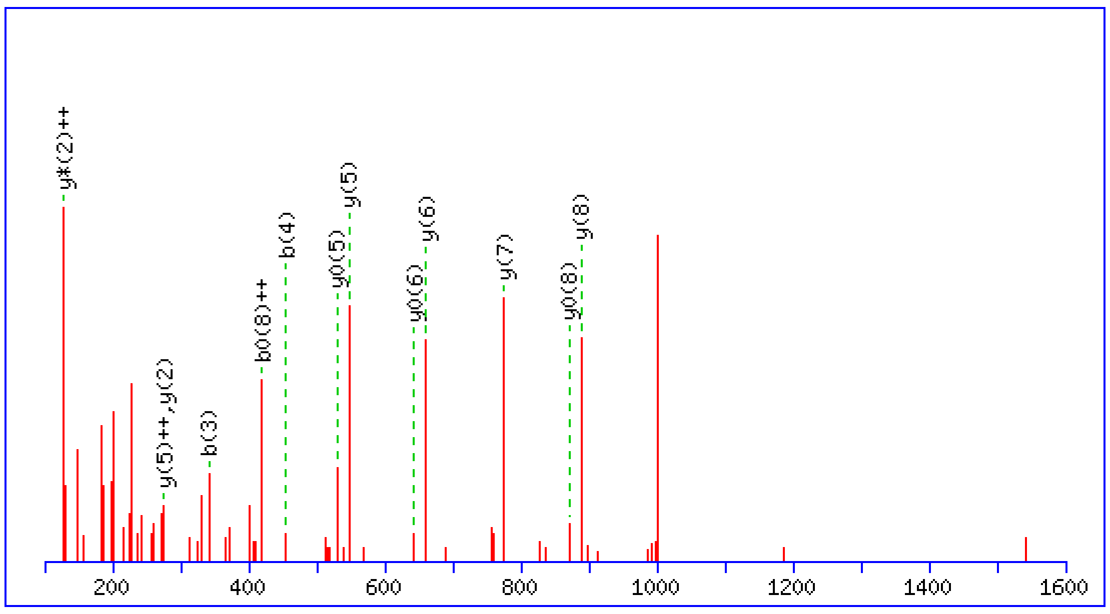
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LIDIVSSQK**
Found in **CHK1_HUMAN**, Serine/threonine-protein kinase Chk1 OS=Homo sapiens GN=CHEK1 PE=1 SV=2

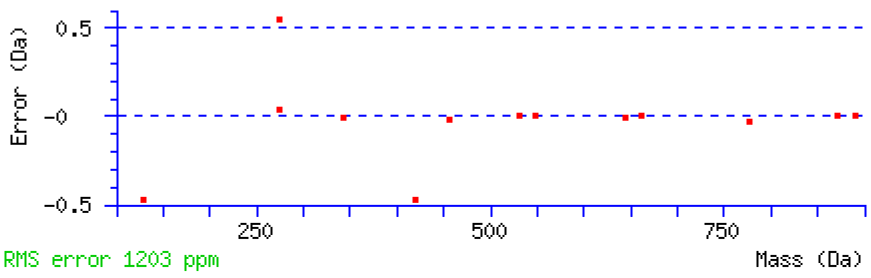
Match to Query 13151: 1001.579188 from(501.796870,2+) rtinseconds(1964) index(22171)
Title: Locus:1.1.1.2117.21
Data file 2011-11-12 - TFD - EP 6-3.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1600] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●

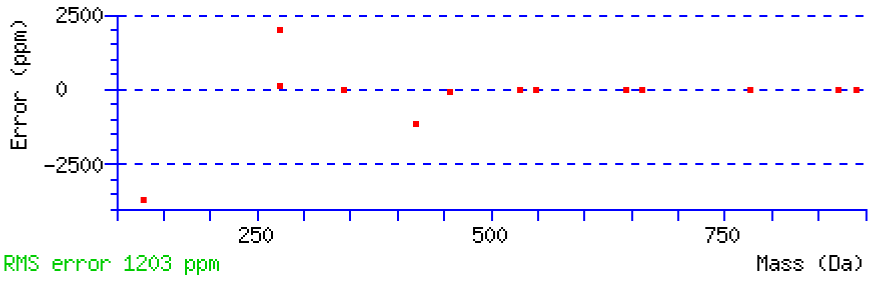


Monoisotopic mass of neutral peptide Mr(calc): 1001.575699
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.0036
Matches : 13/74 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							9
2	227.175404	114.091340					I	*889.498923*	445.253100	872.472374	436.739825	871.488358	436.247817	8
3	**342.202347**	171.604811			324.191782	162.599529	D	*776.414859*	388.711068	759.388310	380.197793	758.404294	379.705785	7
4	**455.286411**	228.146843			437.275846	219.141561	I	*661.387916*	331.197596	644.361367	322.684322	643.377351	322.192314	6
5	554.354825	277.681051			536.344260	268.675768	V	*548.303852*	274.655564	531.277303	266.142290	530.293287	265.650282	5
6	641.386853	321.197065			623.376288	312.191782	S	449.235438	225.121357	432.208889	216.608082	431.224873	216.116074	4
7	728.418881	364.713078			710.408316	355.707796	S	362.203410	181.605343	345.176861	173.092068	344.192845	172.600060	3
8	856.477459	428.742368	839.450910	420.229093	838.466894	419.737085	Q	*275.171382*	138.089329	258.144833	129.576055			2
9							K	147.112804	74.060040	130.086255	65.546765			1



RMS error 1203 ppm



RMS error 1203 ppm

NCBI **BLAST** search of LIDIVSSQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.9	1001.575699	0.003489	LIDIVSSQK
23.0	1001.575699	0.003489	LPDLKSSVK
12.1	1001.586929	-0.007741	LSNNTKVVK
8.4	1001.575699	0.003489	VEELVTGKK
5.5	1001.586929	-0.007741	LLQSTGQKK
5.1	1001.575699	0.003489	LPSSVEVKK
3.4	1001.575684	0.003504	LQTELASLK
3.4	1001.580399	-0.001211	ILSGGRMLR
2.9	1001.569183	0.010005	MPVQIRVK
0.8	1001.575684	0.003504	IDVASIKEK

Mascot: http://www.matrixscience.com/

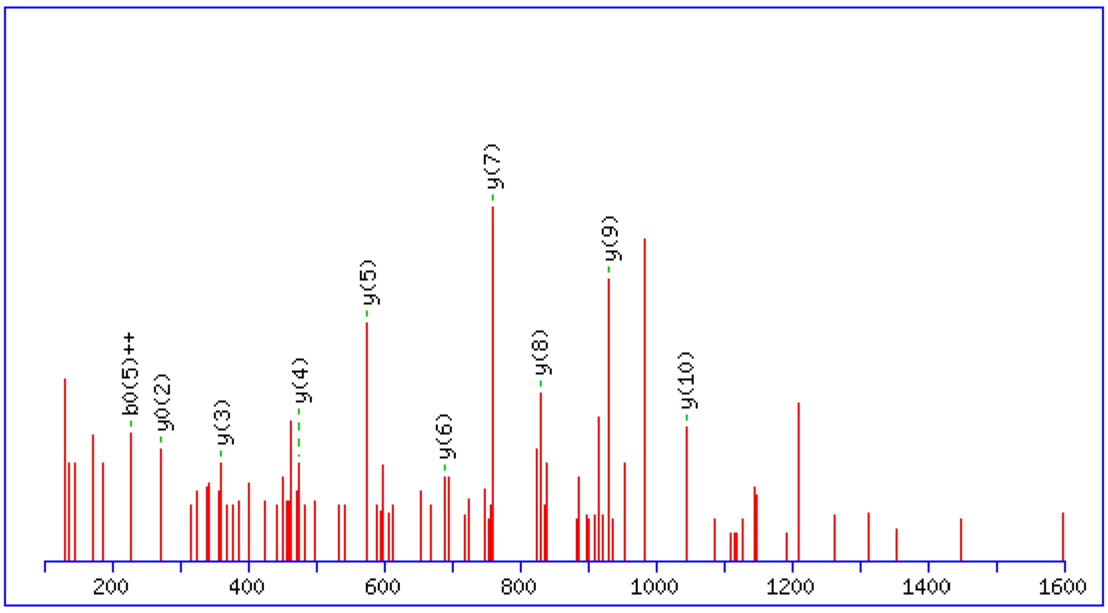
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AILTAAIVDADR**
Found in **MRCKB_HUMAN**, Serine/threonine-protein kinase MRCK beta OS=Homo sapiens GN=CDC42BPB PE=1 SV=2

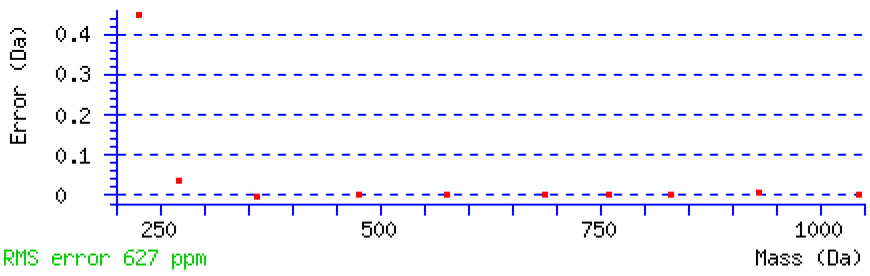
Match to Query 27975: 1227.683308 from(614.848930,2+) rtinseconds(2637) index(31351)
Title: Locus:1.1.1.2556.28
Data file 2011-11-12 - TFD - EP 5-1.mgf

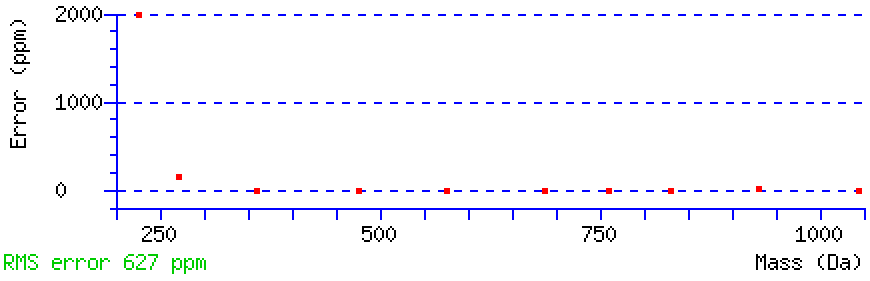
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1227.682281
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 50  Expect: 2.9e-005
Matches : 10/102 fragment ions using 22 most intense peaks   (help)
```

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	72.044390	36.525833			A							12
2	185.128454	93.067865			I	1157.652465	579.329870	1140.625916	570.816596	1139.641900	570.324588	11
3	298.212518	149.609897			L	***1044.568401***	522.787838	1027.541852	514.274564	1026.557836	513.782556	10
4	399.260197	200.133737	381.249632	191.128454	T	***931.484337***	466.245806	914.457788	457.732532	913.473772	457.240524	9
5	470.297311	235.652293	452.286746	226.647011	A	***830.436658***	415.721967	813.410109	407.208692	812.426093	406.716684	8
6	541.334425	271.170851	523.323860	262.165568	A	***759.399544***	380.203410	742.372995	371.690135	741.388979	371.198127	7
7	654.418489	327.712883	636.407924	318.707600	I	***688.362430***	344.684853	671.335881	336.171578	670.351865	335.679570	6
8	753.486903	377.247090	735.476338	368.241807	V	***575.278366***	288.142821	558.251817	279.629546	557.267801	279.137538	5
9	868.513846	434.760561	850.503281	425.755278	D	***476.209952***	238.608614	459.183403	230.095339	458.199387	229.603331	4
10	939.550960	470.279118	921.540395	461.273835	A	***361.183009***	181.095142	344.156460	172.581868	343.172444	172.089860	3
11	1054.577903	527.792589	1036.567338	518.787307	D	290.145895	145.576585	273.119346	137.063311	272.135330	136.571303	2
12					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of AILTAAIVDADR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
50.1	1227.682281	0.001027	AILTAAIVDADR
1.8	1227.682297	0.001011	DLLPTVNSLTR

Mascot: http://www.matrixscience.com/

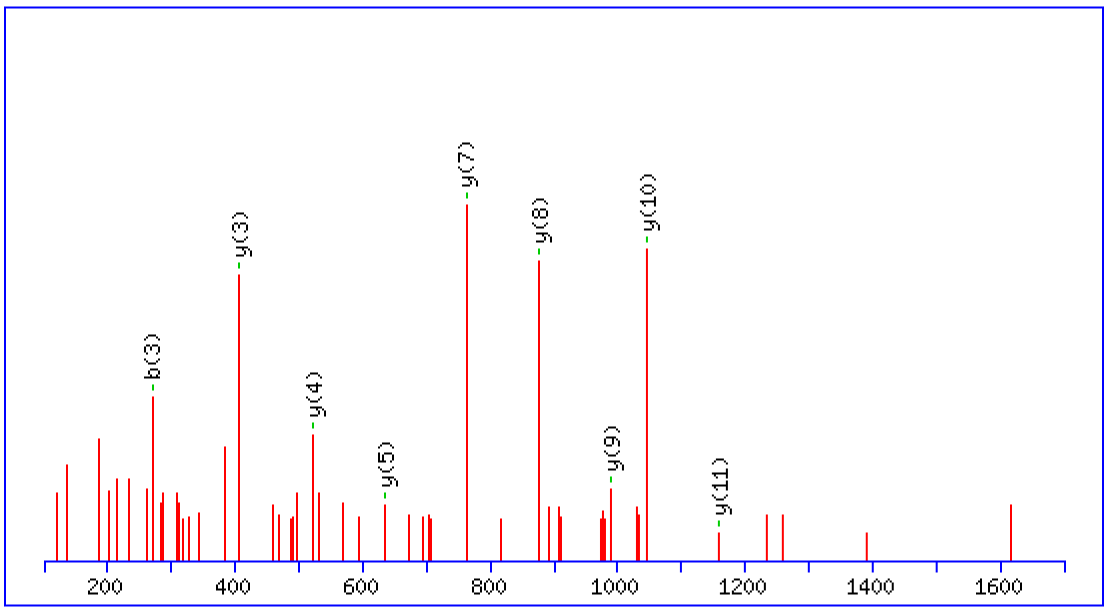
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLGLLGALDPYK**
Found in **MTOR_HUMAN**, Serine/threonine-protein kinase mTOR OS=Homo sapiens GN=MTOR PE=1 SV=1

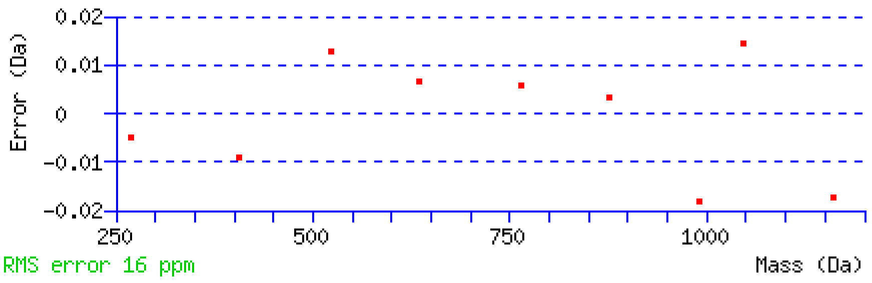
Match to Query 33192: 1257.740188 from(629.877370,2+) rtinseconds(3783) index(56048)
Title: Locus:1.1.1.2741.9
Data file 2011-11-12 - TFD - EP 6-1.mgf

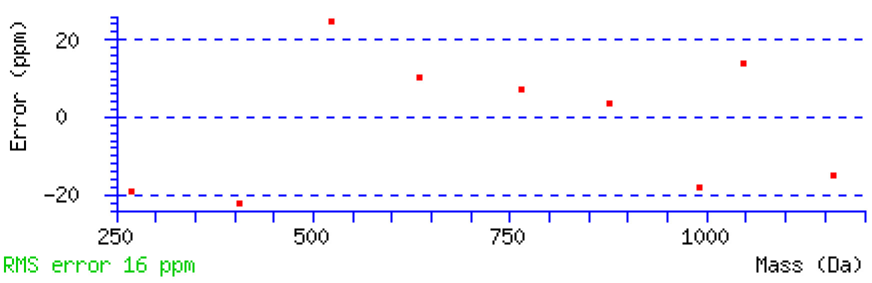
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1257.733261
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 67  Expect: 7.5e-007
Matches : 9/88 fragment ions using 12 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483			V							12
2	213.159754	107.083515			L	*1159.672138*	580.339707	1142.645589	571.826433	1141.661573	571.334425	11
3	270.181218	135.594247			G	*1046.588074*	523.797675	1029.561525	515.284401	1028.577509	514.792393	10
4	383.265282	192.136279			L	*989.566610*	495.286943	972.540061	486.773669	971.556045	486.281661	9
5	496.349346	248.678311			L	*876.482546*	438.744911	859.455997	430.231637	858.471981	429.739629	8
6	553.370810	277.189043			G	*763.398482*	382.202879	746.371933	373.689605	745.387917	373.197597	7
7	624.407924	312.707600			A	706.377018	353.692147	689.350469	345.178873	688.366453	344.686865	6
8	737.491988	369.249632			L	*635.339904*	318.173590	618.313355	309.660316	617.329339	309.168308	5
9	852.518931	426.763104	834.508366	417.757821	D	*522.255840*	261.631558	505.229291	253.118284	504.245275	252.626276	4
10	949.571695	475.289486	931.561130	466.284203	P	*407.228897*	204.118087	390.202348	195.604812			3
11	1112.635024	556.821150	1094.624459	547.815868	Y	310.176133	155.591705	293.149584	147.078430			2
12					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of VLGLLGALDPYK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
66.7	1257.733261	0.006927	VLGLLGALDPYK
11.2	1257.751892	-0.011704	VLQGLLMPLFK

Mascot: http://www.matrixscience.com/

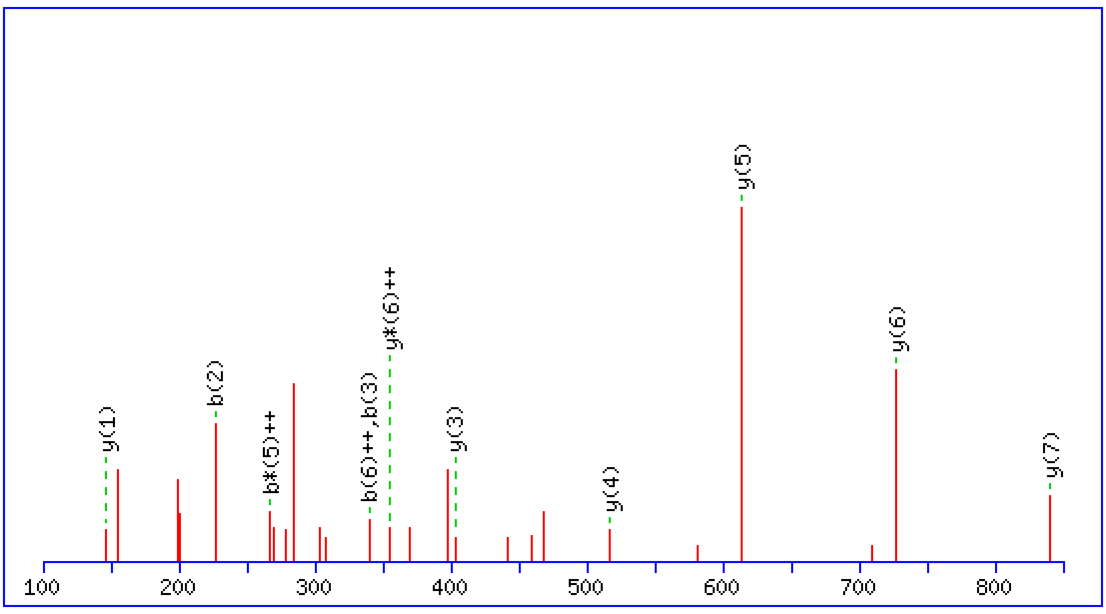
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LILPNKQK**
Found in **NEK10_HUMAN**, Serine/threonine-protein kinase Nek10 OS=Homo sapiens GN=NEK10 PE=2 SV=2

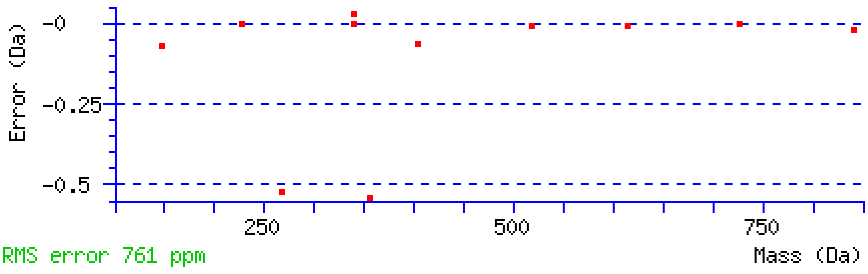
Match to Query 12293: 952.599608 from(477.307080,2+) rtinseconds(3375) index(34417)
Title: Locus:1.1.1.2695.4
Data file 2011-11-10 - TFD - EP 3-7.mgf

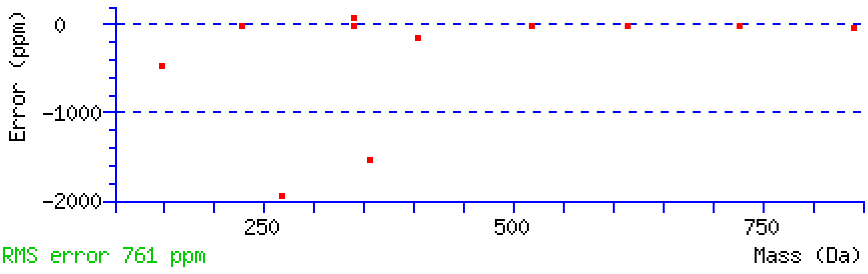
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 952.606918
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.00034
Matches : 11/48 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	114.091340	57.549308			**L**					8
2	**227.175404**	114.091340			**I**	***840.530164***	420.768720	823.503615	412.255446	7
3	**340.259468**	170.633372			**L**	***727.446100***	364.226688	710.419551	355.713414	6
4	437.312232	219.159754			**P**	***614.362036***	307.684656	597.335487	299.171382	5
5	551.355159	276.181218	534.328610	267.667943	**N**	***517.309272***	259.158274	500.282723	250.645000	4
6	679.450122	340.228699	662.423573	331.715424	**K**	***403.266345***	202.136811	386.239796	193.623536	3
7	807.508700	404.257988	790.482151	395.744713	**Q**	275.171382	138.089329	258.144833	129.576055	2
8					**K**	***147.112804***	74.060040	130.086255	65.546765	1





NCBI **BLAST** search of LILPNKQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.6	952.606918	-0.007310	LILPNKQK
30.3	952.595688	0.003920	LLLPGELAK
30.3	952.595688	0.003920	IIIPEIQK
28.9	952.606934	-0.007326	LLLGATLPR
24.0	952.595703	0.003905	ILGILPPSK
24.0	952.595703	0.003905	ILGILPPSK
23.5	952.595688	0.003920	ILLLEAGPK
21.5	952.597031	0.002577	LLIPRWR
19.8	952.595688	0.003920	LLIKEPPK
19.8	952.595688	0.003920	LLIKEPPK

Mascot: http://www.matrixscience.com/

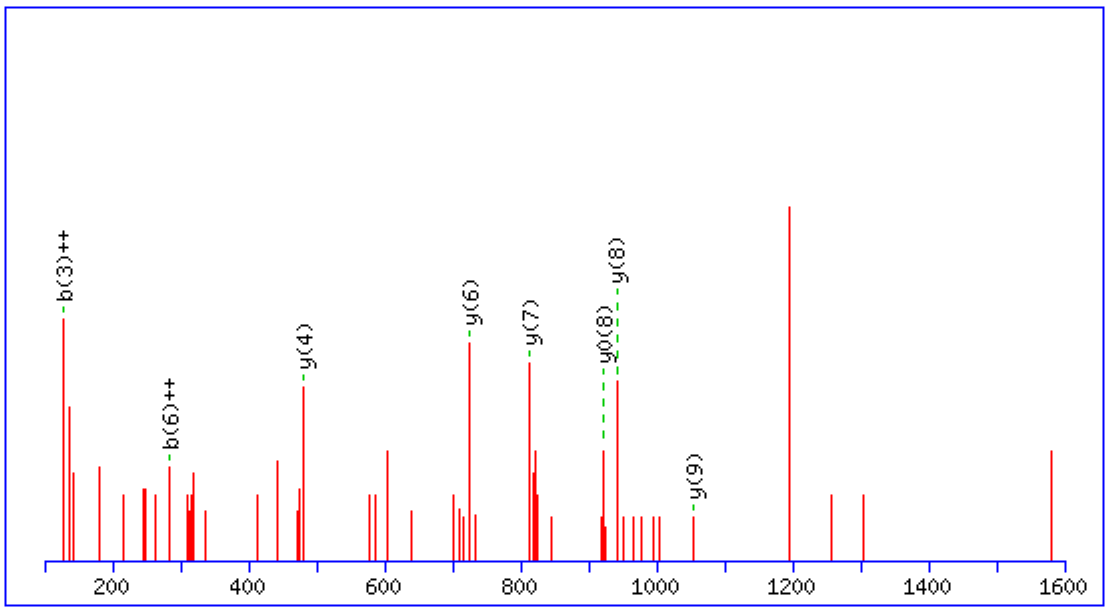
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AALQSPFYGDK**
Found in **NEK6_HUMAN**, Serine/threonine-protein kinase Nek6 OS=Homo sapiens GN=NEK6 PE=1 SV=2

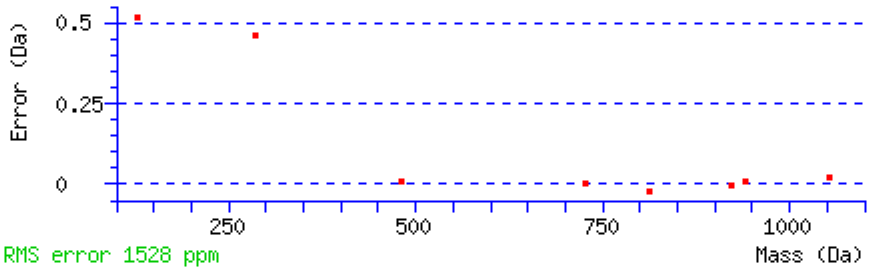
Match to Query 514322: 1195.586368 from(598.800460,2+) rtinseconds(2215) index(680112)
Title: Locus:1.1.1.1514.22
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

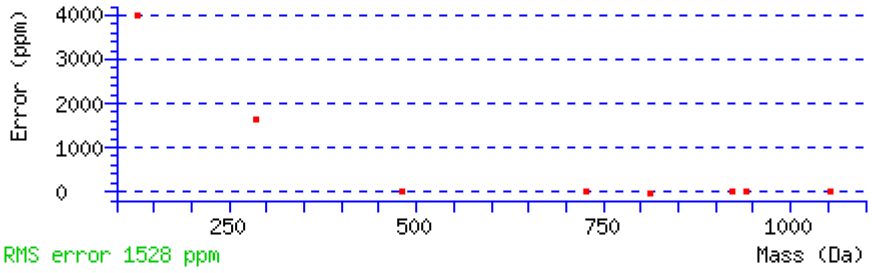
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1195.587326
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.002
Matches : 8/104 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							11
2	143.081504	72.044390					A	1125.557502	563.282389	1108.530953	554.769115	1107.546937	554.277107	10
3	256.165568	**128.586422**					L	*1054.520388*	527.763832	1037.493839	519.250558	1036.509823	518.758550	9
4	384.224146	192.615711	367.197597	184.102437			Q	*941.436324*	471.221800	924.409775	462.708526	923.425759	462.216518	8
5	471.256174	236.131725	454.229625	227.618451	453.245609	227.126443	S	*813.377746*	407.192511	796.351197	398.679237	795.367181	398.187229	7
6	568.308938	**284.658107**	551.282389	276.144833	550.298373	275.652825	P	*726.345718*	363.676497	709.319169	355.163223	708.335153	354.671215	6
7	715.377352	358.192314	698.350803	349.679040	697.366787	349.187032	F	629.292954	315.150115	612.266405	306.636841	611.282389	306.144833	5
8	878.440681	439.723979	861.414132	431.210704	860.430116	430.718696	Y	*482.224540*	241.615908	465.197991	233.102633	464.213975	232.610625	4
9	935.462145	468.234711	918.435596	459.721436	917.451580	459.229428	G	319.161211	160.084243	302.134662	151.570969	301.150646	151.078961	3
10	1050.489088	525.748182	1033.462539	517.234908	1032.478523	516.742900	D	262.139747	131.573511	245.113198	123.060237	244.129182	122.568229	2
11							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of AALQSPFYGDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.6	1195.587326	-0.000958	AALQSPFYGDK

Mascot: http://www.matrixscience.com/

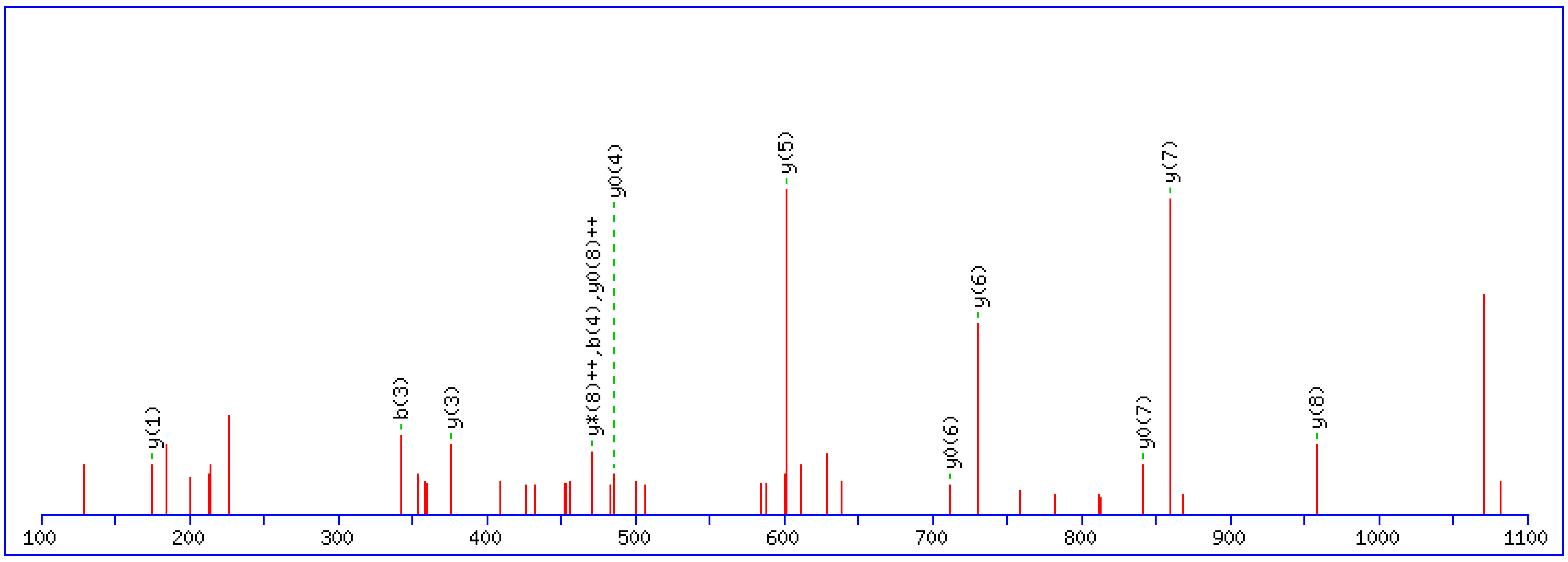
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IVEEPQSNR**
Found in **OXSR1_HUMAN**, Serine/threonine-protein kinase OSR1 OS=Homo sapiens GN=OXSR1 PE=1 SV=1

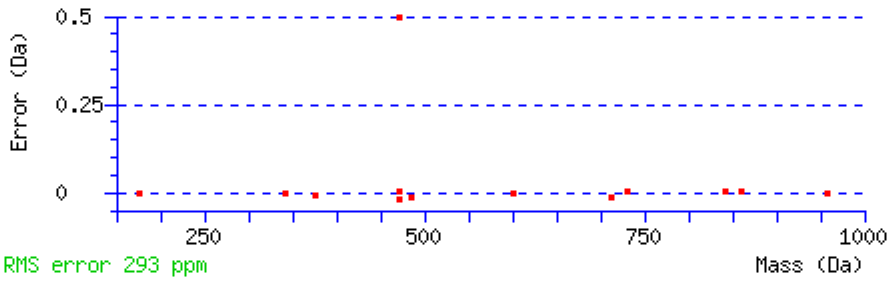
Match to Query 19770: 1070.530748 from(536.272650,2+) rtinseconds(894) index(2014)
Title: Locus:1.1.1.727.27
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 1.mgf

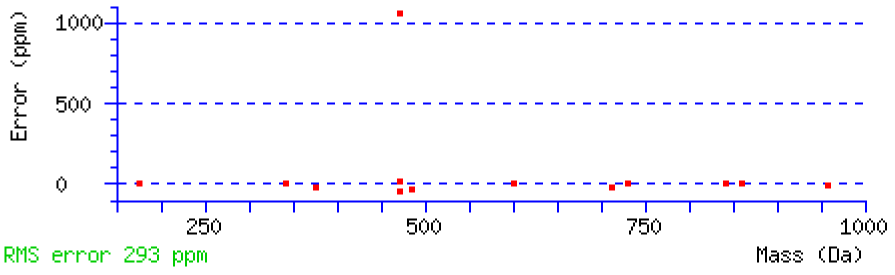
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1070.535614
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.0028
Matches : 13/78 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					I							9
2	213.159754	107.083515					V	***958.458849***	479.733063	941.432300	471.219788	940.448284	470.727780	8
3	**342.202347**	171.604811			324.191782	162.599529	E	***859.390435***	430.198856	842.363886	421.685581	841.379870	421.193573	7
4	**471.244940**	236.126108			453.234375	227.120826	E	***730.347842***	365.677559	713.321293	357.164285	712.337277	356.672277	6
5	568.297704	284.652490			550.287139	275.647208	P	***601.305249***	301.156263	584.278700	292.642988	583.294684	292.150980	5
6	696.356282	348.681779	679.329733	340.168505	678.345717	339.676497	Q	504.252485	252.629880	487.225936	244.116606	486.241920	243.624598	4
7	783.388310	392.197793	766.361761	383.684519	765.377745	383.192511	S	***376.193907***	188.600591	359.167358	180.087317	358.183342	179.595309	3
8	897.431237	449.219257	880.404688	440.705982	879.420672	440.213974	N	289.161879	145.084577	272.135330	136.571303			2
9							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of IVEEPQSNR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.8	1070.535614	-0.004866	IVEEPQSNR
15.2	1070.524384	0.006364	LDLEAPEPR
6.4	1070.525269	0.005479	LVTCYLRM
1.8	1070.535645	-0.004897	LDGSIPPGQR

Mascot: http://www.matrixscience.com/

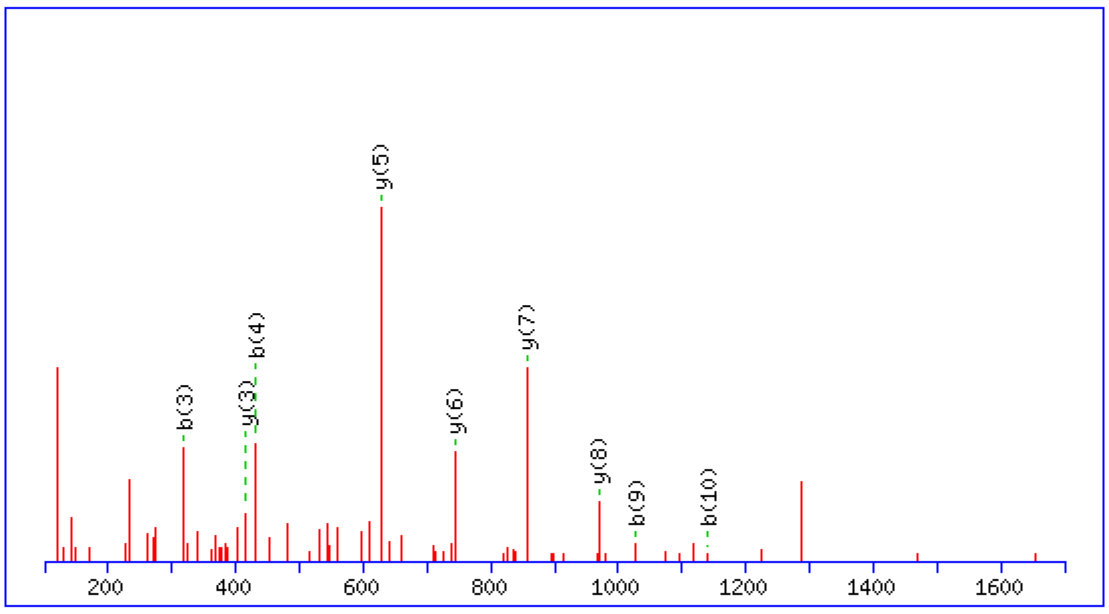
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VMSIPDVIRLK**
Found in **PRKX_HUMAN**, cAMP-dependent protein kinase catalytic subunit PRKX OS=Homo sapiens GN=PRKX PE=1 SV=1

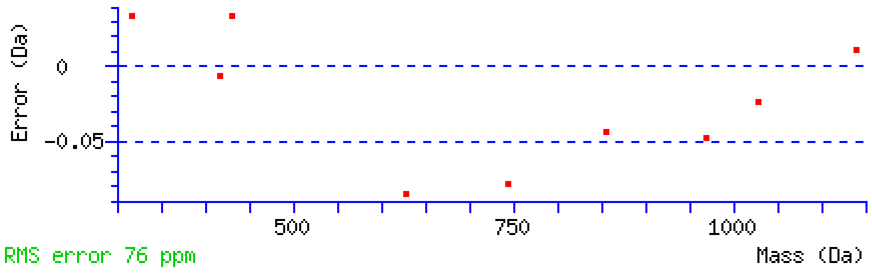
Match to Query 35953: 1285.732528 from(643.873540,2+) rtinseconds(3468) index(48577)
Title: Locus:1.1.1.2641.27
Data file 2011-11-14 - TFD - EP 8-5.mgf

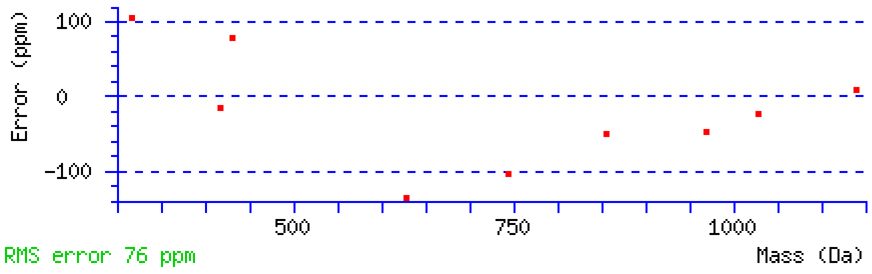
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1285.742783
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P5      : Oxidation (P)
Ions Score: 43  Expect: 0.00035
Matches : 9/90 fragment ions using 12 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							11
2	231.116175	116.061725					M	1187.681656	594.344466	1170.655107	585.831192	1169.671091	585.339183	10
3	*318.148203*	159.577740			300.137638	150.572457	S	1056.641171	528.824224	1039.614622	520.310949	1038.630606	519.818941	9
4	*431.232267*	216.119772			413.221702	207.114489	I	*969.609143*	485.308210	952.582594	476.794935	951.598578	476.302927	8
5	544.279946	272.643611			526.269381	263.638329	P	*856.525079*	428.766178	839.498530	420.252903	838.514514	419.760895	7
6	659.306889	330.157083			641.296324	321.151800	D	*743.477400*	372.242338	726.450851	363.729064	725.466835	363.237056	6
7	758.375303	379.691290			740.364738	370.686007	V	*628.450457*	314.728867	611.423908	306.215592			5
8	871.459367	436.233322			853.448802	427.228039	I	529.382043	265.194660	512.355494	256.681385			4
9	*1027.560478*	514.283877	1010.533929	505.770603	1009.549913	505.278595	R	*416.297979*	208.652627	399.271430	200.139353			3
10	*1140.644542*	570.825909	1123.617993	562.312635	1122.633977	561.820627	L	260.196868	130.602072	243.170319	122.088797			2
11							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of VMSIPDVIRLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
43.0	1285.742783	-0.010255	VMSIPDVIRLK
11.9	1285.742783	-0.010255	VMSIPDVIRLK
4.0	1285.735367	-0.002839	SLELSVNLQRK
2.7	1285.735367	-0.002839	QRTLQEALSLK
2.2	1285.731537	0.000991	ALDMSLPSLVLK

Mascot: http://www.matrixscience.com/

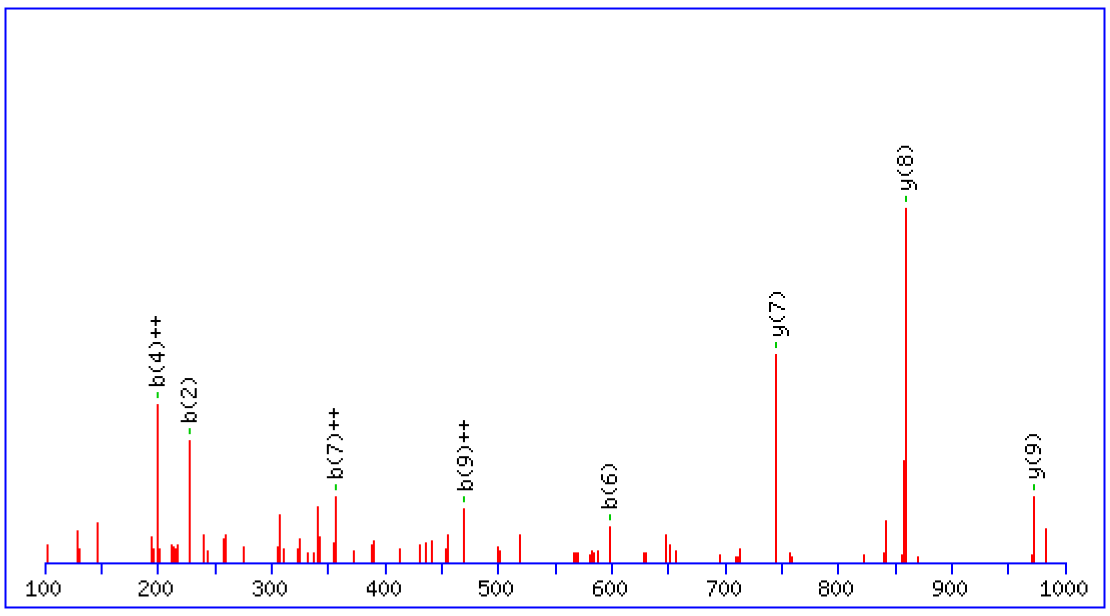
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IPNGEANVKK**
Found in **STK11_HUMAN**, Serine/threonine-protein kinase STK11 OS=Homo sapiens GN=STK11 PE=1 SV=1

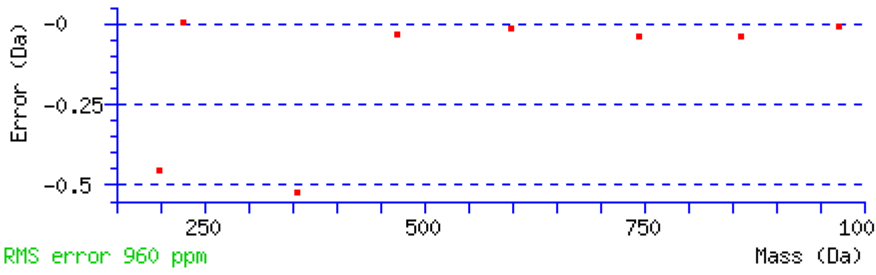
Match to Query 22302: 1084.582608 from(543.298580,2+) rtinseconds(2064) index(22221)
Title: Locus:1.1.1.2101.27
Data file 2011-11-10 - TFD - EP 4-5.mgf

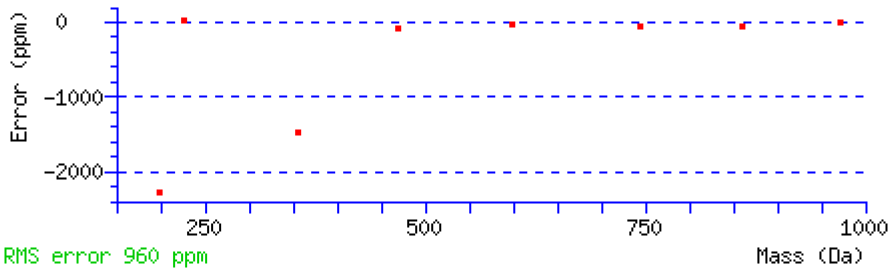
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1084.587646
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P2 : Oxidation (P)
Ions Score: 36 **Expect:** 0.0036
Matches : 8/86 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					I							10
2	**227.139019**	114.073147					P	***972.510885***	486.759081	955.484336	478.245806	954.500320	477.753798	9
3	341.181946	171.094611	324.155397	162.581336			N	***859.463206***	430.235241	842.436657	421.721967	841.452641	421.229959	8
4	398.203410	***199.605343***	381.176861	191.092068			G	***745.420279***	373.213778	728.393730	364.700503	727.409714	364.208495	7
5	527.246003	264.126640	510.219454	255.613365	509.235438	255.121357	E	688.398815	344.703046	671.372266	336.189771	670.388250	335.697763	6
6	**598.283117**	299.645197	581.256568	291.131922	580.272552	290.639914	A	559.356222	280.181749	542.329673	271.668475			5
7	712.326044	***356.666660***	695.299495	348.153385	694.315479	347.661377	N	488.319108	244.663192	471.292559	236.149918			4
8	811.394458	406.200867	794.367909	397.687592	793.383893	397.195584	V	374.276181	187.641729	357.249632	179.128454			3
9	939.489421	***470.248348***	922.462872	461.735074	921.478856	461.243066	K	275.207767	138.107522	258.181218	129.594247			2
10							K	147.112804	74.060040	130.086255	65.546766			1





NCBI **BLAST** search of IPNGEANVKK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.6	1084.587646	-0.005038	IPNGEANVKK
13.2	1084.587662	-0.005054	IPNKPTQQK
13.0	1084.587646	-0.005038	IIEVNQNQK
8.4	1084.587662	-0.005054	LLQDVDINR
5.2	1084.580444	0.002164	FLIDSIYSK
2.9	1084.573730	0.008878	AGRGKPGAEAR
2.7	1084.577286	0.005322	LYMKLVMR
2.2	1084.587662	-0.005054	GAVIQPQSASK
1.2	1084.591660	-0.009052	LSLAPAEAWK
0.1	1084.573746	0.008862	LPGRQTNQR

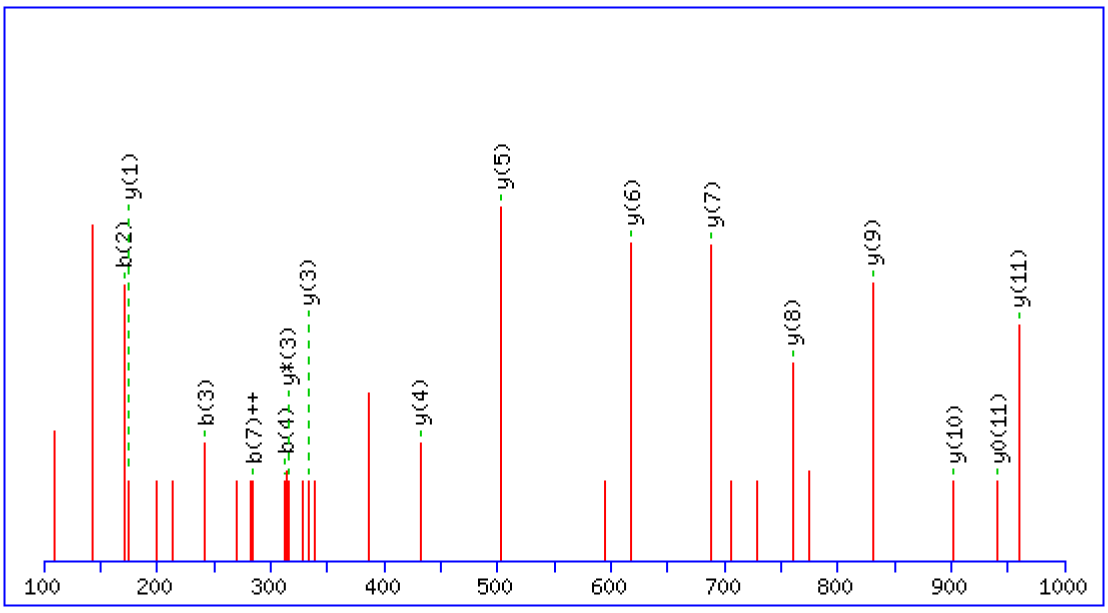
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGAAAADAVTGR**
Found in **WNK1_HUMAN**, Serine/threonine-protein kinase WNK1 OS=Homo sapiens GN=WNK1 PE=1 SV=2

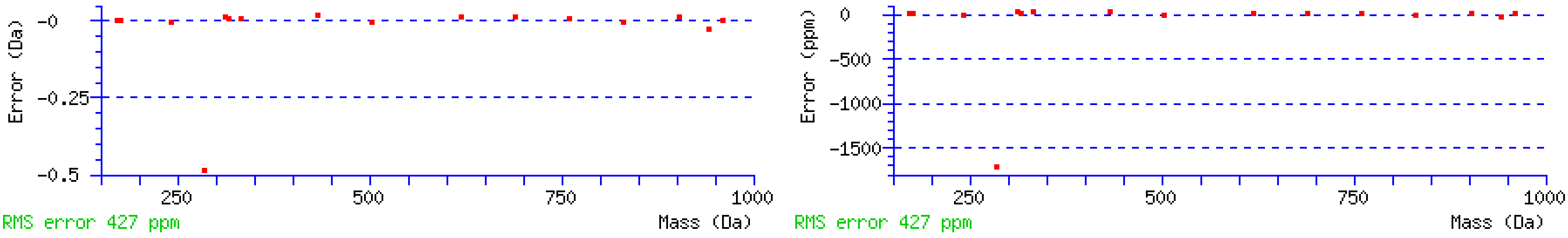
Match to Query 22108: 1071.570508 from(536.792530,2+) rtinseconds(1562) index(11202)
Title: Locus:1.1.1.1866.36
Data file 2011-11-14 - TFD - EP 8-6.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1071.567261
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 74 **Expect:** 1.3e-006
Matches : 16/94 fragment ions using 29 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.091340	57.549308			L							12
2	**171.112804**	86.060040			G	***959.490486***	480.248881	942.463937	471.735607	941.479921	471.243599	11
3	**242.149918**	121.578597			A	***902.469022***	451.738149	885.442473	443.224875	884.458457	442.732867	10
4	**313.187032**	157.097154			A	***831.431908***	416.219592	814.405359	407.706318	813.421343	407.214310	9
5	384.224146	192.615711			A	***760.394794***	380.701035	743.368245	372.187761	742.384229	371.695753	8
6	455.261260	228.134268			A	***689.357680***	345.182478	672.331131	336.669204	671.347115	336.177196	7
7	570.288203	285.647740	552.277638	276.642457	D	***618.320566***	309.663921	601.294017	301.150647	600.310001	300.658639	6
8	641.325317	321.166296	623.314752	312.161014	A	***503.293623***	252.150450	486.267074	243.637175	485.283058	243.145167	5
9	740.393731	370.700503	722.383166	361.695221	V	***432.256509***	216.631893	415.229960	208.118618	414.245944	207.626610	4
10	841.441410	421.224343	823.430845	412.219060	T	***333.188095***	167.097686	316.161546	158.584411	315.177530	158.092403	3
11	898.462874	449.735075	880.452309	440.729792	G	232.140416	116.573846	215.113867	108.060572			2
12					R	***175.118952***	88.063114	158.092403	79.549840			1



NCBI **BLAST** search of LGAAAADAVTGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
74.4	1071.567261	0.003247	LGAAAADAVTGR
23.3	1071.567245	0.003263	LQAKESPQR

Mascot: http://www.matrixscience.com/

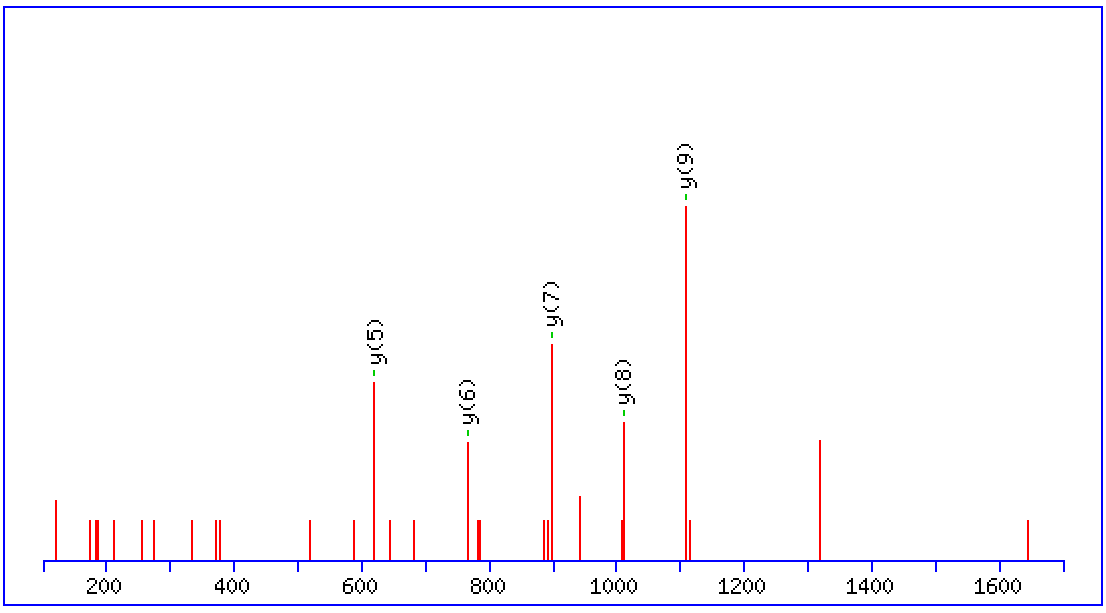
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLPIMFPALYR**
Found in **2A5D_HUMAN**, Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform OS=Homo sapiens GN=PPP2R5D PE=1 SV=1

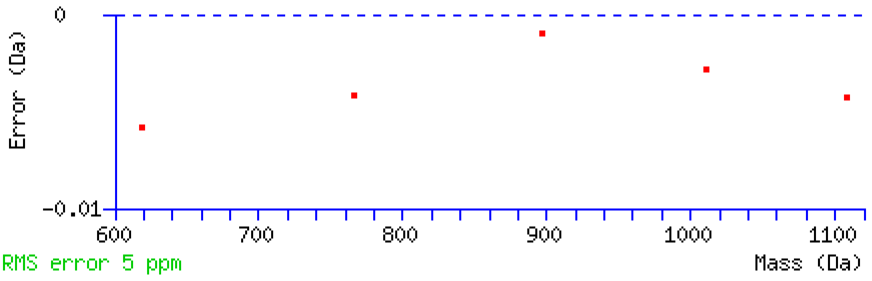
Match to Query 38700: 1318.746568 from(660.380560,2+) rtinseconds(3967) index(58766)
Title: Locus:1.1.1.2923.23
Data file 2011-11-14 - TFD - EP 8-2.mgf

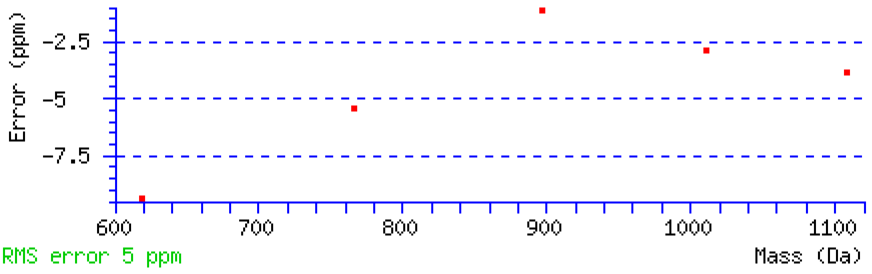
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1318.747131
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 32  Expect: 0.0027
Matches : 5/60 fragment ions using 9 most intense peaks   (help)
```

#	b	b^{++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	100.075690	50.541483	V					11
2	213.159754	107.083515	L	1220.686014	610.846645	1203.659465	602.333371	10
3	310.212518	155.609897	P	***1107.601950***	554.304613	1090.575401	545.791339	9
4	423.296582	212.151929	I	***1010.549186***	505.778231	993.522637	497.264956	8
5	554.337067	277.672172	M	***897.465122***	449.236199	880.438573	440.722924	7
6	701.405481	351.206379	F	***766.424637***	383.715957	749.398088	375.202682	6
7	798.458245	399.732761	P	***619.356223***	310.181750	602.329674	301.668475	5
8	869.495359	435.251318	A	522.303459	261.655368	505.276910	253.142093	4
9	982.579423	491.793350	L	451.266345	226.136810	434.239796	217.623536	3
10	1145.642752	573.325014	Y	338.182281	169.594778	321.155732	161.081504	2
11			R	175.118952	88.063114	158.092403	79.549839	1





NCBI **BLAST** search of VLPIMFPALYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.4	1318.747131	-0.000563	VLPIMFPALYR
1.2	1318.754349	-0.007781	VLGLRVCGLYR

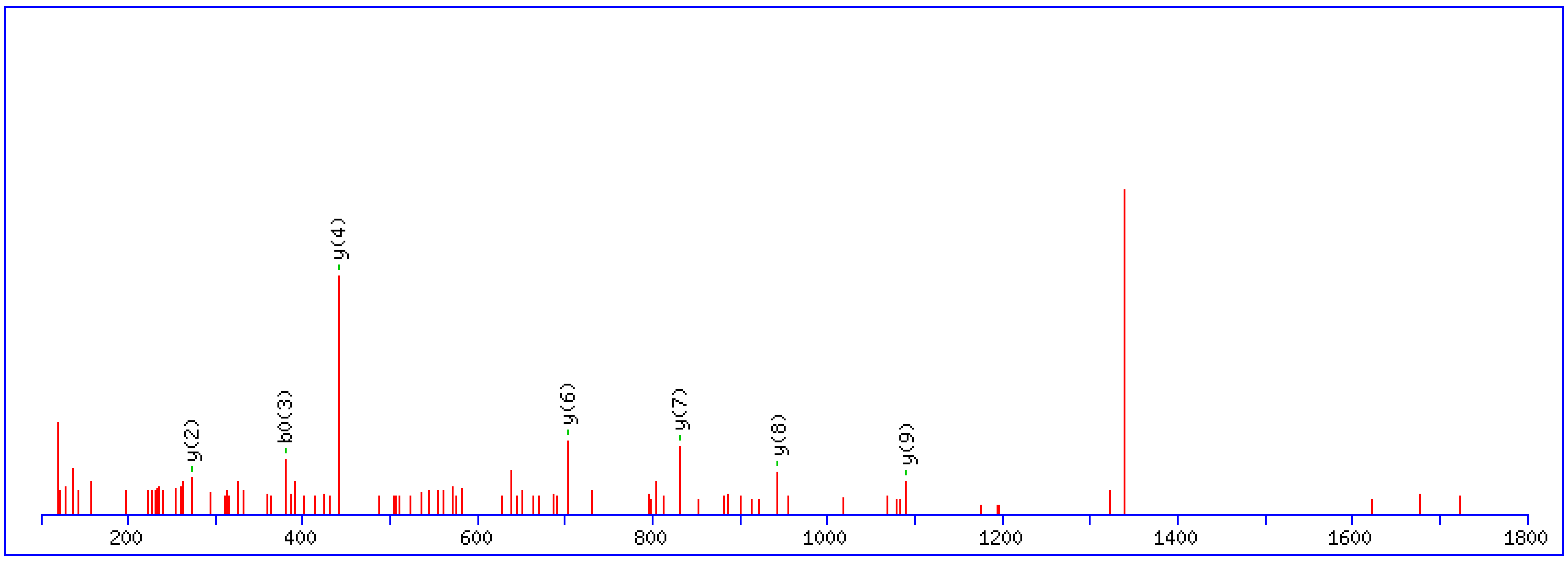
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YSFLQFDPAPR**
Found in **PP2AA_HUMAN**, Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform OS=Homo sapiens GN=PPP2CA PE=1 SV=1

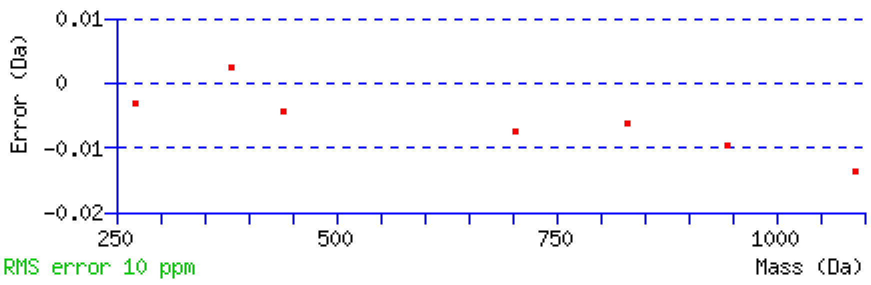
Match to Query 34434: 1339.648248 from(670.831400,2+) rtinseconds(3172) index(44641)
Title: Locus:1.1.1.1648.21
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 3.mgf

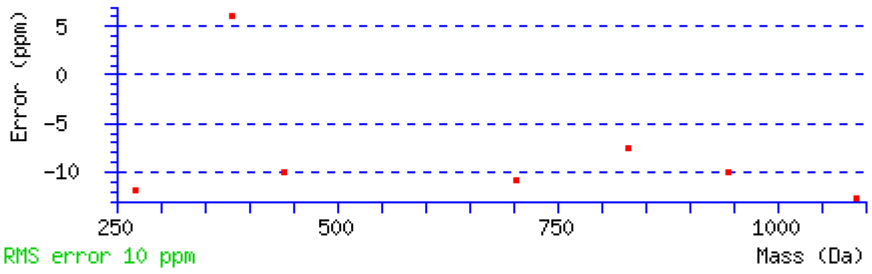
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1339.656082
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 34 **Expect:** 0.0046
Matches : 7/102 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.070605	82.538940					Y							11
2	251.102633	126.054954			233.092068	117.049672	S	1177.600035	589.303655	1160.573486	580.790381	1159.589470	580.298373	10
3	398.171047	199.589161			380.160482	190.583879	F	*1090.568007*	545.787642	1073.541458	537.274367	1072.557442	536.782359	9
4	511.255111	256.131193			493.244546	247.125911	L	*943.499593*	472.253435	926.473044	463.740160	925.489028	463.248152	8
5	639.313689	320.160483	622.287140	311.647208	621.303124	311.155200	Q	*830.415529*	415.711403	813.388980	407.198128	812.404964	406.706120	7
6	786.382103	393.694690	769.355554	385.181415	768.371538	384.689407	F	*702.356951*	351.682114	685.330402	343.168839	684.346386	342.676831	6
7	901.409046	451.208161	884.382497	442.694887	883.398481	442.202879	D	555.288537	278.147907	538.261988	269.634632	537.277972	269.142624	5
8	998.461810	499.734543	981.435261	491.221269	980.451245	490.729261	P	*440.261594*	220.634435	423.235045	212.121160			4
9	1069.498924	535.253100	1052.472375	526.739826	1051.488359	526.247818	A	343.208830	172.108053	326.182281	163.594778			3
10	1166.551688	583.779482	1149.525139	575.266208	1148.541123	574.774200	P	*272.171716*	136.589496	255.145167	128.076221			2
11							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of YSFLQFDPAPR
(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	1339.656082	-0.007834	YSFLQFDPAPR

Mascot: http://www.matrixscience.com/

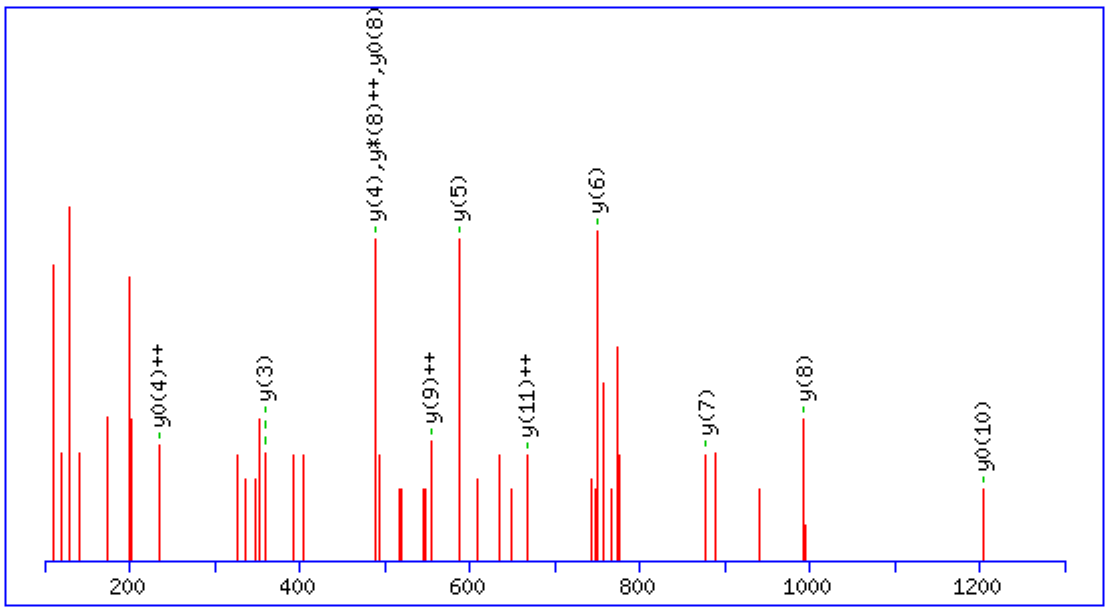
Mascot Search Results

Peptide View

MS/MS Fragmentation of **APLDLDKYVEIAR**
Found in **PPP6_HUMAN**, Serine/threonine-protein phosphatase 6 catalytic subunit OS=Homo sapiens GN=PPP6C PE=1 SV=1

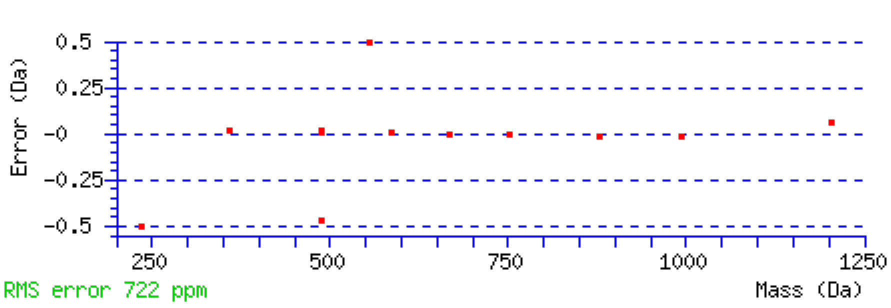
Match to Query 46978: 1501.818282 from(501.613370,3+) rtinseconds(3037) index(42546)
Title: Locus:1.1.1.2451.6
Data file 2011-11-12 - TFD - EP 6-4.mgf

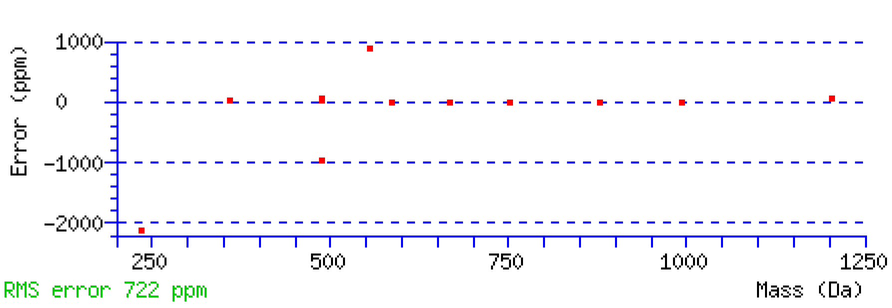
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1300] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1501.814011
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.0053
Matches : 12/120 fragment ions using 18 most intense peaks (help)

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	72.044390	36.525833					A							13
2	169.097154	85.052215					P	1431.784207	716.395741	1414.757658	707.882467	1413.773642	707.390459	12
3	282.181218	141.594247					L	1334.731443	667.869359	1317.704894	659.356085	1316.720878	658.864077	11
4	397.208161	199.107719			379.197596	190.102436	D	1221.647379	611.327327	1204.620830	602.814053	1203.636814	602.322045	10
5	510.292225	255.649751			492.281660	246.644468	L	1106.620436	553.813856	1089.593887	545.300582	1088.609871	544.808573	9
6	625.319168	313.163222			607.308603	304.157940	D	***993.536372***	497.271824	976.509823	488.758549	975.525807	488.266541	8
7	753.414131	377.210704	736.387582	368.697429	735.403566	368.205421	K	***878.509429***	439.758352	861.482880	431.245078	860.498864	430.753070	7
8	916.477460	458.742368	899.450911	450.229094	898.466895	449.737086	Y	***750.414466***	375.710871	733.387917	367.197596	732.403901	366.705588	6
9	1015.545874	508.276575	998.519325	499.763301	997.535309	499.271293	V	***587.351137***	294.179206	570.324588	285.665932	569.340572	285.173924	5
10	1144.588467	572.797872	1127.561918	564.284597	1126.577902	563.792589	E	***488.282723***	244.644999	471.256174	236.131725	470.272158	235.639717	4
11	1257.672531	629.339903	1240.645982	620.826629	1239.661966	620.334621	I	***359.240130***	180.123703	342.213581	171.610428			3
12	1328.709645	664.858460	1311.683096	656.345186	1310.699080	655.853178	A	246.156066	123.581671	229.129517	115.068396			2
13							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of APLDLDKYVEIAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.4	1501.814011	0.004271	APLDLDKYVEIAR

Mascot: http://www.matrixscience.com/

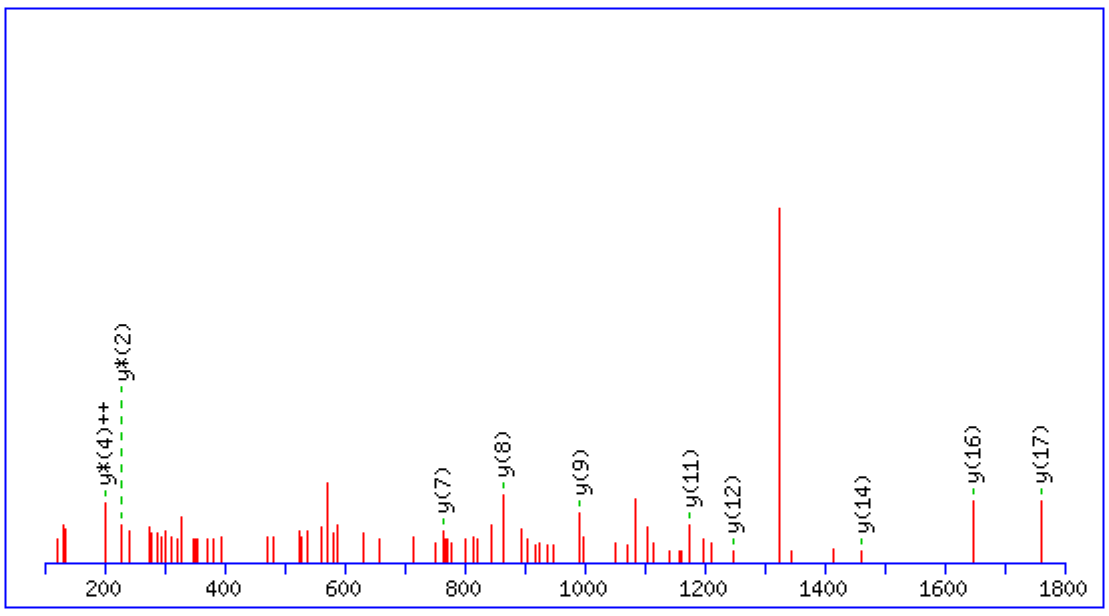
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NLINATNAALQTPLHVAAR**
Found in **ANR28_HUMAN**, Serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit A OS=Homo sapiens GN=ANKRD28 PE=1 SV=5

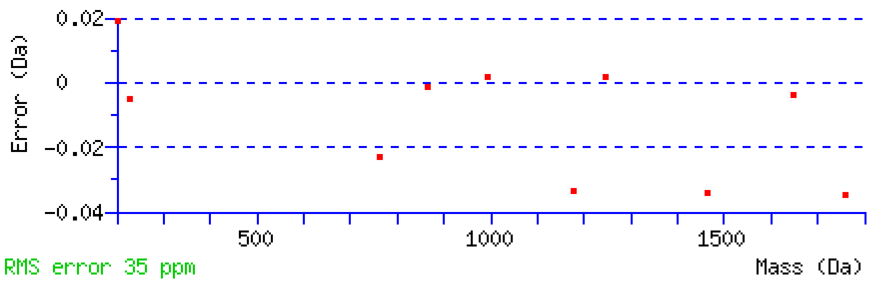
Match to Query 59623: 1987.098972 from(663.373600,3+) rtinseconds(2981) index(40185)
Title: Locus:1.1.1.2555.26
Data file 2011-11-10 - TFD - EP 3-1.mgf

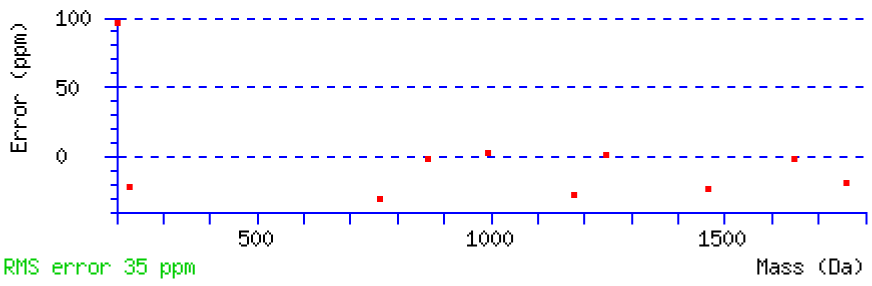
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1987.096268
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 48  Expect: 4.9e-005
Matches : 10/192 fragment ions using 16 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			N							19
2	228.134267	114.570771	211.107718	106.057497			L	1874.060658	937.533967	1857.034109	929.020693	1856.050093	928.528684	18
3	341.218331	171.112803	324.191782	162.599529			I	***1760.976594***	880.991935	1743.950045	872.478660	1742.966029	871.986652	17
4	455.261258	228.134267	438.234709	219.620993			N	***1647.892530***	824.449903	1630.865981	815.936628	1629.881965	815.444620	16
5	526.298372	263.652824	509.271823	255.139550			A	1533.849603	767.428439	1516.823054	758.915165	1515.839038	758.423157	15
6	627.346051	314.176664	610.319502	305.663389	609.335486	305.171381	T	***1462.812489***	731.909882	1445.785940	723.396608	1444.801924	722.904600	14
7	741.388978	371.198127	724.362429	362.684853	723.378413	362.192845	N	1361.764810	681.386043	1344.738261	672.872769	1343.754245	672.380760	13
8	812.426092	406.716684	795.399543	398.203410	794.415527	397.711402	A	***1247.721883***	624.364579	1230.695334	615.851305	1229.711318	615.359297	12
9	883.463206	442.235241	866.436657	433.721967	865.452641	433.229959	A	***1176.684769***	588.846022	1159.658220	580.332748	1158.674204	579.840740	11
10	996.547270	498.777273	979.520721	490.263999	978.536705	489.771991	L	1105.647655	553.327466	1088.621106	544.814191	1087.637090	544.322183	10
11	1124.605848	562.806562	1107.579299	554.293288	1106.595283	553.801279	Q	***992.563591***	496.785433	975.537042	488.272159	974.553026	487.780151	9
12	1225.653527	613.330401	1208.626978	604.817127	1207.642962	604.325119	T	***864.505013***	432.756145	847.478464	424.242870	846.494448	423.750862	8
13	1322.706291	661.856784	1305.679742	653.343509	1304.695726	652.851501	P	***763.457334***	382.232305	746.430785	373.719030			7
14	1435.790355	718.398815	1418.763806	709.885541	1417.779790	709.393533	L	666.404570	333.705923	649.378021	325.192648			6
15	1572.849267	786.928271	1555.822718	778.414997	1554.838702	777.922989	H	553.320506	277.163891	536.293957	268.650617			5
16	1671.917681	836.462478	1654.891132	827.949204	1653.907116	827.457196	V	416.261594	208.634435	399.235045	200.121160			4
17	1742.954795	871.981035	1725.928246	863.467761	1724.944230	862.975753	A	317.193180	159.100228	300.166631	150.586953			3
18	1813.991909	907.499592	1796.965360	898.986318	1795.981344	898.494310	A	246.156066	123.581671	229.129517	115.068396			2
19							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of NLINATNAALQTPLHVAAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.4	1987.096268	0.002704	NLINATNAALQTPLHVAAR

Mascot: http://www.matrixscience.com/

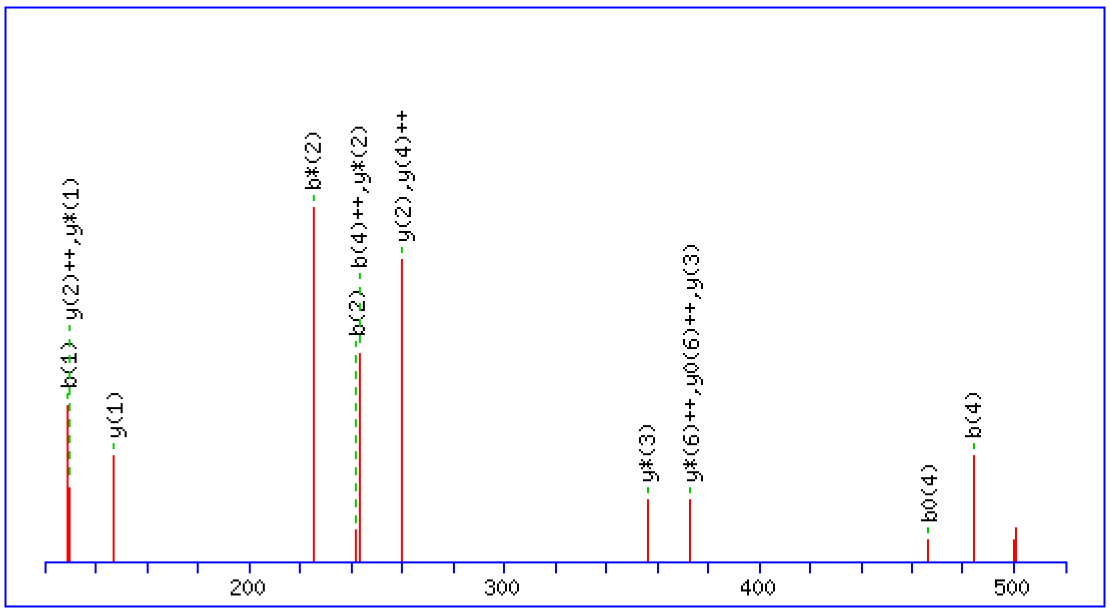
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **KLIEFLLK**
Found in **PP6R3_HUMAN**, Serine/threonine-protein phosphatase 6 regulatory subunit 3 OS=Homo sapiens GN=PPP6R3 PE=1 SV=2

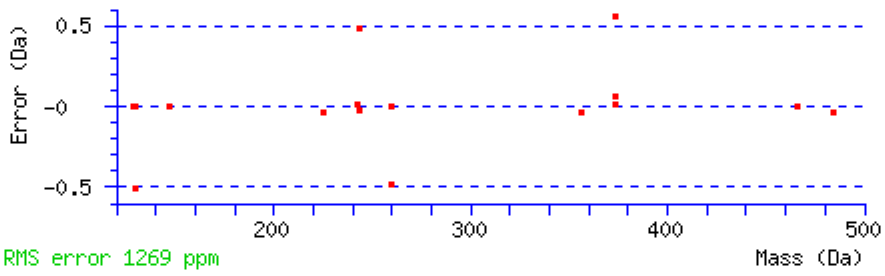
Match to Query 9307: 1002.639188 from(502.326870,2+) rtinseconds(1697) index(4635)
Title: Locus:1.1.1.2294.14
Data file 2011-11-10 - TFD - EP 3-8.mgf

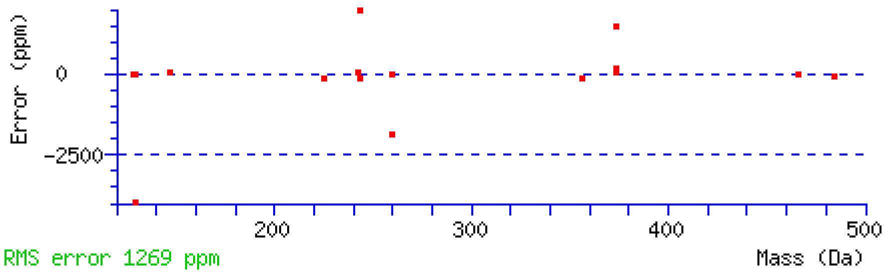
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 120 to 520 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1002.647720
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.00062
Matches : 17/70 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	***129.102239***	65.054757	112.075690	56.541483			K							8
2	***242.186303***	121.596790	225.159754	113.083515			L	875.560067	438.283672	858.533518	429.770397	857.549502	429.278389	7
3	355.270367	178.138822	338.243818	169.625547			I	762.476003	381.741640	745.449454	373.228365	744.465438	372.736357	6
4	***484.312960***	**242.660118**	467.286411	234.146844	466.302395	233.654836	E	649.391939	325.199608	632.365390	316.686333	631.381374	316.194325	5
5	631.381374	316.194325	614.354825	307.681051	613.370809	307.189043	F	520.349346	260.678311	503.322797	252.165037			4
6	744.465438	**372.736357**	727.438889	364.223083	726.454873	363.731075	L	***373.280932***	187.144104	356.254383	178.630830			3
7	857.549502	429.278389	840.522953	420.765115	839.538937	420.273107	L	***260.196868***	130.602072	243.170319	122.088798			2
8							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of KLIEFLLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.1	1002.647720	-0.008532	KLIEFLLK
17.0	1002.647720	-0.008532	LKLFEILK
3.1	1002.647736	-0.008548	IFLLGLSIK

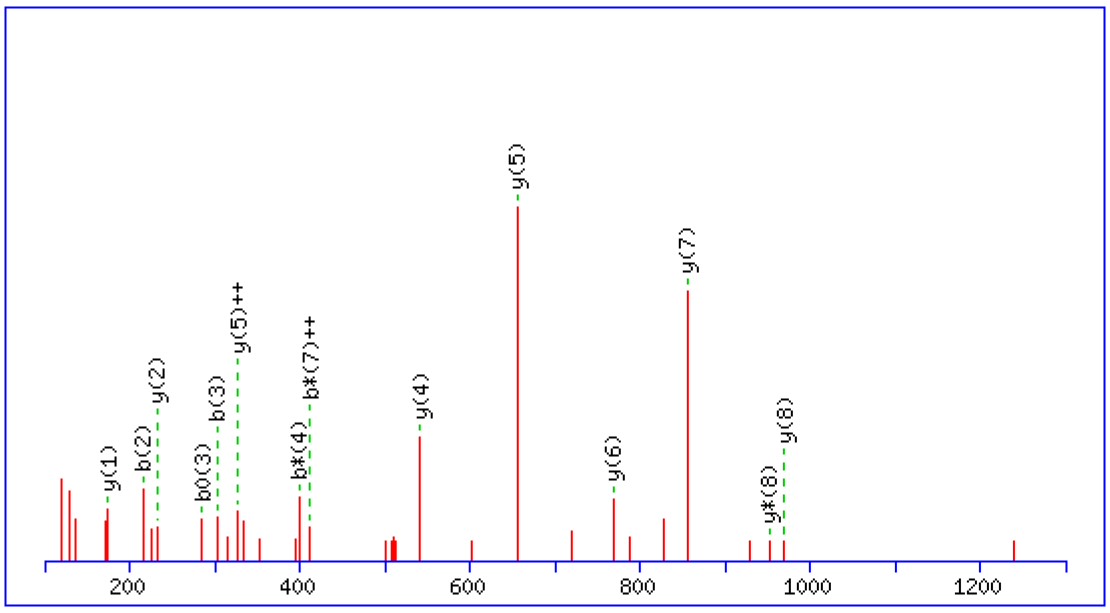
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TNSILFYGR**
Found in **SPB3_HUMAN**, Serpin B3 OS=Homo sapiens GN=SERPINB3 PE=1 SV=2

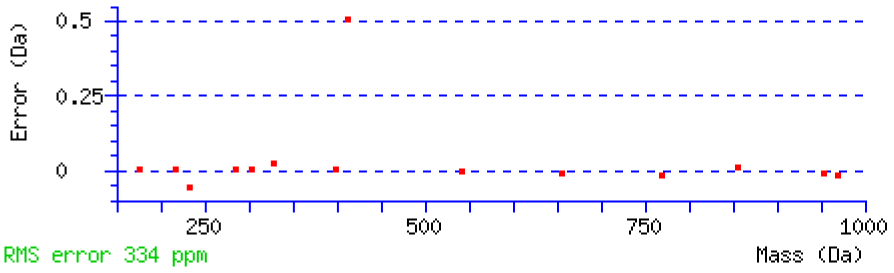
Match to Query 14277: 1069.556128 from(535.785340,2+) rtinseconds(2555) index(15375)
Title: Locus:1.1.1.2695.7
Data file 2011-11-14 - TFD - EP 8-8.mgf

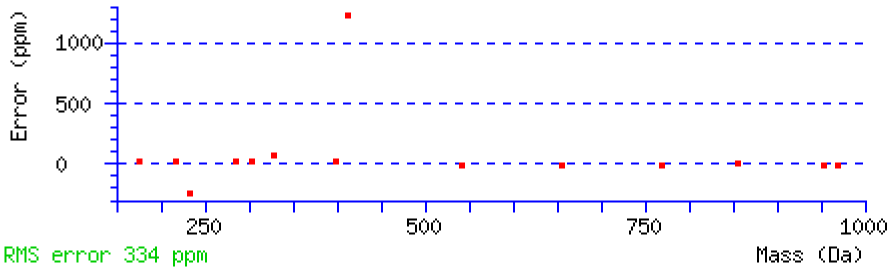
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1300] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1069.555634
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 43 **Expect:** 0.00046
Matches : 14/82 fragment ions using 28 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							9
2	**216.097882**	108.552579	199.071333	100.039305	198.087317	99.547296	N	***969.515242***	485.261259	952.488693	476.747985	951.504677	476.255977	8
3	**303.129910**	152.068593	286.103361	143.555319	285.119345	143.063311	S	***855.472315***	428.239796	838.445766	419.726521	837.461750	419.234513	7
4	416.213974	208.610625	399.187425	200.097351	398.203409	199.605343	I	***768.440287***	384.723782	751.413738	376.210507			6
5	529.298038	265.152657	512.271489	256.639383	511.287473	256.147375	L	***655.356223***	328.181750	638.329674	319.668475			5
6	676.366452	338.686864	659.339903	330.173589	658.355887	329.681581	F	***542.272159***	271.639718	525.245610	263.126443			4
7	839.429781	420.218529	822.403232	411.705254	821.419216	411.213246	Y	395.203745	198.105511	378.177196	189.592236			3
8	896.451245	448.729261	879.424696	440.215986	878.440680	439.723978	G	***232.140416***	116.573846	215.113867	108.060572			2
9							R	***175.118952***	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of TNSILFYGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.9	1069.555634	0.000494	TNSILFYGR
6.8	1069.551620	0.004508	TPLSTGNPQR
5.7	1069.551590	0.004538	QSSKLNEHK
0.4	1069.555618	0.000510	FYQSEIKR
0.0	1069.551590	0.004538	EPRALAEPR

Mascot: http://www.matrixscience.com/

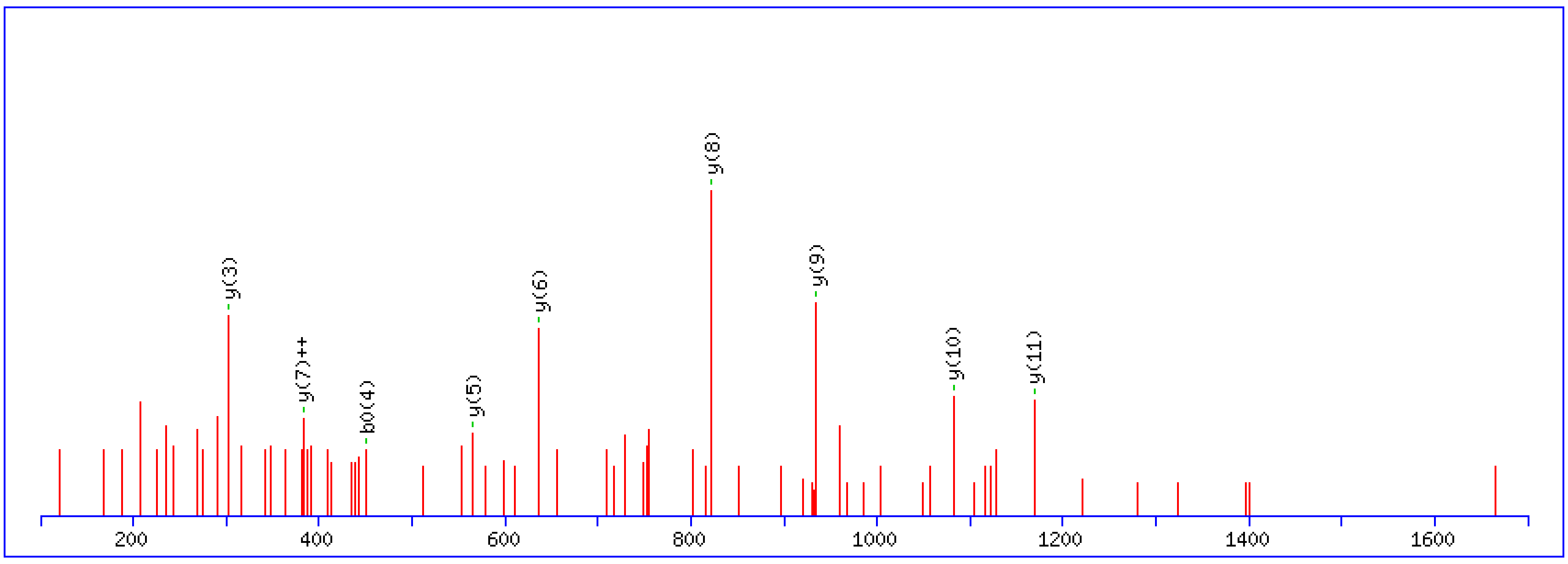
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SFFSFLGEAFDGAR**
Found in **SAA_HUMAN**, Serum amyloid A protein OS=Homo sapiens GN=SAA1 PE=1 SV=2

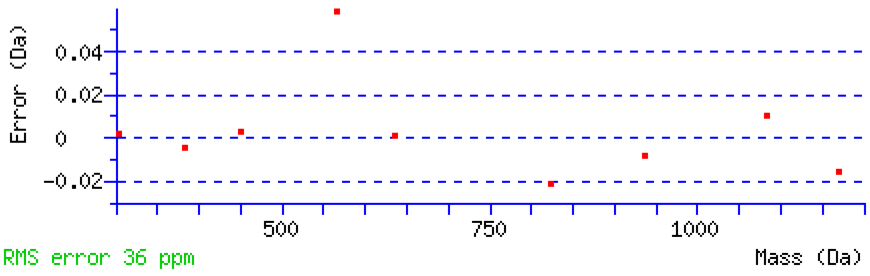
Match to Query 45994: 1549.720128 from(775.867340,2+) rtinseconds(4471) index(69035)
Title: Locus:1.1.1.2070.27
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 2.mgf

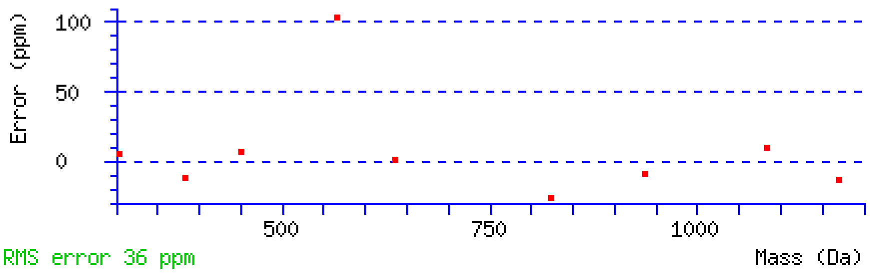
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1700] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1549.720154
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 44  Expect: 0.0005
Matches : 9/124 fragment ions using 13 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	S							14
2	235.107718	118.057497	217.097153	109.052214	F	1463.695392	732.351334	1446.668843	723.838059	1445.684827	723.346051	13
3	382.176132	191.591704	364.165567	182.586422	F	1316.626978	658.817127	1299.600429	650.303853	1298.616413	649.811845	12
4	469.208160	235.107718	451.197595	226.102435	S	***1169.558564***	585.282920	1152.532015	576.769646	1151.547999	576.277637	11
5	616.276574	308.641925	598.266009	299.636642	F	***1082.526536***	541.766906	1065.499987	533.253632	1064.515971	532.761624	10
6	729.360638	365.183957	711.350073	356.178675	L	***935.458122***	468.232699	918.431573	459.719425	917.447557	459.227417	9
7	786.382102	393.694689	768.371537	384.689407	G	***822.374058***	411.690667	805.347509	403.177393	804.363493	402.685385	8
8	915.424695	458.215986	897.414130	449.210703	E	765.352594	383.179935	748.326045	374.666660	747.342029	374.174652	7
9	986.461809	493.734543	968.451244	484.729260	A	***636.310001***	318.658639	619.283452	310.145364	618.299436	309.653356	6
10	1133.530223	567.268750	1115.519658	558.263467	F	***565.272887***	283.140082	548.246338	274.626807	547.262322	274.134799	5
11	1248.557166	624.782221	1230.546601	615.776939	D	418.204473	209.605874	401.177924	201.092600	400.193908	200.600592	4
12	1305.578630	653.292953	1287.568065	644.287670	G	***303.177530***	152.092403	286.150981	143.579128			3
13	1376.615744	688.811510	1358.605179	679.806227	A	246.156066	123.581671	229.129517	115.068396			2
14					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of SFFSFLGEAFDGAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.1	1549.720154	-0.000026	SFFSFLGEAFDGAR

Mascot: http://www.matrixscience.com/

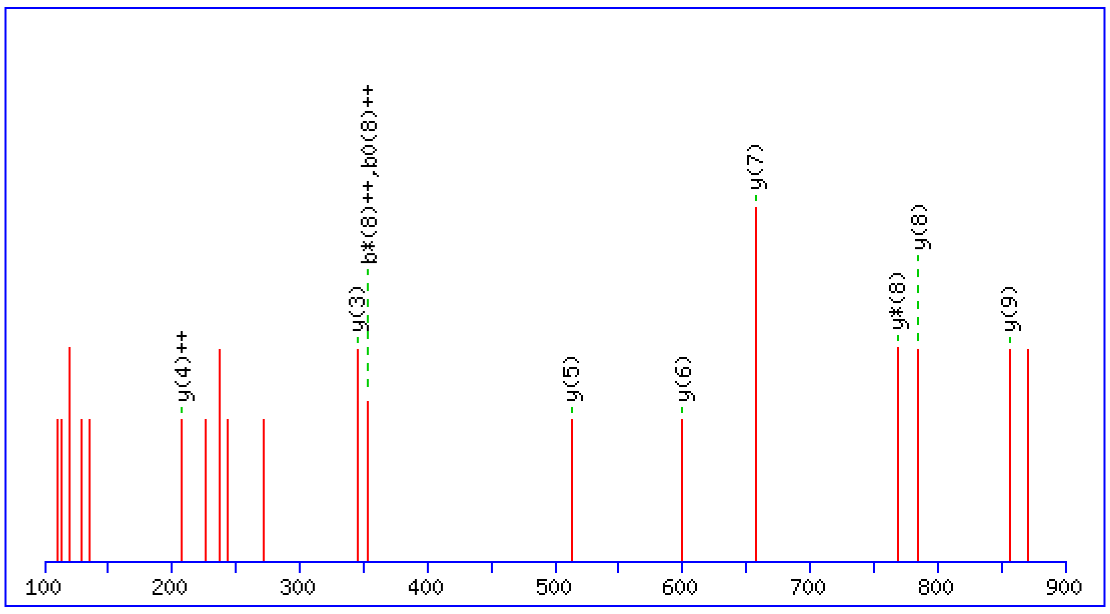
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LAQGSPAVAR**
Found in **SPD2A_HUMAN**, SH3 and PX domain-containing protein 2A OS=Homo sapiens GN=SH3PXD2A PE=1 SV=1

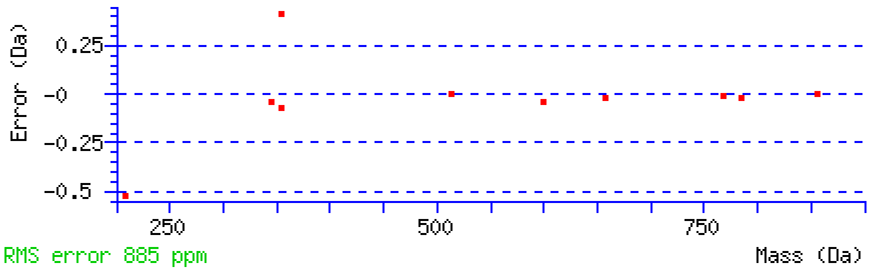
Match to Query 13419: 968.530908 from(485.272730,2+) rtinseconds(967) index(2468)
Title: Locus:1.1.1.1723.23
Data file 2011-11-10 - TFD - EP 4-1.mgf

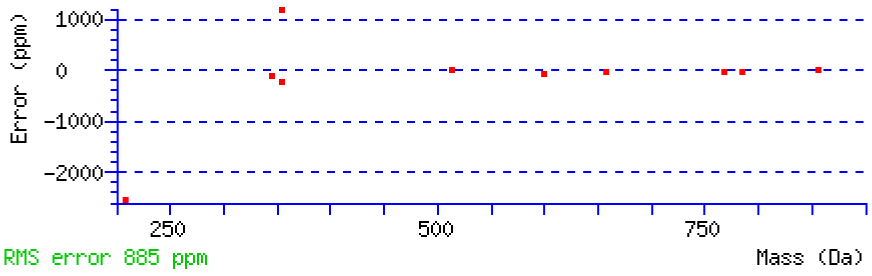
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 968.540314
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.0025
Matches : 10/86 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							10
2	185.128454	93.067865					A	***856.463542***	428.735409	839.436993	420.222135	838.452977	419.730127	9
3	313.187032	157.097154	296.160483	148.583879			Q	***785.426428***	393.216852	768.399879	384.703578	767.415863	384.211570	8
4	370.208496	185.607886	353.181947	177.094611			G	***657.367850***	329.187563	640.341301	320.674289	639.357285	320.182281	7
5	457.240524	229.123900	440.213975	220.610626	439.229959	220.118618	S	***600.346386***	300.676831	583.319837	292.163557	582.335821	291.671549	6
6	554.293288	277.650282	537.266739	269.137008	536.282723	268.645000	P	***513.314358***	257.160817	496.287809	248.647543			5
7	625.330402	313.168839	608.303853	304.655565	607.319837	304.163557	A	416.261594	208.634435	399.235045	200.121160			4
8	724.398816	362.703046	707.372267	354.189772	706.388251	353.697764	V	***345.224480***	173.115878	328.197931	164.602603			3
9	795.435930	398.221603	778.409381	389.708328	777.425365	389.216320	A	246.156066	123.581671	229.129517	115.068397			2
10							R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of LAQGSPAVAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.1	968.540314	-0.009406	LAQGSPAVAR
12.7	968.529099	0.001809	VPDQKGTPK
7.5	968.540314	-0.009406	SPKPSGLQR
7.0	968.529068	0.001840	LAANPDPKK
6.0	968.529068	0.001840	LAANPDPKK
6.0	968.529083	0.001825	IATQPTNPK
2.6	968.533112	-0.002204	LASFLGFSK
2.0	968.540314	-0.009406	IRDSLPPR

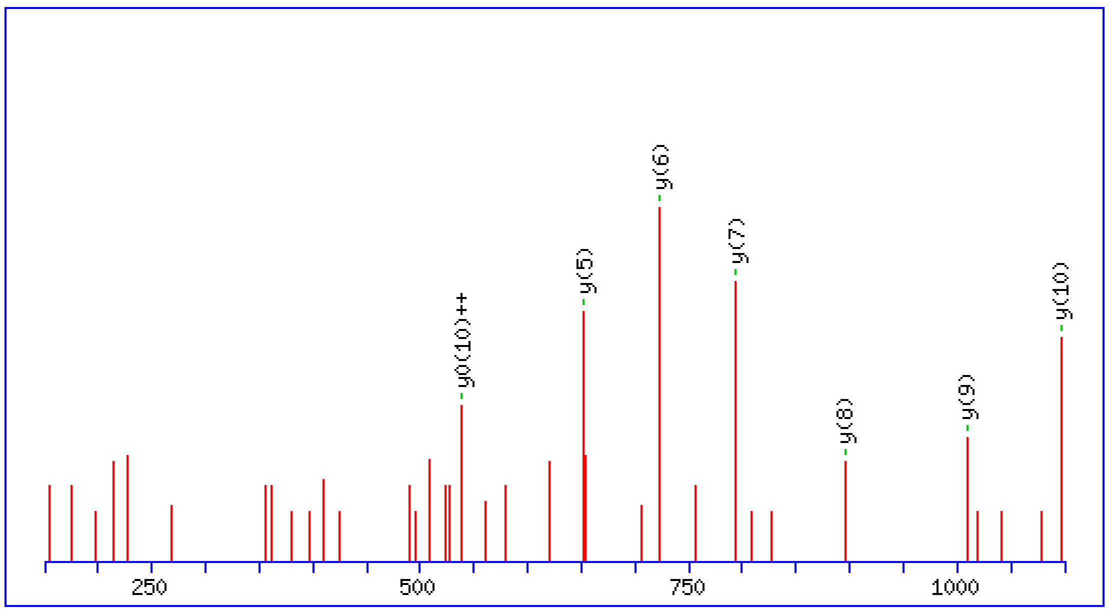
{MATRIX SCIENCE}
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELSNTAAYQSVR**
Found in **SIAE_HUMAN**, Sialate O-acetylesterase OS=Homo sapiens GN=SIAE PE=1 SV=1

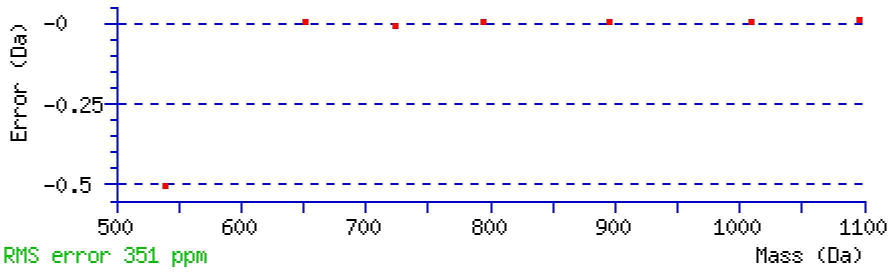
Match to Query 38168: 1337.655108 from(669.834830,2+) rtinseconds(1654) index(14442)
Title: Locus:1.1.1.1945.48
Data file 2011-11-10 - TFD - EP 4-5.mgf

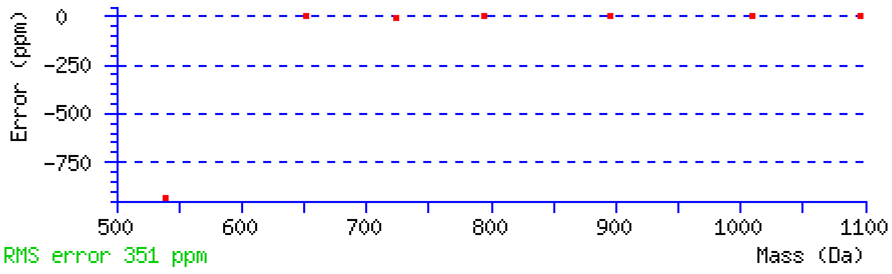
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1337.657516
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 45 **Expect:** 6.9e-005
Matches : 7/122 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	E							12
2	243.133933	122.070605			225.123368	113.065322	L	1209.622227	605.314752	1192.595678	596.801477	1191.611662	596.309469	11
3	330.165961	165.586618			312.155396	156.581336	S	***1096.538163***	548.772719	1079.511614	540.259445	1078.527598	539.767437	10
4	444.208888	222.608082	427.182339	214.094808	426.198323	213.602800	N	***1009.506135***	505.256706	992.479586	496.743431	991.495570	496.251423	9
5	545.256567	273.131922	528.230018	264.618647	527.246002	264.126639	T	***895.463208***	448.235242	878.436659	439.721967	877.452643	439.229959	8
6	616.293681	308.650479	599.267132	300.137204	598.283116	299.645196	A	***794.415529***	397.711403	777.388980	389.198128	776.404964	388.706120	7
7	687.330795	344.169036	670.304246	335.655761	669.320230	335.163753	A	***723.378415***	362.192846	706.351866	353.679571	705.367850	353.187563	6
8	850.394124	425.700700	833.367575	417.187425	832.383559	416.695417	Y	***652.341301***	326.674289	635.314752	318.161014	634.330736	317.669006	5
9	978.452702	489.729989	961.426153	481.216714	960.442137	480.724706	Q	489.277972	245.142624	472.251423	236.629349	471.267407	236.137341	4
10	1065.484730	533.246003	1048.458181	524.732729	1047.474165	524.240720	S	361.219394	181.113335	344.192845	172.600060	343.208829	172.108052	3
11	1164.553144	582.780210	1147.526595	574.266936	1146.542579	573.774927	V	274.187366	137.597321	257.160817	129.084047			2
12							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of ELSNTAAYQSVR
(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	1337.657516	-0.002408	ELSNTAAYQSVR
0.4	1337.651016	0.004092	MAAGPAPPPGRPR
0.4	1337.651016	0.004092	MAAGPAPPPGRPR
0.1	1337.651016	0.004092	MAAGPAPPPGRPR

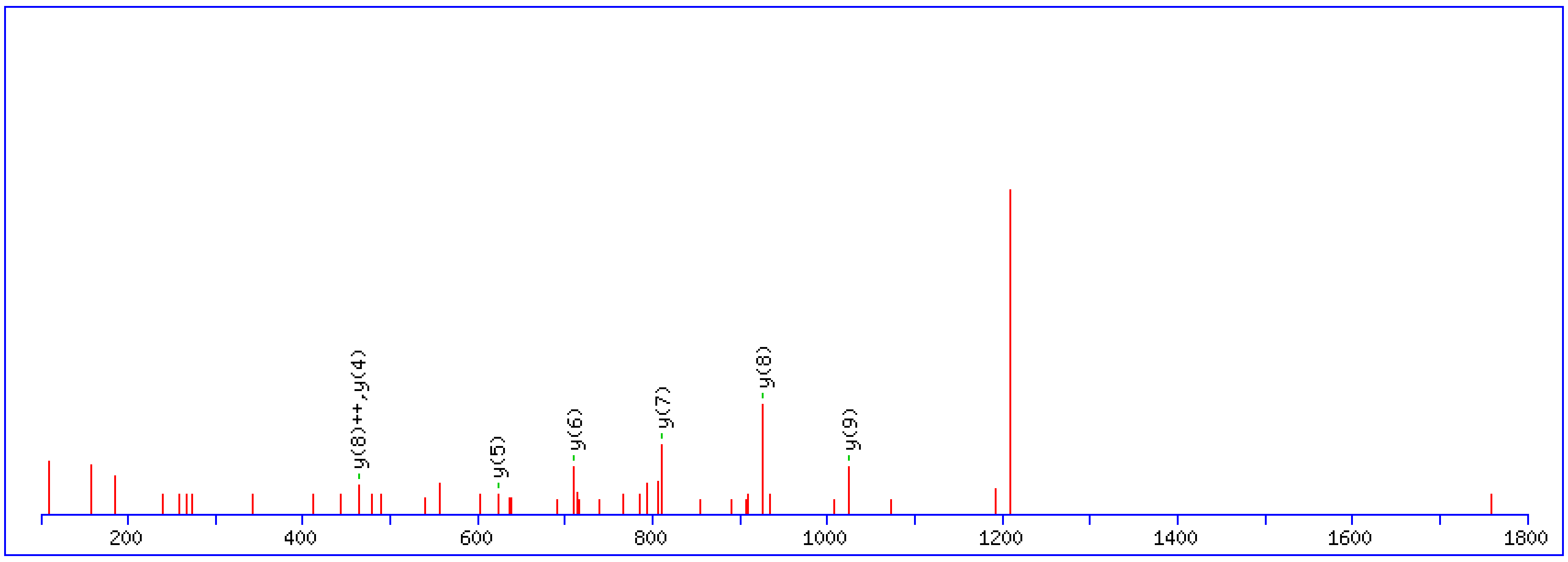
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALVDTSCSSNR**
Found in **SKT_HUMAN**, Sickle tail protein homolog OS=Homo sapiens GN=SKT PE=1 SV=2

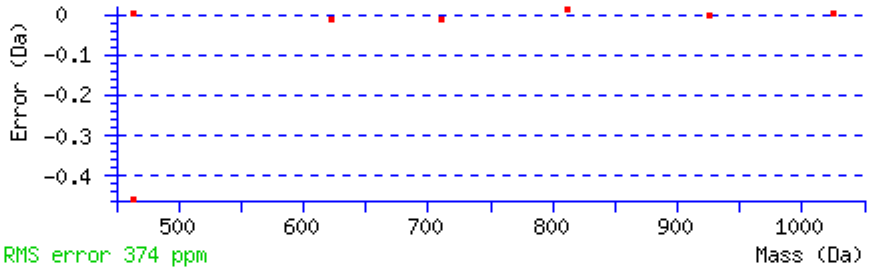
Match to Query 22499: 1208.546588 from(605.280570,2+) rtinseconds(1030) index(4297)
Title: Locus:1.1.1.775.38
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 2.mgf

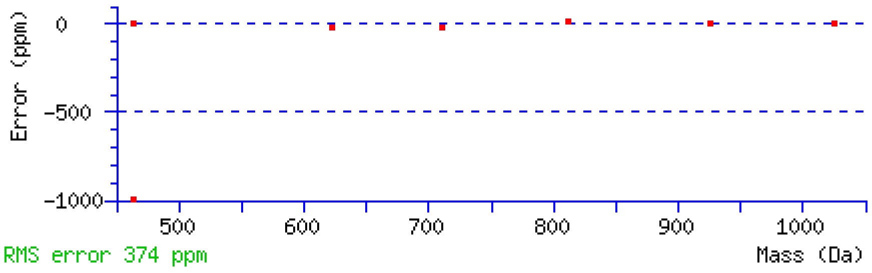
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1208.545547
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 43  Expect: 0.00046
Matches : 7/92 fragment ions using 11 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.044390	36.525833					A							11
2	185.128454	93.067865					L	1138.515712	569.761494	1121.489163	561.248220	1120.505147	560.756212	10
3	284.196868	142.602072					V	***1025.431648***	513.219462	1008.405099	504.706188	1007.421083	504.214180	9
4	399.223811	200.115544			381.213246	191.110261	D	***926.363234***	463.685255	909.336685	455.171981	908.352669	454.679973	8
5	500.271490	250.639383			482.260925	241.634101	T	***811.336291***	406.171784	794.309742	397.658509	793.325726	397.166501	7
6	587.303518	294.155397			569.292953	285.150115	S	***710.288612***	355.647944	693.262063	347.134670	692.278047	346.642662	6
7	747.334167	374.170722			729.323602	365.165439	C	***623.256584***	312.131930	606.230035	303.618656	605.246019	303.126648	5
8	834.366195	417.686736			816.355630	408.681453	S	***463.225935***	232.116605	446.199386	223.603331	445.215370	223.111323	4
9	921.398223	461.202750			903.387658	452.197467	S	376.193907	188.600591	359.167358	180.087317	358.183342	179.595309	3
10	1035.441150	518.224213	1018.414601	509.710939	1017.430585	509.218931	N	289.161879	145.084577	272.135330	136.571303			2
11							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of ALVDTSCSSNR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
43.2	1208.545547	0.001041	ALVDTSCSSNR

Mascot: http://www.matrixscience.com/

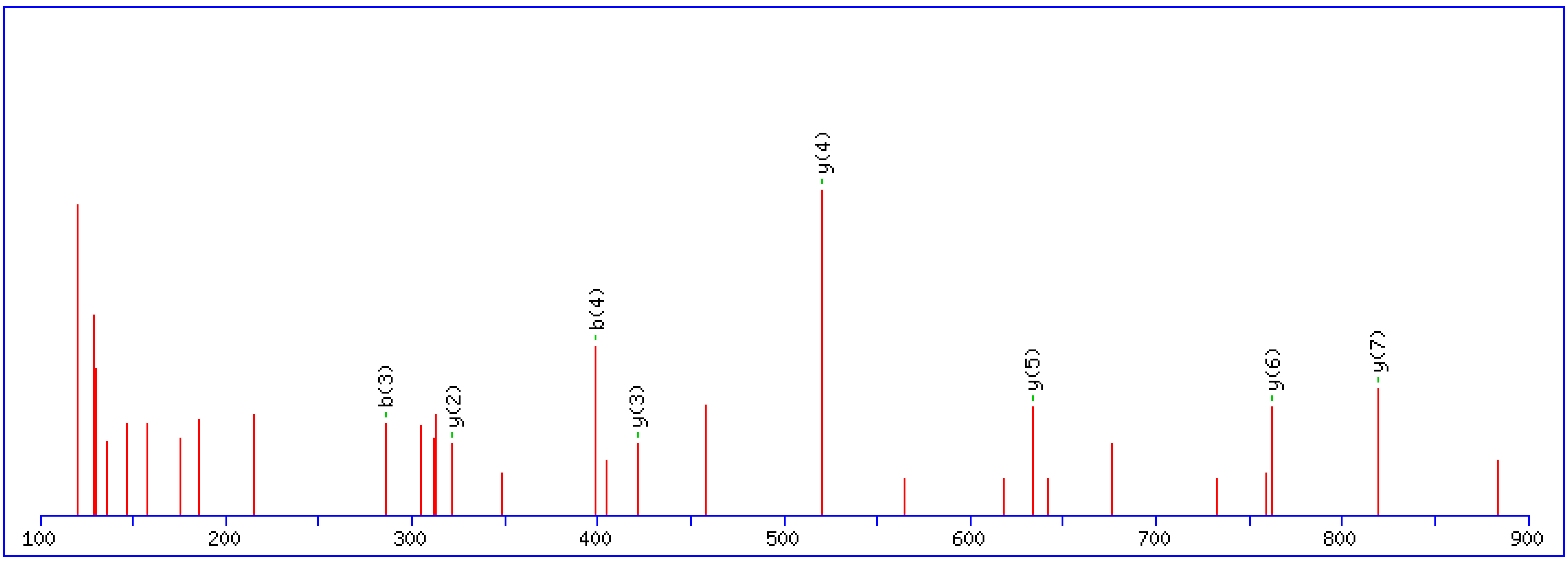
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VGEIVVFR**
Found in **SC11A_HUMAN**, Signal peptidase complex catalytic subunit SEC11A OS=Homo sapiens GN=SEC11A PE=1 SV=1

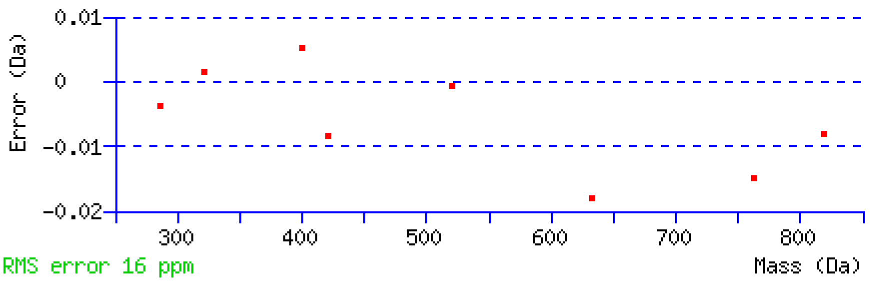
Match to Query 4802: 917.527828 from(459.771190,2+) rtinseconds(2305) index(28467)
Title: Locus:1.1.1.1259.8
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 2.mgf

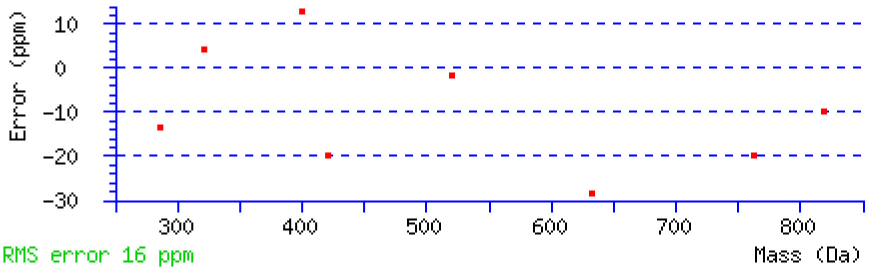
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 917.533463
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 43 **Expect:** 0.00023
Matches : 8/56 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483			V							8
2	157.097154	79.052215			G	***819.472315***	410.239796	802.445766	401.726521	801.461750	401.234513	7
3	**286.139747**	143.573512	268.129182	134.568229	E	***762.450851***	381.729064	745.424302	373.215789	744.440286	372.723781	6
4	**399.223811**	200.115544	381.213246	191.110261	I	***633.408258***	317.207767	616.381709	308.694493			5
5	498.292225	249.649751	480.281660	240.644468	V	***520.324194***	260.665735	503.297645	252.152461			4
6	597.360639	299.183958	579.350074	290.178675	V	***421.255780***	211.131528	404.229231	202.618253			3
7	744.429053	372.718165	726.418488	363.712882	F	***322.187366***	161.597321	305.160817	153.084046			2
8					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of VGEIVVFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
43.3	917.533463	-0.005635	VGEIVVFR
4.2	917.525574	0.002254	VSLVLEKM

Mascot: http://www.matrixscience.com/

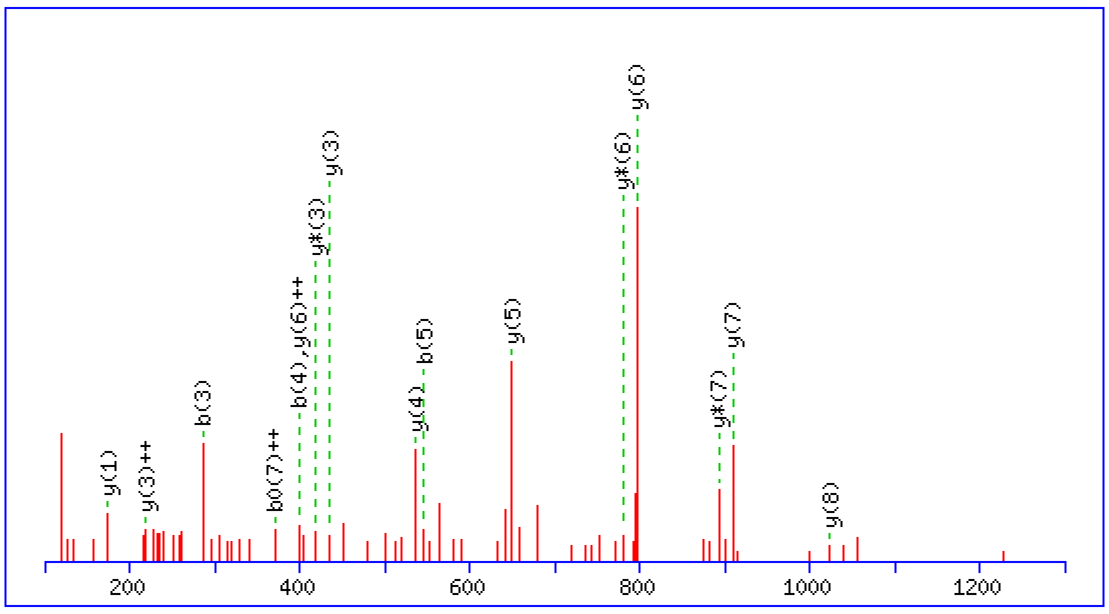
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GDLLFLTNFR**
Found in **SC11C_HUMAN**, Signal peptidase complex catalytic subunit SEC11C OS=Homo sapiens GN=SEC11C PE=1 SV=3

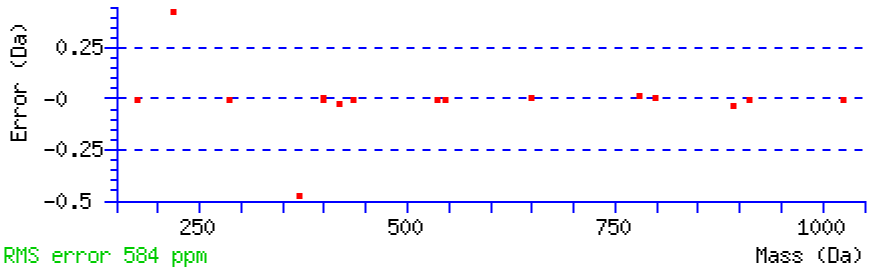
Match to Query 29986: 1194.639608 from(598.327080,2+) rtinseconds(3767) index(51504)
Title: Locus:1.1.1.2583.6
Data file 2011-11-12 - TFD - EP 6-6.mgf

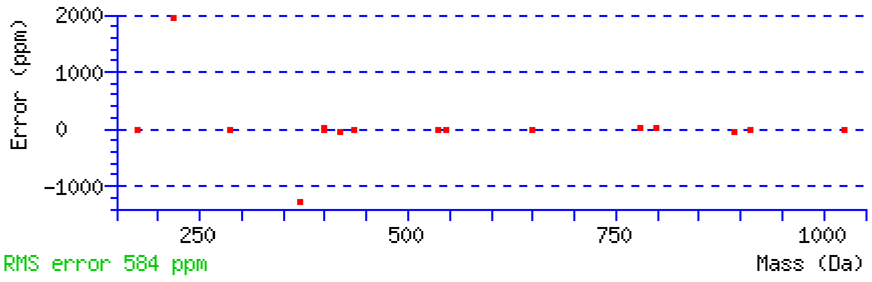
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



`Monoisotopic mass of neutral peptide Mr(calc): 1194.639709`
`Fixed modifications: Propionamide (C) (apply to specified residues or termini only)`
`Ions Score: 43 Expect: 0.00051`
`Matches : 16/86 fragment ions using 28 most intense peaks (help)`

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							10
2	173.055683	87.031479			155.045118	78.026197	D	1138.625521	569.816399	1121.598972	561.303124	1120.614956	560.811116	9
3	**286.139747**	143.573512			268.129182	134.568229	L	***1023.598578***	512.302927	1006.572029	503.789653	1005.588013	503.297645	8
4	**399.223811**	200.115544			381.213246	191.110261	L	***910.514514***	455.760895	893.487965	447.247621	892.503949	446.755613	7
5	**546.292225**	273.649751			528.281660	264.644468	F	***797.430450***	399.218863	780.403901	390.705589	779.419885	390.213581	6
6	659.376289	330.191783			641.365724	321.186500	L	***650.362036***	325.684656	633.335487	317.171382	632.351471	316.679374	5
7	760.423968	380.715622			742.413403	371.710340	T	***537.277972***	269.142624	520.251423	260.629350	519.267407	260.137342	4
8	874.466895	437.737086	857.440346	429.223811	856.456330	428.731803	N	***436.230293***	218.618784	419.203744	210.105510			3
9	1021.535309	511.271293	1004.508760	502.758018	1003.524744	502.266010	F	322.187366	161.597321	305.160817	153.084047			2
10							R	***175.118952***	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of GDLLFLTNFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
43.1	1194.639709	-0.000101	GDLLFLTNFR
8.2	1194.639709	-0.000101	DVIAFPKSFR
4.8	1194.635696	0.003912	GDLGLPGQPGLR
4.7	1194.646912	-0.007304	LSTPGPRPSGAR
3.9	1194.635696	0.003912	GDLGLPGQPGLR

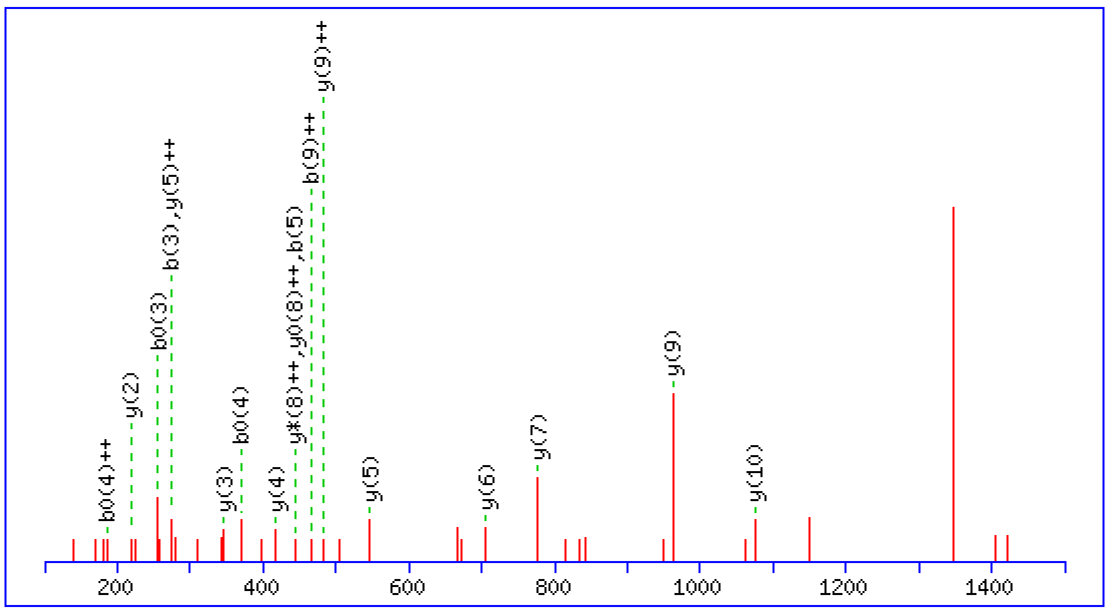
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DASIGQACEAQAK**
Found in **SRP54_HUMAN**, Signal recognition particle 54 kDa protein OS=Homo sapiens GN=SRP54 PE=1 SV=1

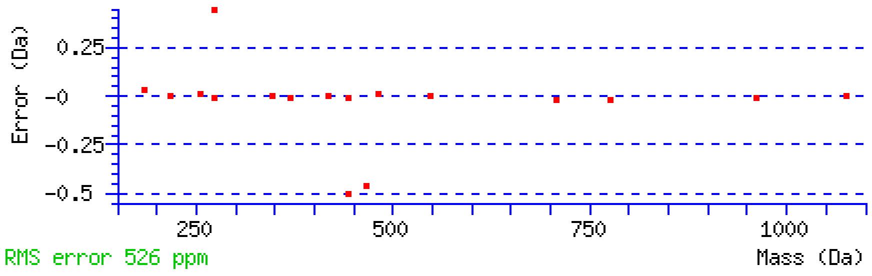
Match to Query 693810: 1347.616348 from(674.815450,2+) rtinseconds(1217) index(247897)
Title: Locus:1.1.1.906.31
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

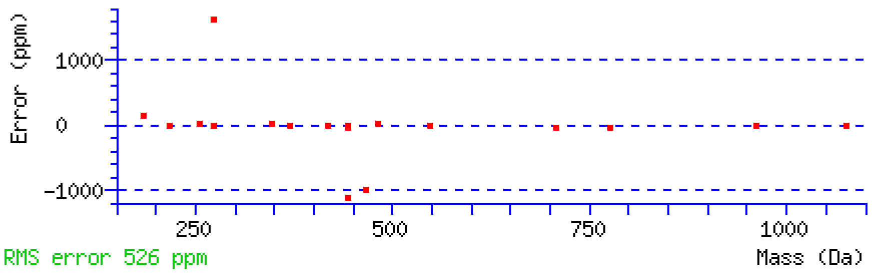
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1347.608856
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 46 **Expect:** 0.00016
Matches : 18/126 fragment ions using 32 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.034219	58.520748			98.023654	49.515465	D							13
2	187.071333	94.039304			169.060768	85.034022	A	1233.589214	617.298245	1216.562665	608.784971	1215.578649	608.292963	12
3	**274.103361**	137.555319			256.092796	128.550036	S	1162.552100	581.779688	1145.525551	573.266414	1144.541535	572.774406	11
4	387.187425	194.097351			369.176860	185.092068	I	***1075.520072***	538.263674	1058.493523	529.750400	1057.509507	529.258392	10
5	**444.208889**	222.608082			426.198324	213.602800	G	***962.436008***	481.721642	945.409459	473.208368	944.425443	472.716360	9
6	572.267467	286.637372	555.240918	278.124097	554.256902	277.632089	Q	905.414544	453.210910	888.387995	444.697636	887.403979	444.205628	8
7	643.304581	322.155929	626.278032	313.642654	625.294016	313.150646	A	***777.355966***	389.181621	760.329417	380.668347	759.345401	380.176339	7
8	803.335230	402.171253	786.308681	393.657979	785.324665	393.165971	C	***706.318852***	353.663064	689.292303	345.149790	688.308287	344.657782	6
9	932.377823	466.692550	915.351274	458.179275	914.367258	457.687267	E	***546.288203***	273.647740	529.261654	265.134465	528.277638	264.642457	5
10	1003.414937	502.211107	986.388388	493.697832	985.404372	493.205824	A	***417.245610***	209.126443	400.219061	200.613168			4
11	1131.473515	566.240396	1114.446966	557.727121	1113.462950	557.235113	Q	***346.208496***	173.607886	329.181947	165.094611			3
12	1202.510629	601.758953	1185.484080	593.245678	1184.500064	592.753670	A	***218.149918***	109.578597	201.123369	101.065322			2
13							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of DASIGQACEAQAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.7	1347.608856	0.007492	DASIGQACEAQAK
4.8	1347.622787	-0.006439	EEDATLSSPAVVM
1.0	1347.626602	-0.010254	QKEGESEDLASR
0.4	1347.627991	-0.011643	GTVHSQGEPSGHR

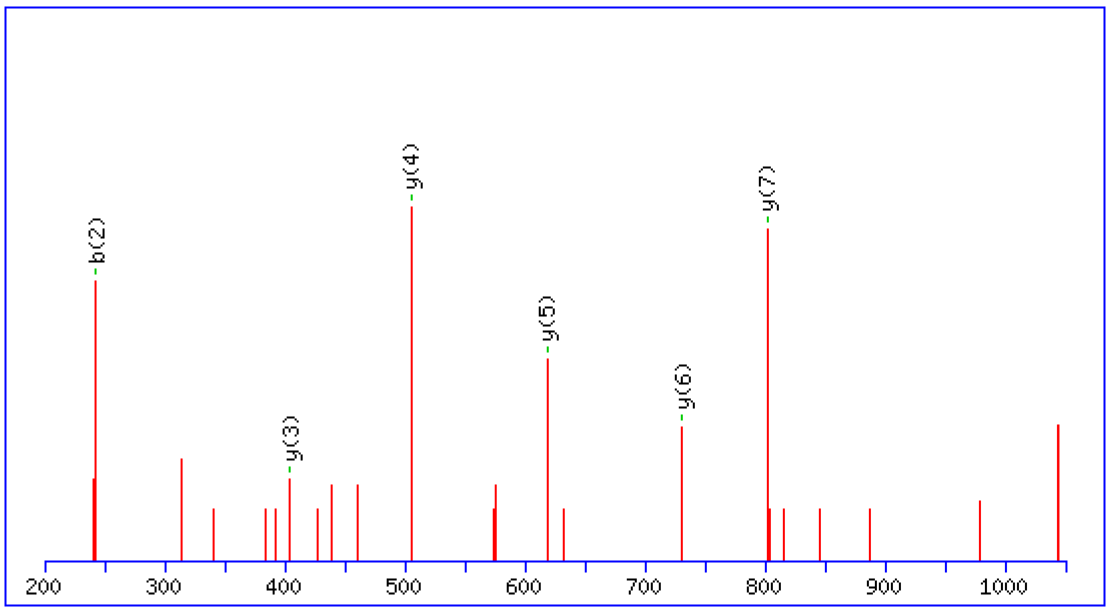
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LEALITQTR**
Found in **SRP68_HUMAN**, Signal recognition particle 68 kDa protein OS=Homo sapiens GN=SRP68 PE=1 SV=2

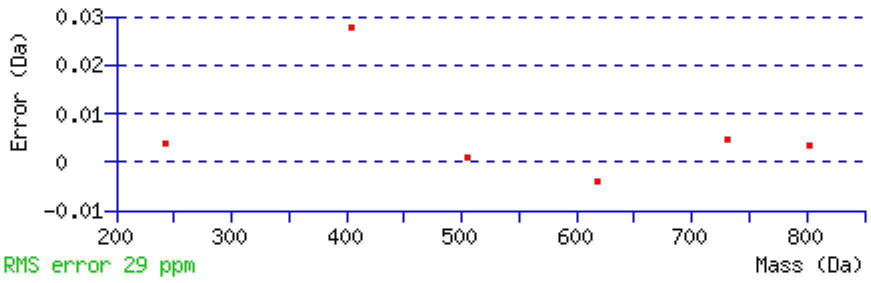
Match to Query 320161: 1043.593168 from(522.803860,2+) rtinseconds(1931) index(593514)
Title: Locus:1.1.1.1059.16
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

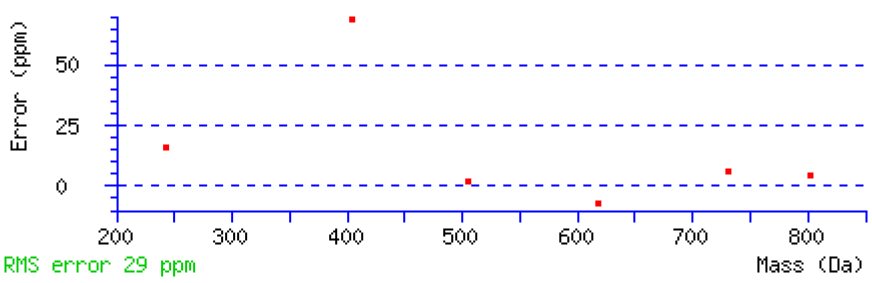
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1043.597488
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 38 **Expect:** 0.002
Matches : 6/80 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.091340	57.549308					**L**							9
2	243.133933	122.070605			225.123368	113.065322	**E**	931.520723	466.264000	914.494174	457.750725	913.510158	457.258717	8
3	314.171047	157.589161			296.160482	148.583879	**A**	***802.478130***	401.742703	785.451581	393.229429	784.467565	392.737421	7
4	427.255111	214.131193			409.244546	205.125911	**L**	***731.441016***	366.224146	714.414467	357.710872	713.430451	357.218864	6
5	540.339175	270.673226			522.328610	261.667943	**I**	***618.356952***	309.682114	601.330403	301.168840	600.346387	300.676832	5
6	641.386854	321.197065			623.376289	312.191783	**T**	***505.272888***	253.140082	488.246339	244.626808	487.262323	244.134800	4
7	769.445432	385.226354	752.418883	376.713080	751.434867	376.221072	**Q**	***404.225209***	202.616243	387.198660	194.102968	386.214644	193.610960	3
8	870.493111	435.750194	853.466562	427.236919	852.482546	426.744911	**T**	276.166631	138.586954	259.140082	130.073679	258.156066	129.581671	2
9							**R**	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of LEALITQTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.6	1043.597488	-0.004320	LEALITQTR
10.6	1043.593643	-0.000475	ILSPLEIIM
0.9	1043.597504	-0.004336	ISPLVKDTR
0.1	1043.587585	0.005583	NKPAFQAIR

Mascot: http://www.matrixscience.com/

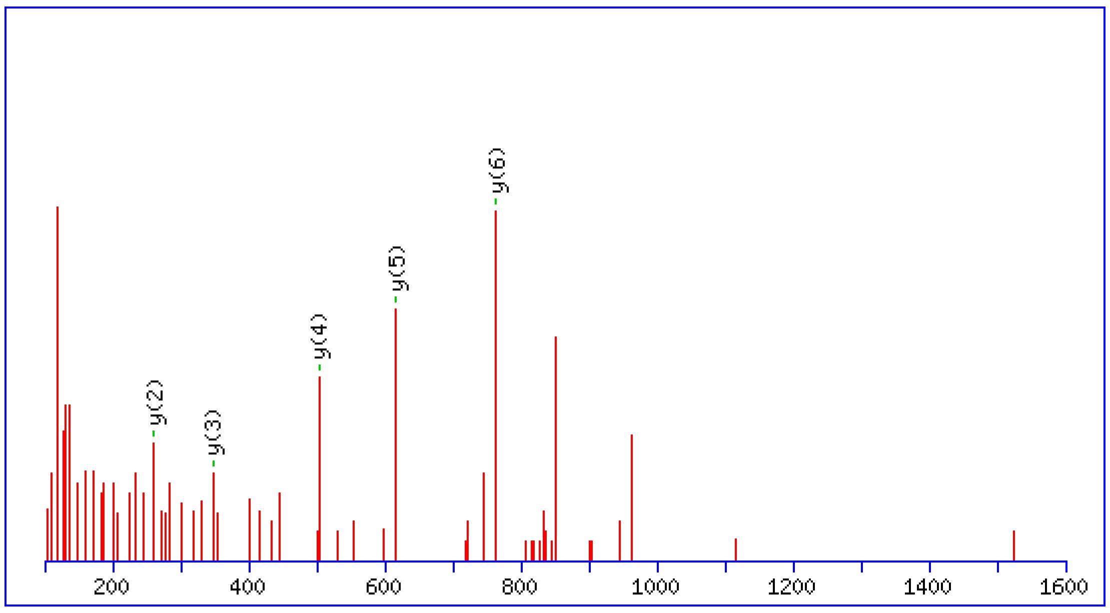
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AAGFLRSNK**
Found in **SGSM1_HUMAN**, Small G protein signaling modulator 1 OS=Homo sapiens GN=SGSM1 PE=1 SV=2

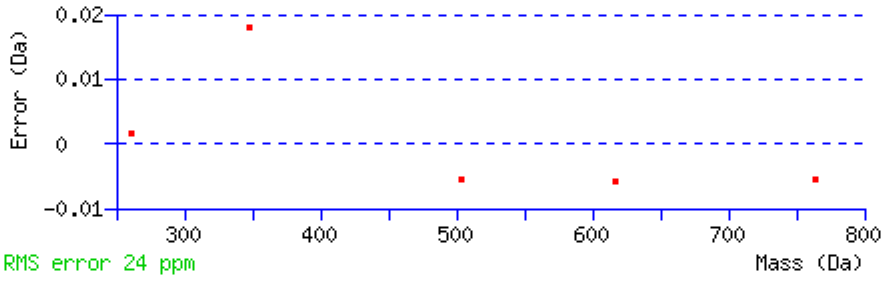
Match to Query 12781: 962.530808 from(482.272680,2+) rtinseconds(2388) index(30257)
Title: Locus:1.1.1.2225.18
Data file 2011-11-12 - TFD - EP 6-1.mgf

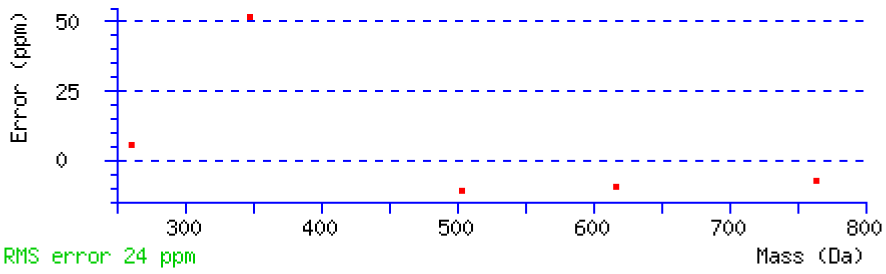
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 962.529739
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.00073
Matches : 5/70 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							9
2	143.081504	72.044390					A	892.499926	446.753601	875.473377	438.240327	874.489361	437.748319	8
3	200.102968	100.555122					G	821.462812	411.235044	804.436263	402.721769	803.452247	402.229762	7
4	347.171382	174.089329					F	*764.441348*	382.724312	747.414799	374.211038	746.430783	373.719030	6
5	460.255446	230.631361					L	*617.372934*	309.190105	600.346385	300.676830	599.362369	300.184823	5
6	616.356557	308.681917	599.330008	300.168642			R	*504.288870*	252.648073	487.262321	244.134798	486.278305	243.642790	4
7	703.388585	352.197931	686.362036	343.684656	685.378020	343.192648	S	*348.187759*	174.597517	331.161210	166.084243	330.177194	165.592235	3
8	817.431512	409.219394	800.404963	400.706120	799.420947	400.214112	N	*261.155731*	131.081503	244.129182	122.568229			2
9							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of AAGFLRSNK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.8	962.529739	0.001069	AAGFLRSNK
2.4	962.539627	-0.008819	LASKSATSAK

Mascot: http://www.matrixscience.com/

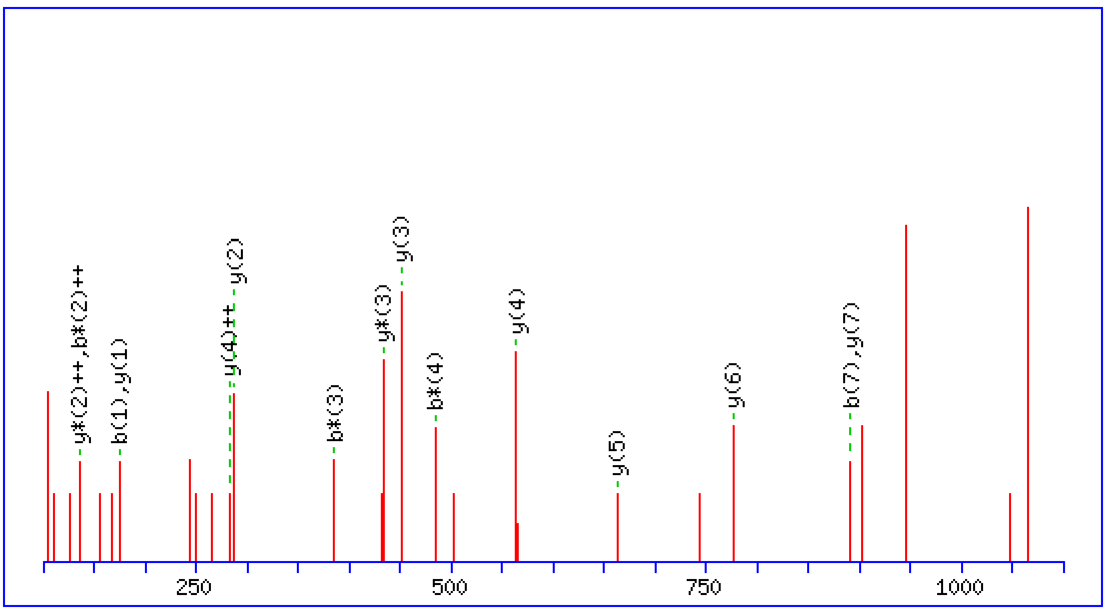
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **CNNVLYIR**
Found in **RUXF_HUMAN**, Small nuclear ribonucleoprotein F OS=Homo sapiens GN=SNRPF PE=1 SV=1

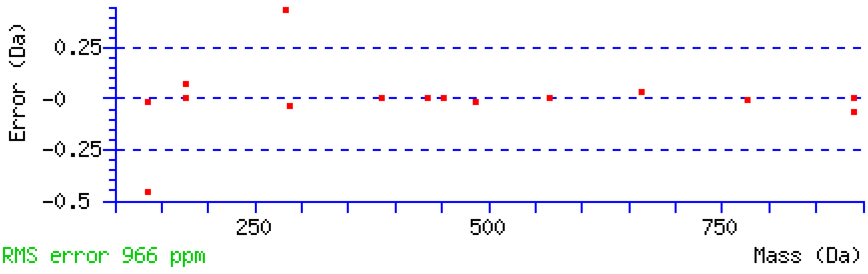
Match to Query 13490: 1064.546448 from(533.280500,2+) rtinseconds(2122) index(10615)
Title: Locus:1.1.1.2324.23
Data file 2011-11-12 - TFD - EP 6-8.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●

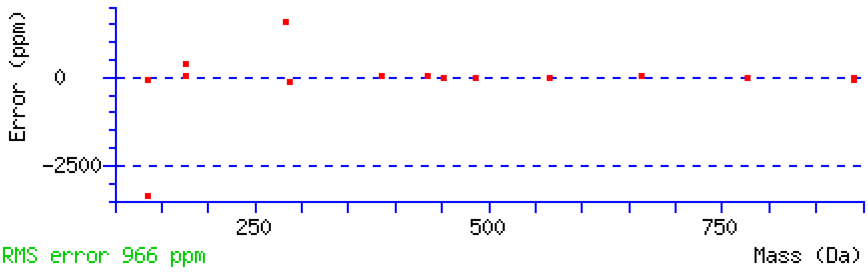


Monoisotopic mass of neutral peptide Mr(calc): 1064.543671
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 54 **Expect:** 4.7e-005
Matches : 15/54 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	**175.053575**	88.030425			C					8
2	289.096502	145.051889	272.069953	136.538614	N	***891.504677***	446.255977	874.478128	437.742702	7
3	403.139429	202.073353	386.112880	193.560078	N	***777.461750***	389.234513	760.435201	380.721239	6
4	502.207843	251.607560	485.181294	243.094285	V	***663.418823***	332.213050	646.392274	323.699775	5
5	615.291907	308.149592	598.265358	299.636317	L	***564.350409***	282.678843	547.323860	274.165568	4
6	778.355236	389.681256	761.328687	381.167982	Y	***451.266345***	226.136811	434.239796	217.623536	3
7	**891.439300**	446.223288	874.412751	437.710014	I	***288.203016***	144.605146	271.176467	136.091872	2
8					R	***175.118952***	88.063114	158.092403	79.549840	1



RMS error 966 ppm

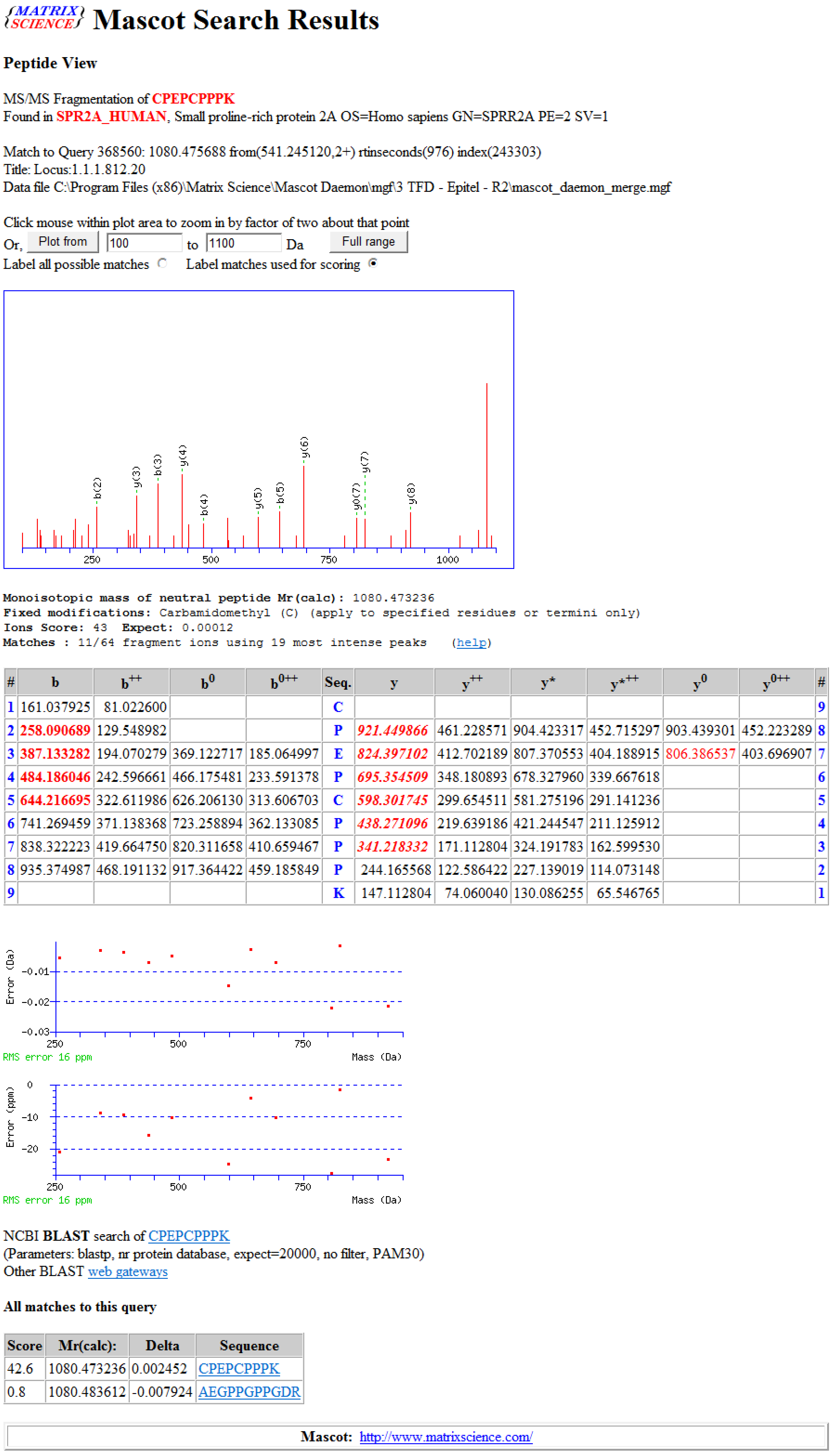


RMS error 966 ppm

NCBI **BLAST** search of CNNVLYIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.1	1064.543671	0.002777	CNNVLYIR
8.6	1064.543671	0.002777	YAKALGCPR
7.3	1064.550217	-0.003769	SPSEVVYLR
7.1	1064.535797	0.010651	KEMILMER
5.9	1064.536270	0.010178	RYITENNR
4.6	1064.536301	0.010147	SSPHPKQPR
4.6	1064.536301	0.010147	SSPHPKQPR
3.8	1064.536301	0.010147	SSPHPKQPR
2.7	1064.554916	-0.008468	CKIQPHPR
2.0	1064.536285	0.010163	AGPGREEPPR



Mascot Search Results

Peptide View

MS/MS Fragmentation of **CPEPCPPPK**
Found in **SPR2A_HUMAN**, Small proline-rich protein 2A OS=Homo sapiens GN=SPRR2A PE=2 SV=1

Match to Query 368560: 1080.475688 from(541.245120,2+) rtinseconds(976) index(243303)
Title: Locus:1.1.1.812.20
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1080.473236
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 43 **Expect:** 0.00012
Matches : 11/64 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	161.037925	81.022600			C							9
2	**258.090689**	129.548982			P	***921.449866***	461.228571	904.423317	452.715297	903.439301	452.223289	8
3	**387.133282**	194.070279	369.122717	185.064997	E	***824.397102***	412.702189	807.370553	404.188915	806.386537	403.696907	7
4	**484.186046**	242.596661	466.175481	233.591378	P	***695.354509***	348.180893	678.327960	339.667618			6
5	**644.216695**	322.611986	626.206130	313.606703	C	***598.301745***	299.654511	581.275196	291.141236			5
6	741.269459	371.138368	723.258894	362.133085	P	***438.271096***	219.639186	421.244547	211.125912			4
7	838.322223	419.664750	820.311658	410.659467	P	***341.218332***	171.112804	324.191783	162.599530			3
8	935.374987	468.191132	917.364422	459.185849	P	244.165568	122.586422	227.139019	114.073148			2
9					K	147.112804	74.060040	130.086255	65.546765			1

NCBI **BLAST** search of CPEPCPPPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.6	1080.473236	0.002452	CPEPCPPPK
0.8	1080.483612	-0.007924	AEGPPGPPGDR

Mascot: http://www.matrixscience.com/

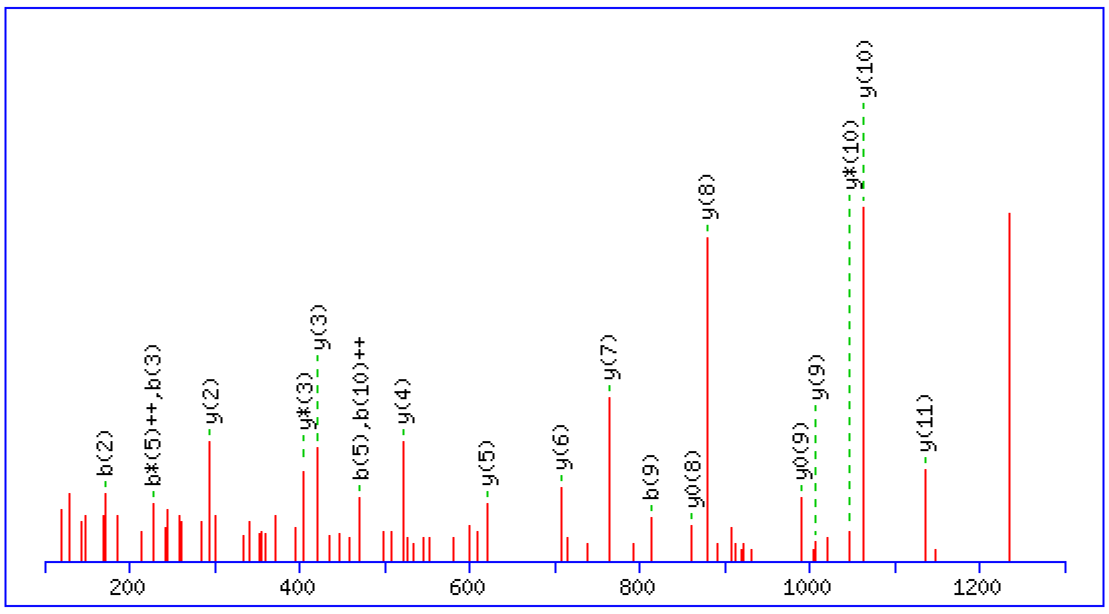
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VAGQDGSVVQFK**
Found in **SUMO2_HUMAN**, Small ubiquitin-related modifier 2 OS=Homo sapiens GN=SUMO2 PE=1 SV=2

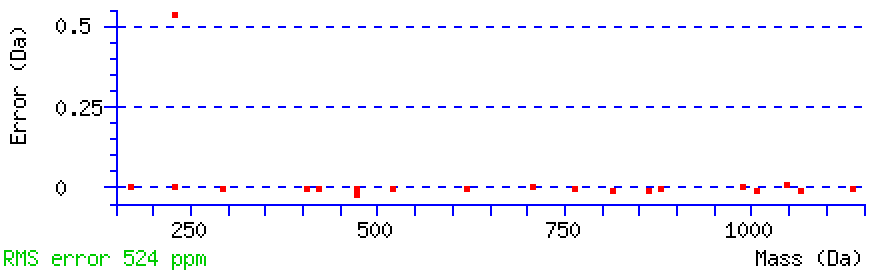
Match to Query 35093: 1233.632608 from(617.823580,2+) rtinseconds(1883) index(18836)
Title: Locus:1.1.1.1935.44
Data file 2011-11-12 - TFD - EP 5-6.mgf

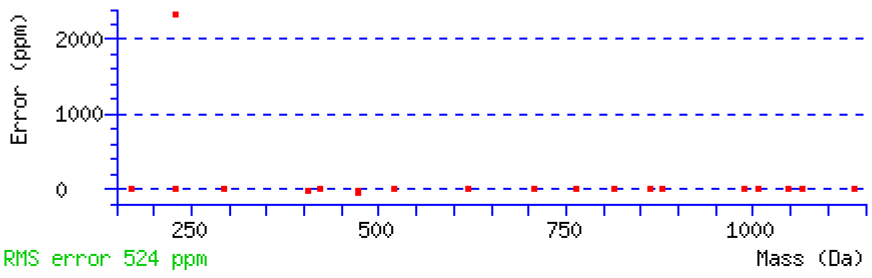
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1233.635376
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 103 **Expect:** 7.7e-010
Matches : 20/108 fragment ions using 22 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	100.075690	50.541483					V							12
2	**171.112804**	86.060040					A	***1135.574215***	568.290745	1118.547666	559.777471	1117.563650	559.285463	11
3	**228.134268**	114.570772					G	***1064.537101***	532.772188	1047.510552	524.258914	1046.526536	523.766906	10
4	356.192846	178.600061	339.166297	170.086786			Q	***1007.515637***	504.261457	990.489088	495.748182	989.505072	495.256174	9
5	**471.219789**	236.113532	454.193240	227.600258	453.209224	227.108250	D	***879.457059***	440.232168	862.430510	431.718893	861.446494	431.226885	8
6	528.241253	264.624265	511.214704	256.110990	510.230688	255.618982	G	***764.430116***	382.718696	747.403567	374.205422	746.419551	373.713414	7
7	615.273281	308.140279	598.246732	299.627004	597.262716	299.134996	S	***707.408652***	354.207964	690.382103	345.694689	689.398087	345.202681	6
8	714.341695	357.674486	697.315146	349.161211	696.331130	348.669203	V	***620.376624***	310.691950	603.350075	302.178676			5
9	**813.410109**	407.208692	796.383560	398.695418	795.399544	398.203410	V	***521.308210***	261.157743	504.281661	252.644469			4
10	941.468687	471.237981	924.442138	462.724707	923.458122	462.232699	Q	***422.239796***	211.623536	405.213247	203.110261			3
11	1088.537101	544.772188	1071.510552	536.258914	1070.526536	535.766906	F	***294.181218***	147.594247	277.154669	139.080972			2
12							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of VAGQDGSVVQFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
102.6	1233.635376	-0.002768	VAGQDGSVVQFK
6.8	1233.635330	-0.002722	NISNTGEKPFK
4.0	1233.627457	0.005151	QLESELQMLK
1.3	1233.621429	0.011179	QVHTSERPHK
0.8	1233.638718	-0.006110	QVLDLMTTAAR

Mascot: http://www.matrixscience.com/

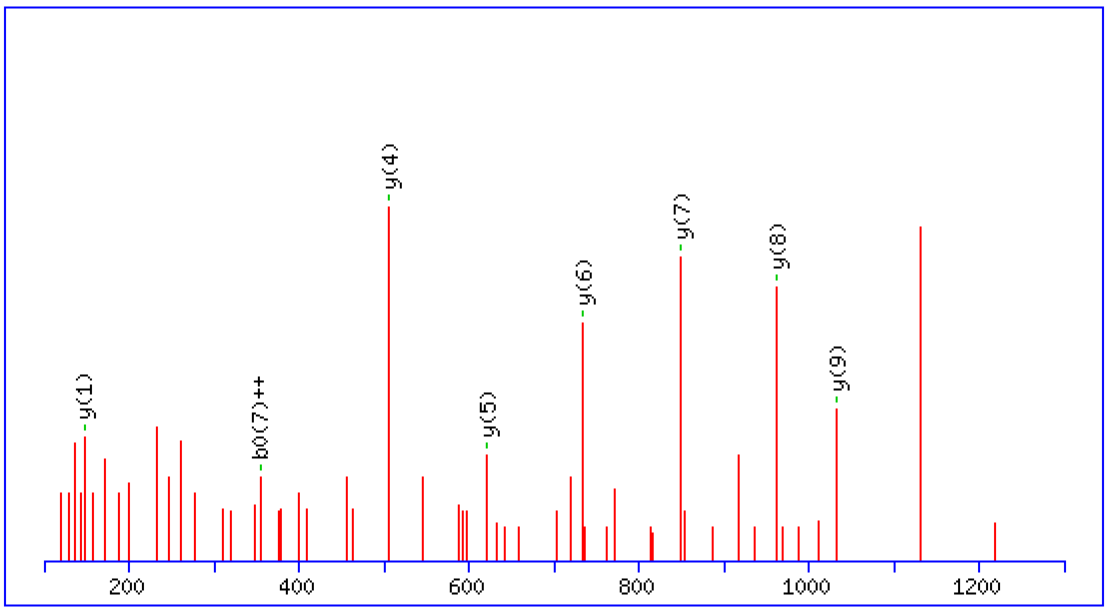
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VALDLDPYVK**
Found in **SNAPN_HUMAN**, SNARE-associated protein Snapin OS=Homo sapiens GN=SNAPIN PE=1 SV=1

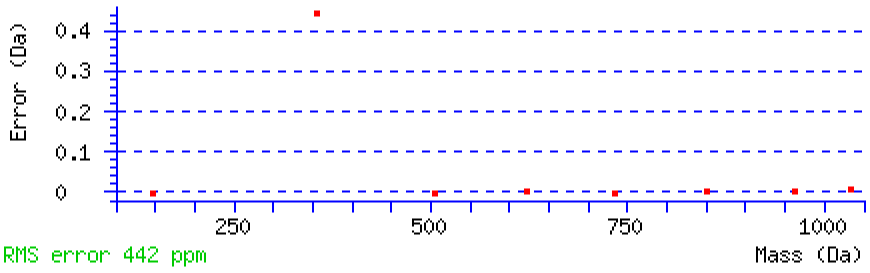
Match to Query 28300: 1131.613088 from(566.813820,2+) rtinseconds(2832) index(36408)
Title: Locus:1.1.1.2298.14
Data file 2011-11-12 - TFD - EP 5-6.mgf

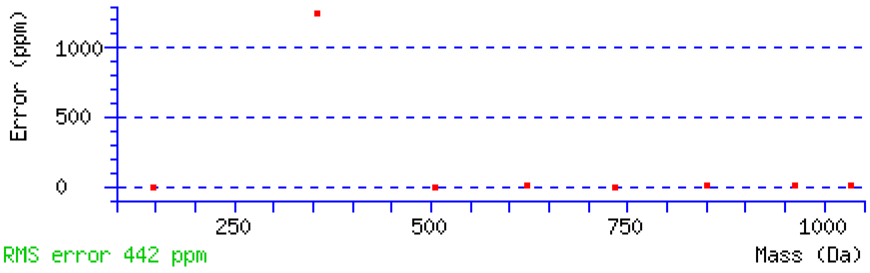
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1131.617569
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 59  Expect: 4.6e-006
Matches : 8/76 fragment ions using 10 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483			V							10
2	171.112804	86.060040			A	***1033.556439***	517.281858	1016.529890	508.768583	1015.545874	508.276575	9
3	284.196868	142.602072			L	***962.519325***	481.763301	945.492776	473.250026	944.508760	472.758018	8
4	399.223811	200.115544	381.213246	191.110261	D	***849.435261***	425.221269	832.408712	416.707994	831.424696	416.215986	7
5	512.307875	256.657576	494.297310	247.652293	L	***734.408318***	367.707797	717.381769	359.194523	716.397753	358.702515	6
6	627.334818	314.171047	609.324253	305.165765	D	***621.324254***	311.165765	604.297705	302.652491	603.313689	302.160483	5
7	724.387582	362.697429	706.377017	353.692147	P	***506.297311***	253.652293	489.270762	245.139019			4
8	887.450911	444.229094	869.440346	435.223811	Y	409.244547	205.125911	392.217998	196.612637			3
9	986.519325	493.763301	968.508760	484.758018	V	246.181218	123.594247	229.154669	115.080972			2
10					K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of VALDLDPYVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.7	1131.617569	-0.004481	VALDLDPYVK
1.8	1131.603668	0.009420	GIPGSHGLPGPK

Mascot: http://www.matrixscience.com/

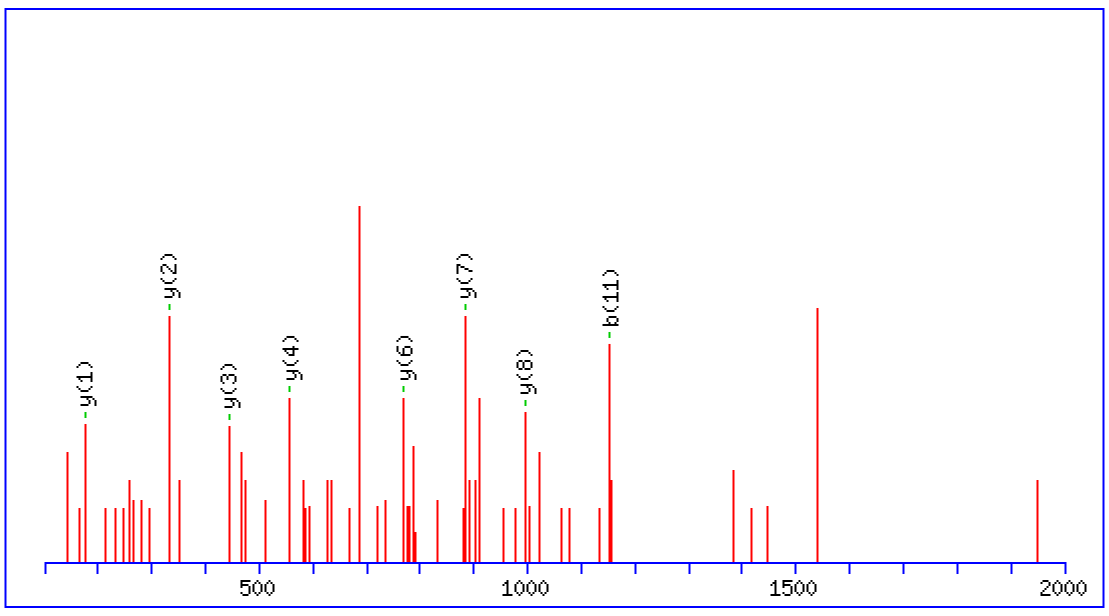
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GTDEVPVPPPVPPRR**
Found in **SOS1_HUMAN**, Son of sevenless homolog 1 OS=Homo sapiens GN=SOS1 PE=1 SV=1

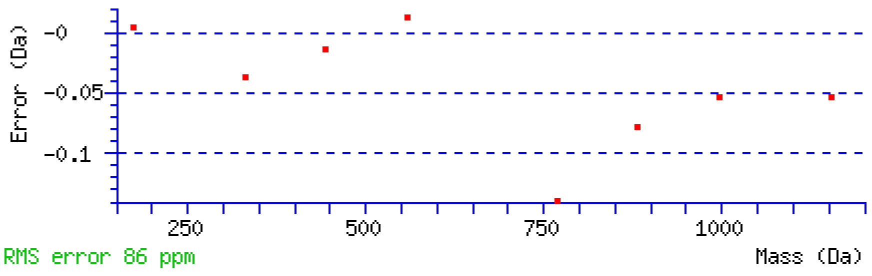
Match to Query 56316: 1707.831012 from(570.284280,3+) rtinseconds(3846) index(57283)
Title: Locus:1.1.1.2844.13
Data file 2011-11-14 - TFD - EP 8-4.mgf

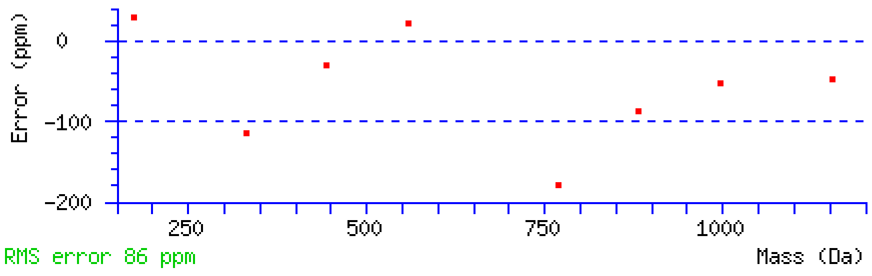
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1707.842819
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P6      : Oxidation (P)
P8      : Oxidation (P)
P9      : Oxidation (P)
P10     : Oxidation (P)
P12     : Oxidation (P)
P13     : Oxidation (P)
Ions Score: 42  Expect: 0.00081
Matches : 8/118 fragment ions using 13 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							15
2	159.076419	80.041847			141.065854	71.036565	T	1651.828594	826.417935	1634.802045	817.904661	1633.818029	817.412653	14
3	274.103362	137.555319			256.092797	128.550037	D	1550.780915	775.894096	1533.754366	767.380821	1532.770350	766.888813	13
4	403.145955	202.076616			385.135390	193.071333	E	1435.753972	718.380624	1418.727423	709.867350	1417.743407	709.375341	12
5	502.214369	251.610823			484.203804	242.605540	V	1306.711379	653.859328	1289.684830	645.346053			11
6	615.262048	308.134662			597.251483	299.129380	P	1207.642965	604.325121	1190.616416	595.811846			10
7	714.330462	357.668869			696.319897	348.663587	V	1094.595286	547.801281	1077.568737	539.288007			9
8	827.378141	414.192709			809.367576	405.187426	P	***995.526872***	498.267074	978.500323	489.753800			8
9	940.425820	470.716548			922.415255	461.711266	P	***882.479193***	441.743235	865.452644	433.229960			7
10	1053.473499	527.240388			1035.462934	518.235105	P	***769.431514***	385.219395	752.404965	376.706121			6
11	1152.541913	576.774595			1134.531348	567.769312	V	656.383835	328.695556	639.357286	320.182281			5
12	1265.589592	633.298434			1247.579027	624.293152	P	***557.315421***	279.161349	540.288872	270.648074			4
13	1378.637271	689.822274			1360.626706	680.816991	P	***444.267742***	222.637509	427.241193	214.124234			3
14	1534.738382	767.872829	1517.711833	759.359555	1516.727817	758.867547	R	***331.220063***	166.113669	314.193514	157.600395			2
15							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of GTDEVPVPPPVPPRR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.8	1707.842819	-0.011807	GTDEVPVPPPVPPRR
18.5	1707.831558	-0.000546	GPPTSEPPPVPANKPK
10.3	1707.831558	-0.000546	GPPTSEPPPVPANKPK
8.7	1707.831558	-0.000546	GPPTSEPPPVPANKPK
6.5	1707.824982	0.006030	GNLFSNKDLEELCR
1.8	1707.846802	-0.015790	AVSSFPDPALYPLGSR
1.6	1707.831558	-0.000546	GPPTSEPPPVPANKPK

Mascot: http://www.matrixscience.com/

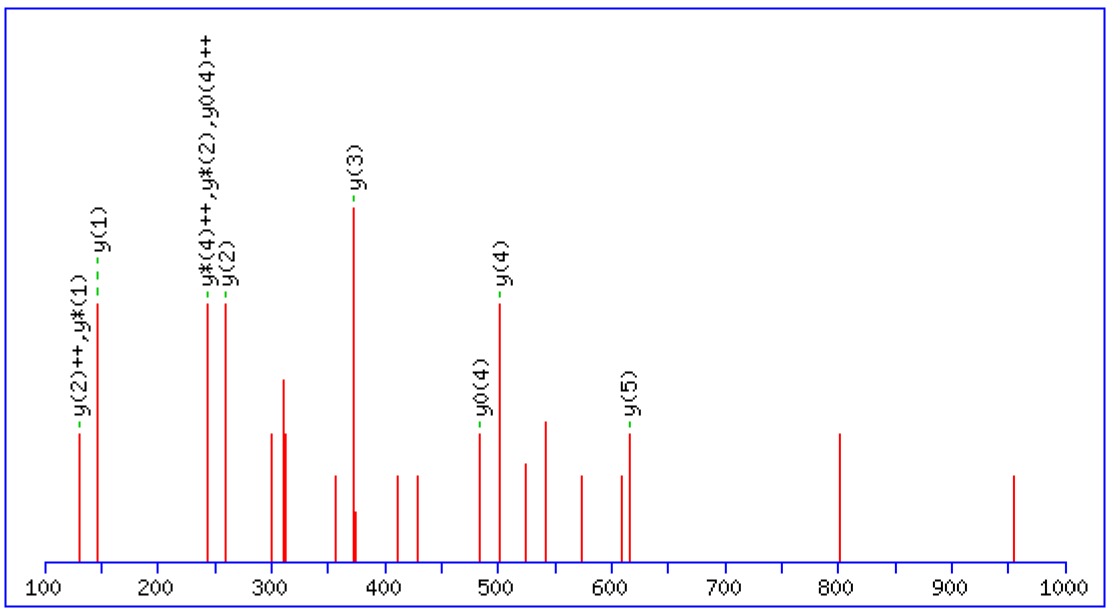
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SAALQPEPIK**
Found in **SORL_HUMAN**, Sortilin-related receptor OS=Homo sapiens GN=SORL1 PE=1 SV=2

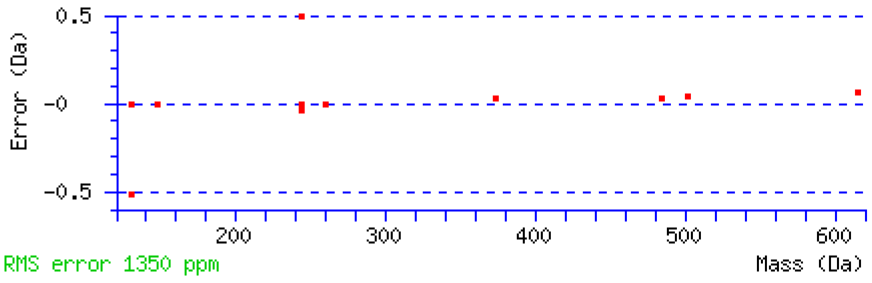
Match to Query 376094: 1084.568848 from(543.291700,2+) rtinseconds(2387) index(843584)
Title: Locus:1.1.1.1457.21
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

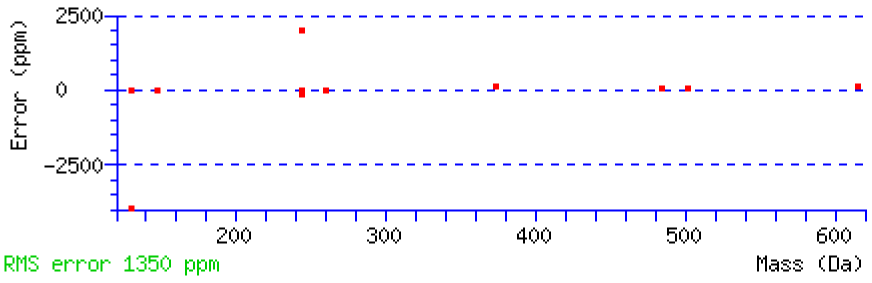
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1084.576416
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
P6      : Oxidation (P)
P8      : Oxidation (P)
Ions Score: 36  Expect: 0.0038
Matches : 11/94 fragment ions using 12 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							10
2	159.076418	80.041847			141.065853	71.036564	A	998.551689	499.779483	981.525140	491.266208	980.541124	490.774200	9
3	230.113532	115.560404			212.102967	106.555121	A	927.514575	464.260926	910.488026	455.747651	909.504010	455.255643	8
4	343.197596	172.102436			325.187031	163.097153	L	856.477461	428.742369	839.450912	420.229094	838.466896	419.737086	7
5	471.256174	236.131725	454.229625	227.618450	453.245609	227.126443	Q	743.393397	372.200337	726.366848	363.687062	725.382832	363.195054	6
6	584.303853	292.655565	567.277304	284.142290	566.293288	283.650282	P	***615.334819***	308.171048	598.308270	299.657773	597.324254	299.165765	5
7	713.346446	357.176861	696.319897	348.663587	695.335881	348.171579	E	***502.287140***	251.647208	485.260591	243.133934	484.276575	242.641926	4
8	826.394125	413.700701	809.367576	405.187426	808.383560	404.695418	P	***373.244547***	187.125912	356.217998	178.612637			3
9	939.478189	470.242733	922.451640	461.729458	921.467624	461.237450	I	***260.196868***	130.602072	243.170319	122.088798			2
10							K	***147.112804***	74.060040	130.086255	65.546766			1





NCBI **BLAST** search of SAALQPEPIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.4	1084.576416	-0.007568	SAALQPEPIK
25.0	1084.558670	0.010178	THTMELLPK
23.7	1084.576431	-0.007583	GLQEGVELPK
13.4	1084.566544	0.002304	FHVQLSNPK
13.2	1084.558685	0.010163	TDIVHMIPK
12.8	1084.576447	-0.007599	DPVDGTQLLK
12.5	1084.576401	-0.007553	APAAEKLEPK
12.5	1084.576416	-0.007568	VENLQPEIK
11.6	1084.576431	-0.007583	EIIDPVLDR
11.2	1084.576431	-0.007583	SPPPKSSLPK

Mascot: http://www.matrixscience.com/

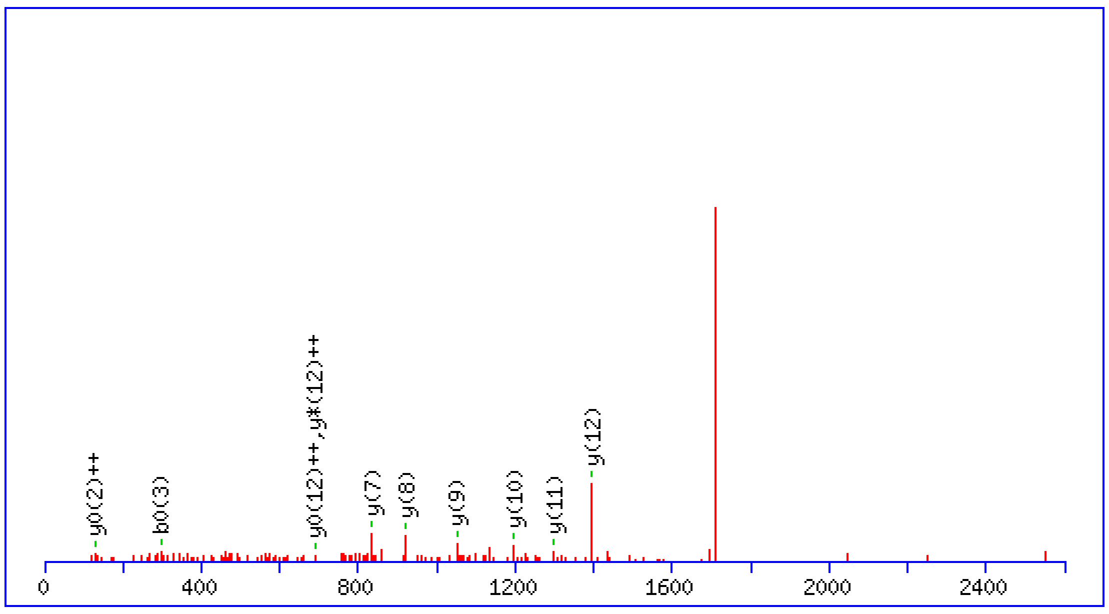
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TTLPTFQSPEFSVTR**
Found in **SNX5_HUMAN**, Sorting nexin-5 OS=Homo sapiens GN=SNX5 PE=1 SV=1

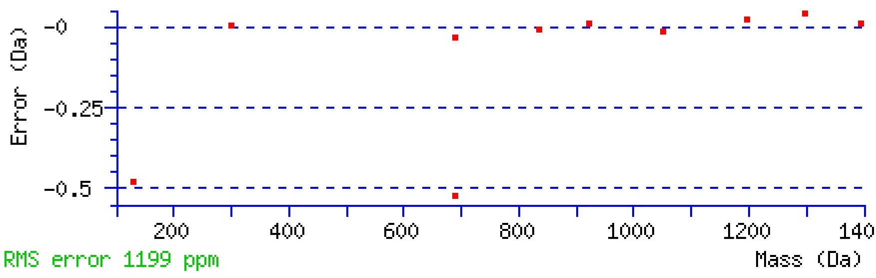
Match to Query 50966: 1709.864248 from(855.939400,2+) rtinseconds(2971) index(41262)
Title: Locus:1.1.1.2619.46
Data file 2011-11-10 - TFD - EP 4-3.mgf

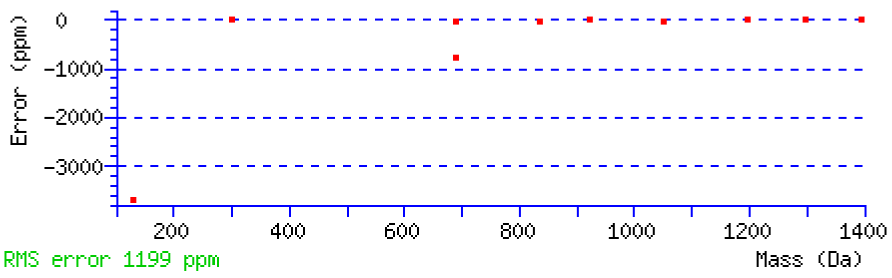
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1709.862473
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.0021
Matches : 10/154 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							15
2	203.102634	102.054955			185.092069	93.049672	T	1609.822050	805.414663	1592.795501	796.901389	1591.811485	796.409381	14
3	316.186698	158.596987			298.176133	149.591704	L	1508.774371	754.890824	1491.747822	746.377549	1490.763806	745.885541	13
4	413.239462	207.123369			395.228897	198.118086	P	***1395.690307***	698.348792	1378.663758	689.835517	1377.679742	689.343509	12
5	514.287141	257.647209			496.276576	248.641926	T	***1298.637543***	649.822410	1281.610994	641.309135	1280.626978	640.817127	11
6	661.355555	331.181416			643.344990	322.176133	F	***1197.589864***	599.298570	1180.563315	590.785296	1179.579299	590.293288	10
7	789.414133	395.210705	772.387584	386.697430	771.403568	386.205422	Q	***1050.521450***	525.764363	1033.494901	517.251089	1032.510885	516.759081	9
8	876.446161	438.726719	859.419612	430.213444	858.435596	429.721436	S	***922.462872***	461.735074	905.436323	453.221800	904.452307	452.729792	8
9	973.498925	487.253101	956.472376	478.739826	955.488360	478.247818	P	***835.430844***	418.219060	818.404295	409.705786	817.420279	409.213778	7
10	1102.541518	551.774397	1085.514969	543.261123	1084.530953	542.769115	E	738.378080	369.692678	721.351531	361.179404	720.367515	360.687396	6
11	1249.609932	625.308604	1232.583383	616.795330	1231.599367	616.303322	F	609.335487	305.171382	592.308938	296.658107	591.324922	296.166099	5
12	1336.641960	668.824618	1319.615411	660.311344	1318.631395	659.819336	S	462.267073	231.637175	445.240524	223.123900	444.256508	222.631892	4
13	1435.710374	718.358825	1418.683825	709.845551	1417.699809	709.353543	V	375.235045	188.121161	358.208496	179.607886	357.224480	179.115878	3
14	1536.758053	768.882665	1519.731504	760.369390	1518.747488	759.877382	T	276.166631	138.586953	259.140082	130.073679	258.156066	129.581671	2
15							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of TTLPTFQSPEFSVTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.5	1709.862473	0.001775	TTLPTFQSPEFSVTR

Mascot: http://www.matrixscience.com/

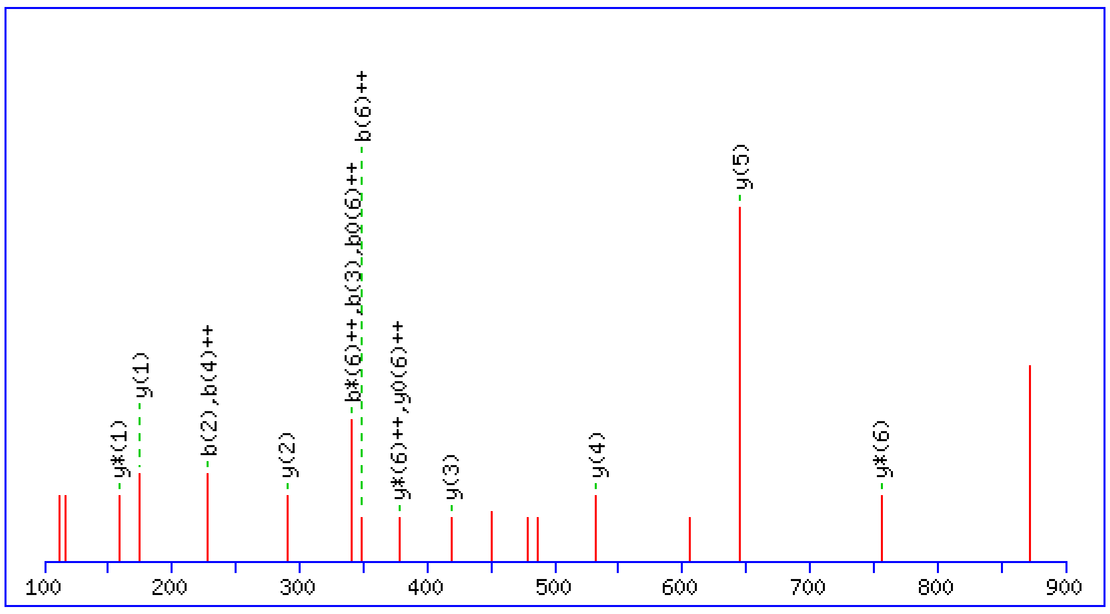
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VQLIEDR**
Found in **SPTB1_HUMAN**, Spectrin beta chain, erythrocyte OS=Homo sapiens GN=SPTB PE=1 SV=5

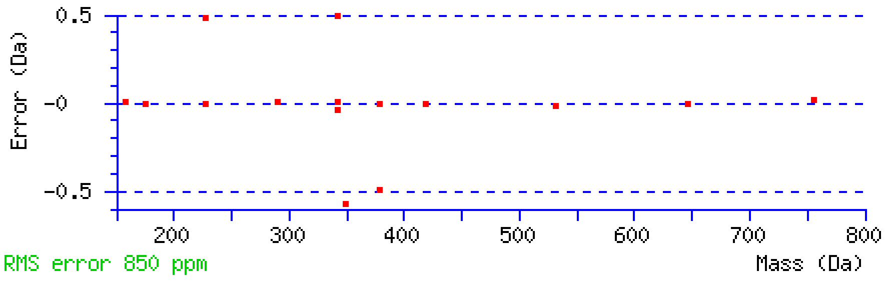
Match to Query 5947: 871.482568 from(436.748560,2+) rtinseconds(1720) index(11883)
Title: Locus:1.1.1.2061.8
Data file 2011-11-10 - TFD - EP 3-7.mgf

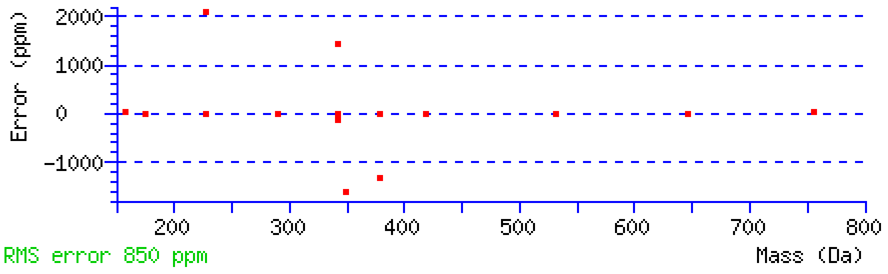
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 871.476318
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 42 **Expect:** 0.0013
Matches : 15/60 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	100.075690	50.541483					V							7
2	**228.134268**	114.570772	211.107719	106.057498			Q	773.415194	387.211235	756.388645	378.697961	755.404629	378.205953	6
3	**341.218332**	171.112804	324.191783	162.599530			L	***645.356616***	323.181946	628.330067	314.668672	627.346051	314.176664	5
4	454.302396	**227.654836**	437.275847	219.141562			I	***532.272552***	266.639914	515.246003	258.126640	514.261987	257.634632	4
5	583.344989	292.176133	566.318440	283.662858	565.334424	283.170850	E	***419.188488***	210.097882	402.161939	201.584608	401.177923	201.092600	3
6	698.371932	**349.689604**	681.345383	341.176330	680.361367	340.684322	D	***290.145895***	145.576585	273.119346	137.063311	272.135330	136.571303	2
7							R	***175.118952***	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of VQLIEDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.8	871.476318	0.006250	VQLIEDR
41.8	871.476318	0.006250	VQLLEDR
26.3	871.476318	0.006250	KVPLDER
20.6	871.487534	-0.004966	LRALEDR
12.8	871.487564	-0.004996	KVQVQDR
9.4	871.487534	-0.004966	LNKINDR
7.5	871.487549	-0.004981	VKNDQLR
7.5	871.487549	-0.004981	VQKSSAPR
7.5	871.487534	-0.004966	ALRELDR
5.8	871.487534	-0.004966	LRADLER

Mascot: http://www.matrixscience.com/

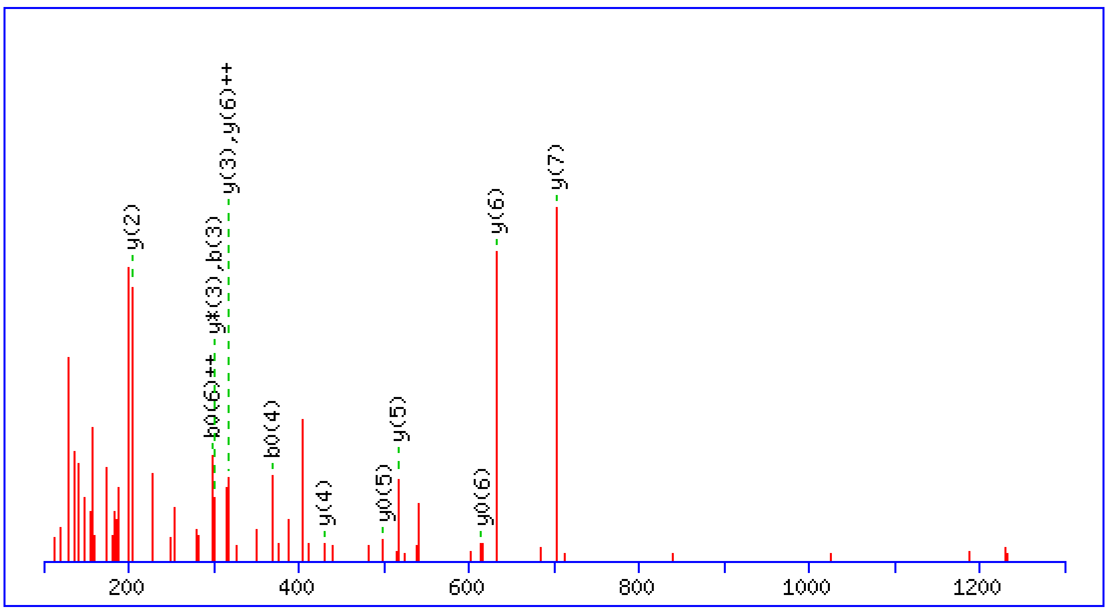
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LADSLIGK**
Found in **SPIN4_HUMAN**, Spindlin-4 OS=Homo sapiens GN=SPIN4 PE=2 SV=1

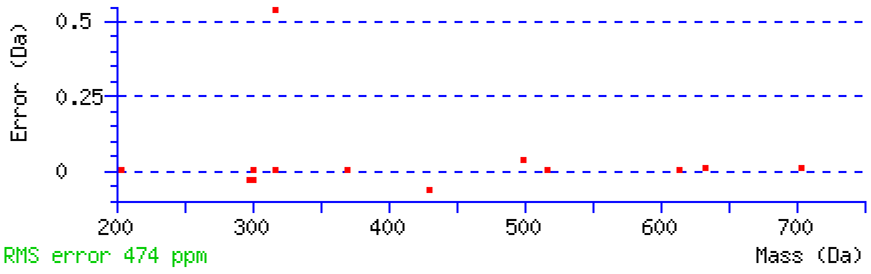
Match to Query 1199: 815.477648 from(408.746100,2+) rtinseconds(1885) index(19811)
Title: Locus:1.1.1.2148.2
Data file 2011-11-10 - TFD - EP 3-1.mgf

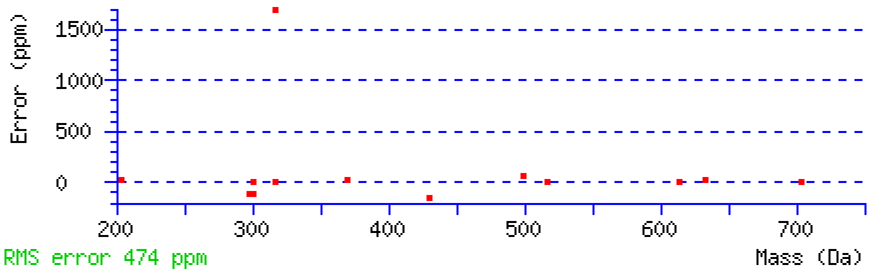
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 815.475250
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.0012
Matches : 13/58 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							8
2	185.128454	93.067865			A	***703.398481***	352.202879	686.371932	343.689604	685.387916	343.197596	7
3	300.155397	150.581336	282.144832	141.576054	D	***632.361367***	316.684322	615.334818	308.171047	614.350802	307.679039	6
4	387.187425	194.097351	369.176860	185.092068	S	***517.334424***	259.170850	500.307875	250.657576	499.323859	250.165568	5
5	500.271489	250.639383	482.260924	241.634100	L	***430.302396***	215.654836	413.275847	207.141562			4
6	613.355553	307.181415	595.344988	298.176132	I	***317.218332***	159.112804	300.191783	150.599530			3
7	670.377017	335.692147	652.366452	326.686864	G	***204.134268***	102.570772	187.107719	94.057498			2
8					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of LADSLIGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.9	815.475250	0.002398	LADSLIGK
38.7	815.475250	0.002398	LADISLGK
12.5	815.475266	0.002382	EGIIVTGK
6.6	815.475266	0.002382	EAVTVAVK
5.9	815.475235	0.002413	LKEEIGK
5.9	815.475235	0.002413	LKEELGK
5.0	815.475235	0.002413	IEEKLGK

Mascot: http://www.matrixscience.com/

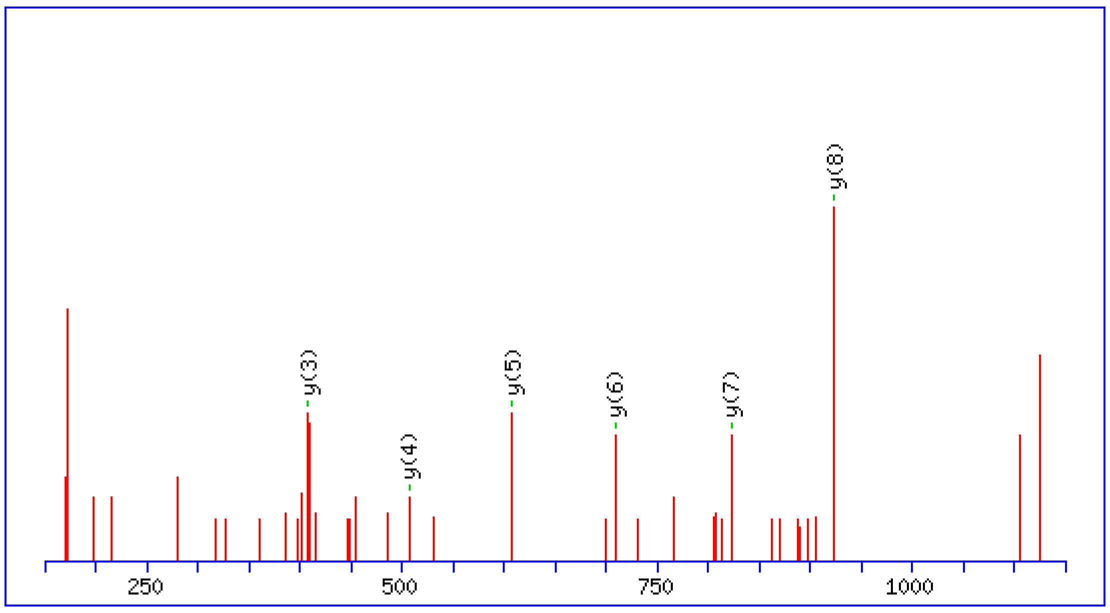
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SITNTTVCTK**
Found in **SF01_HUMAN**, Splicing factor 1 OS=Homo sapiens GN=SF1 PE=1 SV=4

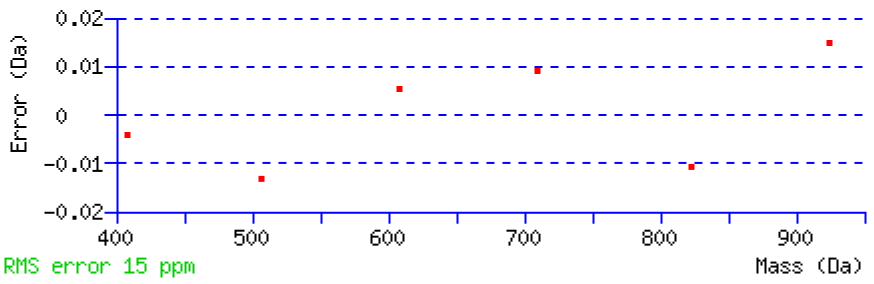
Match to Query 423843: 1123.551188 from(562.782870,2+) rtinseconds(1140) index(246387)
Title: Locus:1.1.1.876.21
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●

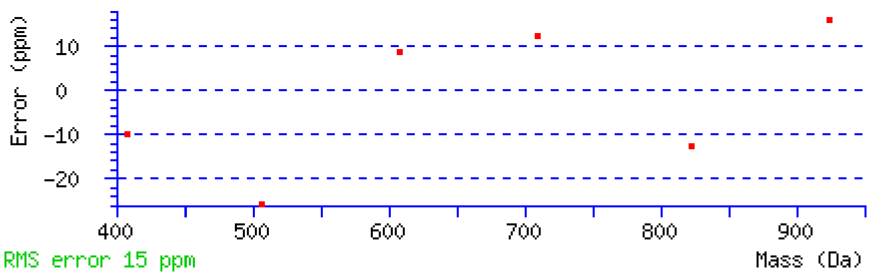


Monoisotopic mass of neutral peptide Mr(calc): 1123.554337
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 50 **Expect:** 2.2e-005
Matches : 6/100 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							10
2	201.123368	101.065322			183.112803	92.060039	I	1037.529574	519.268425	1020.503025	510.755151	1019.519009	510.263143	9
3	302.171047	151.589161			284.160482	142.583879	T	***924.445510***	462.726393	907.418961	454.213119	906.434945	453.721111	8
4	416.213974	208.610625	399.187425	200.097351	398.203409	199.605343	N	***823.397831***	412.202554	806.371282	403.689279	805.387266	403.197271	7
5	517.261653	259.134465	500.235104	250.621190	499.251088	250.129182	T	***709.354904***	355.181090	692.328355	346.667816	691.344339	346.175808	6
6	618.309332	309.658304	601.282783	301.145030	600.298767	300.653022	T	***608.307225***	304.657251	591.280676	296.143976	590.296660	295.651968	5
7	717.377746	359.192511	700.351197	350.679237	699.367181	350.187229	V	***507.259546***	254.133411	490.232997	245.620136	489.248981	245.128128	4
8	877.408395	439.207836	860.381846	430.694561	859.397830	430.202553	C	***408.191132***	204.599204	391.164583	196.085929	390.180567	195.593921	3
9	978.456074	489.731675	961.429525	481.218401	960.445509	480.726393	T	248.160483	124.583879	231.133934	116.070605	230.149918	115.578597	2
10							K	147.112804	74.060040	130.086255	65.546765			1



RMS error 15 ppm



RMS error 15 ppm

NCBI **BLAST** search of SITNTTVCTK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
50.3	1123.554337	-0.003149	SITNTTVCTK
0.6	1123.546951	0.004237	TVTTSGTSQSR

Mascot: http://www.matrixscience.com/

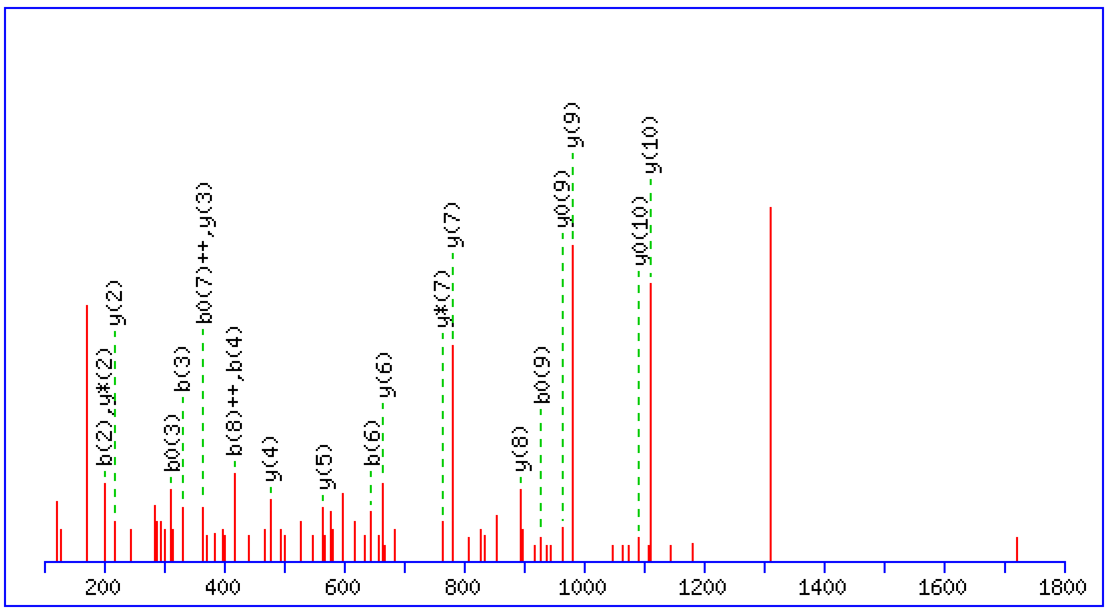
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SLESLDTSLFAK**
Found in **SF3A3_HUMAN**, Splicing factor 3A subunit 3 OS=Homo sapiens GN=SF3A3 PE=1 SV=1

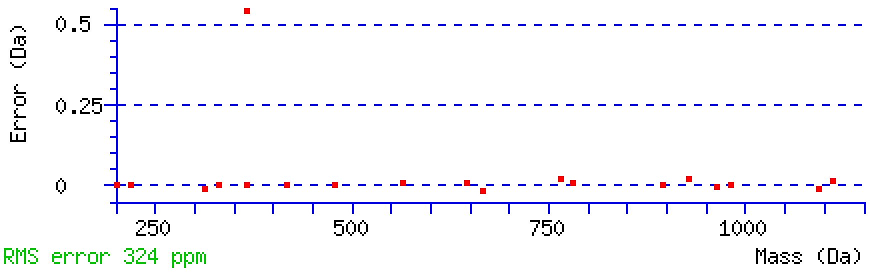
Match to Query 33099: 1309.676228 from(655.845390,2+) rtinseconds(3088) index(43560)
Title: Locus:1.1.1.2724.28
Data file 2011-11-13 - TFD - EP 7-3.mgf

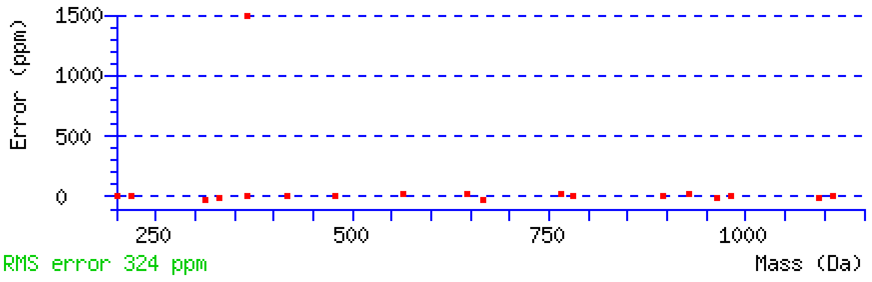
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1309.676529
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 52 **Expect:** 8.2e-005
Matches : 21/102 fragment ions using 41 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	S							12
2	**201.123368**	101.065322	183.112803	92.060039	L	1223.651795	612.329536	1206.625246	603.816261	1205.641230	603.324253	11
3	**330.165961**	165.586618	312.155396	156.581336	E	***1110.567731***	555.787504	1093.541182	547.274229	1092.557166	546.782221	10
4	**417.197989**	209.102632	399.187424	200.097350	S	***981.525138***	491.266207	964.498589	482.752933	963.514573	482.260925	9
5	530.282053	265.644665	512.271488	256.639382	L	***894.493110***	447.750193	877.466561	439.236919	876.482545	438.744911	8
6	**645.308996**	323.158136	627.298431	314.152853	D	***781.409046***	391.208161	764.382497	382.694887	763.398481	382.202879	7
7	746.356675	373.681976	728.346110	364.676693	T	***666.382103***	333.694690	649.355554	325.181415	648.371538	324.689407	6
8	833.388703	417.197990	815.378138	408.192707	S	***565.334424***	283.170850	548.307875	274.657576	547.323859	274.165568	5
9	946.472767	473.740022	928.462202	464.734739	L	***478.302396***	239.654836	461.275847	231.141562			4
10	1093.541181	547.274229	1075.530616	538.268946	F	***365.218332***	183.112804	348.191783	174.599530			3
11	1164.578295	582.792786	1146.567730	573.787503	A	***218.149918***	109.578597	201.123369	101.065322			2
12					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of SLESLDTSLFAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.6	1309.676529	-0.000301	SLESLDTSLFAK
8.7	1309.687790	-0.011562	DTLSILVPHGDK
1.3	1309.667313	0.008915	MNHNRLGSLPR

Mascot: http://www.matrixscience.com/

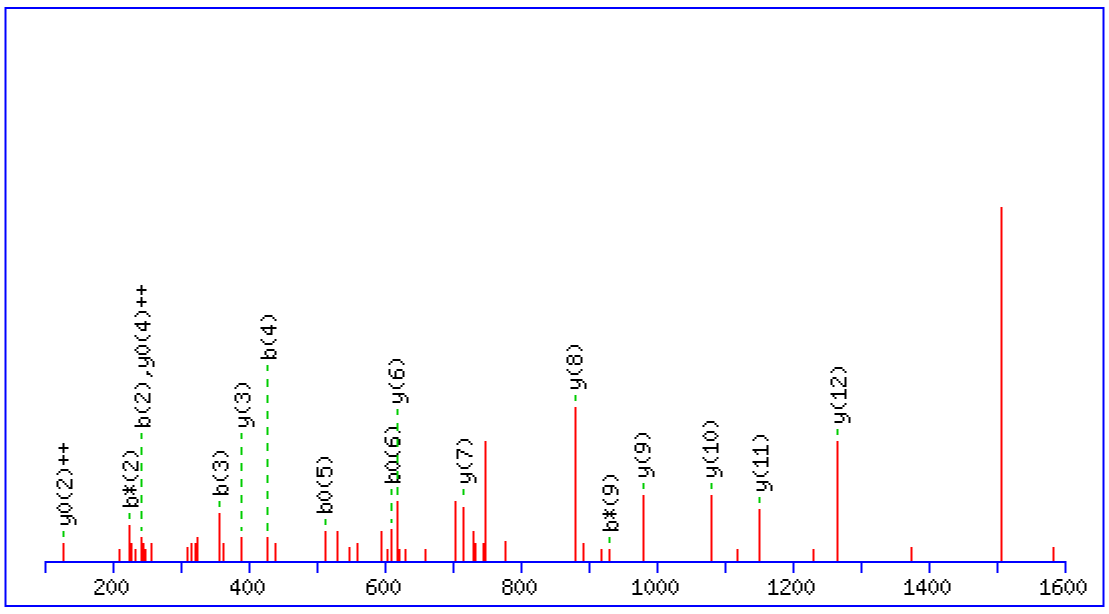
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NQDATVYVGGLDEK**
Found in **SF3B4_HUMAN**, Splicing factor 3B subunit 4 OS=Homo sapiens GN=SF3B4 PE=1 SV=1

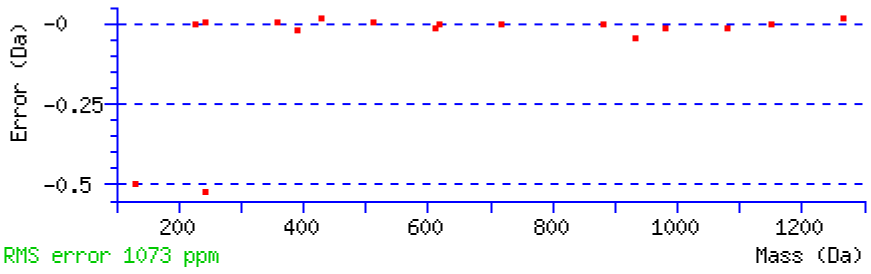
Match to Query 842887: 1507.718348 from(754.866450,2+) rtinseconds(2139) index(349969)
Title: Locus:1.1.1.1155.35
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1600] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●

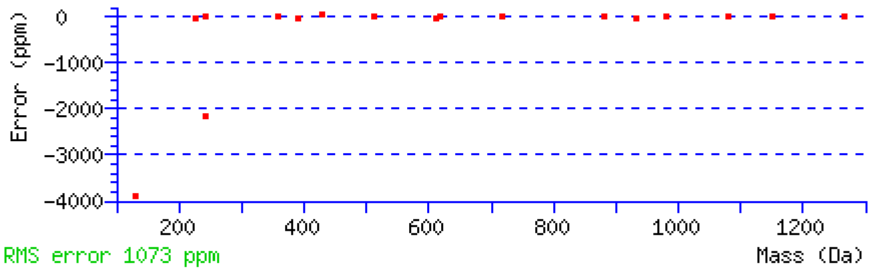


Monoisotopic mass of neutral peptide Mr(calc): 1507.715454
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 58 **Expect:** 1.9e-005
Matches : 17/150 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			N							14
2	**243.108781**	122.058029	226.082232	113.544754			Q	1394.679803	697.843540	1377.653254	689.330265	1376.669238	688.838257	13
3	**358.135724**	179.571500	341.109175	171.058226	340.125159	170.566218	D	***1266.621225***	633.814251	1249.594676	625.300976	1248.610660	624.808968	12
4	**429.172838**	215.090057	412.146289	206.576783	411.162273	206.084775	A	***1151.594282***	576.300779	1134.567733	567.787505	1133.583717	567.295497	11
5	530.220517	265.613897	513.193968	257.100622	512.209952	256.608614	T	***1080.557168***	540.782222	1063.530619	532.268948	1062.546603	531.776940	10
6	629.288931	315.148104	612.262382	306.634829	611.278366	306.142821	V	***979.509489***	490.258383	962.482940	481.745108	961.498924	481.253100	9
7	792.352260	396.679768	775.325711	388.166494	774.341695	387.674486	Y	***880.441075***	440.724176	863.414526	432.210901	862.430510	431.718893	8
8	891.420674	446.213975	874.394125	437.700701	873.410109	437.208693	V	***717.377746***	359.192511	700.351197	350.679237	699.367181	350.187229	7
9	948.442138	474.724707	931.415589	466.211433	930.431573	465.719425	G	***618.309332***	309.658304	601.282783	301.145030	600.298767	300.653022	6
10	1005.463602	503.235439	988.437053	494.722165	987.453037	494.230157	G	561.287868	281.147572	544.261319	272.634298	543.277303	272.142290	5
11	1118.547666	559.777471	1101.521117	551.264197	1100.537101	550.772189	L	504.266404	252.636840	487.239855	244.123565	486.255839	243.631557	4
12	1233.574609	617.290943	1216.548060	608.777668	1215.564044	608.285660	D	***391.182340***	196.094808	374.155791	187.581533	373.171775	187.089525	3
13	1362.617202	681.812239	1345.590653	673.298965	1344.606637	672.806957	E	276.155397	138.581336	259.128848	130.068062	258.144832	129.576054	2
14							K	147.112804	74.060040	130.086255	65.546765			1



RMS error 1073 ppm



RMS error 1073 ppm

NCBI **BLAST** search of NQDATVYVGGLDEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
57.6	1507.715454	0.002894	NQDATVYVGGLDEK

Mascot: http://www.matrixscience.com/

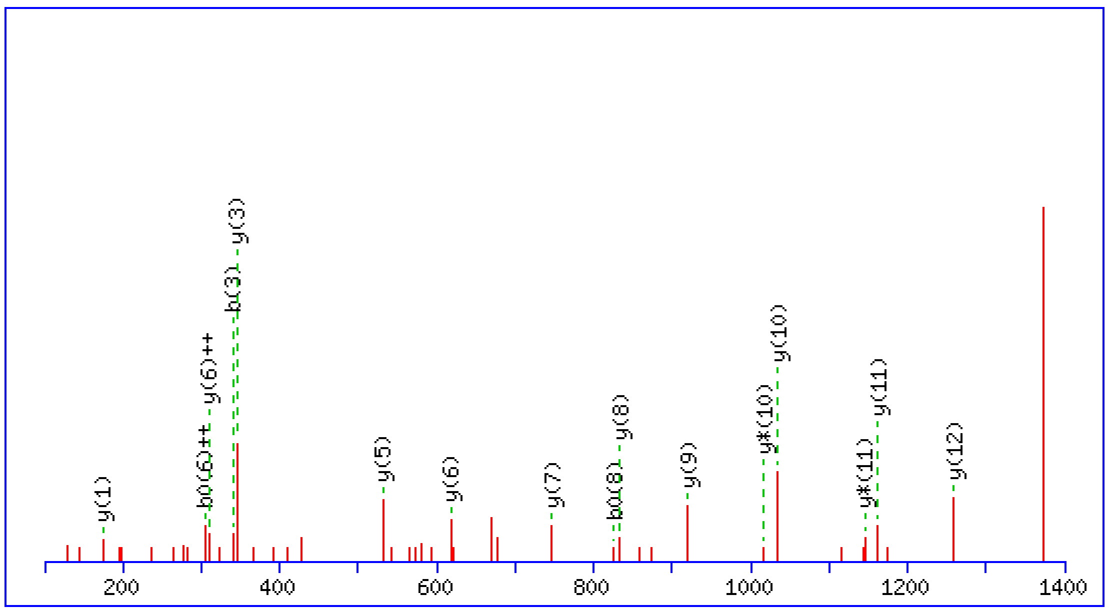
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NPQNSSQSADGLR**
Found in **U2AF1_HUMAN**, Splicing factor U2AF 35 kDa subunit OS=Homo sapiens GN=U2AF1 PE=1 SV=3

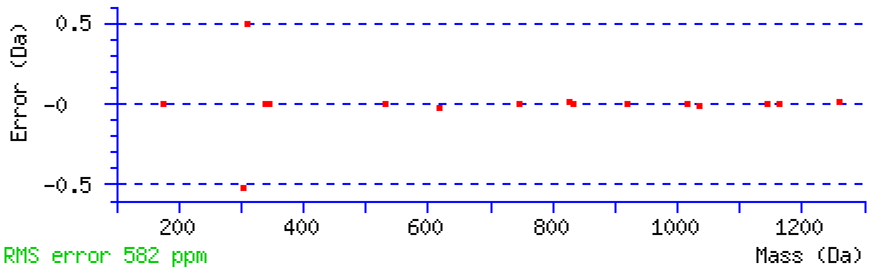
Match to Query 720013: 1372.634948 from(687.324750,2+) rtinseconds(979) index(243364)
Title: Locus:1.1.1.813.43
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

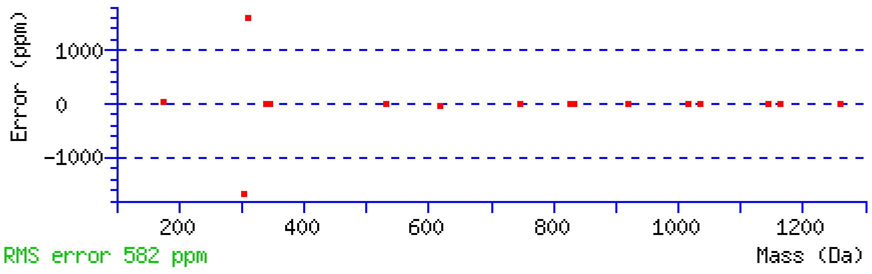
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1372.633102
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 86 **Expect:** 3.5e-008
Matches : 16/130 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			N							13
2	212.102967	106.555121	195.076418	98.041847			P	**1259.597468**	630.302372	1242.570919	621.789098	1241.586903	621.297089	12
3	340.161545	170.584410	323.134996	162.071136			Q	**1162.544704**	581.775990	1145.518155	573.262716	1144.534139	572.770707	11
4	454.204472	227.605874	437.177923	219.092600			N	**1034.486126**	517.746701	1017.459577	509.233427	1016.475561	508.741419	10
5	541.236500	271.121888	524.209951	262.608614	523.225935	262.116606	S	**920.443199**	460.725237	903.416650	452.211963	902.432634	451.719955	9
6	628.268528	314.637902	611.241979	306.124628	610.257963	305.632620	S	**833.411171**	417.209223	816.384622	408.695949	815.400606	408.203941	8
7	756.327106	378.667191	739.300557	370.153917	738.316541	369.661909	Q	**746.379143**	373.693209	729.352594	365.179935	728.368578	364.687927	7
8	843.359134	422.183205	826.332585	413.669931	825.348569	413.177923	S	**618.320565**	309.663920	601.294016	301.150646	600.310000	300.658638	6
9	914.396248	457.701762	897.369699	449.188488	896.385683	448.696480	A	**531.288537**	266.147906	514.261988	257.634632	513.277972	257.142624	5
10	1029.423191	515.215234	1012.396642	506.701959	1011.412626	506.209951	D	460.251423	230.629349	443.224874	222.116075	442.240858	221.624067	4
11	1086.444655	543.725966	1069.418106	535.212691	1068.434090	534.720683	G	**345.224480**	173.115878	328.197931	164.602603			3
12	1199.528719	600.267997	1182.502170	591.754723	1181.518154	591.262715	L	288.203016	144.605146	271.176467	136.091871			2
13							R	**175.118952**	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of NPQNSSQSADGLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
85.5	1372.633102	0.001846	NPQNSSQSADGLR
7.3	1372.648361	-0.013413	DLQPRSHSYDR
5.7	1372.648361	-0.013413	NKPSQGDPFNNR
2.4	1372.637115	-0.002167	DHLNEYAGEGLR
0.0	1372.621887	0.013061	QDSPKPSGSGEPR

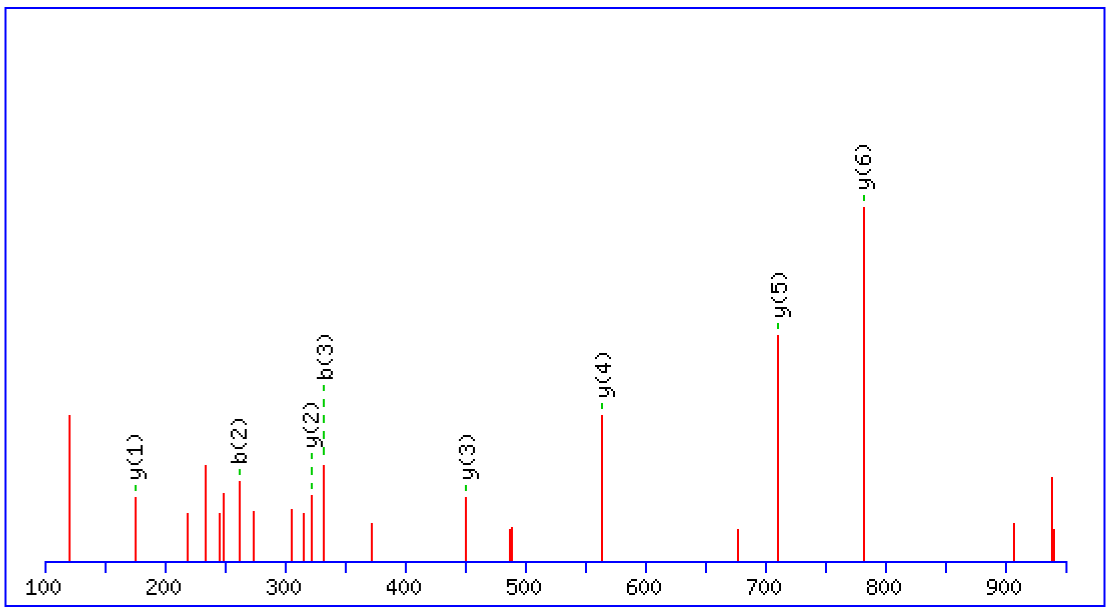
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NFAFLEFR**
Found in **U2AF2_HUMAN**, Splicing factor U2AF 65 kDa subunit OS=Homo sapiens GN=U2AF2 PE=1 SV=4

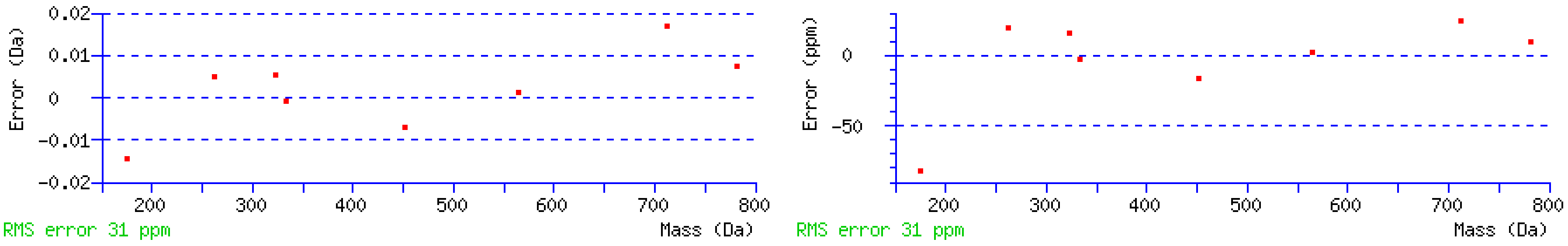
Match to Query 15785: 1042.529388 from(522.271970,2+) rtinseconds(3528) index(52347)
Title: Locus:1.1.1.2762.3
Data file 2011-11-10 - TFD - EP 3-3.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1042.523605
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 41  Expect: 0.00036
Matches : 8/70 fragment ions using 15 most intense peaks   (help)
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			N							8
2	**262.118617**	131.562946	245.092068	123.049672			F	929.487965	465.247621	912.461416	456.734346	911.477400	456.242338	7
3	**333.155731**	167.081504	316.129182	158.568229			A	***782.419551***	391.713414	765.393002	383.200139	764.408986	382.708131	6
4	480.224145	240.615710	463.197596	232.102436			F	***711.382437***	356.194857	694.355888	347.681582	693.371872	347.189574	5
5	593.308209	297.157743	576.281660	288.644468			L	***564.314023***	282.660650	547.287474	274.147375	546.303458	273.655367	4
6	722.350802	361.679039	705.324253	353.165765	704.340237	352.673757	E	***451.229959***	226.118617	434.203410	217.605343	433.219394	217.113335	3
7	869.419216	435.213246	852.392667	426.699972	851.408651	426.207964	F	***322.187366***	161.597321	305.160817	153.084046			2
8							R	***175.118952***	88.063114	158.092403	79.549839			1



NCBI **BLAST** search of NFAFLEFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.7	1042.523605	0.005783	NFAFLEFR
3.7	1042.522949	0.006439	MAASLPGPGSR
3.5	1042.522964	0.006424	CVVQHTASK
3.4	1042.533508	-0.004120	EVATYFSKV
0.7	1042.534180	-0.004792	RCQPPLSR
0.2	1042.534836	-0.005448	AGWWPALSR
0.1	1042.534180	-0.004792	CSLKHQTR

Mascot: http://www.matrixscience.com/

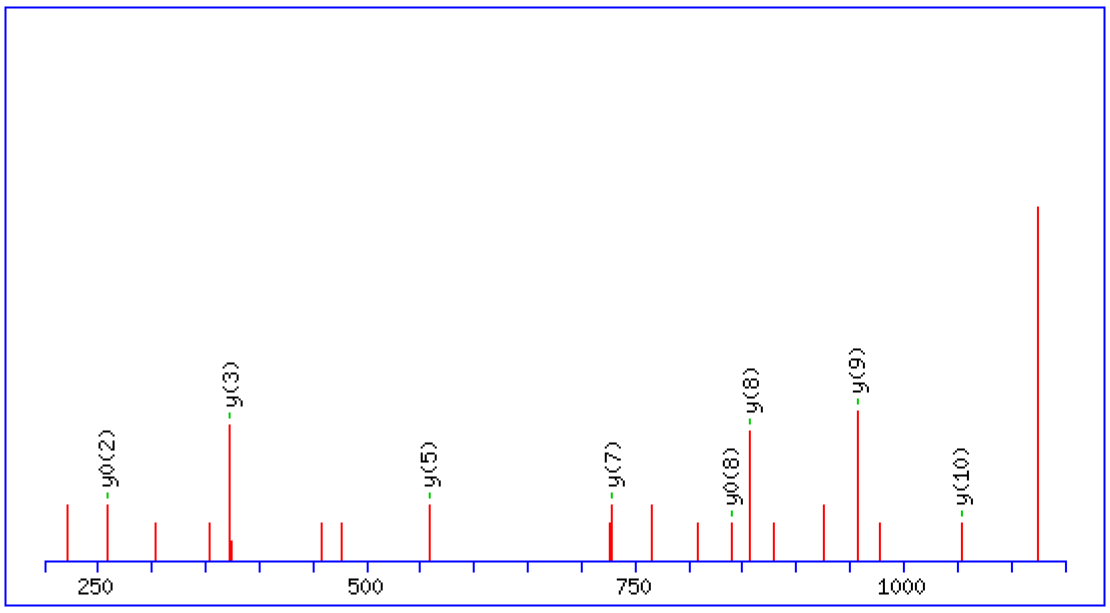
Mascot Search Results

Peptide View

MS/MS Fragmentation of **APVEGIGQPEK**
Found in **SPRY4_HUMAN**, SPRY domain-containing protein 4 OS=Homo sapiens GN=SPRYD4 PE=1 SV=2

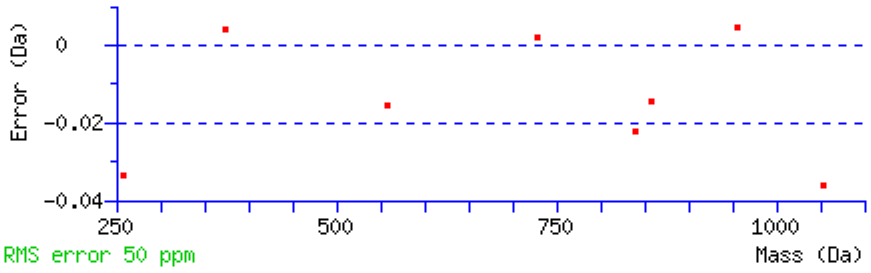
Match to Query 29768: 1123.586688 from(562.800620,2+) rtinseconds(1362) index(8775)
Title: Locus:1.1.1.1773.41
Data file 2011-11-10 - TFD - EP 4-6.mgf

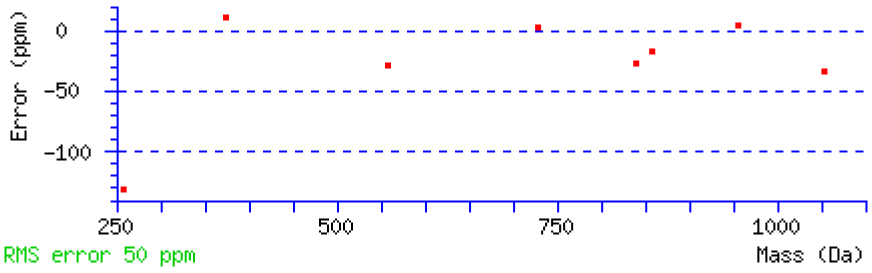
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1123.587326
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.0003
Matches : 8/98 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							11
2	169.097154	85.052215					P	***1053.557502***	527.282389	1036.530953	518.769115	1035.546937	518.277107	10
3	268.165568	134.586422					V	***956.504738***	478.756007	939.478189	470.242733	938.494173	469.750725	9
4	397.208161	199.107719			379.197596	190.102436	E	***857.436324***	429.221800	840.409775	420.708526	839.425759	420.216518	8
5	454.229625	227.618450			436.219060	218.613168	G	***728.393731***	364.700504	711.367182	356.187229	710.383166	355.695221	7
6	567.313689	284.160483			549.303124	275.155200	I	671.372267	336.189772	654.345718	327.676497	653.361702	327.184489	6
7	624.335153	312.671215			606.324588	303.665932	G	***558.288203***	279.647740	541.261654	271.134465	540.277638	270.642457	5
8	752.393731	376.700504	735.367182	368.187229	734.383166	367.695221	Q	501.266739	251.137007	484.240190	242.623733	483.256174	242.131725	4
9	849.446495	425.226886	832.419946	416.713611	831.435930	416.221603	P	***373.208161***	187.107718	356.181612	178.594444	355.197596	178.102436	3
10	978.489088	489.748182	961.462539	481.234908	960.478523	480.742900	E	276.155397	138.581336	259.128848	130.068062	258.144832	129.576054	2
11							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of APVEGIGQPEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.3	1123.587326	-0.000638	APVEGIGQPEK
3.8	1123.584625	0.002063	APRPREQDR

Mascot: http://www.matrixscience.com/

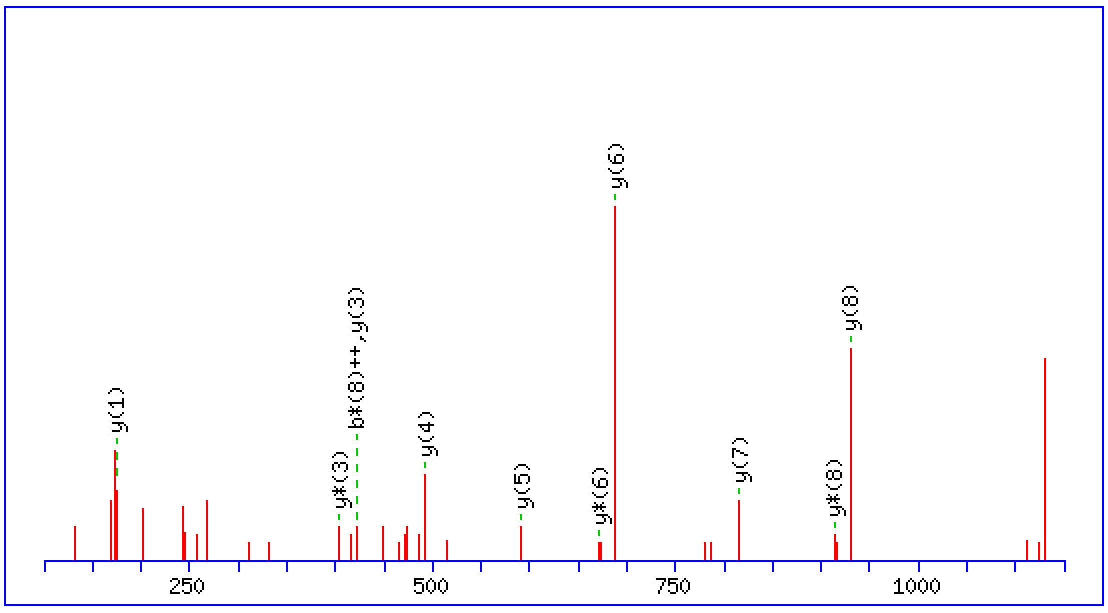
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SINQPVAFVR**
Found in **SLIRP_HUMAN**, SRA stem-loop-interacting RNA-binding protein, mitochondrial OS=Homo sapiens GN=SLIRP PE=1 SV=1

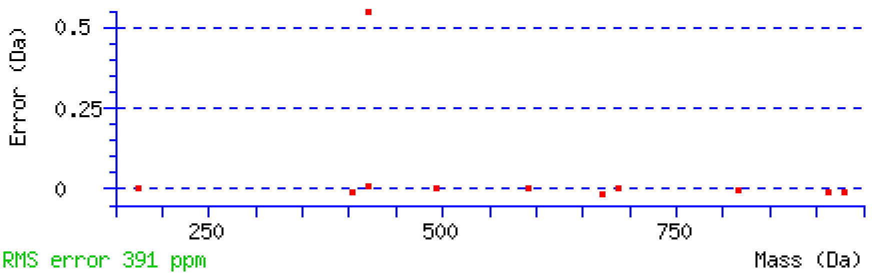
Match to Query 24208: 1129.624168 from(565.819360,2+) rtinseconds(2206) index(18980)
Title: Locus:1.1.1.2296.29
Data file 2011-11-10 - TFD - EP 4-7.mgf

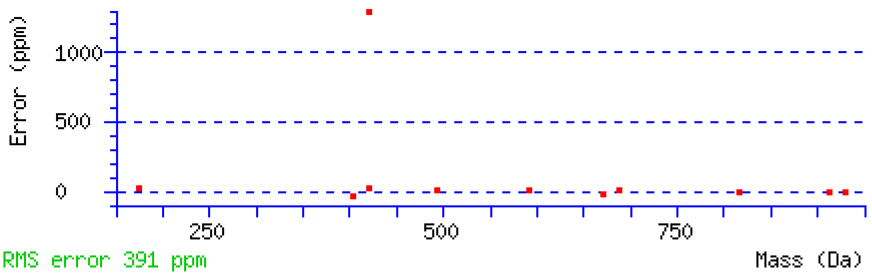
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1129.624390
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 51 **Expect:** 2.9e-005
Matches : 11/86 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	88.039304	44.523290			70.028739	35.518008	S					10
2	201.123368	101.065322			183.112803	92.060039	I	1043.599641	522.303458	1026.573092	513.790184	9
3	315.166295	158.086785	298.139746	149.573511	297.155730	149.081503	N	***930.515577***	465.761426	913.489028	457.248152	8
4	443.224873	222.116075	426.198324	213.602800	425.214308	213.110792	Q	***816.472650***	408.739963	799.446101	400.226688	7
5	540.277637	270.642457	523.251088	262.129182	522.267072	261.637174	P	***688.414072***	344.710674	671.387523	336.197399	6
6	639.346051	320.176664	622.319502	311.663389	621.335486	311.171381	V	***591.361308***	296.184292	574.334759	287.671017	5
7	710.383165	355.695221	693.356616	347.181946	692.372600	346.689938	A	***492.292894***	246.650085	475.266345	238.136810	4
8	857.451579	429.229427	840.425030	420.716153	839.441014	420.224145	F	***421.255780***	211.131528	404.229231	202.618253	3
9	956.519993	478.763634	939.493444	470.250360	938.509428	469.758352	V	274.187366	137.597321	257.160817	129.084046	2
10							R	***175.118952***	88.063114	158.092403	79.549839	1





NCBI **BLAST** search of SINQPVAFVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.0	1129.624390	-0.000222	SINQPVAFVR
2.7	1129.616516	0.007652	CGLDLIVQAK

Mascot: http://www.matrixscience.com/

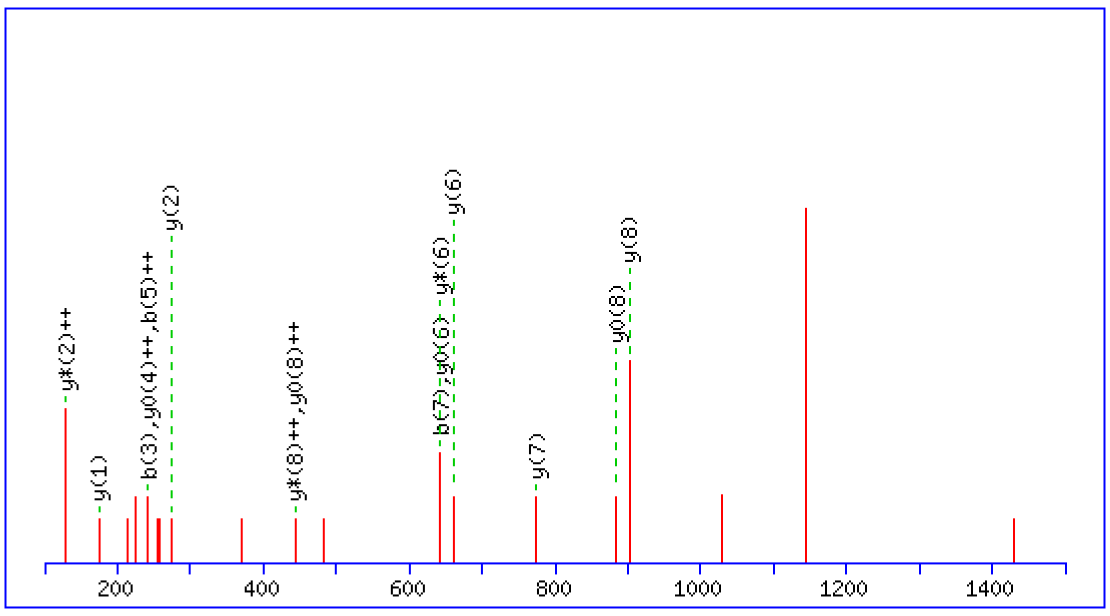
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VAAQNSAEVVR**
Found in **STC1_HUMAN**, Stanniocalcin-1 OS=Homo sapiens GN=STC1 PE=1 SV=1

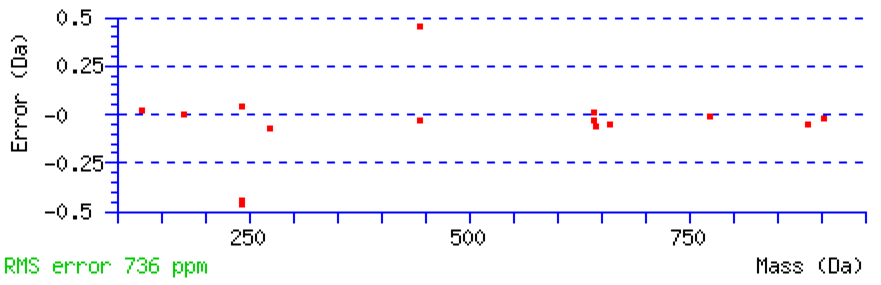
Match to Query 25846: 1142.605808 from(572.310180,2+) rtinseconds(920) index(1588)
Title: Locus:1.1.1.1705.40
Data file 2011-11-10 - TFD - EP 4-1.mgf

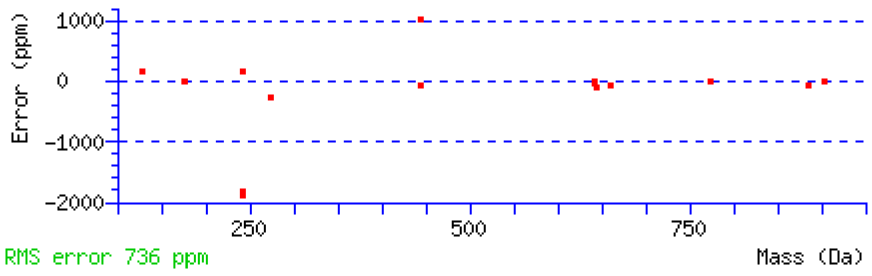
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1142.604370
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 33  Expect: 0.0063
Matches : 15/98 fragment ions using 17 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	100.075690	50.541483					V							11
2	171.112804	86.060040					A	1044.543248	522.775262	1027.516699	514.261988	1026.532683	513.769979	10
3	**242.149918**	121.578597					A	973.506134	487.256705	956.479585	478.743430	955.495569	478.251422	9
4	370.208496	185.607886	353.181947	177.094612			Q	***902.469020***	451.738148	885.442471	443.224874	884.458455	442.732866	8
5	484.251423	242.629350	467.224874	234.116075			N	***774.410442***	387.708859	757.383893	379.195585	756.399877	378.703577	7
6	571.283451	286.145364	554.256902	277.632089	553.272886	277.140081	S	***660.367515***	330.687395	643.340966	322.174121	642.356950	321.682113	6
7	**642.320565**	321.663921	625.294016	313.150646	624.310000	312.658638	A	573.335487	287.171382	556.308938	278.658107	555.324922	278.166099	5
8	771.363158	386.185217	754.336609	377.671943	753.352593	377.179935	E	502.298373	251.652824	485.271824	243.139550	484.287808	242.647542	4
9	870.431572	435.719424	853.405023	427.206150	852.421007	426.714142	V	373.255780	187.131528	356.229231	178.618253			3
10	969.499986	485.253631	952.473437	476.740357	951.489421	476.248349	V	***274.187366***	137.597321	257.160817	129.084046			2
11							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of VAAQNSAEVVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.0	1142.604370	0.001438	VAAQNSAEVVR
25.1	1142.604355	0.001453	IKELQNAGDR
19.3	1142.615601	-0.009793	LQQDNIRTR
14.3	1142.604355	0.001453	LKQQNEDLR
11.6	1142.615601	-0.009793	QLQRSQQQK
10.3	1142.608383	-0.002575	IGAEVYHNLK
8.1	1142.604385	0.001423	KLVGSDQAPGR
7.5	1142.608398	-0.002590	QPSYVPAPLR
6.5	1142.604370	0.001438	QLIVANAGDSR
6.5	1142.615601	-0.009793	KPSASQRPTR

Mascot: http://www.matrixscience.com/

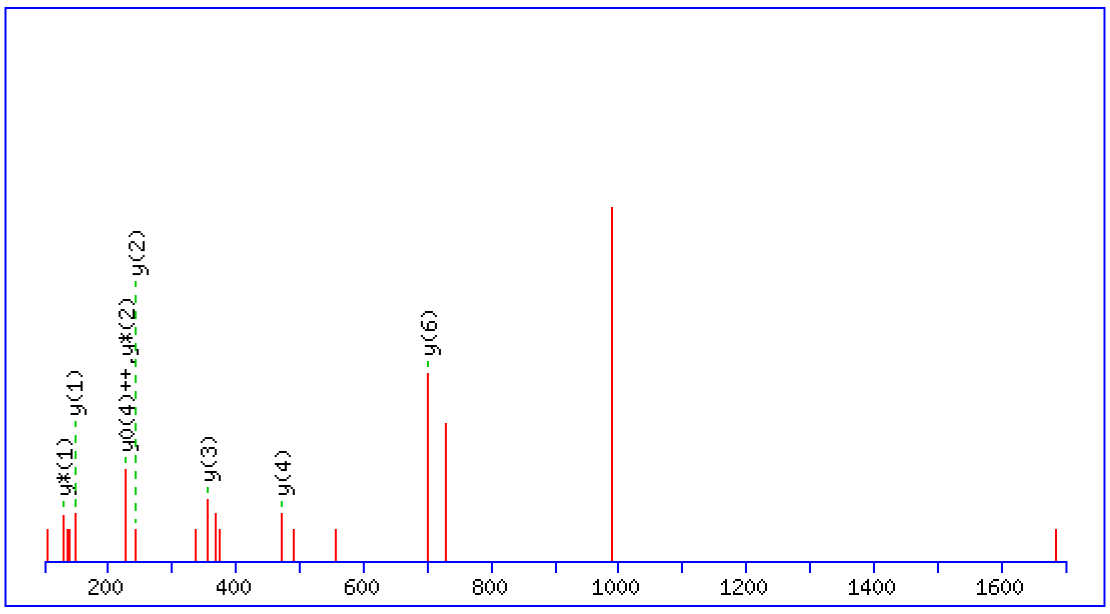
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TWKTDLPK**
Found in **STA13_HUMAN**, StAR-related lipid transfer protein 13 OS=Homo sapiens GN=STARD13 PE=1 SV=2

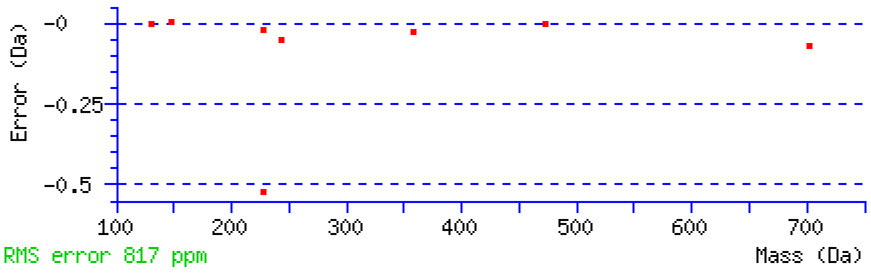
Match to Query 15485: 987.535628 from(494.775090,2+) rtinseconds(1222) index(5006)
Title: Locus:1.1.1.1732.26
Data file 2011-11-10 - TFD - EP 3-6.mgf

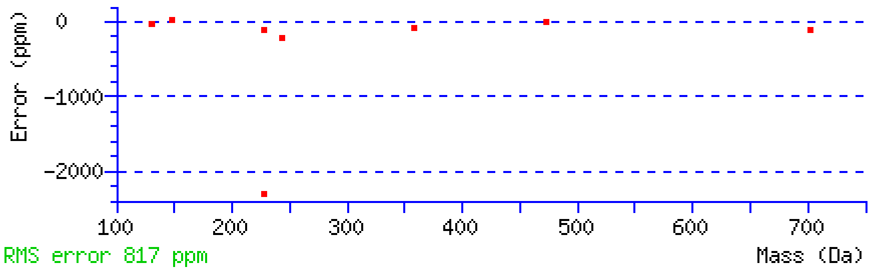
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1700] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 987.538925
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 37  Expect: 0.0031
Matches : 8/74 fragment ions using 11 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	**T**							8
2	288.134268	144.570772			270.123703	135.565490	**W**	887.498530	444.252903	870.471981	435.739629	869.487965	435.247621	7
3	416.229231	208.618254	399.202682	200.104979	398.218666	199.612971	**K**	***701.419217***	351.213247	684.392668	342.699972	683.408652	342.207964	6
4	517.276910	259.142093	500.250361	250.628819	499.266345	250.136811	**T**	573.324254	287.165765	556.297705	278.652491	555.313689	278.160483	5
5	632.303853	316.655565	615.277304	308.142290	614.293288	307.650282	**D**	***472.276575***	236.641925	455.250026	228.128651	454.266010	227.636643	4
6	745.387917	373.197597	728.361368	364.684322	727.377352	364.192314	**L**	***357.249632***	179.128454	340.223083	170.615180			3
7	842.440681	421.723979	825.414132	413.210704	824.430116	412.718696	**P**	***244.165568***	122.586422	227.139019	114.073148			2
8							**K**	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of TWKTDLPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.8	987.538925	-0.003297	TWKTDLPK
22.2	987.542282	-0.006654	ASTAGMILPK
21.2	987.534882	0.000746	SRLDQELK
20.8	987.534866	0.000762	ENLESRLK
12.3	987.534882	0.000746	RISAEDGLK
11.8	987.534897	0.000731	DAGKAGQTLK
10.8	987.534897	0.000731	ERTLQTPK
8.8	987.542267	-0.006639	KINELMPK
8.2	987.542267	-0.006639	KINELMPK
8.1	987.534882	0.000746	ENDLTLKR

Mascot: http://www.matrixscience.com/

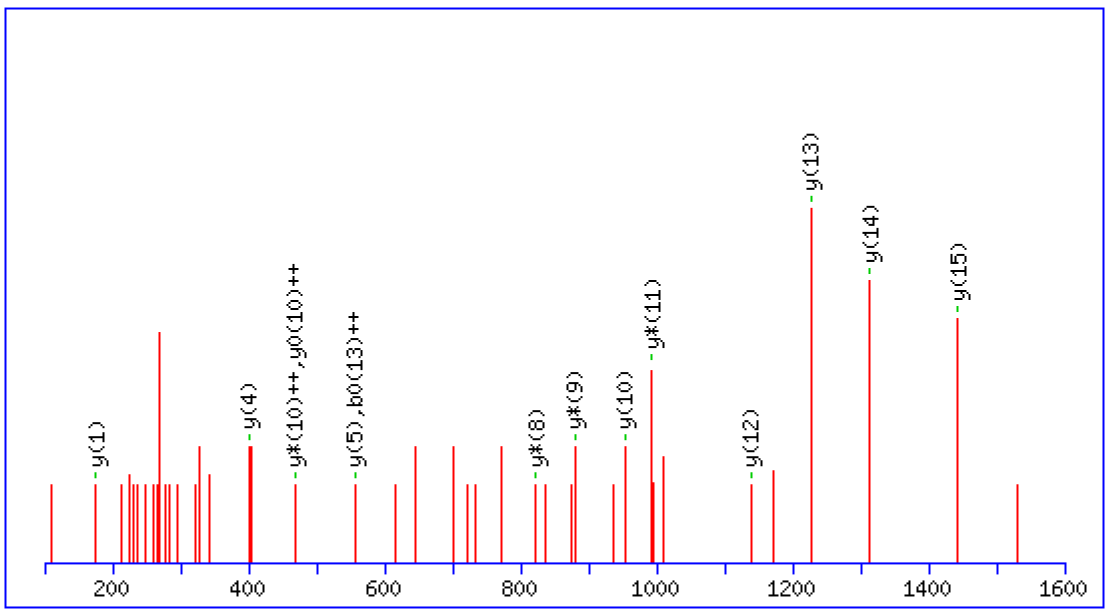
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AGLESSEGGGGPERPGAR**
Found in **SCD5_HUMAN**, Stearoyl-CoA desaturase 5 OS=Homo sapiens GN=SCD5 PE=2 SV=2

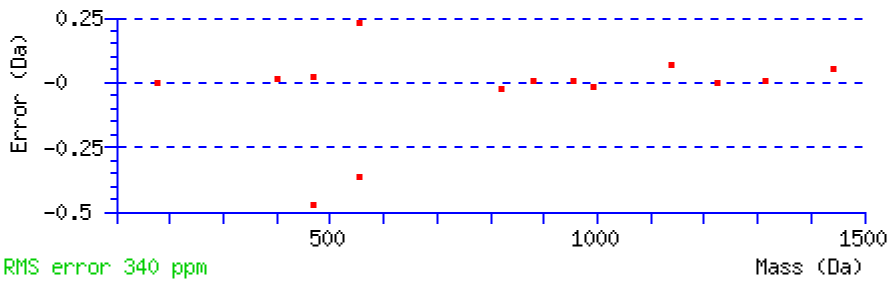
Match to Query 45837: 1682.800992 from(561.940940,3+) rtinseconds(1182) index(2310)
Title: Locus:1.1.1.2073.35
Data file 2011-11-10 - TFD - EP 3-5.mgf

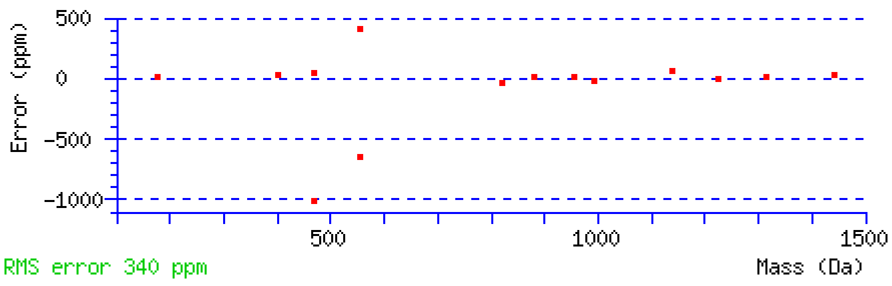
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1682.797211
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 44  Expect: 9.1e-005
Matches : 14/162 fragment ions using 23 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	72.044390	36.525833					A							18
2	129.065854	65.036565					G	1612.767388	806.887332	1595.740839	798.374058	1594.756823	797.882049	17
3	242.149918	121.578597					L	1555.745924	778.376600	1538.719375	769.863326	1537.735359	769.371318	16
4	371.192511	186.099894			353.181946	177.094611	E	***1442.661860***	721.834568	1425.635311	713.321294	1424.651295	712.829285	15
5	458.224539	229.615907			440.213974	220.610625	S	***1313.619267***	657.313271	1296.592718	648.799997	1295.608702	648.307989	14
6	545.256567	273.131922			527.246002	264.126639	S	***1226.587239***	613.797258	1209.560690	605.283983	1208.576674	604.791975	13
7	674.299160	337.653218			656.288595	328.647936	E	***1139.555211***	570.281244	1122.528662	561.767969	1121.544646	561.275961	12
8	731.320624	366.163950			713.310059	357.158668	G	1010.512618	505.759947	993.486069	497.246672	992.502053	496.754664	11
9	788.342088	394.674682			770.331523	385.669400	G	***953.491154***	477.249215	936.464605	468.735940	935.480589	468.243932	10
10	845.363552	423.185414			827.352987	414.180132	G	896.469690	448.738483	879.443141	440.225208	878.459125	439.733200	9
11	902.385016	451.696146			884.374451	442.690864	G	839.448226	420.227751	822.421677	411.714476	821.437661	411.222468	8
12	999.437780	500.222528			981.427215	491.217246	P	782.426762	391.717019	765.400213	383.203744	764.416197	382.711736	7
13	1128.480373	564.743825			1110.469808	555.738542	E	685.373998	343.190637	668.347449	334.677362	667.363433	334.185354	6
14	1284.581484	642.794380	1267.554935	634.281106	1266.570919	633.789098	R	***556.331405***	278.669340	539.304856	270.156066			5
15	1381.634248	691.320762	1364.607699	682.807488	1363.623683	682.315480	P	***400.230294***	200.618785	383.203745	192.105510			4
16	1438.655712	719.831494	1421.629163	711.318220	1420.645147	710.826212	G	303.177530	152.092403	286.150981	143.579128			3
17	1509.692826	755.350051	1492.666277	746.836777	1491.682261	746.344768	A	246.156066	123.581671	229.129517	115.068396			2
18							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of AGLESSEGGGGPERPGAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
43.8	1682.797211	0.003781	AGLESSEGGGGPERPGAR
0.7	1682.804626	-0.003634	IPMPPSSPQPRGAPR

Mascot: http://www.matrixscience.com/

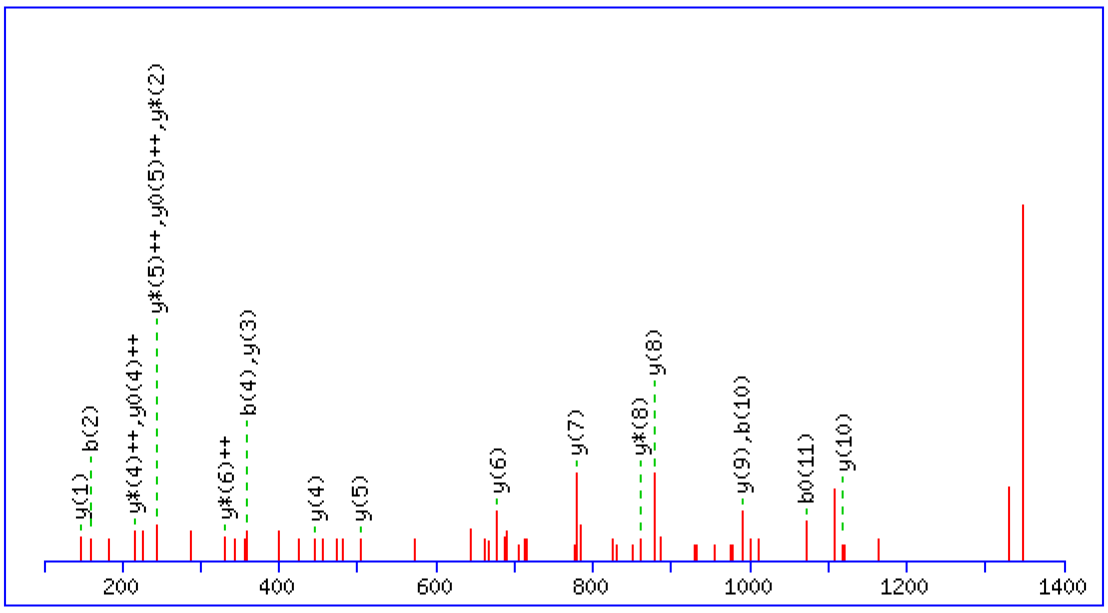
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TGAELVTCGSVLK**
Found in **SDF2L_HUMAN**, Stromal cell-derived factor 2-like protein 1 OS=Homo sapiens GN=SDF2L1 PE=1 SV=2

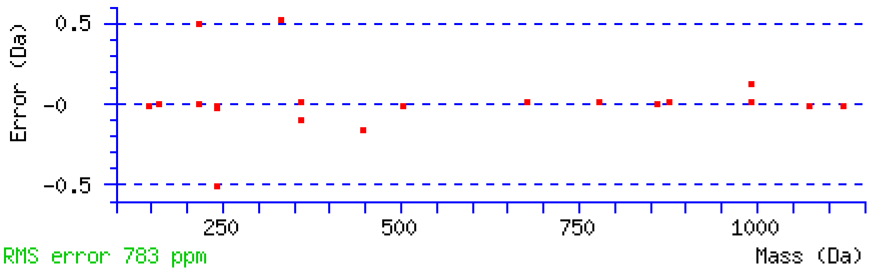
Match to Query 38509: 1347.696768 from(674.855660,2+) rtinseconds(2239) index(24003)
Title: Locus:1.1.1.2125.42
Data file 2011-11-14 - TFD - EP 8-6.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●

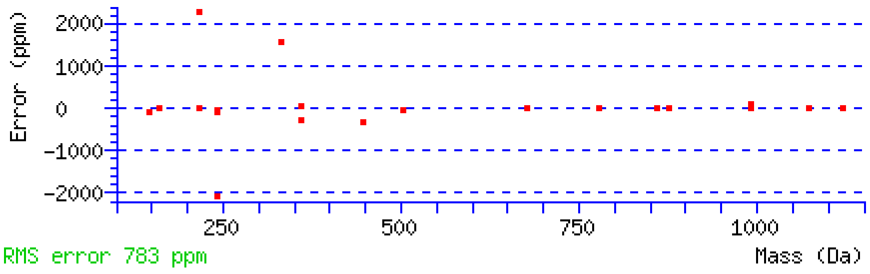


Monoisotopic mass of neutral peptide Mr(calc): 1347.706802
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 42 **Expect:** 0.0009
Matches : 20/114 fragment ions using 45 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116	84.044390	42.525833	T							13
2	**159.076419**	80.041847	141.065854	71.036565	G	1247.666401	624.336839	1230.639852	615.823564	1229.655836	615.331556	12
3	230.113533	115.560404	212.102968	106.555122	A	1190.644937	595.826107	1173.618388	587.312832	1172.634372	586.820824	11
4	**359.156126**	180.081701	341.145561	171.076419	E	***1119.607823***	560.307550	1102.581274	551.794275	1101.597258	551.302267	10
5	472.240190	236.623733	454.229625	227.618451	L	***990.565230***	495.786253	973.538681	487.272978	972.554665	486.780970	9
6	571.308604	286.157940	553.298039	277.152658	V	***877.481166***	439.244221	860.454617	430.730946	859.470601	430.238938	8
7	672.356283	336.681780	654.345718	327.676497	T	***778.412752***	389.710014	761.386203	381.196739	760.402187	380.704731	7
8	846.402582	423.704929	828.392017	414.699647	C	***677.365073***	339.186174	660.338524	330.672900	659.354508	330.180892	6
9	903.424046	452.215661	885.413481	443.210379	G	***503.318774***	252.163025	486.292225	243.649750	485.308209	243.157742	5
10	**990.456074**	495.731675	972.445509	486.726393	S	***446.297310***	223.652293	429.270761	215.139018	428.286745	214.647010	4
11	1089.524488	545.265882	1071.513923	536.260600	V	***359.265282***	180.136279	342.238733	171.623004			3
12	1202.608552	601.807914	1184.597987	592.802631	L	260.196868	130.602072	243.170319	122.088797			2
13					K	***147.112804***	74.060040	130.086255	65.546765			1



RMS error 783 ppm



RMS error 783 ppm

NCBI **BLAST** search of TGAELVTCGSVLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.7	1347.706802	-0.010034	TGAELVTCGSVLK

Mascot: http://www.matrixscience.com/

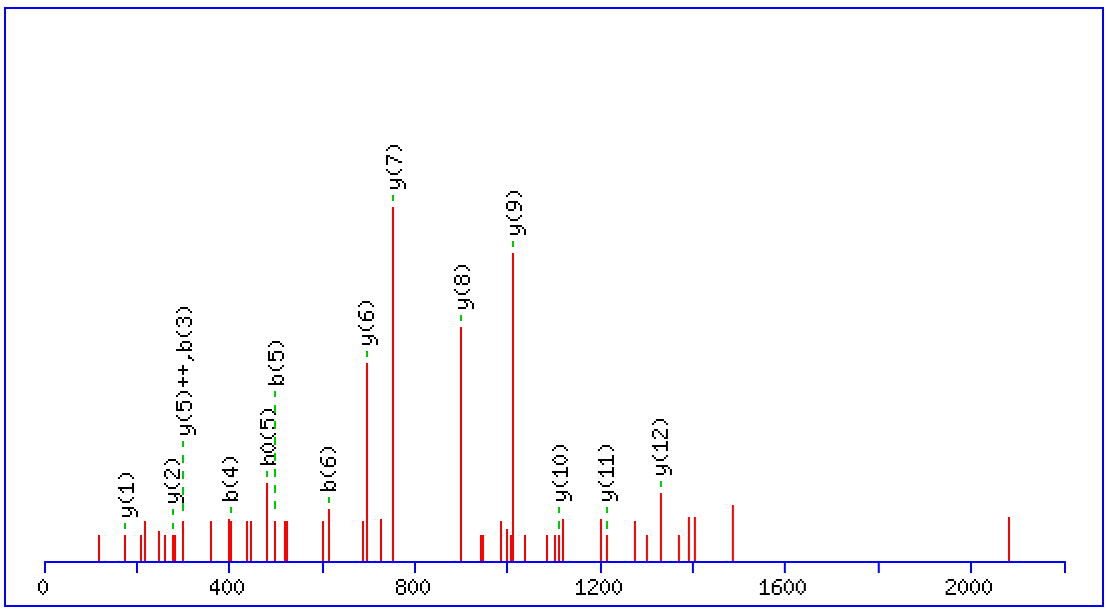
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALDTVLFGPPLLTR**
Found in **STIM1_HUMAN**, Stromal interaction molecule 1 OS=Homo sapiens GN=STIM1 PE=1 SV=3

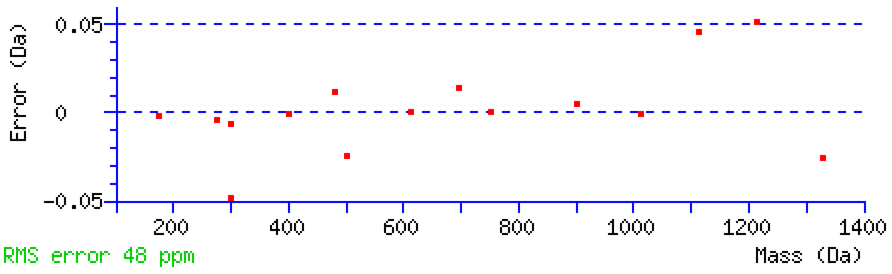
Match to Query 48118: 1511.879448 from(756.947000,2+) rtinseconds(3859) index(57073)
Title: Locus:1.1.1.2897.38
Data file 2011-11-10 - TFD - EP 3-2.mgf

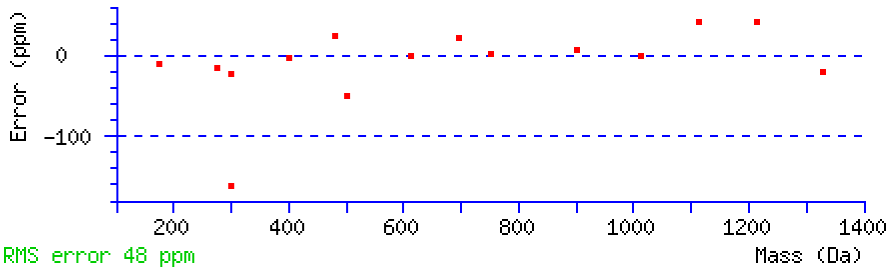
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1511.871170
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 42 **Expect:** 0.00021
Matches : 15/124 fragment ions using 40 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	72.044390	36.525833			A							14
2	185.128454	93.067865			L	1441.841329	721.424303	1424.814780	712.911028	1423.830764	712.419020	13
3	**300.155397**	150.581336	282.144832	141.576054	D	***1328.757265***	664.882271	1311.730716	656.368996	1310.746700	655.876988	12
4	**401.203076**	201.105176	383.192511	192.099894	T	***1213.730322***	607.368799	1196.703773	598.855525	1195.719757	598.363517	11
5	**500.271490**	250.639383	482.260925	241.634101	V	***1112.682643***	556.844960	1095.656094	548.331685	1094.672078	547.839677	10
6	**613.355554**	307.181415	595.344989	298.176133	L	***1013.614229***	507.310753	996.587680	498.797478	995.603664	498.305470	9
7	760.423968	380.715622	742.413403	371.710340	F	***900.530165***	450.768721	883.503616	442.255446	882.519600	441.763438	8
8	817.445432	409.226354	799.434867	400.221072	G	***753.461751***	377.234514	736.435202	368.721239	735.451186	368.229231	7
9	914.498196	457.752736	896.487631	448.747454	P	***696.440287***	348.723782	679.413738	340.210507	678.429722	339.718499	6
10	1011.550960	506.279118	993.540395	497.273836	P	599.387523	300.197400	582.360974	291.684125	581.376958	291.192117	5
11	1124.635024	562.821150	1106.624459	553.815868	L	502.334759	251.671017	485.308210	243.157743	484.324194	242.665735	4
12	1237.719088	619.363182	1219.708523	610.357900	L	389.250695	195.128985	372.224146	186.615711	371.240130	186.123703	3
13	1338.766767	669.887022	1320.756202	660.881739	T	***276.166631***	138.586953	259.140082	130.073679	258.156066	129.581671	2
14					R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of ALDTVLFGPPLLTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.2	1511.871170	0.008278	ALDTVLFGPPLLTR

Mascot: http://www.matrixscience.com/

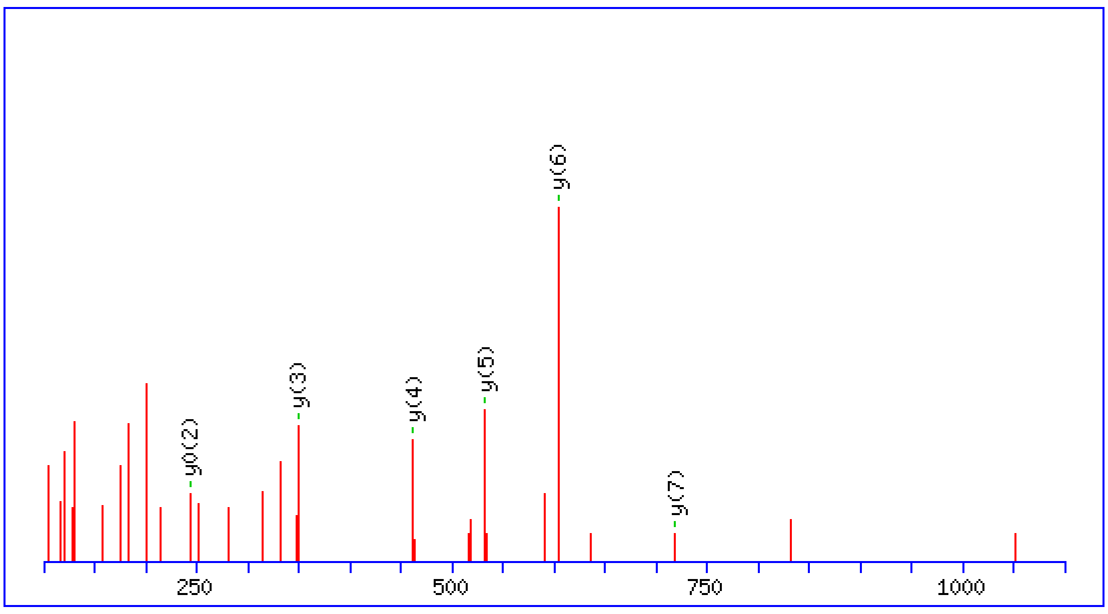
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IDAAISDK**
Found in **MMP3_HUMAN**, Stromelysin-1 OS=Homo sapiens GN=MMP3 PE=1 SV=2

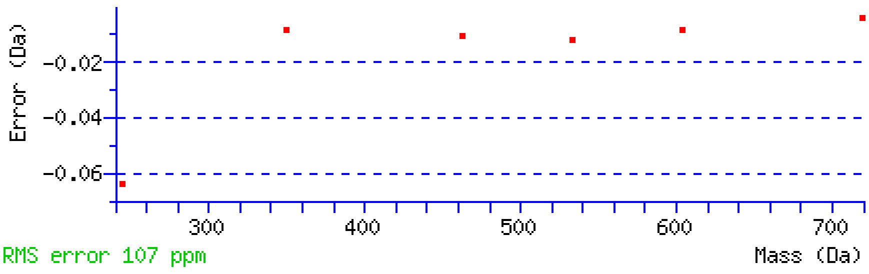
Match to Query 2622: 831.426488 from(416.720520,2+) rtinseconds(1214) index(7059)
Title: Locus:1.1.1.1859.7
Data file 2011-11-12 - TFD - EP 6-2.mgf

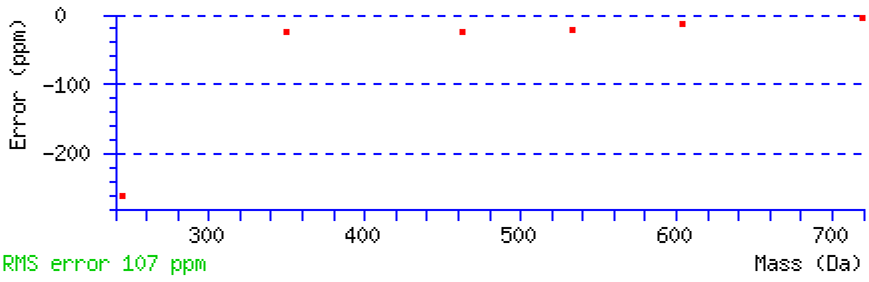
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 831.433777
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 42 **Expect:** 0.0011
Matches : 6/66 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^0	y^{0++}	#
1	114.091340	57.549308			I							8
2	229.118283	115.062779	211.107718	106.057497	D	*719.357010*	360.182143	702.330461	351.668869	701.346445	351.176861	7
3	300.155397	150.581336	282.144832	141.576054	A	*604.330067*	302.668672	587.303518	294.155397	586.319502	293.663389	6
4	371.192511	186.099894	353.181946	177.094611	A	*533.292953*	267.150115	516.266404	258.636840	515.282388	258.144832	5
5	484.276575	242.641926	466.266010	233.636643	I	*462.255839*	231.631557	445.229290	223.118283	444.245274	222.626275	4
6	571.308603	286.157940	553.298038	277.152657	S	*349.171775*	175.089525	332.145226	166.576251	331.161210	166.084243	3
7	686.335546	343.671411	668.324981	334.666129	D	262.139747	131.573511	245.113198	123.060237	244.129182	122.568229	2
8					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of IDAAISDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.3	831.433777	-0.007289	IDAAISDK
23.6	831.427246	-0.000758	EVAALCR
15.2	831.427246	-0.000758	LEQLCR
10.6	831.427246	-0.000758	NQQLMAK
10.4	831.427246	-0.000758	LDLAACR
10.3	831.427261	-0.000773	LVSSPCR
8.3	831.423874	0.002614	LWAESAR
8.0	831.427902	-0.001414	LWAWEK
7.8	831.427246	-0.000758	LQELCR
4.6	831.433792	-0.007304	IGEVSSPK

Mascot: http://www.matrixscience.com/

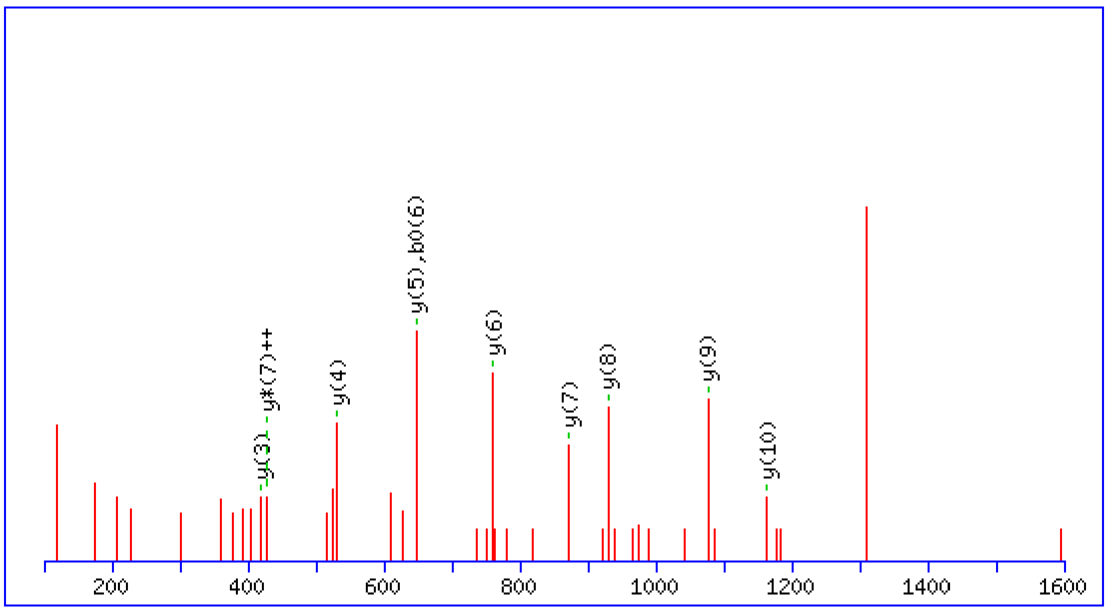
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **FSFGLLDLPFR**
Found in **SMHD1_HUMAN**, Structural maintenance of chromosomes flexible hinge domain-containing protein 1 OS=Homo sapiens GN=SMCHD1 PE=1 SV=2

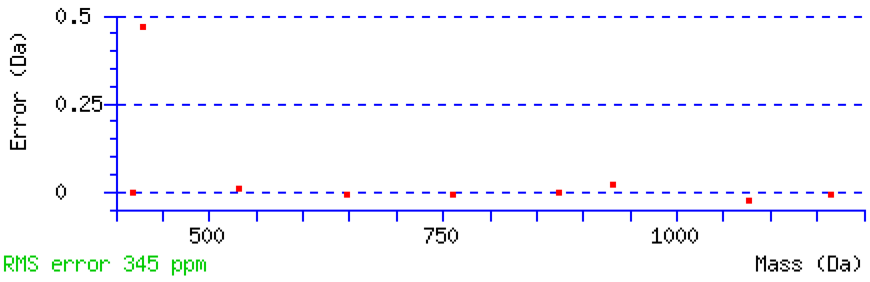
Match to Query 36265: 1310.702028 from(656.358290,2+) rtinseconds(4496) index(65850)
Title: Locus:1.1.1.3095.12
Data file 2011-11-14 - TFD - EP 8-1.mgf

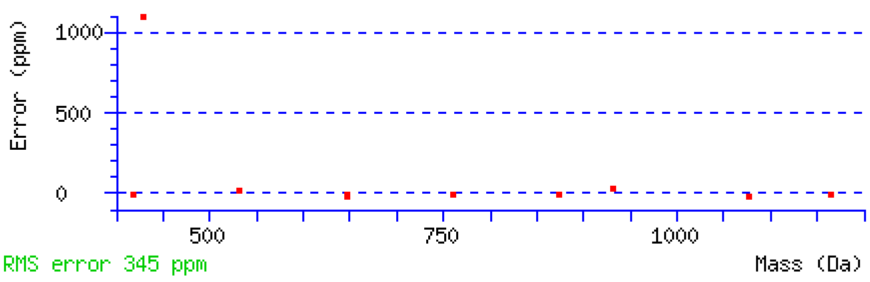
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1600] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1310.702316
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 76  Expect: 1.4e-007
Matches : 10/90 fragment ions using 11 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.075690	74.541483			F							11
2	235.107718	118.057497	217.097153	109.052214	S	***1164.641171***	582.824224	1147.614622	574.310949	1146.630606	573.818941	10
3	382.176132	191.591704	364.165567	182.586422	F	***1077.609143***	539.308210	1060.582594	530.794935	1059.598578	530.302927	9
4	439.197596	220.102436	421.187031	211.097153	G	***930.540729***	465.774003	913.514180	457.260728	912.530164	456.768720	8
5	552.281660	276.644468	534.271095	267.639186	L	***873.519265***	437.263271	856.492716	428.749996	855.508700	428.257988	7
6	665.365724	333.186500	647.355159	324.181218	L	***760.435201***	380.721239	743.408652	372.207964	742.424636	371.715956	6
7	780.392667	390.699972	762.382102	381.694689	D	***647.351137***	324.179207	630.324588	315.665932	629.340572	315.173924	5
8	893.476731	447.242004	875.466166	438.236721	L	***532.324194***	266.665735	515.297645	258.152461			4
9	990.529495	495.768386	972.518930	486.763103	P	***419.240130***	210.123703	402.213581	201.610429			3
10	1137.597909	569.302593	1119.587344	560.297310	F	322.187366	161.597321	305.160817	153.084047			2
11					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of FSFGLLDLPFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
75.6	1310.702316	-0.000288	FSFGLLDLPFR
2.5	1310.709503	-0.007475	AYQLHSRPVPK
0.9	1310.701630	0.000398	MPPLIADSPKAR

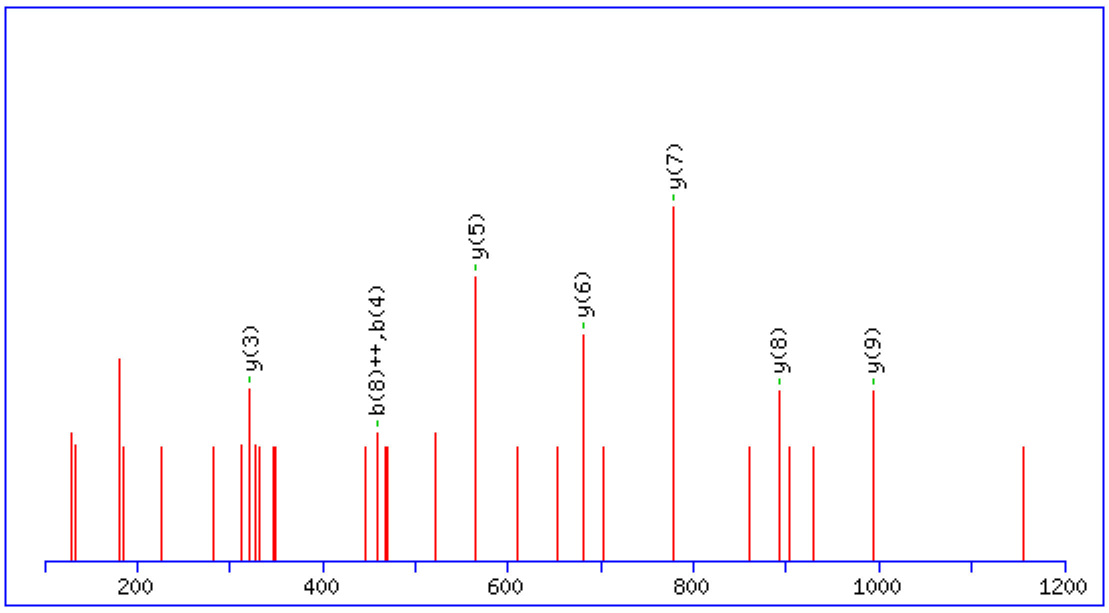
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DQTIVDPFSSK**
Found in **SMC3_HUMAN**, Structural maintenance of chromosomes protein 3 OS=Homo sapiens GN=SMC3 PE=1 SV=2

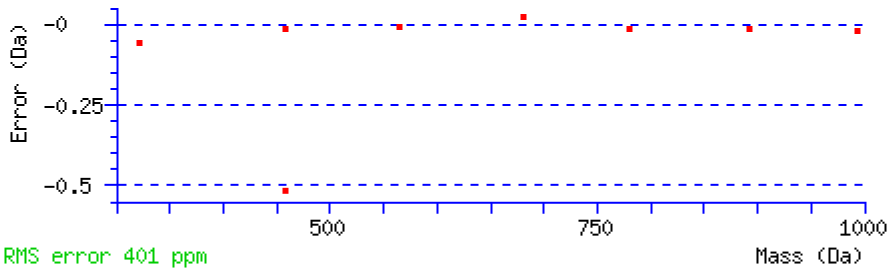
Match to Query 564143: 1235.600608 from(618.807580,2+) rtinseconds(2620) index(687579)
Title: Locus:1.1.1.1669.26
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

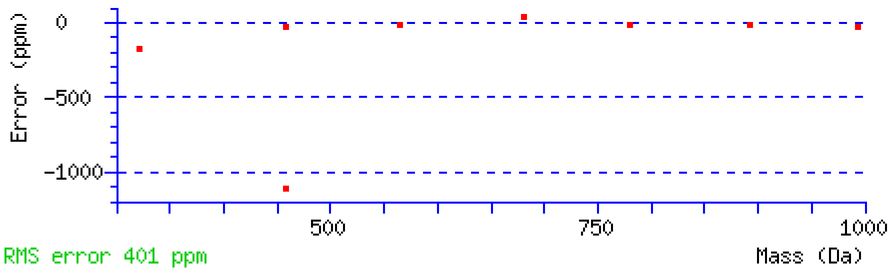
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1235.603394
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 42 **Expect:** 0.0009
Matches : 8/116 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	116.034219	58.520748			98.023654	49.515465	D							11
2	244.092797	122.550037	227.066248	114.036762	226.082232	113.544754	Q	1121.583716	561.295496	1104.557167	552.782222	1103.573151	552.290214	10
3	345.140476	173.073876	328.113927	164.560602	327.129911	164.068594	T	***993.525138***	497.266207	976.498589	488.752933	975.514573	488.260925	9
4	458.224540	229.615908	441.197991	221.102634	440.213975	220.610626	I	***892.477459***	446.742368	875.450910	438.229093	874.466894	437.737085	8
5	557.292954	279.150115	540.266405	270.636841	539.282389	270.144833	V	***779.393395***	390.200336	762.366846	381.687061	761.382830	381.195053	7
6	672.319897	336.663587	655.293348	328.150312	654.309332	327.658304	D	***680.324981***	340.666129	663.298432	332.152854	662.314416	331.660846	6
7	769.372661	385.189969	752.346112	376.676694	751.362096	376.184686	P	***565.298038***	283.152657	548.271489	274.639383	547.287473	274.147375	5
8	916.441075	458.724176	899.414526	450.210901	898.430510	449.718893	F	468.245274	234.626275	451.218725	226.113001	450.234709	225.620993	4
9	1003.473103	502.240190	986.446554	493.726915	985.462538	493.234907	S	***321.176860***	161.092068	304.150311	152.578794	303.166295	152.086786	3
10	1090.505131	545.756204	1073.478582	537.242929	1072.494566	536.750921	S	234.144832	117.576054	217.118283	109.062780	216.134267	108.570772	2
11							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of DQTIVDPFSSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.6	1235.603394	-0.002786	DQTIVDPFSSK

Mascot: http://www.matrixscience.com/

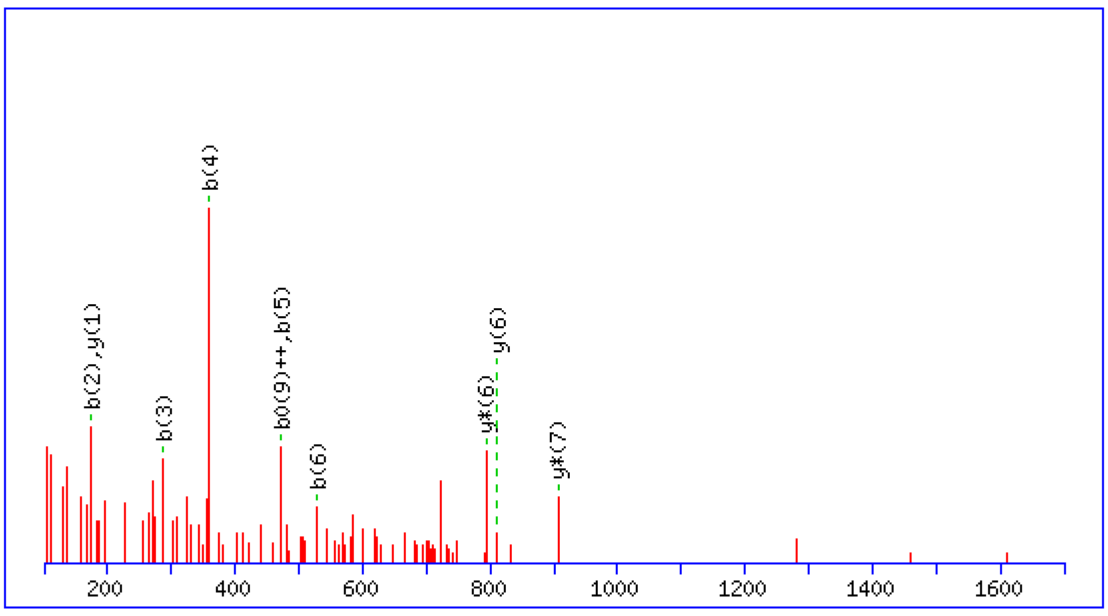
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SSLAPGVWFFR**
Found in **SPX2_HUMAN**, Sugar phosphate exchanger 2 OS=Homo sapiens GN=SLC37A2 PE=2 SV=2

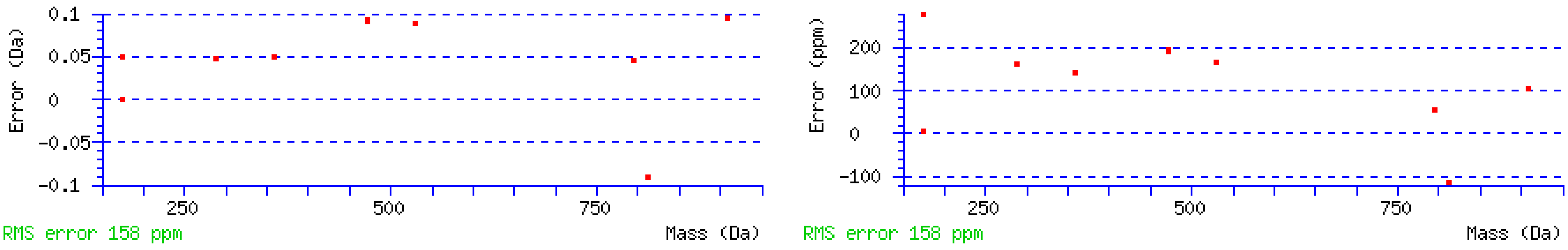
Match to Query 33792: 1281.640632 from(428.220820,3+) rtinseconds(1721) index(16716)
Title: Locus:1.1.1.2086.7
Data file 2011-11-10 - TFD - EP 3-1.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1281.650620
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P5 : Oxidation (P)
Ions Score: 41 **Expect:** 0.00086
Matches : 10/82 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	S							11
2	*175.071332*	88.039304	157.060767	79.034021	S	1195.625856	598.316566	1178.599307	589.803292	1177.615291	589.311283	10
3	*288.155396*	144.581336	270.144831	135.576054	L	1108.593828	554.800552	1091.567279	546.287278			9
4	*359.192510*	180.099893	341.181945	171.094611	A	995.509764	498.258520	978.483215	489.745245			8
5	*472.240189*	236.623733	454.229624	227.618450	P	924.472650	462.739963	907.446101	454.226688			7
6	*529.261653*	265.134465	511.251088	256.129182	G	811.424971	406.216123	794.398422	397.702849			6
7	628.330067	314.668672	610.319502	305.663389	V	754.403507	377.705391	737.376958	369.192117			5
8	814.409380	407.708328	796.398815	398.703046	W	655.335093	328.171184	638.308544	319.657910			4
9	961.477794	481.242535	943.467229	472.237253	F	469.255780	235.131528	452.229231	226.618253			3
10	1108.546208	554.776742	1090.535643	545.771459	F	322.187366	161.597321	305.160817	153.084046			2
11					R	175.118952	88.063114	158.092403	79.549839			1



NCBI **BLAST** search of SSLAPGVWFFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.7	1281.650620	-0.009988	SSLAPGVWFFR
24.9	1281.638672	0.001960	MKYENELALR
6.9	1281.649933	-0.009301	AQLPSAQMPAPR
6.9	1281.631317	0.009315	DSQLHLDDALR
6.9	1281.649918	-0.009286	MQYIERSALR
5.3	1281.649933	-0.009301	KFMAASVASTNR
4.9	1281.646591	-0.005959	WHQVETTPLR
4.1	1281.647446	-0.006814	MMLIPTHHFR
3.8	1281.631332	0.009300	SVDIHDSIQPR
3.6	1281.631332	0.009300	AGSPAAGPPLQPR

Mascot: http://www.matrixscience.com/

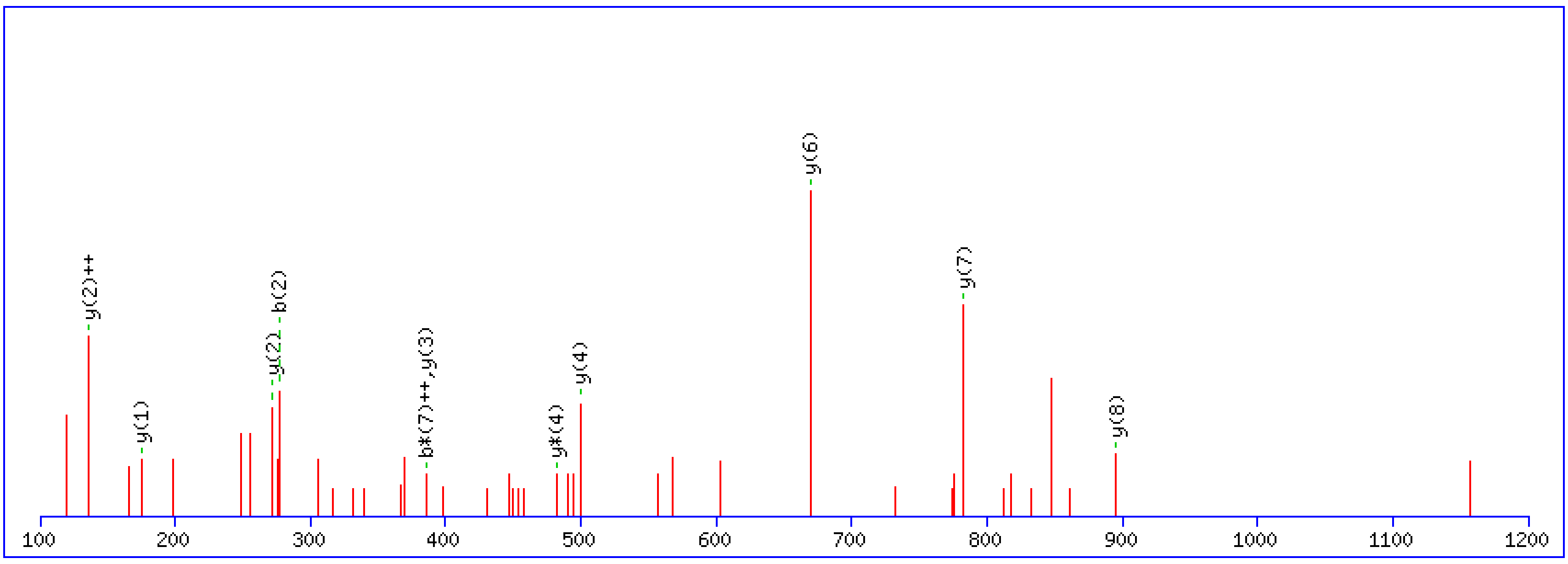
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YLLGLNLPR**
Found in **S26A2_HUMAN**, Sulfate transporter OS=Homo sapiens GN=SLC26A2 PE=1 SV=2

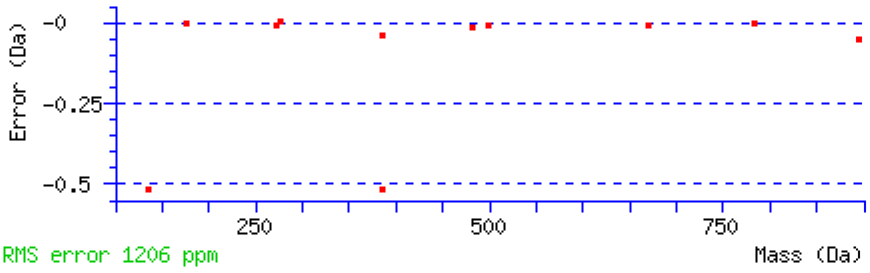
Match to Query 12394: 1057.632448 from(529.823500,2+) rtinseconds(3157) index(44463)
Title: Locus:1.1.1.1579.4
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 2.mgf

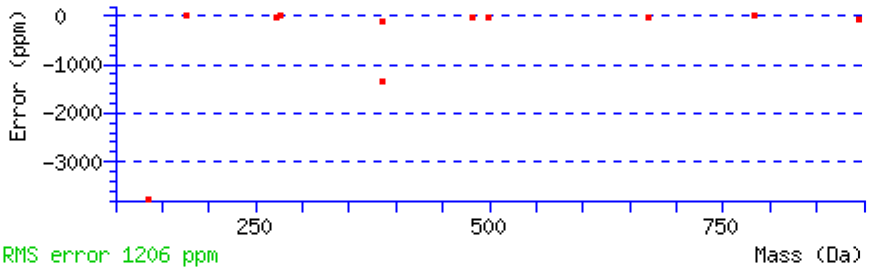
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1057.628387
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 38 **Expect:** 0.00068
Matches : 11/54 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	164.070605	82.538940			Y					9
2	277.154669	139.080973			L	***895.572363***	448.289820	878.545814	439.776545	8
3	390.238733	195.623005			L	***782.488299***	391.747788	765.461750	383.234513	7
4	447.260197	224.133737			G	***669.404235***	335.205756	652.377686	326.692481	6
5	560.344261	280.675769			L	612.382771	306.695024	595.356222	298.181749	5
6	674.387188	337.697232	657.360639	329.183958	N	***499.298707***	250.152991	482.272158	241.639717	4
7	787.471252	394.239264	770.444703	385.725990	L	***385.255780***	193.131528	368.229231	184.618253	3
8	884.524016	442.765646	867.497467	434.252372	P	***272.171716***	136.589496	255.145167	128.076221	2
9					R	***175.118952***	88.063114	158.092403	79.549839	1





NCBI **BLAST** search of YLLGLNLPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.5	1057.628387	0.004061	YLLGLNLPR

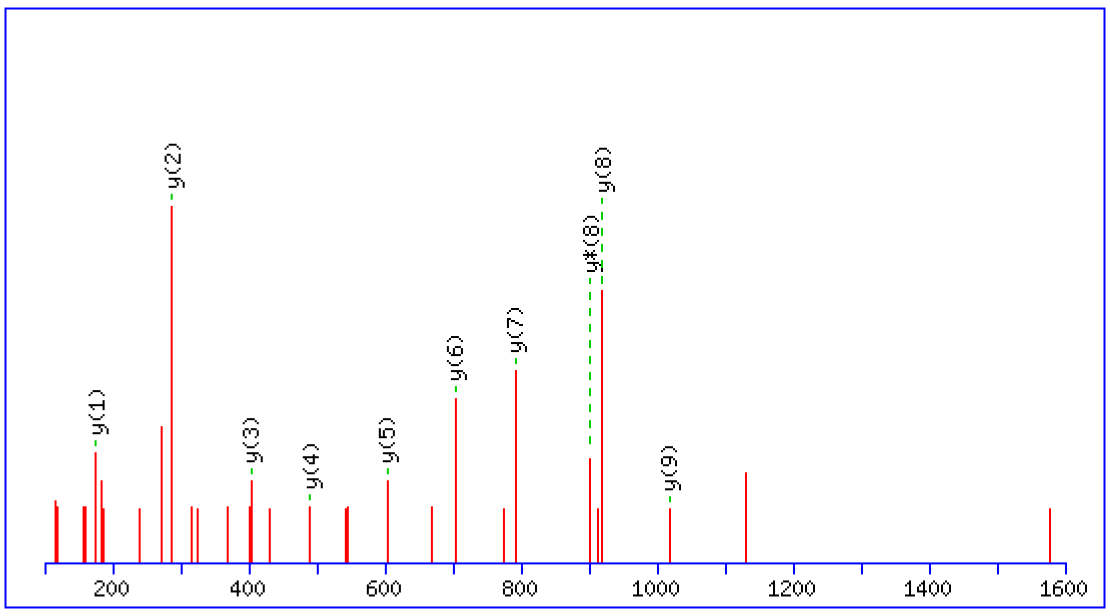
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LVQSTLSDLR**
Found in **SRXN1_HUMAN**, Sulfiredoxin-1 OS=Homo sapiens GN=SRXN1 PE=1 SV=2

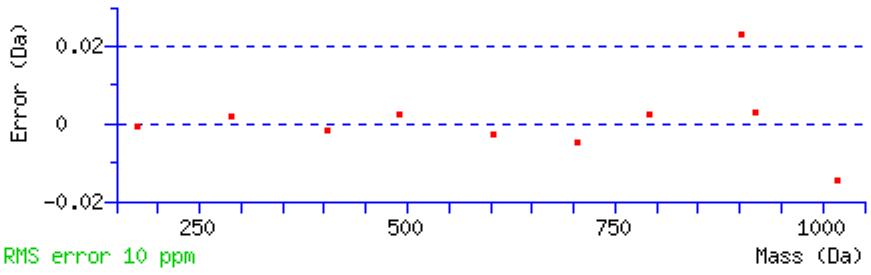
Match to Query 22786: 1130.631428 from(566.322990,2+) rtinseconds(2119) index(19262)
Title: Locus:1.1.1.2214.27
Data file 2011-11-10 - TFD - EP 3-7.mgf

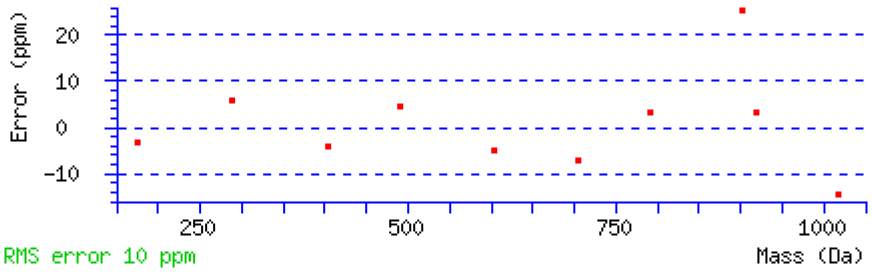
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1600] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1130.629532
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 105  Expect: 2e-010
Matches : 10/94 fragment ions using 10 most intense peaks   (help)
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							10
2	213.159754	107.083515					V	***1018.552750***	509.780013	1001.526201	501.266738	1000.542185	500.774730	9
3	341.218332	171.112804	324.191783	162.599529			Q	***919.484336***	460.245806	902.457787	451.732531	901.473771	451.240523	8
4	428.250360	214.628818	411.223811	206.115543	410.239795	205.623535	S	***791.425758***	396.216517	774.399209	387.703242	773.415193	387.211234	7
5	529.298039	265.152658	512.271490	256.639383	511.287474	256.147375	T	***704.393730***	352.700503	687.367181	344.187229	686.383165	343.695221	6
6	642.382103	321.694690	625.355554	313.181415	624.371538	312.689407	L	***603.346051***	302.176664	586.319502	293.663389	585.335486	293.171381	5
7	729.414131	365.210704	712.387582	356.697429	711.403566	356.205421	S	***490.261987***	245.634631	473.235438	237.121357	472.251422	236.629349	4
8	844.441074	422.724175	827.414525	414.210900	826.430509	413.718892	D	***403.229959***	202.118617	386.203410	193.605343	385.219394	193.113335	3
9	957.525138	479.266207	940.498589	470.752932	939.514573	470.260924	L	***288.203016***	144.605146	271.176467	136.091871			2
10							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LVQSTLSDLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
105.0	1130.629532	0.001896	LVQSTLSDLR
28.9	1130.640762	-0.009334	RAPSTTLTLR
15.5	1130.623642	0.007786	LAAFPWAALR
9.1	1130.622986	0.008442	LTRGLCIER
8.8	1130.629517	0.001911	LSNDITSILR
8.7	1130.629532	0.001896	LVQTQGTKEK
8.6	1130.622971	0.008457	LREINSMIR
8.1	1130.622986	0.008442	LVEALRQMR
8.1	1130.629517	0.001911	LVETSLKGER
7.2	1130.630371	0.001057	LQNIMMLLR

Mascot: http://www.matrixscience.com/

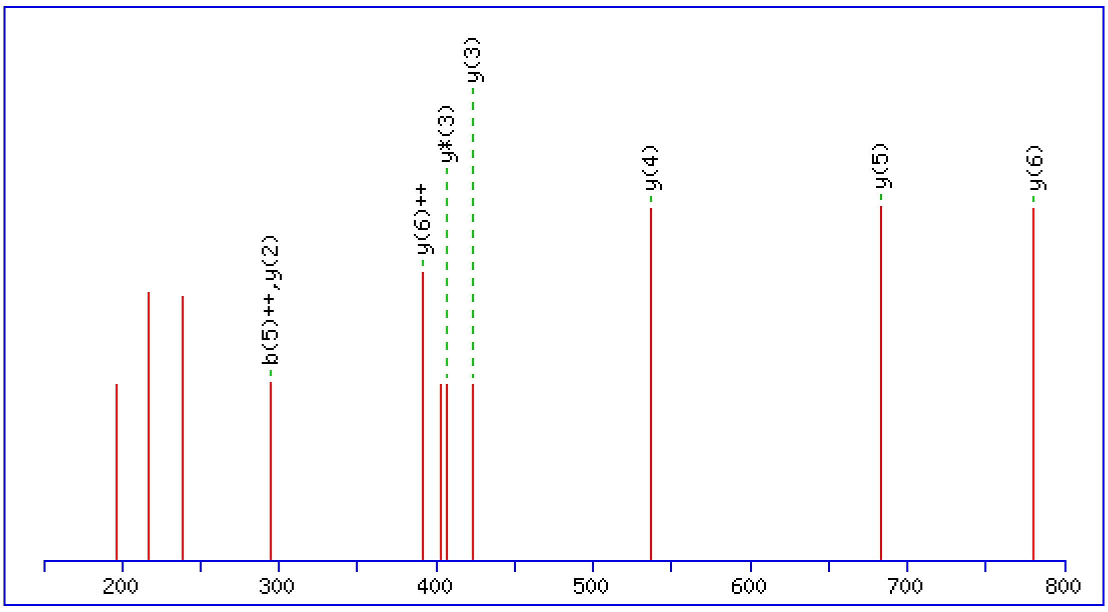
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VPFLEFK**
Found in **ST1A1_HUMAN**, Sulfotransferase 1A1 OS=Homo sapiens GN=SULT1A1 PE=1 SV=3

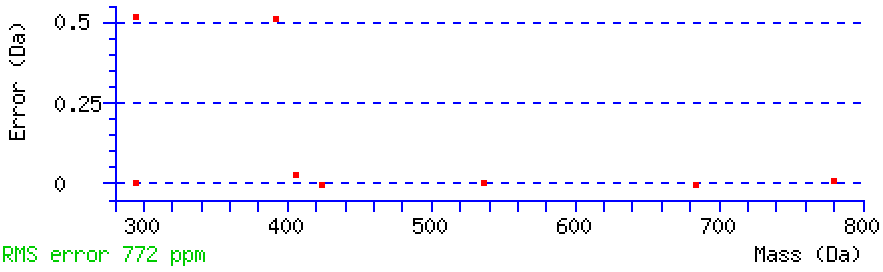
Match to Query 5545: 878.496788 from(440.255670,2+) rtinseconds(3004) index(36614)
Title: Locus:1.1.1.2762.4
Data file 2011-11-10 - TFD - EP 3-5.mgf

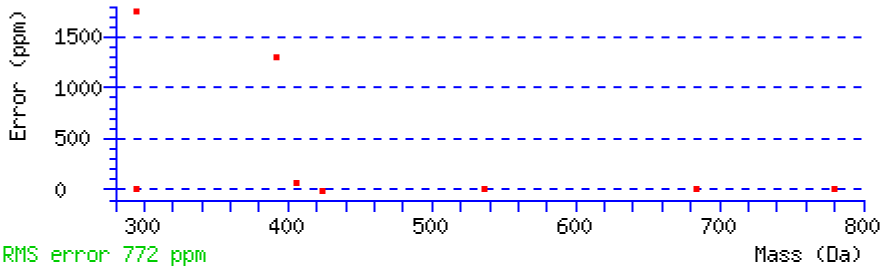
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 878.490189
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.00041
Matches : 8/48 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	100.075690	50.541483			V							7
2	197.128454	99.067865			P	***780.429053***	390.718165	763.402504	382.204890	762.418488	381.712882	6
3	344.196868	172.602072			F	***683.376289***	342.191783	666.349740	333.678508	665.365724	333.186500	5
4	457.280932	229.144104			L	***536.307875***	268.657576	519.281326	260.144301	518.297310	259.652293	4
5	586.323525	293.665401	568.312960	284.660118	E	***423.223811***	212.115543	406.197262	203.602269	405.213246	203.110261	3
6	733.391939	367.199608	715.381374	358.194325	F	***294.181218***	147.594247	277.154669	139.080972			2
7					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of VPFLEFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.1	878.490189	0.006599	VPFLEFK
3.1	878.497391	-0.000603	VPAATPAPR

Mascot: http://www.matrixscience.com/

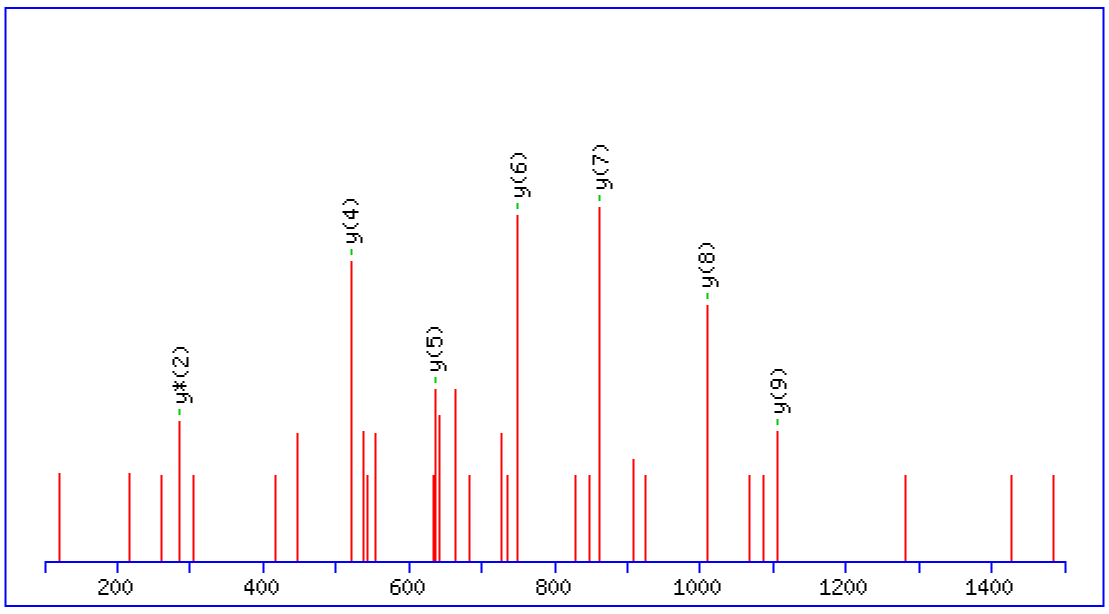
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EYPFILDAFQR**
Found in **SK2L2_HUMAN**, Superkiller viralicidic activity 2-like 2 OS=Homo sapiens GN=SKIV2L2 PE=1 SV=3

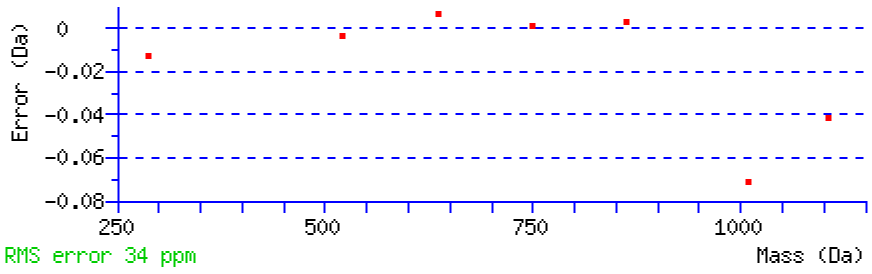
Match to Query 41529: 1397.700828 from(699.857690,2+) rtinseconds(3881) index(56773)
Title: Locus:1.1.1.2809.31
Data file 2011-11-10 - TFD - EP 4-1.mgf

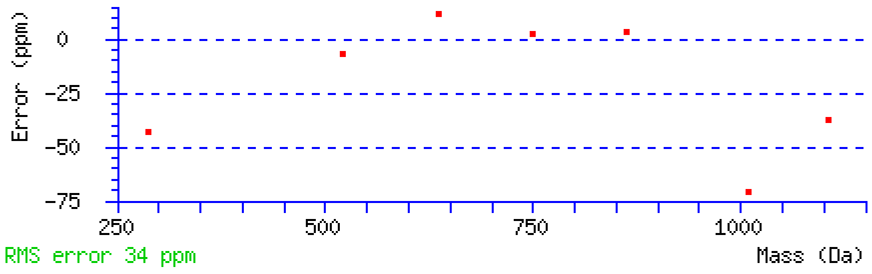
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1397.697937
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 42 **Expect:** 0.00055
Matches : 7/94 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	E							11
2	293.113198	147.060237			275.102633	138.054955	Y	1269.662636	635.334956	1252.636087	626.821681	1251.652071	626.329673	10
3	390.165962	195.586619			372.155397	186.581336	P	***1106.599307***	553.803292	1089.572758	545.290017	1088.588742	544.798009	9
4	537.234376	269.120826			519.223811	260.115544	F	***1009.546543***	505.276909	992.519994	496.763635	991.535978	496.271627	8
5	650.318440	325.662858			632.307875	316.657576	I	***862.478129***	431.742703	845.451580	423.229428	844.467564	422.737420	7
6	763.402504	382.204890			745.391939	373.199608	L	***749.394065***	375.200671	732.367516	366.687396	731.383500	366.195388	6
7	878.429447	439.718362			860.418882	430.713079	D	***636.310001***	318.658639	619.283452	310.145364	618.299436	309.653356	5
8	949.466561	475.236919			931.455996	466.231636	A	***521.283058***	261.145167	504.256509	252.631892			4
9	1096.534975	548.771126			1078.524410	539.765843	F	450.245944	225.626610	433.219395	217.113335			3
10	1224.593553	612.800414	1207.567004	604.287140	1206.582988	603.795132	Q	303.177530	152.092403	286.150981	143.579128			2
11							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of EYPFILDAFQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.8	1397.697937	0.002891	EYPFILDAFQR
6.8	1397.707825	-0.006997	VEEYITPEKFK
2.6	1397.693939	0.006889	AGSPPPPPPPPAR
0.7	1397.693939	0.006889	AGSPPPPPPPPAR

Mascot: http://www.matrixscience.com/

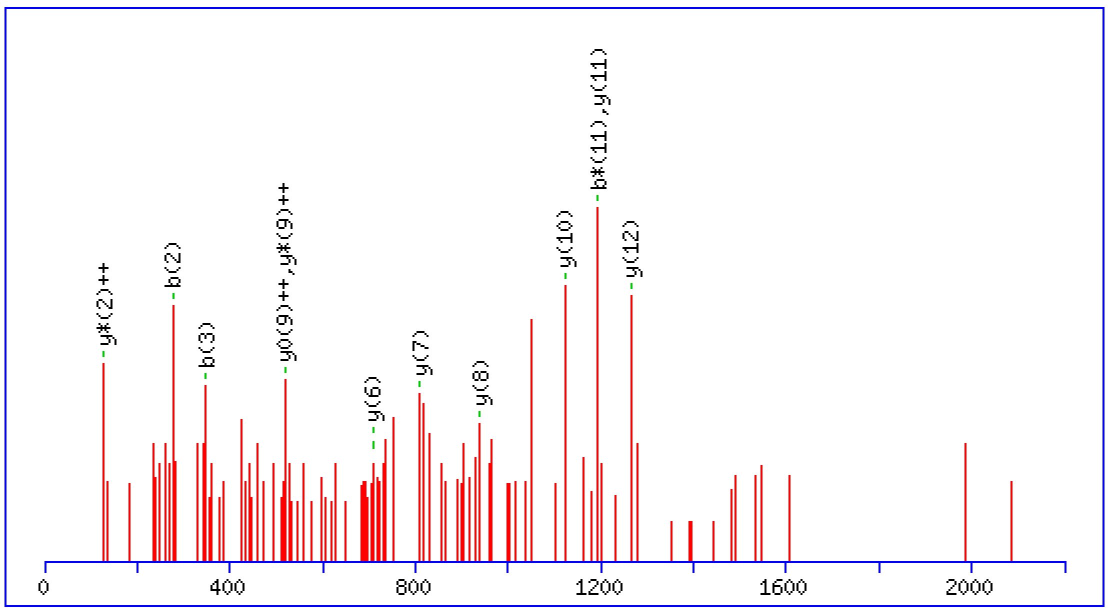
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NYAAALETFTEGQK**
Found in **SUGT1_HUMAN**, Suppressor of G2 allele of SKP1 homolog OS=Homo sapiens GN=SUGT1 PE=1 SV=3

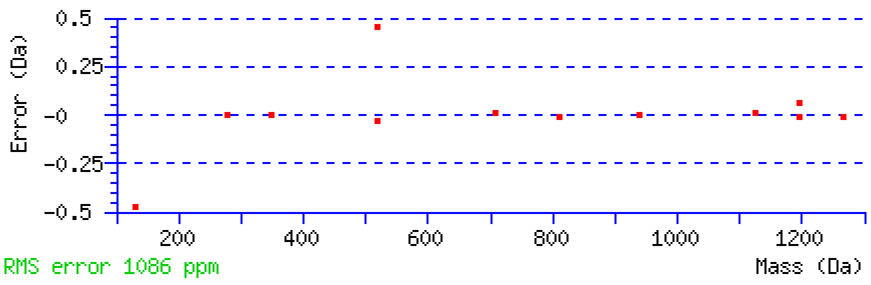
Match to Query 48696: 1541.723268 from(771.868910,2+) rtinseconds(2971) index(40377)
Title: Locus:1.1.1.2545.41
Data file 2011-11-12 - TFD - EP 5-4.mgf

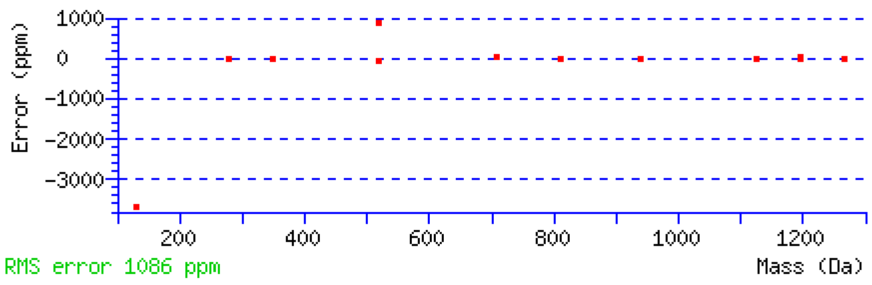
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1541.736160
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 37 **Expect:** 0.00043
Matches : 12/138 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			N							14
2	**278.113532**	139.560404	261.086983	131.047130			Y	1428.700539	714.853908	1411.673990	706.340633	1410.689974	705.848625	13
3	**349.150646**	175.078961	332.124097	166.565687			A	***1265.637210***	633.322243	1248.610661	624.808969	1247.626645	624.316961	12
4	420.187760	210.597518	403.161211	202.084243			A	***1194.600096***	597.803686	1177.573547	589.290412	1176.589531	588.798404	11
5	491.224874	246.116075	474.198325	237.602800			A	***1123.562982***	562.285129	1106.536433	553.771855	1105.552417	553.279847	10
6	604.308938	302.658107	587.282389	294.144833			L	1052.525868	526.766572	1035.499319	518.253298	1034.515303	517.761290	9
7	733.351531	367.179404	716.324982	358.666129	715.340966	358.174121	E	***939.441804***	470.224540	922.415255	461.711266	921.431239	461.219258	8
8	834.399210	417.703243	817.372661	409.189969	816.388645	408.697961	T	***810.399211***	405.703244	793.372662	397.189969	792.388646	396.697961	7
9	981.467624	491.237450	964.441075	482.724176	963.457059	482.232168	F	***709.351532***	355.179404	692.324983	346.666130	691.340967	346.174122	6
10	1082.515303	541.761289	1065.488754	533.248015	1064.504738	532.756007	T	562.283118	281.645197	545.256569	273.131923	544.272553	272.639915	5
11	1211.557896	606.282586	1194.531347	597.769312	1193.547331	597.277304	E	461.235439	231.121358	444.208890	222.608083	443.224874	222.116075	4
12	1268.579360	634.793318	1251.552811	626.280044	1250.568795	625.788035	G	332.192846	166.600061	315.166297	158.086787			3
13	1396.637938	698.822607	1379.611389	690.309333	1378.627373	689.817325	Q	275.171382	138.089329	258.144833	129.576055			2
14							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of NYAAALETFTEGQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.2	1541.736160	-0.012892	NYAAALETFTEGQK

Mascot: http://www.matrixscience.com/

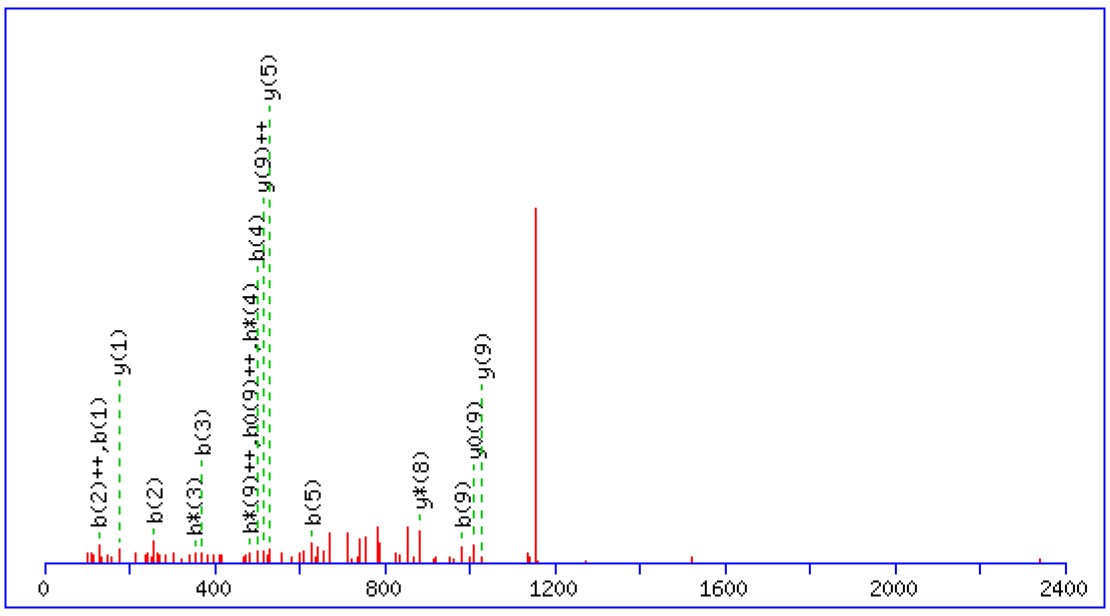
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QELEQALGIR**
Found in **SMRD1_HUMAN**, SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 1 OS=Homo sapiens GN=SMARCD1 PE=1 SV=2

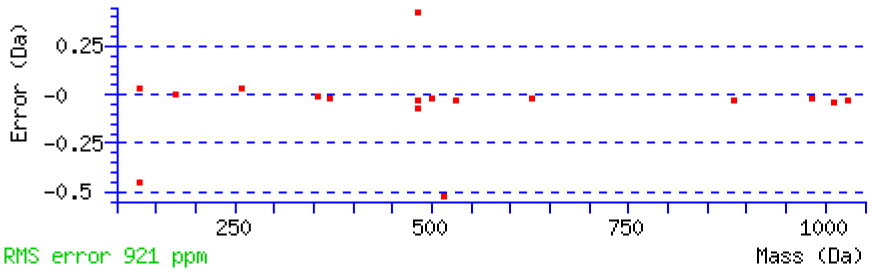
Match to Query 23390: 1155.618108 from(578.816330,2+) rtinseconds(1666) index(11476)
Title: Locus:1.1.1.2257.40
Data file 2011-11-10 - TFD - EP 3-5.mgf

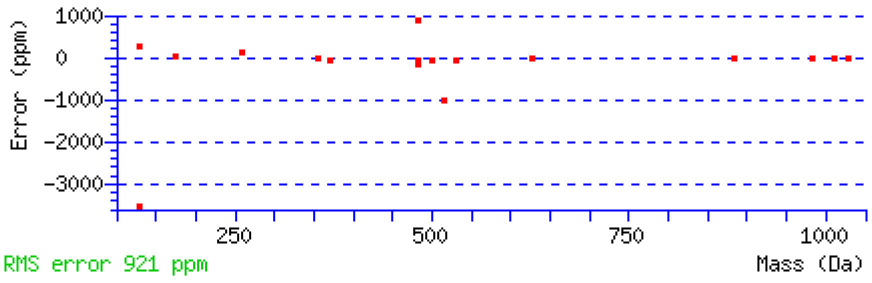
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1155.624756
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 37  Expect: 0.0026
Matches : 17/94 fragment ions using 22 most intense peaks    (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	*129.065854*	65.036565	112.039305	56.523291			Q							10
2	*258.108447*	129.557862	241.081898	121.044587	240.097882	120.552579	E	**1028.573486**	514.790381	1011.546937	506.277107	1010.562921	505.785099	9
3	*371.192511*	186.099894	354.165962	177.586619	353.181946	177.094611	L	899.530893	450.269085	882.504344	441.755810	881.520328	441.263802	8
4	*500.235104*	250.621190	483.208555	242.107916	482.224539	241.615908	E	786.446829	393.727053	769.420280	385.213778	768.436264	384.721770	7
5	*628.293682*	314.650479	611.267133	306.137205	610.283117	305.645197	Q	657.404236	329.205756	640.377687	320.692482			6
6	699.330796	350.169036	682.304247	341.655762	681.320231	341.163754	A	**529.345658**	265.176467	512.319109	256.663193			5
7	812.414860	406.711068	795.388311	398.197794	794.404295	397.705786	L	458.308544	229.657910	441.281995	221.144635			4
8	869.436324	435.221800	852.409775	426.708526	851.425759	426.216518	G	345.224480	173.115878	328.197931	164.602603			3
9	*982.520388*	491.763832	965.493839	483.250558	964.509823	482.758550	I	288.203016	144.605146	271.176467	136.091871			2
10							R	**175.118952**	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of QELEQALGIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.8	1155.624756	-0.006648	QELEQALGIR
18.2	1155.610840	0.007268	QQQQEALRR
15.2	1155.618240	-0.000132	AGKPPCGATKR
14.3	1155.610855	0.007253	GAGAGLSRPGSAR
13.4	1155.624771	-0.006663	KEIPSQAVPR
12.6	1155.624771	-0.006663	SSPQLDPLRK
12.4	1155.624756	-0.006648	ELEQQLAAVR
12.3	1155.624771	-0.006663	SSPQLDPLRK
10.0	1155.607010	0.011098	CGIPEALVQR
9.2	1155.607010	0.011098	QKPCDLPLR

Mascot: http://www.matrixscience.com/

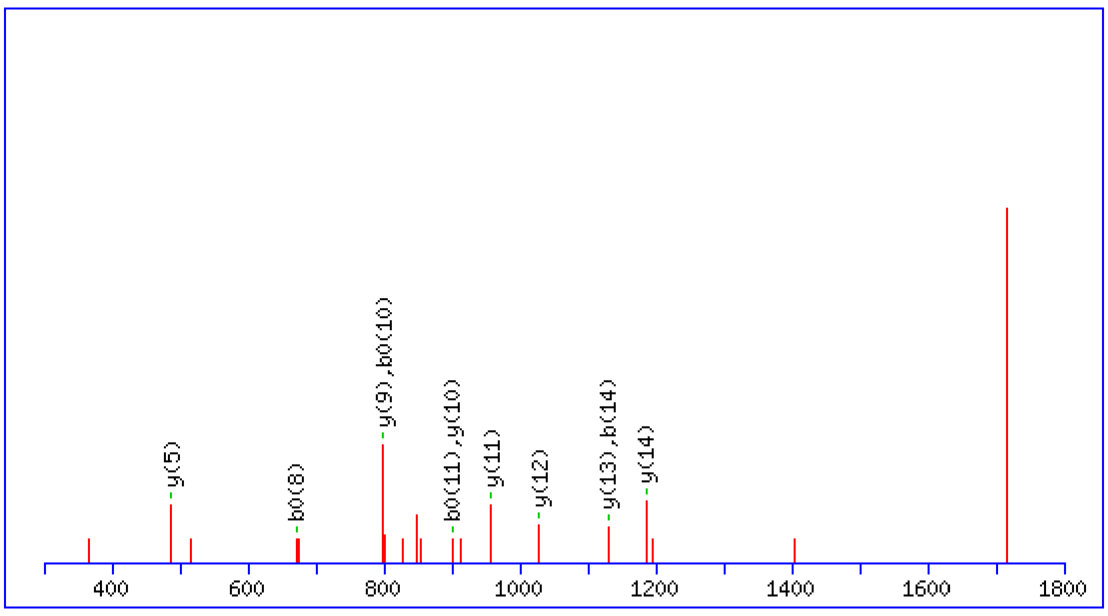
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AEGDSAGTAGTPGGTPAGDK**
Found in **SMRD2_HUMAN**, SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 2 OS=Homo sapiens GN=SMARCD2 PE=1 SV=3

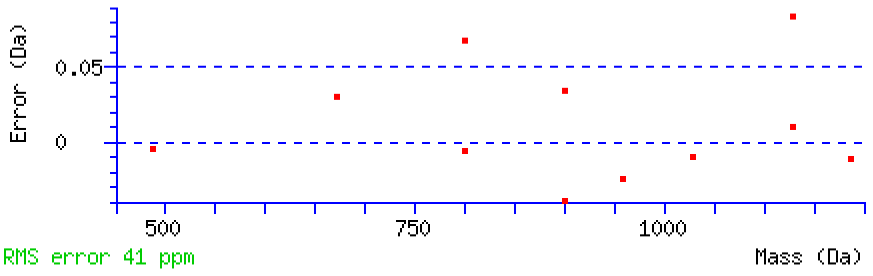
Match to Query 966130: 1715.764828 from(858.889690,2+) rtinseconds(1045) index(158856)
Title: Locus:1.1.1.1082.41
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

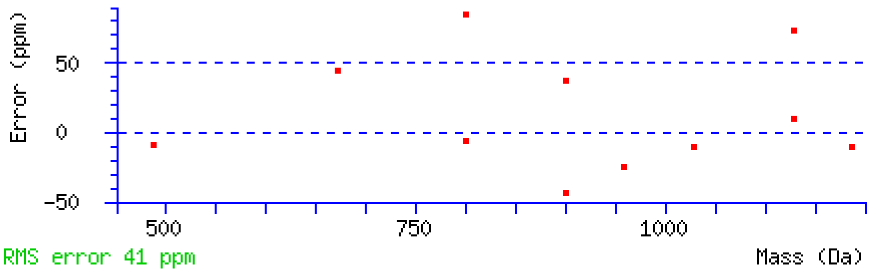
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1715.759857
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 43  Expect: 0.00017
Matches : 11/186 fragment ions using 14 most intense peaks   (help)
```

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	72.044390	36.525833			A							20
2	201.086983	101.047130	183.076418	92.041847	E	1645.730002	823.368639	1628.703453	814.855365	1627.719437	814.363357	19
3	258.108447	129.557862	240.097882	120.552579	G	1516.687409	758.847343	1499.660860	750.334068	1498.676844	749.842060	18
4	373.135390	187.071333	355.124825	178.066051	D	1459.665945	730.336611	1442.639396	721.823336	1441.655380	721.331328	17
5	460.167418	230.587347	442.156853	221.582065	S	1344.639002	672.823139	1327.612453	664.309865	1326.628437	663.817857	16
6	531.204532	266.105904	513.193967	257.100622	A	1257.606974	629.307125	1240.580425	620.793851	1239.596409	620.301843	15
7	588.225996	294.616636	570.215431	285.611354	G	***1186.569860***	593.788568	1169.543311	585.275294	1168.559295	584.783286	14
8	689.273675	345.140476	671.263110	336.135193	T	***1129.548396***	565.277836	1112.521847	556.764562	1111.537831	556.272554	13
9	760.310789	380.659033	742.300224	371.653750	A	***1028.500717***	514.753997	1011.474168	506.240722	1010.490152	505.748714	12
10	817.332253	409.169765	799.321688	400.164482	G	***957.463603***	479.235440	940.437054	470.722165	939.453038	470.230157	11
11	918.379932	459.693604	900.369367	450.688322	T	***900.442139***	450.724708	883.415590	442.211433	882.431574	441.719425	10
12	1015.432696	508.219986	997.422131	499.214704	P	***799.394460***	400.200868	782.367911	391.687594	781.383895	391.195586	9
13	1072.454160	536.730718	1054.443595	527.725436	G	702.341696	351.674486	685.315147	343.161212	684.331131	342.669204	8
14	1129.475624	565.241450	1111.465059	556.236168	G	645.320232	323.163754	628.293683	314.650480	627.309667	314.158472	7
15	1230.523303	615.765290	1212.512738	606.760007	T	588.298768	294.653022	571.272219	286.139748	570.288203	285.647740	6
16	1327.576067	664.291672	1309.565502	655.286389	P	***487.251089***	244.129182	470.224540	235.615908	469.240524	235.123900	5
17	1398.613181	699.810229	1380.602616	690.804946	A	390.198325	195.602800	373.171776	187.089526	372.187760	186.597518	4
18	1455.634645	728.320961	1437.624080	719.315678	G	319.161211	160.084243	302.134662	151.570969	301.150646	151.078961	3
19	1570.661588	785.834432	1552.651023	776.829150	D	262.139747	131.573512	245.113198	123.060237	244.129182	122.568229	2
20					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of AEGDSAGTAGTPGGTPAGDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.7	1715.759857	0.004971	AEGDSAGTAGTPGGTPAGDK
2.3	1715.775970	-0.011142	ECCRFFGDNGLTLK
0.3	1715.778458	-0.013630	PAAALNAAGSVHSPSTSM

Mascot: http://www.matrixscience.com/

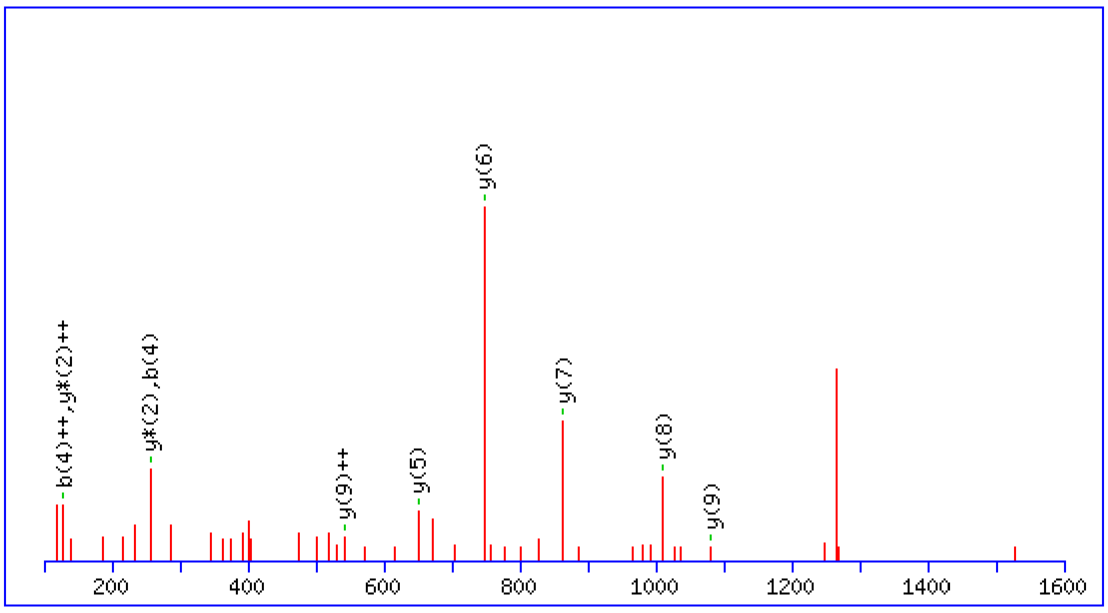
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AGGAFDPYTLVR**
Found in **SNG1_HUMAN**, Synaptogyrin-1 OS=Homo sapiens GN=SYNGR1 PE=1 SV=2

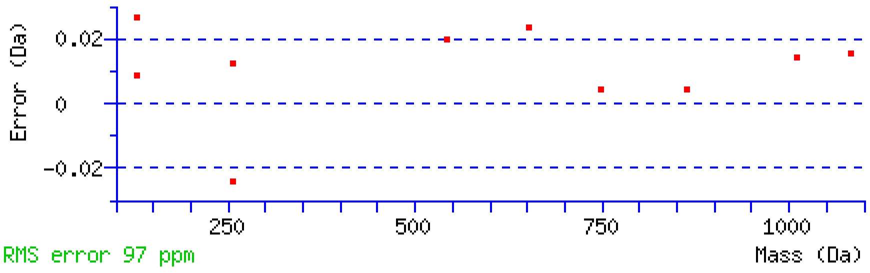
Match to Query 34368: 1265.640668 from(633.827610,2+) rtinseconds(2972) index(39232)
Title: Locus:1.1.1.2283.32
Data file 2011-11-12 - TFD - EP 6-6.mgf

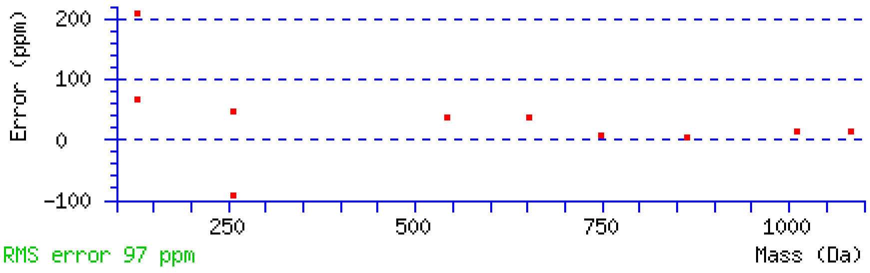
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1265.640442
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 37 **Expect:** 0.0025
Matches : 11/94 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			A							12
2	**129.065854**	65.036565			G	1195.610601	598.308939	1178.584052	589.795664	1177.600036	589.303656	11
3	186.087318	93.547297			G	1138.589137	569.798207	1121.562588	561.284932	1120.578572	560.792924	10
4	**257.124432**	129.065854			A	***1081.567673***	541.287475	1064.541124	532.774200	1063.557108	532.282192	9
5	404.192846	202.600061			F	***1010.530559***	505.768918	993.504010	497.255643	992.519994	496.763635	8
6	519.219789	260.113533	501.209224	251.108250	D	***863.462145***	432.234711	846.435596	423.721436	845.451580	423.229428	7
7	616.272553	308.639915	598.261988	299.634632	P	***748.435202***	374.721239	731.408653	366.207965	730.424637	365.715957	6
8	779.335882	390.171579	761.325317	381.166297	Y	***651.382438***	326.194857	634.355889	317.681583	633.371873	317.189575	5
9	880.383561	440.695419	862.372996	431.690136	T	488.319109	244.663192	471.292560	236.149918	470.308544	235.657910	4
10	993.467625	497.237451	975.457060	488.232168	L	387.271430	194.139353	370.244881	185.626078			3
11	1092.536039	546.771658	1074.525474	537.766375	V	274.187366	137.597321	257.160817	129.084046			2
12					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of AGGAFDPYTLVR
(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	1265.640442	0.000226	AGGAFDPYTLVR

Mascot: http://www.matrixscience.com/

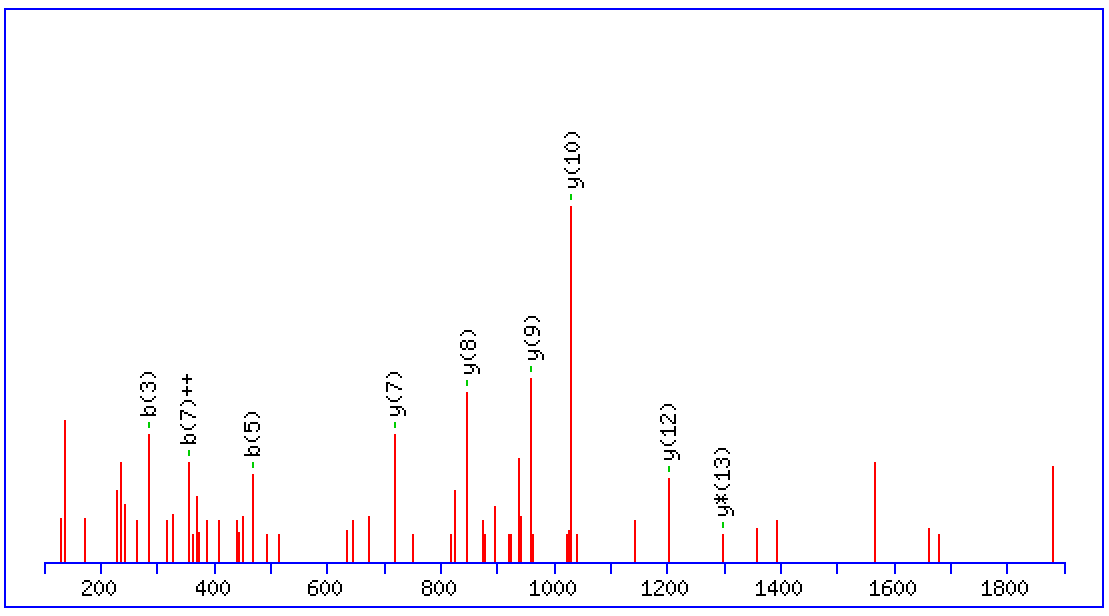
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILGLAIESQDAGIK**
Found in **SNP23_HUMAN**, Synaptosomal-associated protein 23 OS=Homo sapiens GN=SNAP23 PE=1 SV=1

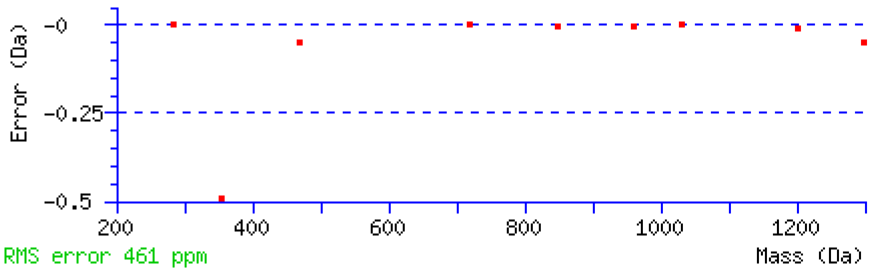
Match to Query 42372: 1426.791248 from(714.402900,2+) rtinseconds(2933) index(38718)
Title: Locus:1.1.1.2431.41
Data file 2011-11-10 - TFD - EP 4-5.mgf

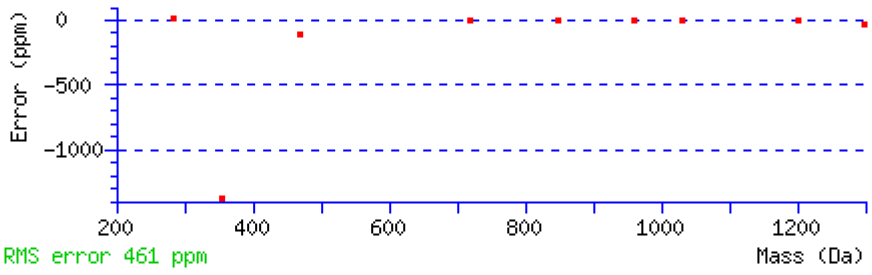
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1426.803116
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 34  Expect: 0.0046
Matches : 9/120 fragment ions using 12 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					I							14
2	227.175404	114.091340					L	1314.726358	657.866817	1297.699809	649.353543	1296.715793	648.861535	13
3	**284.196868**	142.602072					G	***1201.642294***	601.324785	1184.615745	592.811511	1183.631729	592.319503	12
4	397.280932	199.144104					L	1144.620830	572.814053	1127.594281	564.300779	1126.610265	563.808771	11
5	**468.318046**	234.662661					A	***1031.536766***	516.272021	1014.510217	507.758746	1013.526201	507.266738	10
6	581.402110	291.204693					I	***960.499652***	480.753464	943.473103	472.240189	942.489087	471.748181	9
7	710.444703	355.725990			692.434138	346.720707	E	***847.415588***	424.211432	830.389039	415.698157	829.405023	415.206149	8
8	797.476731	399.242004			779.466166	390.236721	S	***718.372995***	359.690136	701.346446	351.176861	700.362430	350.684853	7
9	925.535309	463.271293	908.508760	454.758018	907.524744	454.266010	Q	631.340967	316.174122	614.314418	307.660847	613.330402	307.168839	6
10	1040.562252	520.784764	1023.535703	512.271490	1022.551687	511.779482	D	503.282389	252.144832	486.255840	243.631558	485.271824	243.139550	5
11	1111.599366	556.303321	1094.572817	547.790047	1093.588801	547.298039	A	388.255446	194.631361	371.228897	186.118086			4
12	1168.620830	584.814053	1151.594281	576.300779	1150.610265	575.808771	G	317.218332	159.112804	300.191783	150.599529			3
13	1281.704894	641.356085	1264.678345	632.842811	1263.694329	632.350802	I	260.196868	130.602072	243.170319	122.088797			2
14							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of ILGLAIESQDAGIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.9	1426.803116	-0.011868	ILGLAIESQDAGIK
11.3	1426.785370	0.005878	LLQPAQVCDILK
11.1	1426.793243	-0.001995	HLAELSVPPVPPR
7.2	1426.793243	-0.001995	HLAELSVPPVPPR
7.2	1426.803986	-0.012738	QILHLITMMALK
5.8	1426.803986	-0.012738	QILHLITMMALK
4.4	1426.793228	-0.001980	VSPLAAFLASAPQR
3.1	1426.793243	-0.001995	HLAELSVPPVPPR
0.3	1426.785370	0.005878	IPGLCPDGKSILK

Mascot: http://www.matrixscience.com/

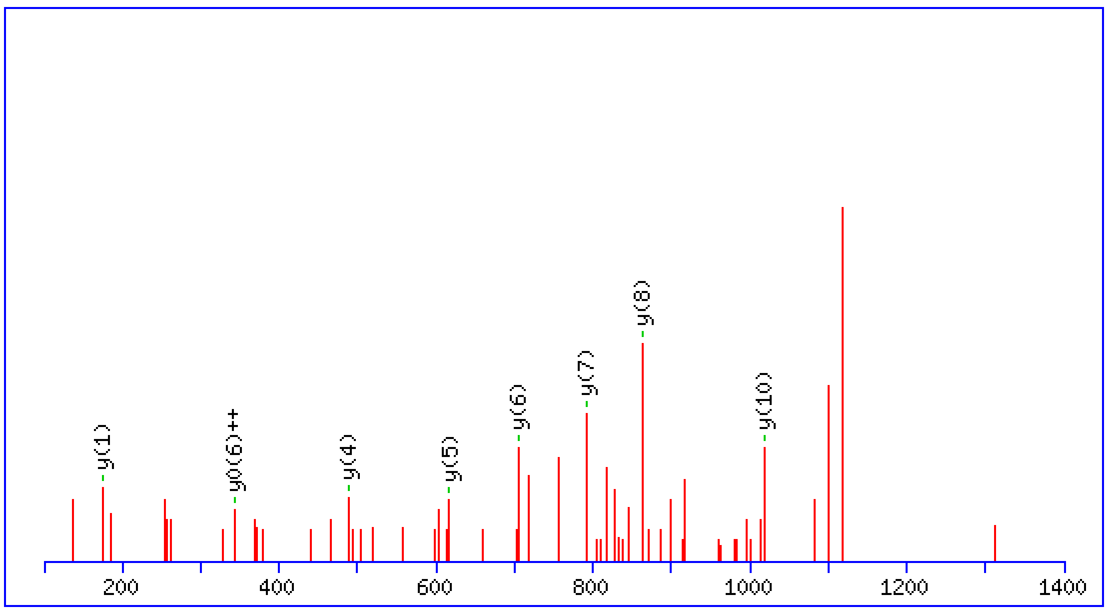
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VGVASSEELAR**
Found in **SNP29_HUMAN**, Synaptosomal-associated protein 29 OS=Homo sapiens GN=SNAP29 PE=1 SV=1

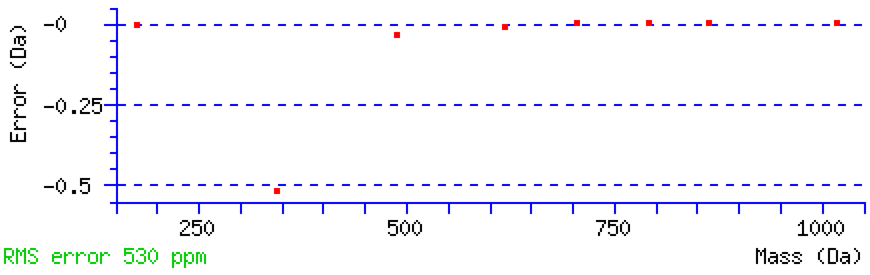
Match to Query 416426: 1116.577328 from(559.295940,2+) rtinseconds(1567) index(339117)
Title: Locus:1.1.1.934.26
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

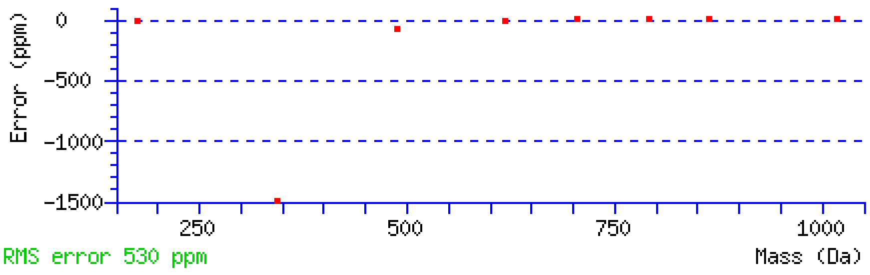
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1116.577484
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 68  Expect: 3e-006
Matches : 8/86 fragment ions using 10 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483			V							11
2	157.097154	79.052215			G	*1018.516364*	509.761820	1001.489815	501.248546	1000.505799	500.756538	10
3	256.165568	128.586422			V	961.494900	481.251088	944.468351	472.737814	943.484335	472.245806	9
4	327.202682	164.104979			A	*862.426486*	431.716881	845.399937	423.203607	844.415921	422.711599	8
5	414.234710	207.620993	396.224145	198.615711	S	*791.389372*	396.198324	774.362823	387.685050	773.378807	387.193042	7
6	501.266738	251.137007	483.256173	242.131724	S	*704.357344*	352.682310	687.330795	344.169036	686.346779	343.677028	6
7	630.309331	315.658304	612.298766	306.653021	E	*617.325316*	309.166296	600.298767	300.653022	599.314751	300.161014	5
8	759.351924	380.179600	741.341359	371.174318	E	*488.282723*	244.645000	471.256174	236.131725	470.272158	235.639717	4
9	872.435988	436.721632	854.425423	427.716350	L	359.240130	180.123703	342.213581	171.610429			3
10	943.473102	472.240189	925.462537	463.234907	A	246.156066	123.581671	229.129517	115.068397			2
11					R	*175.118952*	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of VGVASSEELAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
67.9	1116.577484	-0.000156	VGVASSEELAR
36.0	1116.577515	-0.000187	VTVVDVNESR
3.6	1116.567612	0.009716	AAPAFKGGGGPR
2.8	1116.584930	-0.007602	VTCPPTVTVK

Mascot: http://www.matrixscience.com/

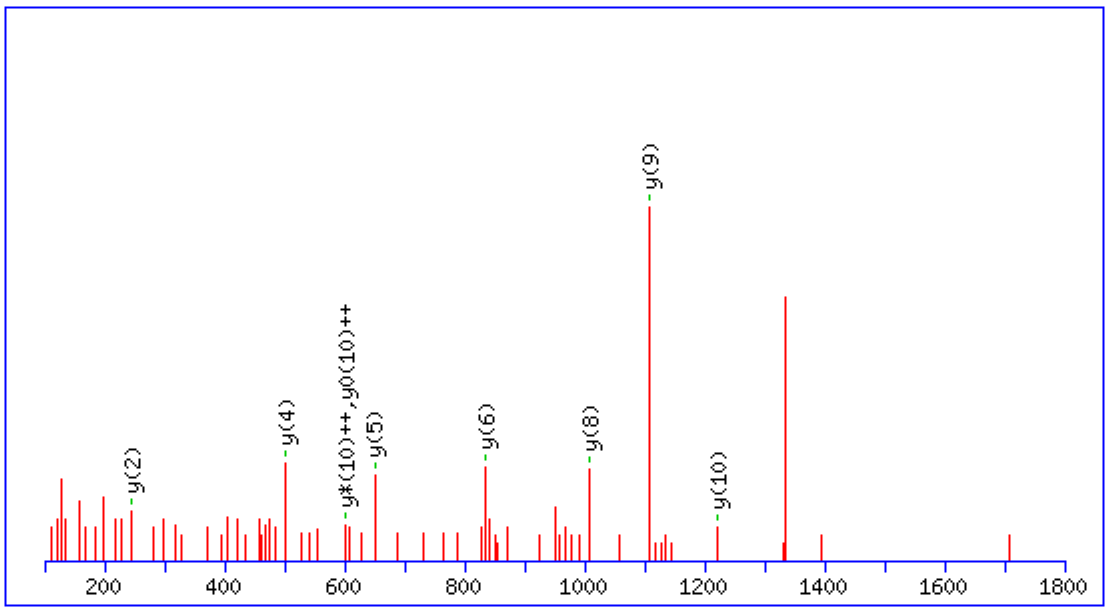
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILTGDWFQEAR**
Found in **SYTL1_HUMAN**, Synaptotagmin-like protein 1 OS=Homo sapiens GN=SYTL1 PE=1 SV=1

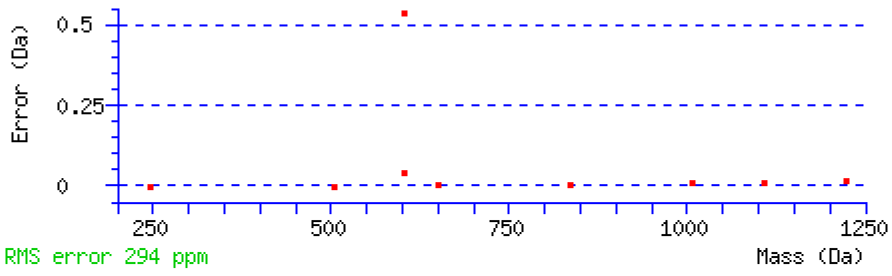
Match to Query 39543: 1334.666528 from(668.340540,2+) rtinseconds(3065) index(42076)
Title: Locus:1.1.1.2589.31
Data file 2011-11-14 - TFD - EP 8-2.mgf

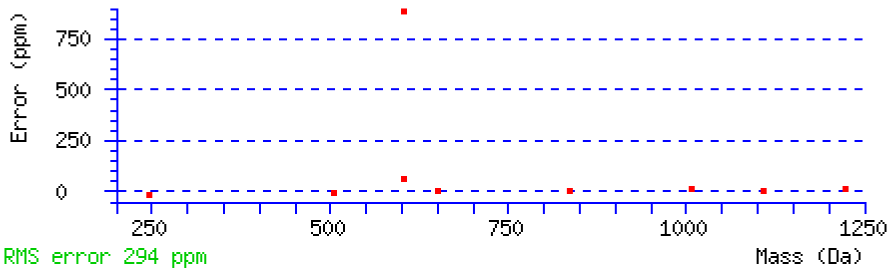
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1334.661896
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 49 **Expect:** 3.3e-005
Matches : 9/98 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					I							11
2	227.175404	114.091340					L	***1222.585114***	611.796195	1205.558565	603.282921	1204.574549	602.790913	10
3	328.223083	164.615179			310.212518	155.609897	T	***1109.501050***	555.254163	1092.474501	546.740889	1091.490485	546.248881	9
4	385.244547	193.125911			367.233982	184.120629	G	***1008.453371***	504.730324	991.426822	496.217049	990.442806	495.725041	8
5	500.271490	250.639383			482.260925	241.634100	D	951.431907	476.219592	934.405358	467.706317	933.421342	467.214309	7
6	686.350803	343.679040			668.340238	334.673757	W	***836.404964***	418.706120	819.378415	410.192846	818.394399	409.700838	6
7	833.419217	417.213247			815.408652	408.207964	F	***650.325651***	325.666464	633.299102	317.153189	632.315086	316.661181	5
8	961.477795	481.242536	944.451246	472.729261	943.467230	472.237253	Q	***503.257237***	252.132257	486.230688	243.618982	485.246672	243.126974	4
9	1090.520388	545.763832	1073.493839	537.250558	1072.509823	536.758550	E	375.198659	188.102968	358.172110	179.589693	357.188094	179.097685	3
10	1161.557502	581.282389	1144.530953	572.769115	1143.546937	572.277107	A	***246.156066***	123.581671	229.129517	115.068396			2
11							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of ILTGDWFQEAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.2	1334.661896	0.004632	ILTGDWFQEAR
1.4	1334.675827	-0.009299	LPPDYVPFEVK
1.4	1334.675827	-0.009299	LPPDYVPFEVK

Mascot: http://www.matrixscience.com/

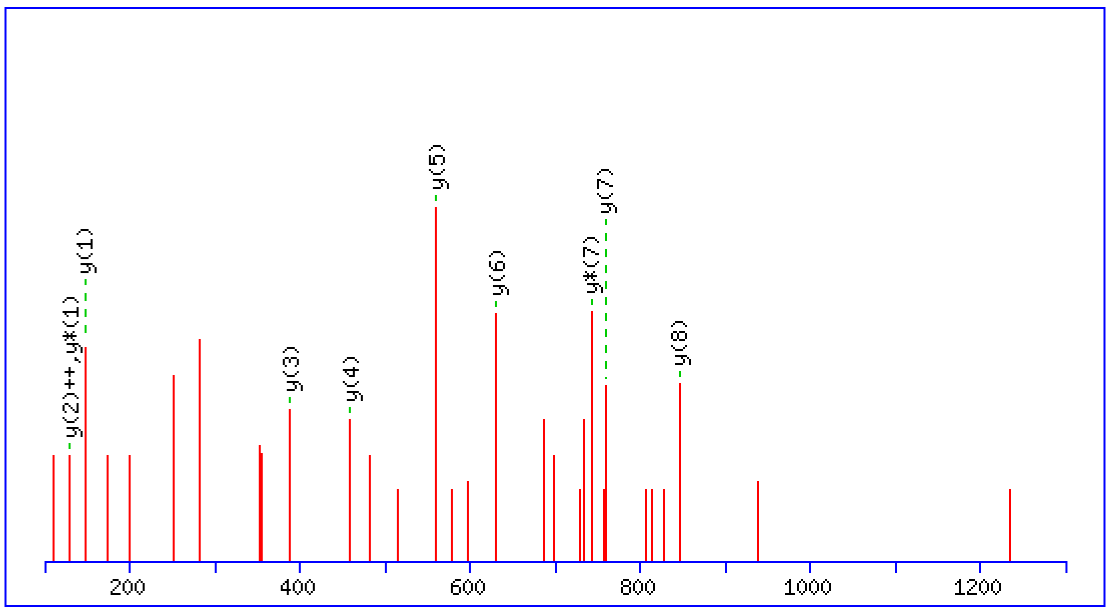
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ISQATAQIK**
Found in **STX12_HUMAN**, Syntaxin-12 OS=Homo sapiens GN=STX12 PE=1 SV=1

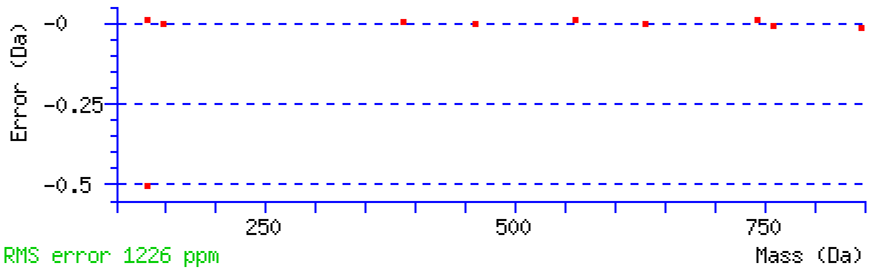
Match to Query 12874: 958.542988 from(480.278770,2+) rtinseconds(1077) index(4508)
Title: Locus:1.1.1.1828.22
Data file 2011-11-12 - TFD - EP 5-4.mgf

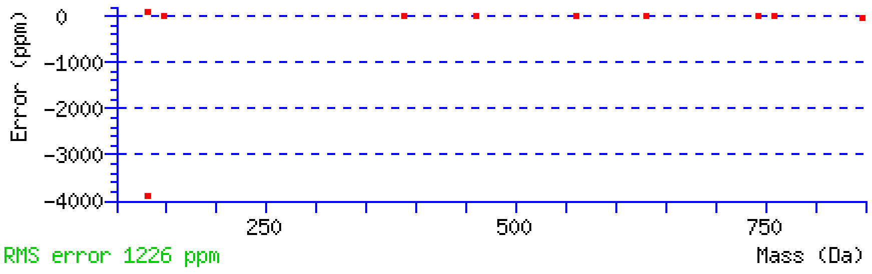
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 958.544724
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 52  Expect: 9.2e-005
Matches : 10/82 fragment ions using 17 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					I							9
2	201.123368	101.065322			183.112803	92.060039	S	*846.467959*	423.737618	829.441410	415.224343	828.457394	414.732335	8
3	329.181946	165.094611	312.155397	156.581336	311.171381	156.089328	Q	*759.435931*	380.221604	742.409382	371.708329	741.425366	371.216321	7
4	400.219060	200.613168	383.192511	192.099893	382.208495	191.607885	A	*631.377353*	316.192315	614.350804	307.679040	613.366788	307.187032	6
5	501.266739	251.137007	484.240190	242.623733	483.256174	242.131725	T	*560.340239*	280.673758	543.313690	272.160483	542.329674	271.668475	5
6	572.303853	286.655565	555.277304	278.142290	554.293288	277.650282	A	*459.292560*	230.149918	442.266011	221.636643			4
7	700.362431	350.684854	683.335882	342.171579	682.351866	341.679571	Q	*388.255446*	194.631361	371.228897	186.118087			3
8	813.446495	407.226886	796.419946	398.713611	795.435930	398.221603	I	260.196868	130.602072	243.170319	122.088798			2
9							K	*147.112804*	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of ISQATAQIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.7	958.544724	-0.001736	ISQATAQIK
13.4	958.533478	0.009510	ISLEEQLK
10.9	958.533478	0.009510	SPKEELLK
7.7	958.544724	-0.001736	ATKSPAKPK
7.0	958.533493	0.009495	LLDDATLAK
6.2	958.544739	-0.001751	LSIIGPTSR
5.2	958.533463	0.009525	EAELEKLK
5.1	958.544739	-0.001751	ISGVNLTQK
5.1	958.533508	0.009480	ISLAPTDVK
5.1	958.544724	-0.001736	ISLDDLRK

Mascot: http://www.matrixscience.com/

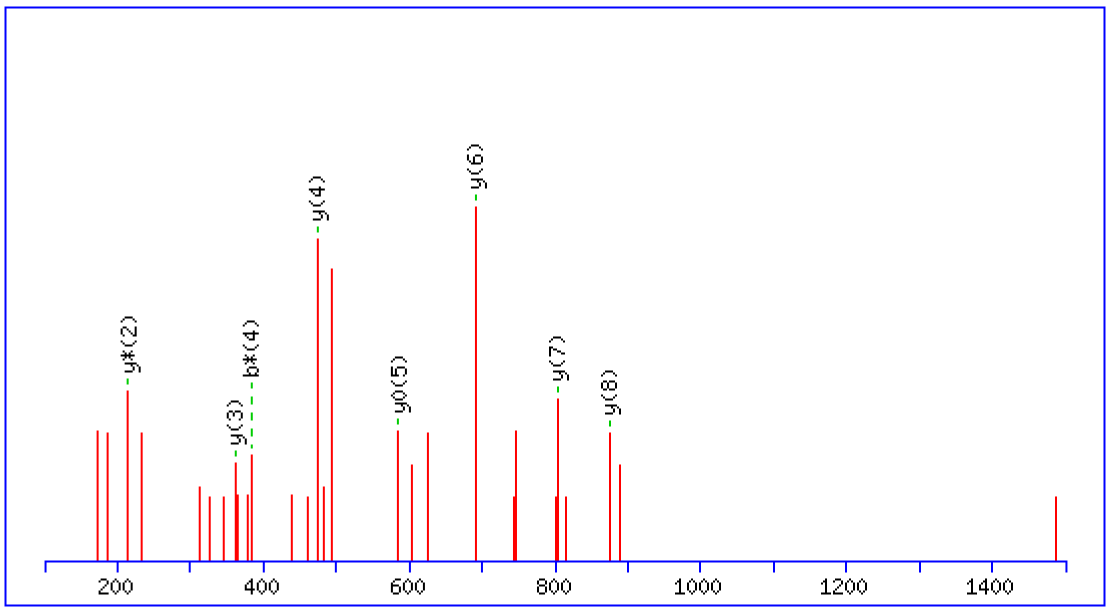
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QALSEIEGR**
Found in **STX3_HUMAN**, Syntaxin-3 OS=Homo sapiens GN=STX3 PE=1 SV=3

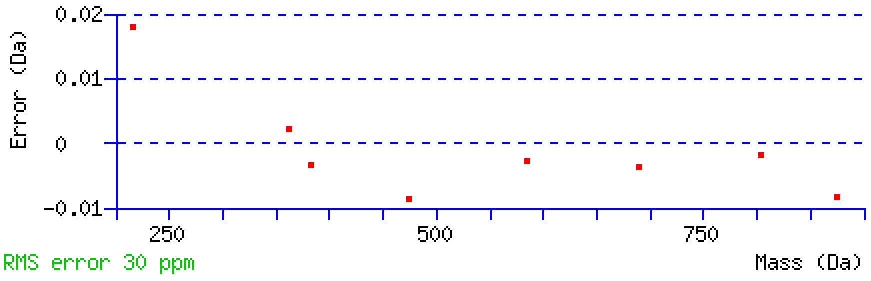
Match to Query 263343: 1001.513508 from(501.764030,2+) rtinseconds(1593) index(504132)
Title: Locus:1.1.1.936.13
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

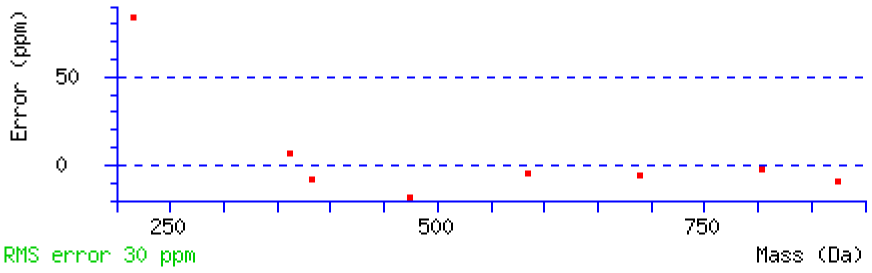
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1001.514145
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 44  Expect: 0.00034
Matches : 8/86 fragment ions using 8 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	129.065854	65.036565	112.039305	56.523291			Q							9
2	200.102968	100.555122	183.076419	92.041848			A	***874.462872***	437.735074	857.436323	429.221800	856.452307	428.729792	8
3	313.187032	157.097154	296.160483	148.583879			L	***803.425758***	402.216517	786.399209	393.703243	785.415193	393.211235	7
4	400.219060	200.613168	383.192511	192.099893	382.208495	191.607885	S	***690.341694***	345.674485	673.315145	337.161211	672.331129	336.669203	6
5	529.261653	265.134465	512.235104	256.621190	511.251088	256.129182	E	603.309666	302.158471	586.283117	293.645197	585.299101	293.153189	5
6	642.345717	321.676497	625.319168	313.163222	624.335152	312.671214	I	***474.267073***	237.637175	457.240524	229.123900	456.256508	228.631892	4
7	771.388310	386.197793	754.361761	377.684519	753.377745	377.192511	E	***361.183009***	181.095143	344.156460	172.581868	343.172444	172.089860	3
8	828.409774	414.708525	811.383225	406.195251	810.399209	405.703243	G	232.140416	116.573846	215.113867	108.060572			2
9							R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of QALSEIEGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.0	1001.514145	-0.000637	QALSEIEGR
6.6	1001.521545	-0.008037	KAPQSLEVM
1.1	1001.503799	0.009709	SVATLLMHM
0.5	1001.514145	-0.000637	AALSDAELGR
0.1	1001.514145	-0.000637	KSPLAEEGR

Mascot: http://www.matrixscience.com/

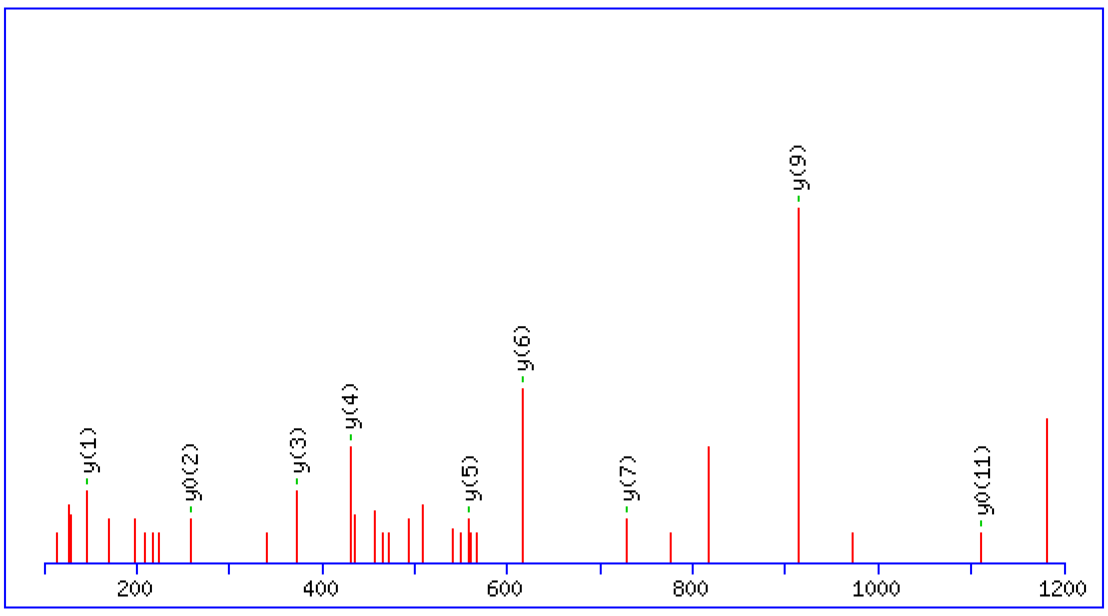
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ADTPSLGEGPEK**
Found in **STXB2_HUMAN**, Syntaxin-binding protein 2 OS=Homo sapiens GN=STXBP2 PE=1 SV=2

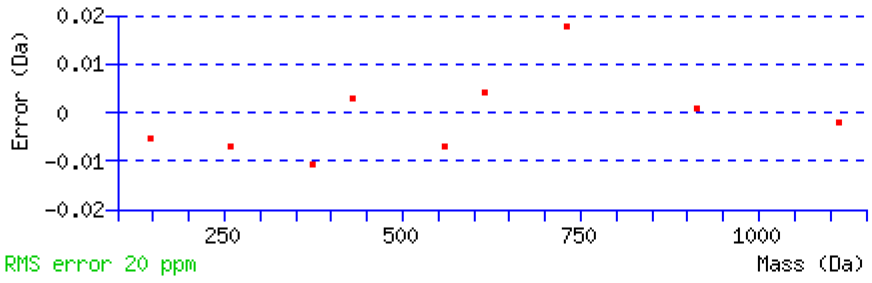
Match to Query 519922: 1199.569668 from(600.792110,2+) rtinseconds(1486) index(252851)
Title: Locus:1.1.1.1011.24
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

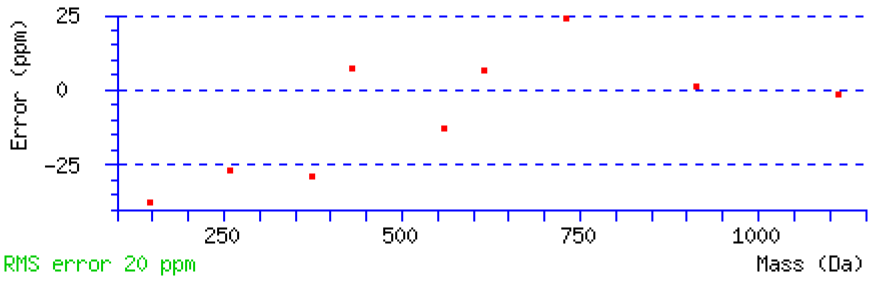
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1199.566986
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 68  Expect: 1.7e-006
Matches : 9/106 fragment ions using 11 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			A							12
2	187.071333	94.039304	169.060768	85.034022	D	1129.537160	565.272218	1112.510611	556.758944	1111.526595	556.266936	11
3	288.119012	144.563144	270.108447	135.557862	T	1014.510217	507.758747	997.483668	499.245472	996.499652	498.753464	10
4	385.171776	193.089526	367.161211	184.084243	P	***913.462538***	457.234907	896.435989	448.721633	895.451973	448.229625	9
5	472.203804	236.605540	454.193239	227.600257	S	816.409774	408.708525	799.383225	400.195251	798.399209	399.703243	8
6	585.287868	293.147572	567.277303	284.142290	L	***729.377746***	365.192511	712.351197	356.679237	711.367181	356.187229	7
7	642.309332	321.658304	624.298767	312.653022	G	***616.293682***	308.650479	599.267133	300.137205	598.283117	299.645197	6
8	771.351925	386.179601	753.341360	377.174318	E	***559.272218***	280.139747	542.245669	271.626473	541.261653	271.134465	5
9	828.373389	414.690333	810.362824	405.685050	G	***430.229625***	215.618451	413.203076	207.105176	412.219060	206.613168	4
10	925.426153	463.216715	907.415588	454.211432	P	***373.208161***	187.107719	356.181612	178.594444	355.197596	178.102436	3
11	1054.468746	527.738011	1036.458181	518.732729	E	276.155397	138.581337	259.128848	130.068062	258.144832	129.576054	2
12					K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of ADTPSLGEGPEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
68.1	1199.566986	0.002682	ADTPSLGEGPEK
10.3	1199.578217	-0.008549	INDEPVSAAPR
8.5	1199.578217	-0.008549	GEAPGAETPSLR
8.3	1199.578201	-0.008533	EAASSPAGEPLR
7.2	1199.578217	-0.008549	EEDRAGLGPPK
6.9	1199.567001	0.002667	VPEPEGQTSPK
3.3	1199.578217	-0.008549	GNVLNSPEDQK
0.8	1199.578232	-0.008564	SSPQPQQTSPK
0.7	1199.571701	-0.002033	PGMGINTQNPR
0.1	1199.567001	0.002667	VGPDEDKPPSK

Mascot: http://www.matrixscience.com/

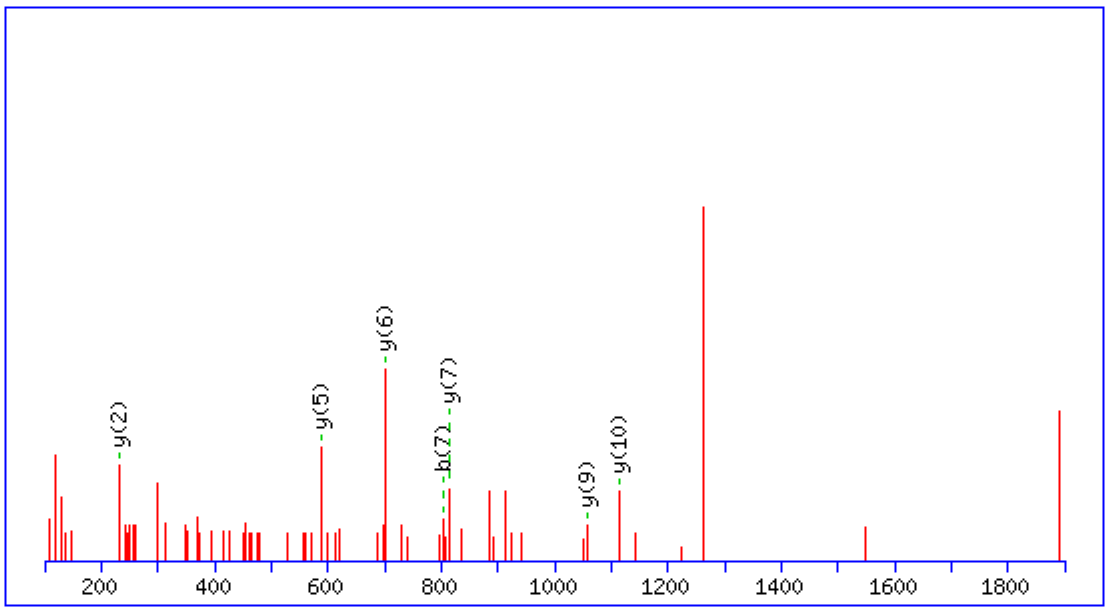
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FGDQLLQIDGR**
Found in **SDCB2_HUMAN**, Syntenin-2 OS=Homo sapiens GN=SDCBP2 PE=2 SV=2

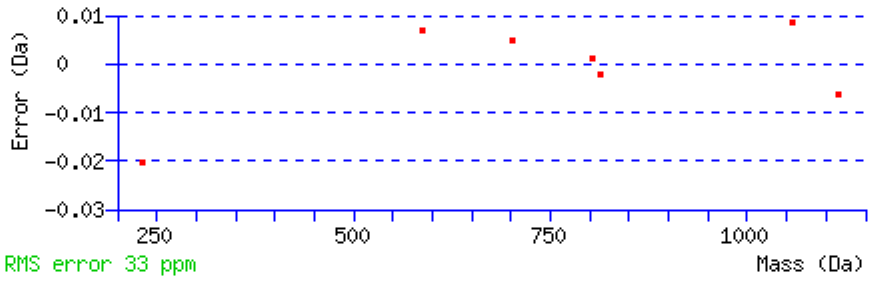
Match to Query 33568: 1260.649488 from(631.332020,2+) rtinseconds(2777) index(36714)
Title: Locus:1.1.1.2472.28
Data file 2011-11-12 - TFD - EP 5-4.mgf

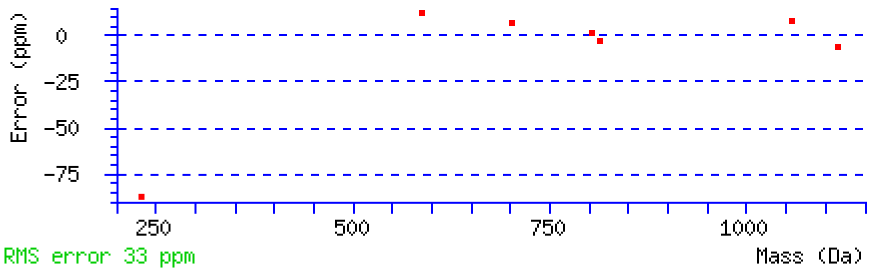
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1260.646255
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 35  Expect: 0.0022
Matches : 7/106 fragment ions using 12 most intense peaks    (help)
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	148.075690	74.541483					F							11
2	205.097154	103.052215					G	***1114.585114***	557.796195	1097.558565	549.282921	1096.574549	548.790912	10
3	320.124097	160.565687			302.113532	151.560404	D	***1057.563650***	529.285463	1040.537101	520.772189	1039.553085	520.280181	9
4	448.182675	224.594976	431.156126	216.081701	430.172110	215.589693	Q	942.536707	471.771992	925.510158	463.258717	924.526142	462.766709	8
5	561.266739	281.137008	544.240190	272.623733	543.256174	272.131725	L	***814.478129***	407.742703	797.451580	399.229428	796.467564	398.737420	7
6	674.350803	337.679040	657.324254	329.165765	656.340238	328.673757	L	***701.394065***	351.200671	684.367516	342.687396	683.383500	342.195388	6
7	802.409381	401.708329	785.382832	393.195054	784.398816	392.703046	Q	***588.310001***	294.658639	571.283452	286.145364	570.299436	285.653356	5
8	915.493445	458.250361	898.466896	449.737086	897.482880	449.245078	I	460.251423	230.629349	443.224874	222.116075	442.240858	221.624067	4
9	1030.520388	515.763832	1013.493839	507.250558	1012.509823	506.758550	D	347.167359	174.087317	330.140810	165.574043	329.156794	165.082035	3
10	1087.541852	544.274564	1070.515303	535.761290	1069.531287	535.269282	G	***232.140416***	116.573846	215.113867	108.060571			2
11							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of FGDQLLQIDGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.0	1260.646255	0.003233	FGDQLLQIDGR
6.7	1260.646255	0.003233	KFLGDLQPDGR

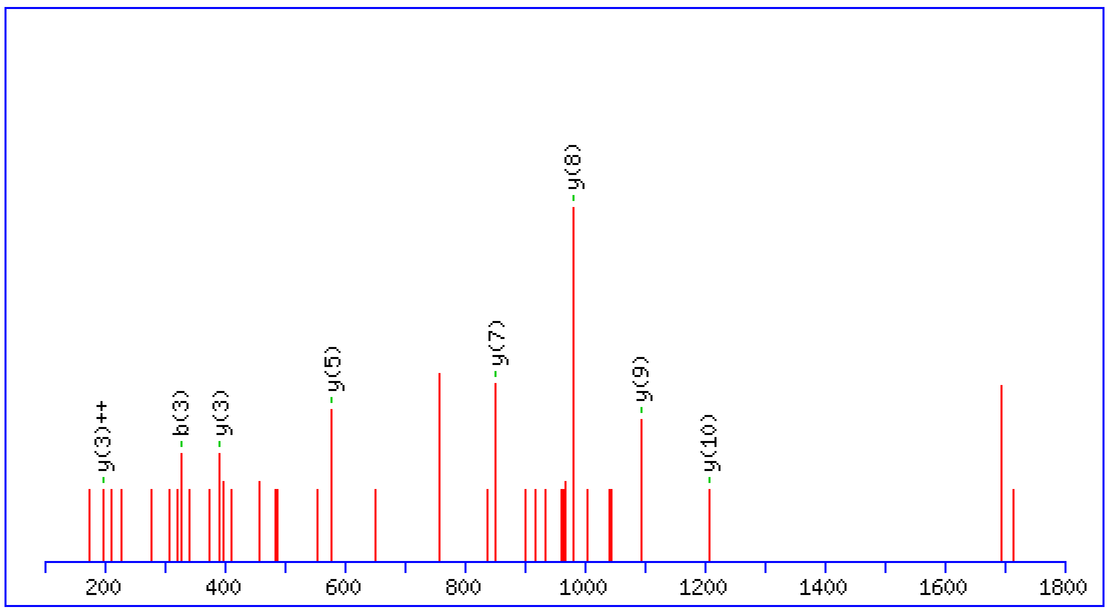
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLNLIQSWADAFR**
Found in **TOM1_HUMAN**, Target of Myb protein 1 OS=Homo sapiens GN=TOM1 PE=1 SV=2

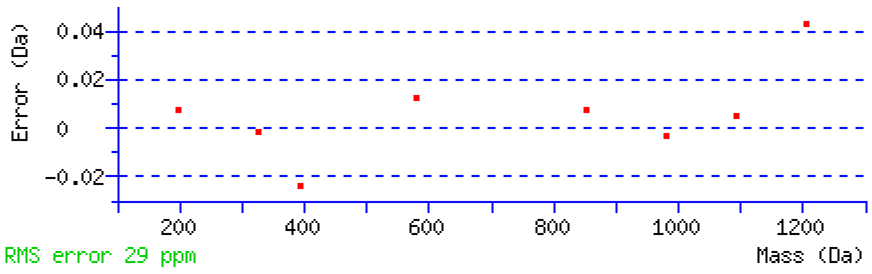
Match to Query 47250: 1531.826368 from(766.920460,2+) rtinseconds(4563) index(69268)
Title: Locus:1.1.1.3158.16
Data file 2011-11-14 - TFD - EP 8-3.mgf

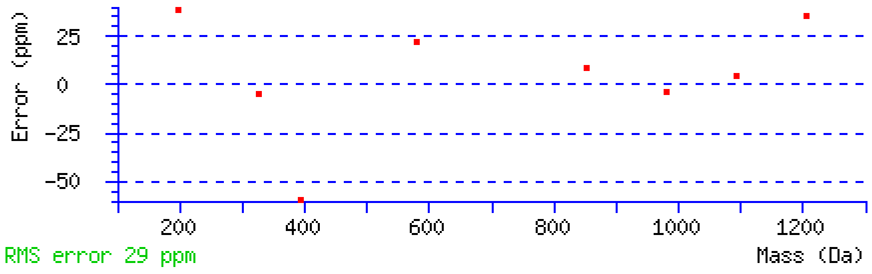
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1531.814697
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.00081
Matches : 8/122 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							13
2	213.159754	107.083515					L	1433.753575	717.380426	1416.727026	708.867151	1415.743010	708.375143	12
3	327.202681	164.104978	310.176132	155.591704			N	1320.669511	660.838394	1303.642962	652.325119	1302.658946	651.833111	11
4	440.286745	220.647010	423.260196	212.133736			L	***1206.626584***	603.816930	1189.600035	595.303656	1188.616019	594.811648	10
5	553.370809	277.189043	536.344260	268.675768			I	***1093.542520***	547.274898	1076.515971	538.761624	1075.531955	538.269615	9
6	681.429387	341.218332	664.402838	332.705057			Q	***980.458456***	490.732866	963.431907	482.219592	962.447891	481.727584	8
7	768.461415	384.734346	751.434866	376.221071	750.450850	375.729063	S	***852.399878***	426.703577	835.373329	418.190303	834.389313	417.698295	7
8	954.540728	477.774002	937.514179	469.260727	936.530163	468.768719	W	765.367850	383.187563	748.341301	374.674289	747.357285	374.182281	6
9	1025.577842	513.292559	1008.551293	504.779284	1007.567277	504.287276	A	***579.288537***	290.147907	562.261988	281.634632	561.277972	281.142624	5
10	1140.604785	570.806031	1123.578236	562.292756	1122.594220	561.800748	D	508.251423	254.629350	491.224874	246.116075	490.240858	245.624067	4
11	1211.641899	606.324588	1194.615350	597.811313	1193.631334	597.319305	A	***393.224480***	197.115878	376.197931	188.602603			3
12	1358.710313	679.858795	1341.683764	671.345520	1340.699748	670.853512	F	322.187366	161.597321	305.160817	153.084047			2
13							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of VLNLIQSWADAFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.6	1531.814697	0.011671	VLNLIQSWADAFR
7.2	1531.814697	0.011671	APAAPAAPPPPPPPPR

Mascot: http://www.matrixscience.com/

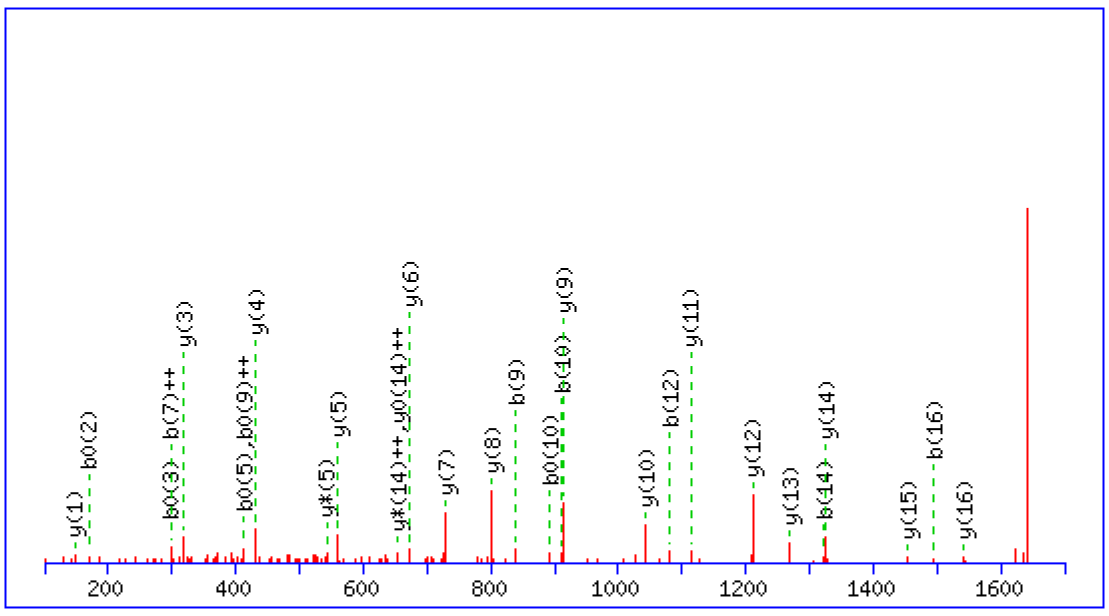
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VSEGGPAEIAGLQIGDK**
Found in **TX1B3_HUMAN**, Tax1-binding protein 3 OS=Homo sapiens GN=TAX1BP3 PE=1 SV=2

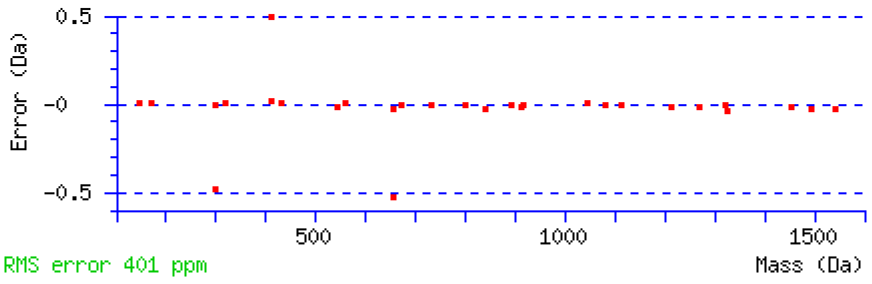
Match to Query 41263: 1639.836048 from(820.925300,2+) rtinseconds(2709) index(27167)
Title: Locus:1.1.1.2490.48
Data file 2011-11-10 - TFD - EP 4-7.mgf

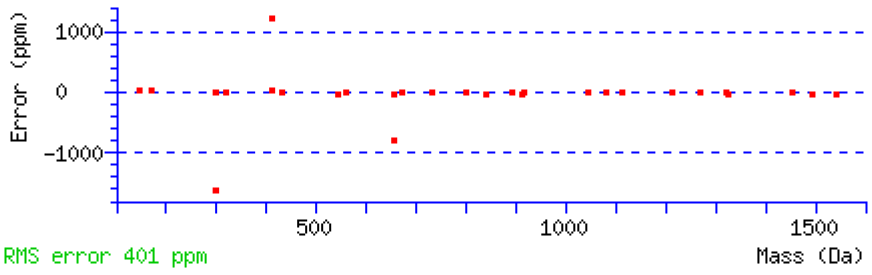
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1639.841705
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 155  Expect: 3.2e-015
Matches : 29/164 fragment ions using 32 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	100.075690	50.541483					V							17
2	187.107718	94.057497			169.097153	85.052214	S	***1541.780579***	771.393927	1524.754030	762.880653	1523.770014	762.388645	16
3	316.150311	158.578793			298.139746	149.573511	E	***1454.748551***	727.877913	1437.722002	719.364639	1436.737986	718.872631	15
4	373.171775	187.089525			355.161210	178.084243	G	***1325.705958***	663.356617	1308.679409	654.843342	1307.695393	654.351334	14
5	430.193239	215.600257			412.182674	206.594975	G	***1268.684494***	634.845885	1251.657945	626.332610	1250.673929	625.840602	13
6	527.246003	264.126640			509.235438	255.121357	P	***1211.663030***	606.335153	1194.636481	597.821879	1193.652465	597.329870	12
7	598.283117	299.645197			580.272552	290.639914	A	***1114.610266***	557.808771	1097.583717	549.295497	1096.599701	548.803488	11
8	727.325710	364.166493			709.315145	355.161210	E	***1043.573152***	522.290214	1026.546603	513.776940	1025.562587	513.284931	10
9	**840.409774**	420.708525			822.399209	411.703242	I	***914.530559***	457.768917	897.504010	449.255643	896.519994	448.763635	9
10	**911.446888**	456.227082			893.436323	447.221799	A	***801.446495***	401.226885	784.419946	392.713611	783.435930	392.221603	8
11	968.468352	484.737814			950.457787	475.732531	G	***730.409381***	365.708328	713.382832	357.195054	712.398816	356.703046	7
12	**1081.552416**	541.279846			1063.541851	532.274564	L	***673.387917***	337.197596	656.361368	328.684322	655.377352	328.192314	6
13	1209.610994	605.309135	1192.584445	596.795861	1191.600429	596.303852	Q	***560.303853***	280.655564	543.277304	272.142290	542.293288	271.650282	5
14	**1322.695058**	661.851167	1305.668509	653.337892	1304.684493	652.845884	I	***432.245275***	216.626275	415.218726	208.113001	414.234710	207.620993	4
15	1379.716522	690.361899	1362.689973	681.848624	1361.705957	681.356616	G	***319.161211***	160.084243	302.134662	151.570969	301.150646	151.078961	3
16	**1494.743465**	747.875370	1477.716916	739.362096	1476.732900	738.870088	D	262.139747	131.573512	245.113198	123.060237	244.129182	122.568229	2
17							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of VSEGGPAEIAGLQIGDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
155.5	1639.841705	-0.005657	VSEGGPAEIAGLQIGDK
3.8	1639.820572	0.015476	LSDGSAYRFEVPTAK
2.8	1639.831818	0.004230	GQHLSDAFAQVNPLK

Mascot: http://www.matrixscience.com/

{MATRIX SCIENCE}

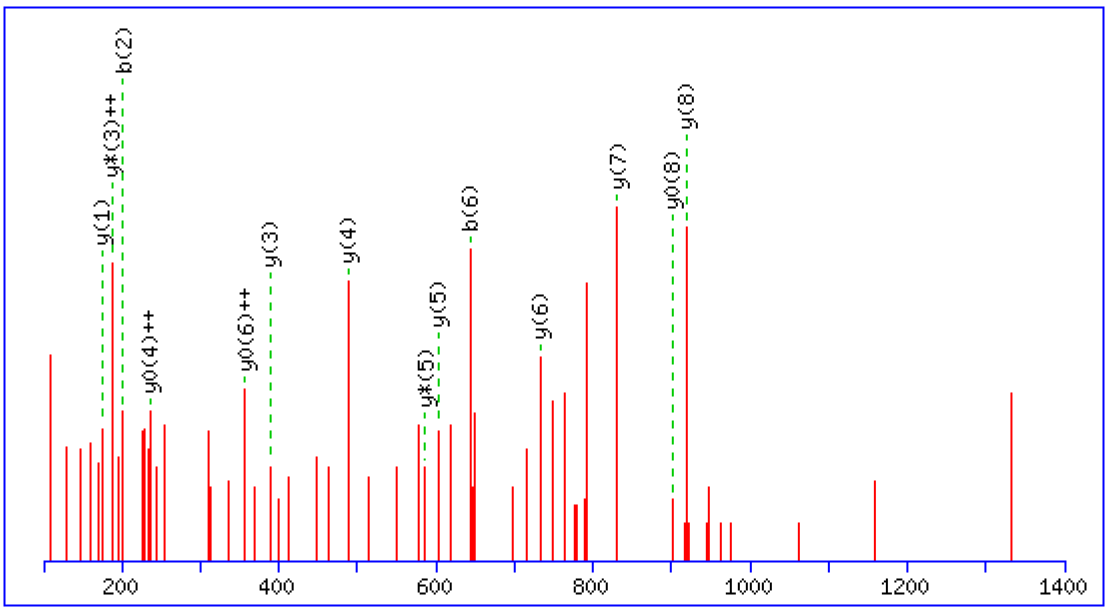
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSVEDVLTR**
Found in **TBC17_HUMAN**, TBC1 domain family member 17 OS=Homo sapiens GN=TBC1D17 PE=2 SV=2

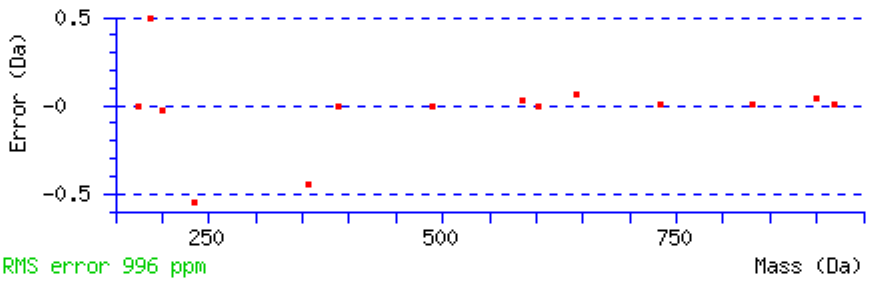
Match to Query 18752: 1030.560228 from(516.287390,2+) rtinseconds(2775) index(36270)
Title: Locus:1.1.1.2545.10
Data file 2011-11-10 - TFD - EP 4-2.mgf

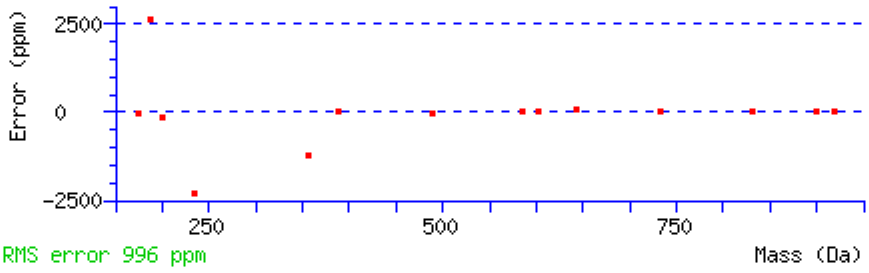
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1030.565872
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 36  Expect: 0.001
Matches : 14/76 fragment ions using 34 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							9
2	**201.123368**	101.065322	183.112803	92.060039	S	***918.489087***	459.748182	901.462538	451.234907	900.478522	450.742899	8
3	300.191782	150.599529	282.181217	141.594247	V	***831.457059***	416.232168	814.430510	407.718893	813.446494	407.226885	7
4	429.234375	215.120826	411.223810	206.115543	E	***732.388645***	366.697961	715.362096	358.184686	714.378080	357.692678	6
5	544.261318	272.634297	526.250753	263.629015	D	***603.346052***	302.176664	586.319503	293.663390	585.335487	293.171382	5
6	**643.329732**	322.168504	625.319167	313.163222	V	***488.319109***	244.663192	471.292560	236.149918	470.308544	235.657910	4
7	756.413796	378.710536	738.403231	369.705254	L	***389.250695***	195.128985	372.224146	186.615711	371.240130	186.123703	3
8	857.461475	429.234376	839.450910	420.229093	T	276.166631	138.586953	259.140082	130.073679	258.156066	129.581671	2
9					R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LSVEDVLTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.8	1030.565872	-0.005644	LSVEDVLTR
3.8	1030.559341	0.000887	IGAGRLMGPK
3.6	1030.554626	0.005602	LSDLLEVDK
2.7	1030.565842	-0.005614	LSQNISELK
2.7	1030.555969	0.004259	SLVHAYVSR

Mascot: http://www.matrixscience.com/

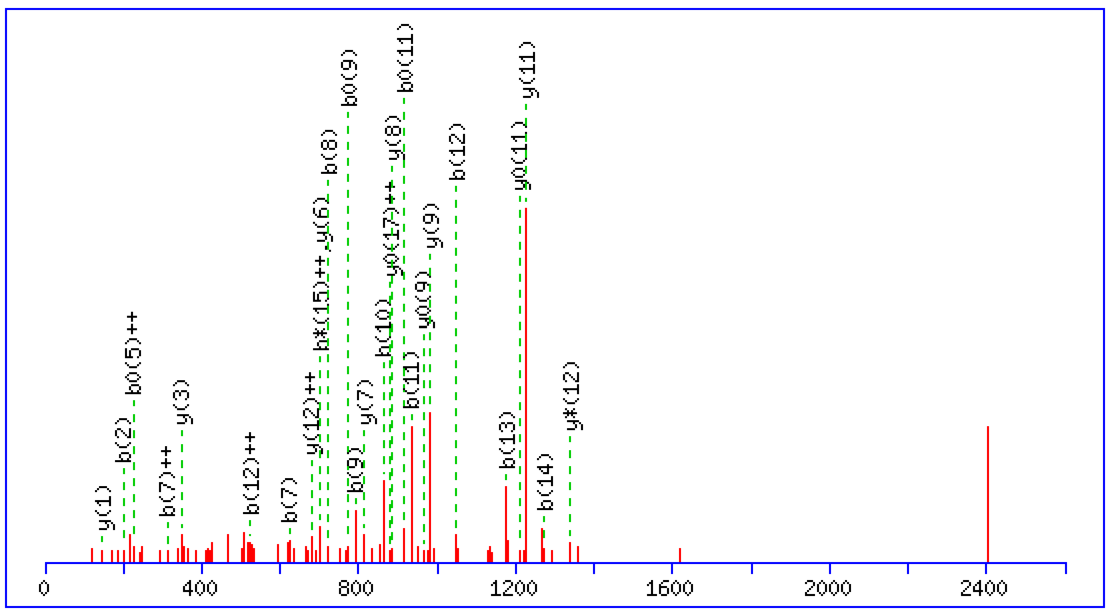
{MATRIX} {SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TPPGLVGVAAALQPFPALQNISLK**
Found in **TBD2A_HUMAN**, TBC1 domain family member 2A OS=Homo sapiens GN=TBC1D2 PE=1 SV=3

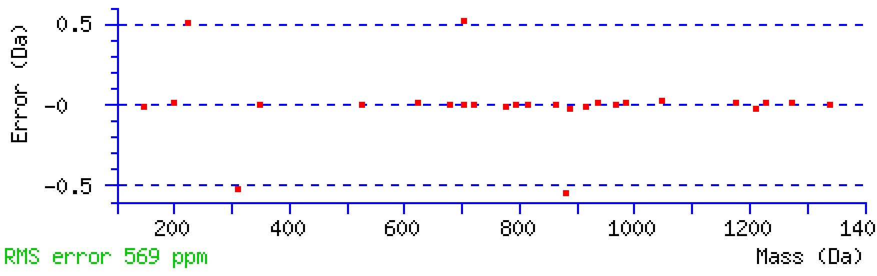
Match to Query 70396: 2401.376292 from(801.466040,3+) rtinseconds(4420) index(67225)
Title: Locus:1.1.1.2976.21
Data file 2011-11-12 - TFD - EP 6-1.mgf

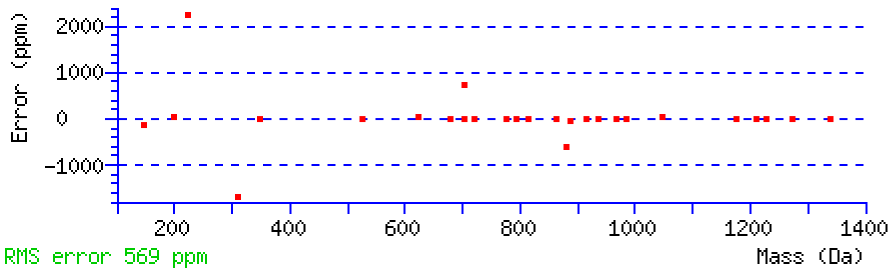
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2401.373306
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.00033
Matches : 27/248 fragment ions using 70 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	102.054955	51.531116			84.044390	42.525833	T							24
2	***199.107719***	100.057497			181.097154	91.052215	P	2301.332917	1151.170096	2284.306368	1142.656822	2283.322352	1142.164814	23
3	296.160483	148.583879			278.149918	139.578597	P	2204.280153	1102.643714	2187.253604	1094.130440	2186.269588	1093.638432	22
4	353.181947	177.094611			335.171382	168.089329	G	2107.227389	1054.117332	2090.200840	1045.604058	2089.216824	1045.112050	21
5	466.266011	233.636643			448.255446	224.631361	L	2050.205925	1025.606600	2033.179376	1017.093326	2032.195360	1016.601318	20
6	565.334425	283.170851			547.323860	274.165568	V	1937.121861	969.064569	1920.095312	960.551294	1919.111296	960.059286	19
7	***622.355889***	311.681583			604.345324	302.676300	G	1838.053447	919.530362	1821.026898	911.017087	1820.042882	910.525079	18
8	***721.424303***	361.215790			703.413738	352.210507	V	1781.031983	891.019630	1764.005434	882.506355	1763.021418	882.014347	17
9	***792.461417***	396.734347			774.450852	387.729064	A	1681.963569	841.485423	1664.937020	832.972148	1663.953004	832.480140	16
10	***863.498531***	432.252904			845.487966	423.247621	A	1610.926455	805.966866	1593.899906	797.453591	1592.915890	796.961583	15
11	***934.535645***	467.771460			916.525080	458.766178	A	1539.889341	770.448309	1522.862792	761.935034	1521.878776	761.443026	14
12	***1047.619709***	524.313492			1029.609144	515.308210	L	1468.852227	734.929752	1451.825678	726.416477	1450.841662	725.924469	13
13	***1175.678287***	588.342782	1158.651738	579.829507	1157.667722	579.337499	Q	1355.768163	678.387720	1338.741614	669.874445	1337.757598	669.382437	12
14	***1272.731051***	636.869164	1255.704502	628.355889	1254.720486	627.863881	P	***1227.709585***	614.358431	1210.683036	605.845156	1209.699020	605.353148	11
15	1419.799465	710.403371	1402.772916	701.890096	1401.788900	701.398088	F	1130.656821	565.832049	1113.630272	557.318774	1112.646256	556.826766	10
16	1516.852229	758.929753	1499.825680	750.416478	1498.841664	749.924470	P	***983.588407***	492.297842	966.561858	483.784567	965.577842	483.292559	9
17	1587.889343	794.448310	1570.862794	785.935035	1569.878778	785.443027	A	***886.535643***	443.771460	869.509094	435.258185	868.525078	434.766177	8
18	1700.973407	850.990342	1683.946858	842.477067	1682.962842	841.985059	L	***815.498529***	408.252903	798.471980	399.739628	797.487964	399.247620	7
19	1829.031985	915.019630	1812.005436	906.506356	1811.021420	906.014348	Q	***702.414465***	351.710871	685.387916	343.197596	684.403900	342.705588	6
20	1943.074912	972.041094	1926.048363	963.527819	1925.064347	963.035811	N	574.355887	287.681582	557.329338	279.168307	556.345322	278.676299	5
21	2056.158976	1028.583126	2039.132427	1020.069851	2038.148411	1019.577843	I	460.312960	230.660118	443.286411	222.146844	442.302395	221.654836	4
22	2143.191004	1072.099140	2126.164455	1063.585865	2125.180439	1063.093857	S	***347.228896***	174.118086	330.202347	165.604812	329.218331	165.112804	3
23	2256.275068	1128.641172	2239.248519	1120.127897	2238.264503	1119.635889	L	260.196868	130.602072	243.170319	122.088798			2
24							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of TPPGLVGVAAALQPFPALQNISLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.6	2401.373306	0.002986	TPPGLVGVAAALQPFPALQNISLK

Mascot: http://www.matrixscience.com/

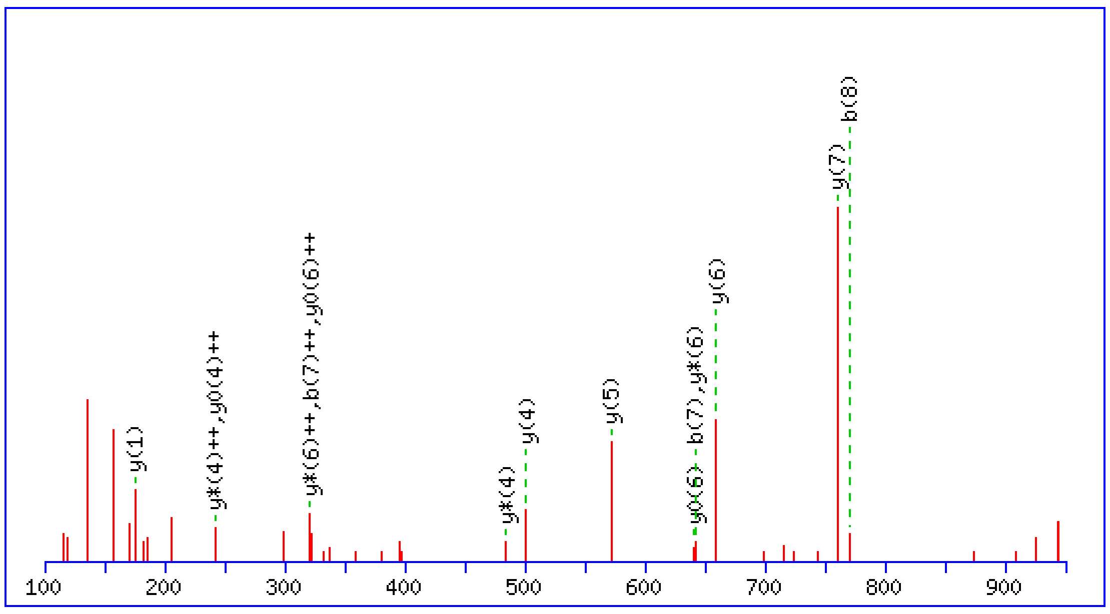
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SPTSAPTQR**
Found in **TENC1_HUMAN**, Tensin-like C1 domain-containing phosphatase OS=Homo sapiens GN=TENC1 PE=1 SV=2

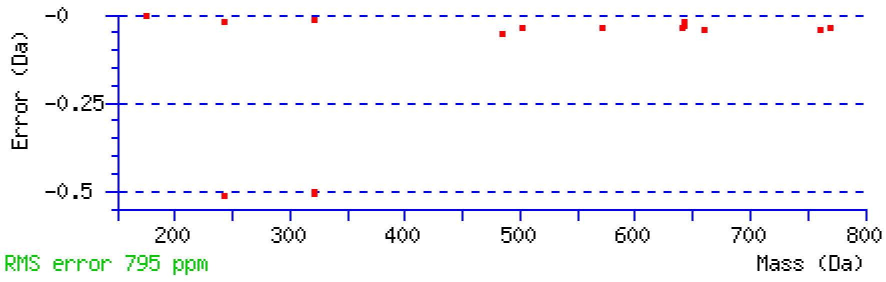
Match to Query 184468: 943.476508 from(472.745530,2+) rtinseconds(1646) index(748867)
Title: Locus:1.1.1.970.16
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

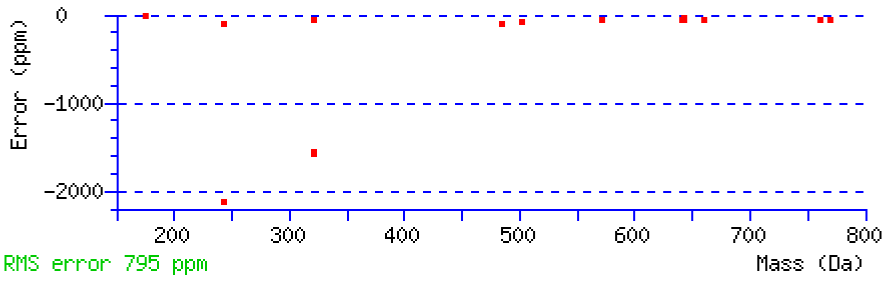
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 943.472305
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.004
Matches : 15/78 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							9
2	185.092068	93.049672			167.081503	84.044389	P	857.447558	429.227417	840.421009	420.714143	839.436993	420.222135	8
3	286.139747	143.573512			268.129182	134.568229	T	**760.394794**	380.701035	743.368245	372.187761	742.384229	371.695753	7
4	373.171775	187.089525			355.161210	178.084243	S	**659.347115**	330.177196	642.320566	321.663921	641.336550	321.171913	6
5	444.208889	222.608082			426.198324	213.602800	A	**572.315087**	286.661182	555.288538	278.147907	554.304522	277.655899	5
6	541.261653	271.134465			523.251088	262.129182	P	**501.277973**	251.142625	484.251424	242.629350	483.267408	242.137342	4
7	**642.309332**	321.658304			624.298767	312.653022	T	404.225209	202.616243	387.198660	194.102968	386.214644	193.610960	3
8	**770.367910**	385.687593	753.341361	377.174319	752.357345	376.682311	Q	303.177530	152.092403	286.150981	143.579129			2
9							R	**175.118952**	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of SPTSAPTQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.4	943.476303	0.000205	AITSAYYR
36.0	943.472305	0.004203	SPTSAPTQR
13.9	943.472305	0.004203	SPPGPASKR
13.7	943.483536	-0.007028	RSGPSPTAR
11.6	943.483521	-0.007013	ALGDRDAAR
11.0	943.483521	-0.007013	REVADAQR
11.0	943.483521	-0.007013	REVEQQR
9.5	943.483505	-0.006997	RENGLEAR
9.4	943.483536	-0.007028	AASPTGRPR
8.7	943.483536	-0.007028	RSGPSPTAR

Mascot: http://www.matrixscience.com/

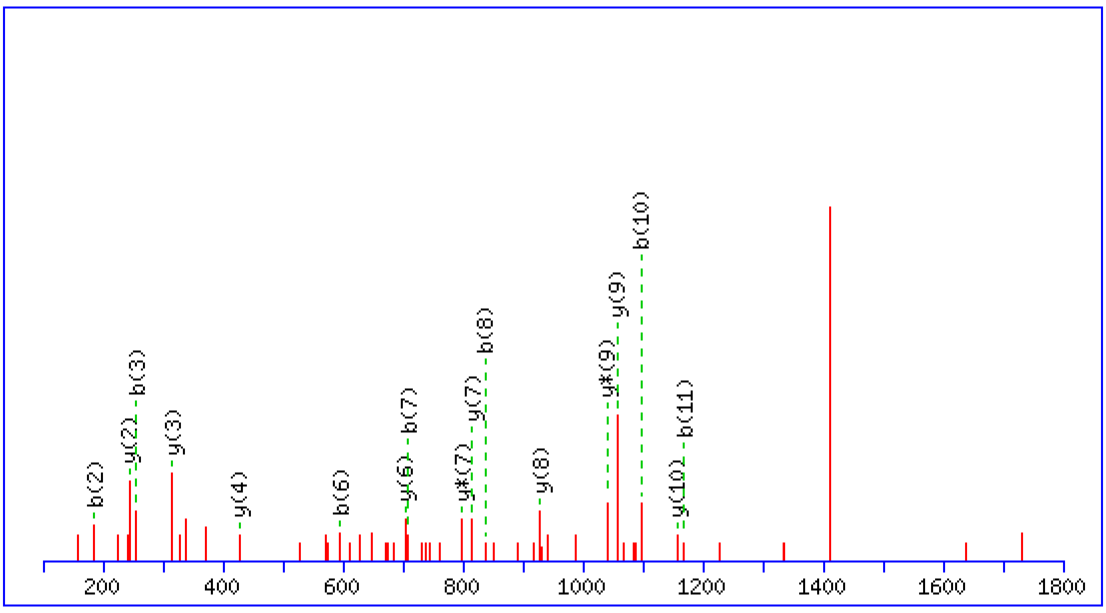
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LAAVQLLQFLAPK**
Found in **TEX10_HUMAN**, Testis-expressed sequence 10 protein OS=Homo sapiens GN=TEX10 PE=1 SV=2

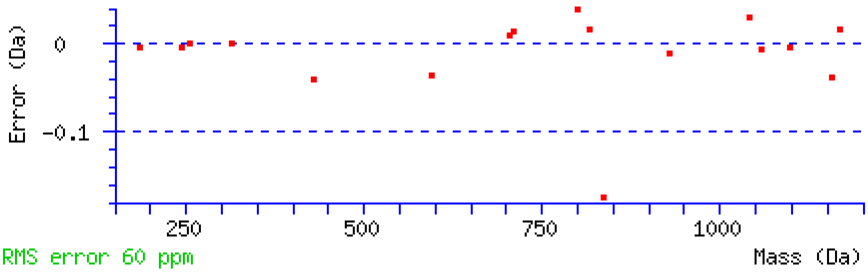
Match to Query 43661: 1410.859828 from(706.437190,2+) rtinseconds(4394) index(64533)
Title: Locus:1.1.1.3081.13
Data file 2011-11-14 - TFD - EP 8-2.mgf

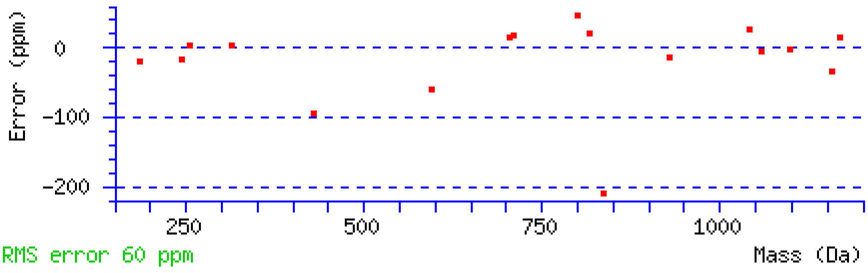
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1410.859848
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 59 **Expect:** 1.3e-006
Matches : 17/88 fragment ions using 29 most intense peaks (help)

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	114.091340	57.549308			**L**					**13**
2	***185.128454***	93.067865			**A**	1298.783086	649.895181	1281.756537	641.381907	**12**
3	***256.165568***	128.586422			**A**	1227.745972	614.376624	1210.719423	605.863350	**11**
4	355.233982	178.120629			**V**	***1156.708858***	578.858067	1139.682309	570.344793	**10**
5	483.292560	242.149918	466.266011	233.636643	**Q**	***1057.640444***	529.323860	1040.613895	520.810586	**9**
6	***596.376624***	298.691950	579.350075	290.178676	**L**	***929.581866***	465.294571	912.555317	456.781297	**8**
7	***709.460688***	355.233982	692.434139	346.720708	**L**	***816.497802***	408.752539	799.471253	400.239265	**7**
8	***837.519266***	419.263271	820.492717	410.749997	**Q**	***703.413738***	352.210507	686.387189	343.697233	**6**
9	984.587680	492.797478	967.561131	484.284203	**F**	575.355160	288.181218	558.328611	279.667944	**5**
10	***1097.671744***	549.339510	1080.645195	540.826236	**L**	***428.286746***	214.647011	411.260197	206.133737	**4**
11	***1168.708858***	584.858067	1151.682309	576.344793	**A**	***315.202682***	158.104979	298.176133	149.591704	**3**
12	1265.761622	633.384449	1248.735073	624.871175	**P**	***244.165568***	122.586422	227.139019	114.073148	**2**
13					**K**	147.112804	74.060040	130.086255	65.546765	**1**





NCBI **BLAST** search of LAAVQLLQFLAPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.7	1410.859848	-0.000020	LAAVQLLQFLAPK

Mascot: http://www.matrixscience.com/

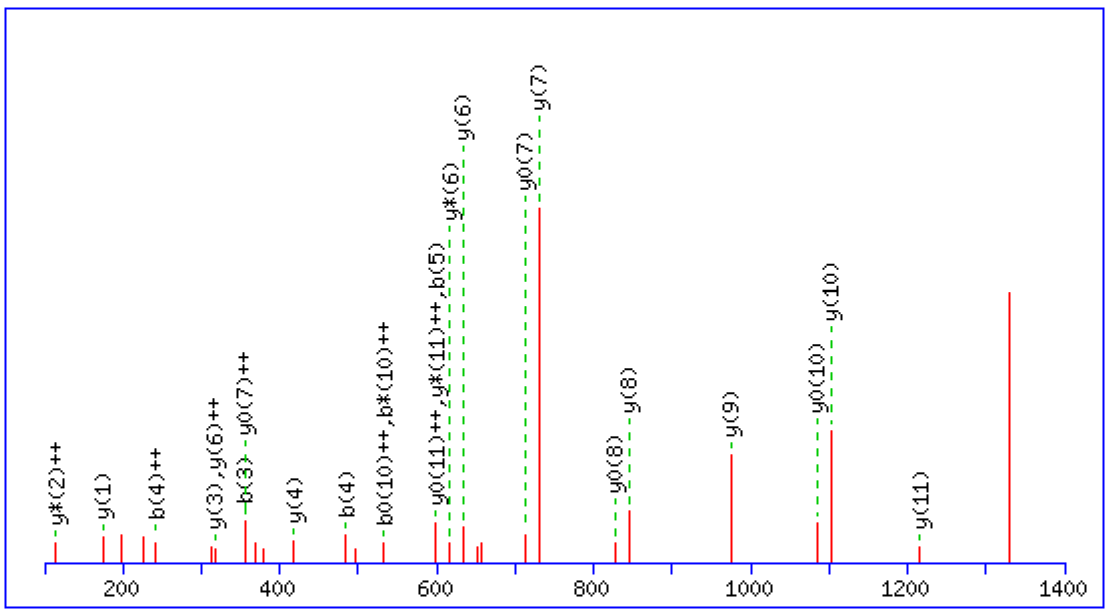
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILQEDPTNTAAR**
Found in **TTC35_HUMAN**, Tetratricopeptide repeat protein 35 OS=Homo sapiens GN=TTC35 PE=1 SV=1

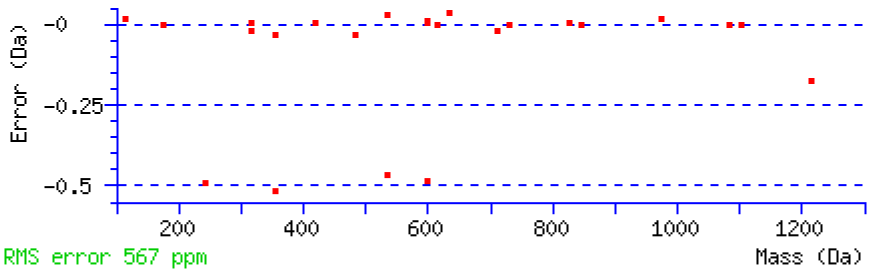
Match to Query 37731: 1327.674828 from(664.844690,2+) rtinseconds(1372) index(10609)
Title: Locus:1.1.1.1865.40
Data file 2011-11-10 - TFD - EP 3-4.mgf

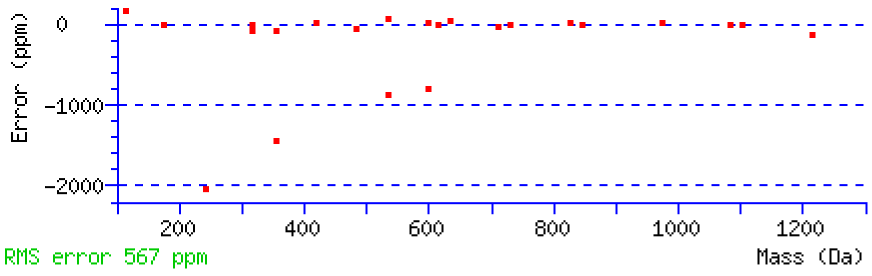
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1327.673172
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 77  Expect: 2.8e-007
Matches : 24/116 fragment ions using 28 most intense peaks    (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					I							12
2	227.175404	114.091340					L	***1215.596407***	608.301842	1198.569858	599.788567	1197.585842	599.296559	11
3	**355.233982**	178.120629	338.207433	169.607355			Q	***1102.512343***	551.759810	1085.485794	543.246535	1084.501778	542.754527	10
4	**484.276575**	242.641926	467.250026	234.128651	466.266010	233.636643	E	***974.453765***	487.730521	957.427216	479.217246	956.443200	478.725238	9
5	**599.303518**	300.155397	582.276969	291.642123	581.292953	291.150115	D	***845.411172***	423.209224	828.384623	414.695950	827.400607	414.203942	8
6	696.356282	348.681779	679.329733	340.168505	678.345717	339.676497	P	***730.384229***	365.695753	713.357680	357.182478	712.373664	356.690470	7
7	797.403961	399.205619	780.377412	390.692344	779.393396	390.200336	T	***633.331465***	317.169371	616.304916	308.656096	615.320900	308.164088	6
8	911.446888	456.227082	894.420339	447.713808	893.436323	447.221800	N	532.283786	266.645531	515.257237	258.132257	514.273221	257.640249	5
9	1012.494567	506.750922	995.468018	498.237647	994.484002	497.745639	T	***418.240859***	209.624068	401.214310	201.110793	400.230294	200.618785	4
10	1083.531681	542.269479	1066.505132	533.756204	1065.521116	533.264196	A	***317.193180***	159.100228	300.166631	150.586953			3
11	1154.568795	577.788036	1137.542246	569.274761	1136.558230	568.782753	A	246.156066	123.581671	229.129517	115.068396			2
12							R	***175.118952***	88.063114	158.092403	79.549839			1



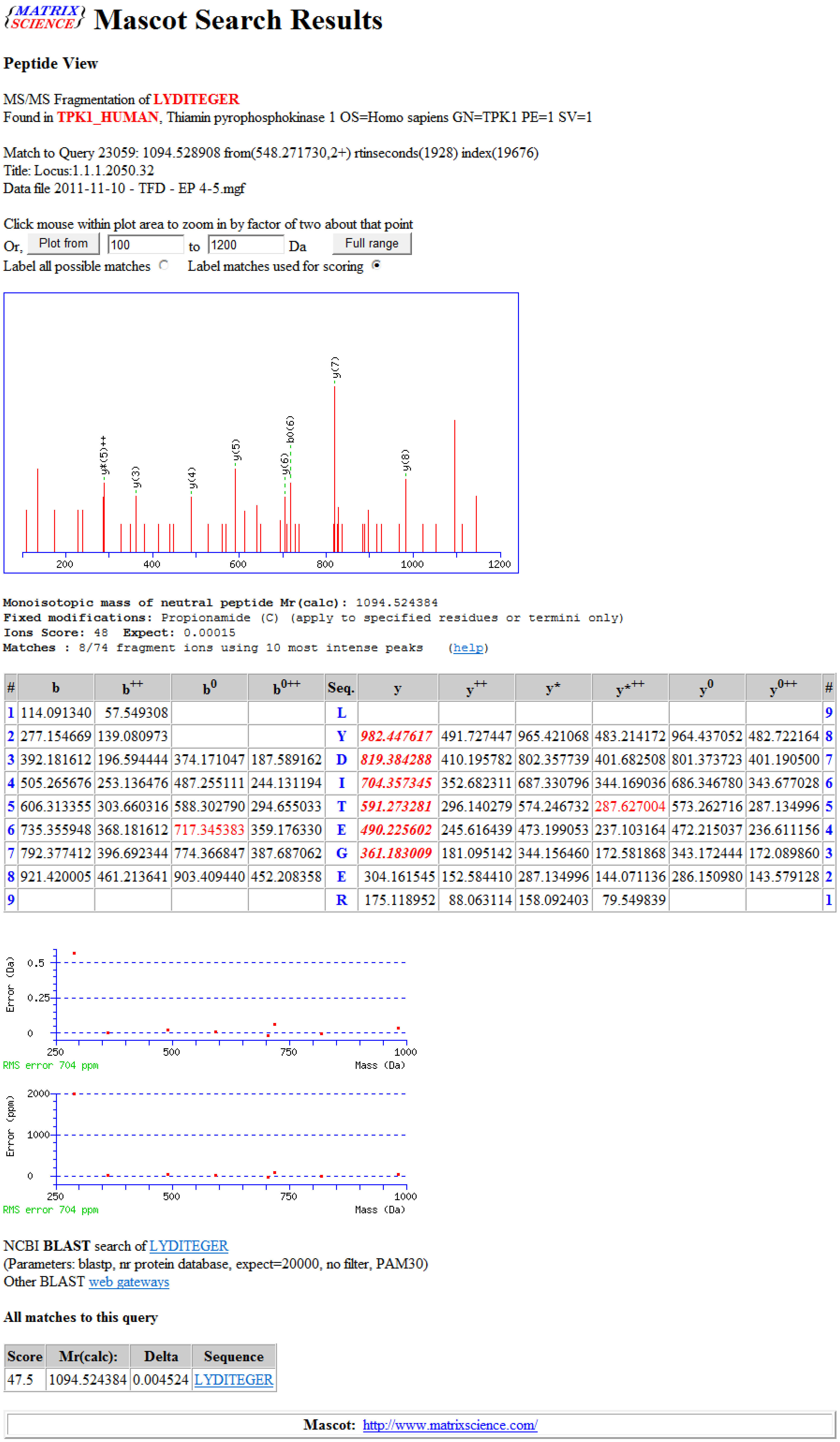


NCBI **BLAST** search of ILQEDPTNTAAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
76.7	1327.673172	0.001656	ILQEDPTNTAAR
8.4	1327.684418	-0.009590	QLNSTVSSLHSR
7.3	1327.674698	0.000130	LQNPMYFFLR
5.4	1327.674713	0.000115	LLSYMFFHVR
4.4	1327.677185	-0.002357	QPEEALPFLER
4.3	1327.670654	0.004174	LIREMFNYAR
4.3	1327.661957	0.012871	QLLIDPEDDVR
2.8	1327.670654	0.004174	YIIYNSRPMR
2.5	1327.687088	-0.012260	KLDPEIVPEEK
2.3	1327.677872	-0.003044	SSARSLQHLCR

Mascot: http://www.matrixscience.com/



{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LYDITEGER**
Found in **TPK1_HUMAN**, Thiamin pyrophosphokinase 1 OS=Homo sapiens GN=TPK1 PE=1 SV=1

Match to Query 23059: 1094.528908 from(548.271730,2+) rtinseconds(1928) index(19676)
Title: Locus:1.1.1.2050.32
Data file 2011-11-10 - TFD - EP 4-5.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
Label all possible matches ○ Label matches used for scoring ●

```
Monoisotopic mass of neutral peptide Mr(calc): 1094.524384
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 48  Expect: 0.00015
Matches : 8/74 fragment ions using 10 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							9
2	277.154669	139.080973			Y	***982.447617***	491.727447	965.421068	483.214172	964.437052	482.722164	8
3	392.181612	196.594444	374.171047	187.589162	D	***819.384288***	410.195782	802.357739	401.682508	801.373723	401.190500	7
4	505.265676	253.136476	487.255111	244.131194	I	***704.357345***	352.682311	687.330796	344.169036	686.346780	343.677028	6
5	606.313355	303.660316	588.302790	294.655033	T	***591.273281***	296.140279	574.246732	287.627004	573.262716	287.134996	5
6	735.355948	368.181612	717.345383	359.176330	E	***490.225602***	245.616439	473.199053	237.103164	472.215037	236.611156	4
7	792.377412	396.692344	774.366847	387.687062	G	***361.183009***	181.095142	344.156460	172.581868	343.172444	172.089860	3
8	921.420005	461.213641	903.409440	452.208358	E	304.161545	152.584410	287.134996	144.071136	286.150980	143.579128	2
9					R	175.118952	88.063114	158.092403	79.549839			1

NCBI **BLAST** search of LYDITEGER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.5	1094.524384	0.004524	LYDITEGER

Mascot: http://www.matrixscience.com/

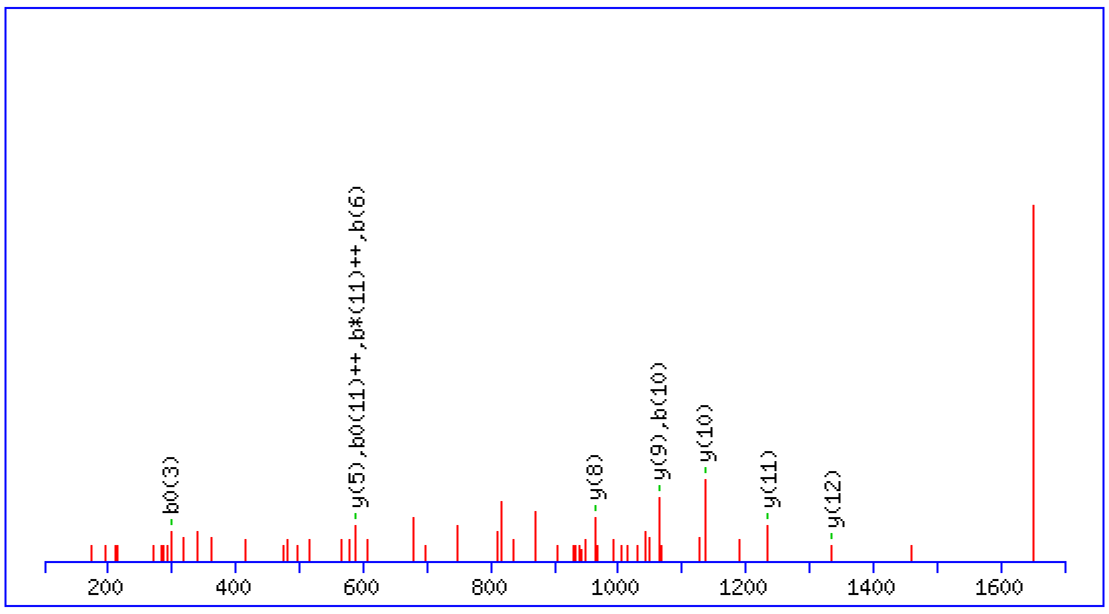
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TSQTVATFLDELAQK**
Found in **THOP1_HUMAN**, Thimet oligopeptidase OS=Homo sapiens GN=THOP1 PE=1 SV=2

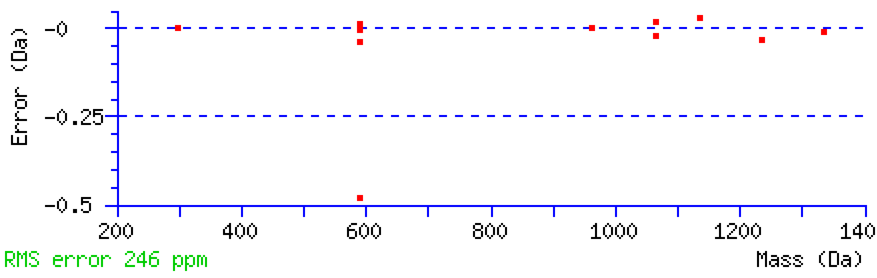
Match to Query 54295: 1650.838808 from(826.426680,2+) rtinseconds(3878) index(57135)
Title: Locus:1.1.1.2890.41
Data file 2011-11-14 - TFD - EP 8-2.mgf

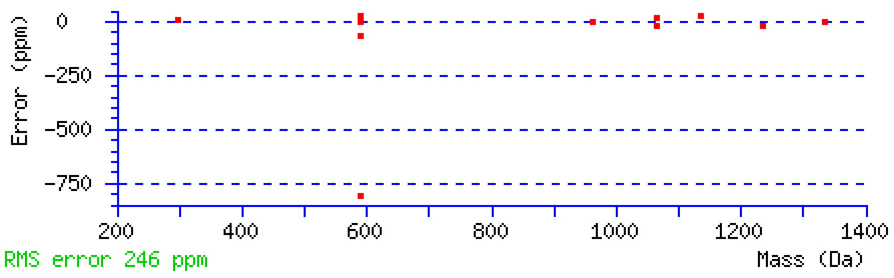
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1650.846466
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.0018
Matches : 11/156 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							15
2	189.086983	95.047129			171.076418	86.041847	S	1550.806066	775.906671	1533.779517	767.393397	1532.795501	766.901389	14
3	317.145561	159.076418	300.119012	150.563144	299.134996	150.071136	Q	1463.774038	732.390657	1446.747489	723.877383	1445.763473	723.385375	13
4	418.193240	209.600258	401.166691	201.086984	400.182675	200.594976	T	***1335.715460***	668.361368	1318.688911	659.848094	1317.704895	659.356086	12
5	517.261654	259.134465	500.235105	250.621191	499.251089	250.129183	V	***1234.667781***	617.837529	1217.641232	609.324254	1216.657216	608.832246	11
6	**588.298768**	294.653022	571.272219	286.139748	570.288203	285.647740	A	***1135.599367***	568.303322	1118.572818	559.790047	1117.588802	559.298039	10
7	689.346447	345.176862	672.319898	336.663587	671.335882	336.171579	T	***1064.562253***	532.784765	1047.535704	524.271490	1046.551688	523.779482	9
8	836.414861	418.711069	819.388312	410.197794	818.404296	409.705786	F	***963.514574***	482.260925	946.488025	473.747651	945.504009	473.255643	8
9	949.498925	475.253101	932.472376	466.739826	931.488360	466.247818	L	816.446160	408.726718	799.419611	400.213444	798.435595	399.721436	7
10	**1064.525868**	532.766572	1047.499319	524.253298	1046.515303	523.761289	D	703.362096	352.184686	686.335547	343.671412	685.351531	343.179404	6
11	1193.568461	597.287869	1176.541912	588.774594	1175.557896	588.282586	E	***588.335153***	294.671215	571.308604	286.157940	570.324588	285.665932	5
12	1306.652525	653.829901	1289.625976	645.316626	1288.641960	644.824618	L	459.292560	230.149918	442.266011	221.636643			4
13	1377.689639	689.348457	1360.663090	680.835183	1359.679074	680.343175	A	346.208496	173.607886	329.181947	165.094612			3
14	1505.748217	753.377747	1488.721668	744.864472	1487.737652	744.372464	Q	275.171382	138.089329	258.144833	129.576055			2
15							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of TSQTVATFLDELAQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.2	1650.846466	-0.007658	TSQTVATFLDELAQK
0.8	1650.836609	0.002199	GFPGPKGGPGDPGPTGLK
0.1	1650.836594	0.002214	FFQTSAVPPGTSLSGR

Mascot: http://www.matrixscience.com/

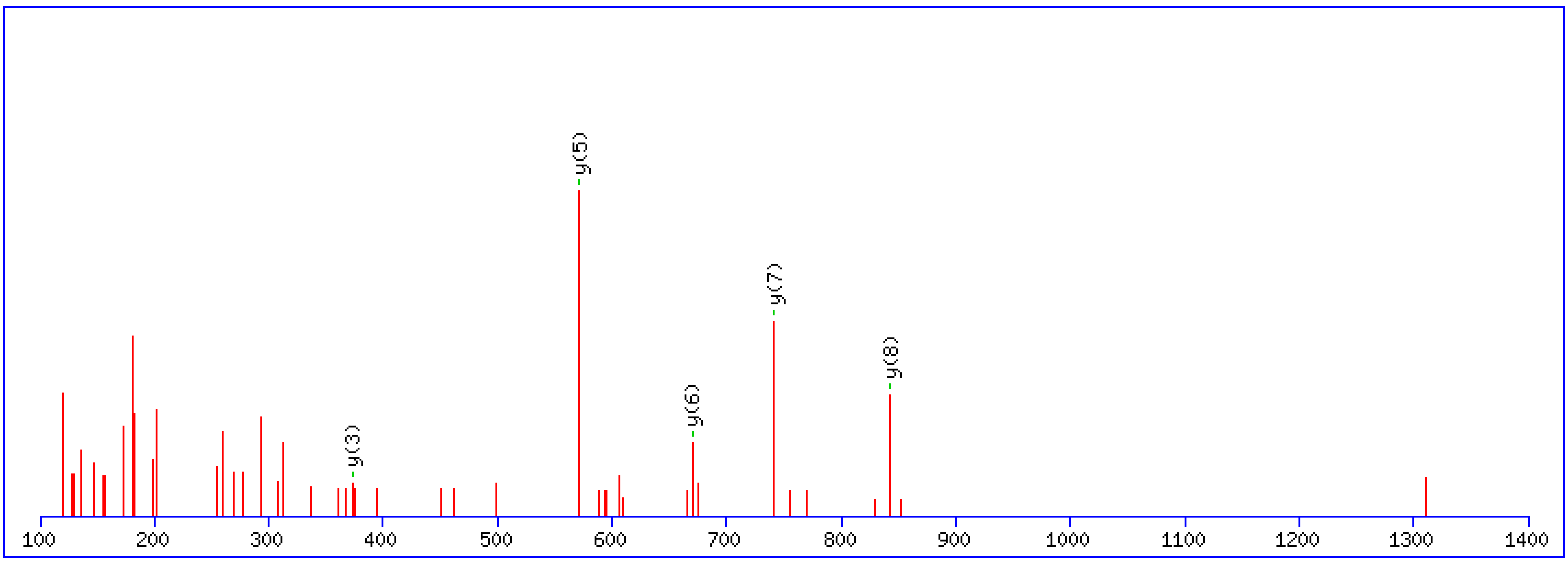
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VTAVPTLLK**
Found in **TXD17_HUMAN**, Thioredoxin domain-containing protein 17 OS=Homo sapiens GN=TXNDC17 PE=1 SV=1

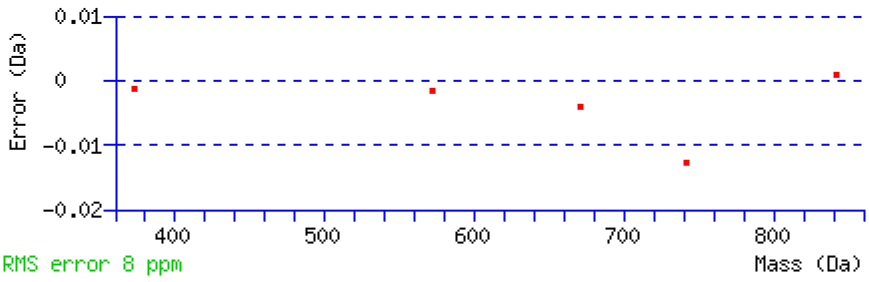
Match to Query 9328: 940.594028 from(471.304290,2+) rtinseconds(2255) index(28047)
Title: Locus:1.1.1.1248.10
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 1.mgf

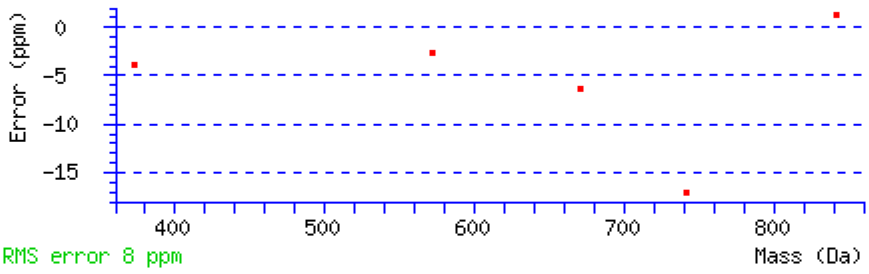
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 940.595718
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 36  Expect: 0.00034
Matches : 5/72 fragment ions using 8 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483			**V**							9
2	201.123369	101.065322	183.112804	92.060040	**T**	*842.534582*	421.770929	825.508033	413.257655	824.524017	412.765647	8
3	272.160483	136.583879	254.149918	127.578597	**A**	*741.486903*	371.247090	724.460354	362.733815	723.476338	362.241807	7
4	371.228897	186.118087	353.218332	177.112804	**V**	*670.449789*	335.728533	653.423240	327.215258	652.439224	326.723250	6
5	468.281661	234.644469	450.271096	225.639186	**P**	*571.381375*	286.194326	554.354826	277.681051	553.370810	277.189043	5
6	569.329340	285.168308	551.318775	276.163026	**T**	474.328611	237.667944	457.302062	229.154669	456.318046	228.662661	4
7	682.413404	341.710340	664.402839	332.705058	**L**	*373.280932*	187.144104	356.254383	178.630830			3
8	795.497468	398.252372	777.486903	389.247090	**L**	260.196868	130.602072	243.170319	122.088798			2
9					**K**	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of VTAVPTLLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.0	940.595718	-0.001690	VTAVPTLLK

Mascot: http://www.matrixscience.com/

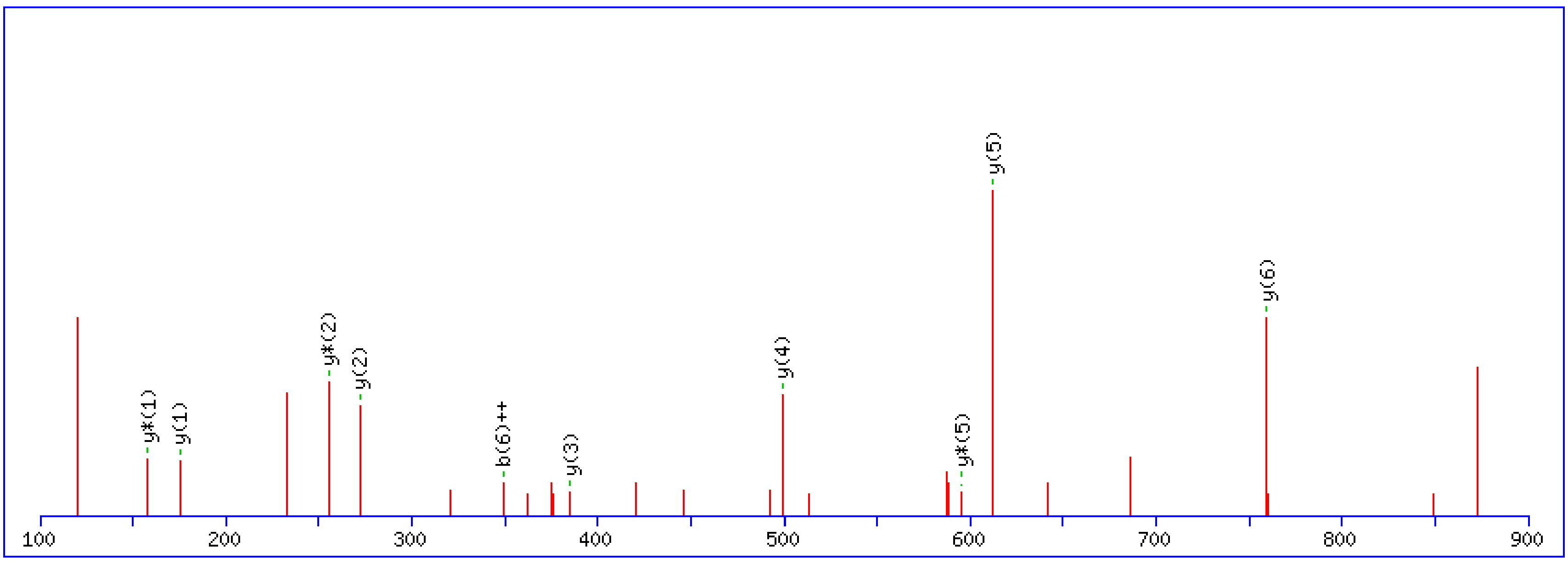
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IFINLPR**
Found in **TXNL1_HUMAN**, Thioredoxin-like protein 1 OS=Homo sapiens GN=TXNL1 PE=1 SV=3

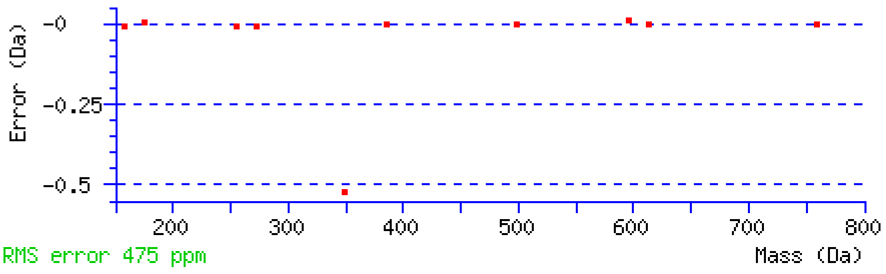
Match to Query 4530: 871.525568 from(436.770060,2+) rtinseconds(2746) index(37394)
Title: Locus:1.1.1.1435.7
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 1.mgf

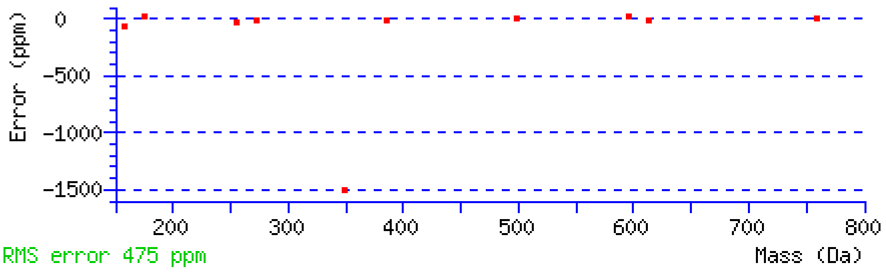
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 900 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 871.527954
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 35  Expect: 0.0022
Matches : 10/42 fragment ions using 23 most intense peaks   (help)
```

#	b	b^{++}	b^*	b^{*++}	Seq.	y	y^{++}	y^*	y^{*++}	#
1	114.091340	57.549308			I					7
2	261.159754	131.083515			F	***759.451185***	380.229231	742.424636	371.715956	6
3	374.243818	187.625547			I	***612.382771***	306.695024	595.356222	298.181749	5
4	488.286745	244.647010	471.260196	236.133736	N	***499.298707***	250.152991	482.272158	241.639717	4
5	601.370809	301.189043	584.344260	292.675768	L	***385.255780***	193.131528	368.229231	184.618253	3
6	698.423573	349.715425	681.397024	341.202150	P	***272.171716***	136.589496	255.145167	128.076221	2
7					R	***175.118952***	88.063114	158.092403	79.549839	1





NCBI **BLAST** search of IFINLPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.0	871.527954	-0.002386	IFINLPR
8.0	871.523926	0.001642	ISAKKPGR
6.9	871.527969	-0.002401	LLVFAPGR
5.4	871.527954	-0.002386	LFNPLIR
5.3	871.523926	0.001642	LSDILRR
4.0	871.523926	0.001642	KNAALVTR
3.2	871.523926	0.001642	IAQLKSGR
2.1	871.523941	0.001627	TLVLRDR
2.0	871.523941	0.001627	LLVDTRR
1.4	871.523926	0.001642	IAIQSKGR

Mascot: http://www.matrixscience.com/

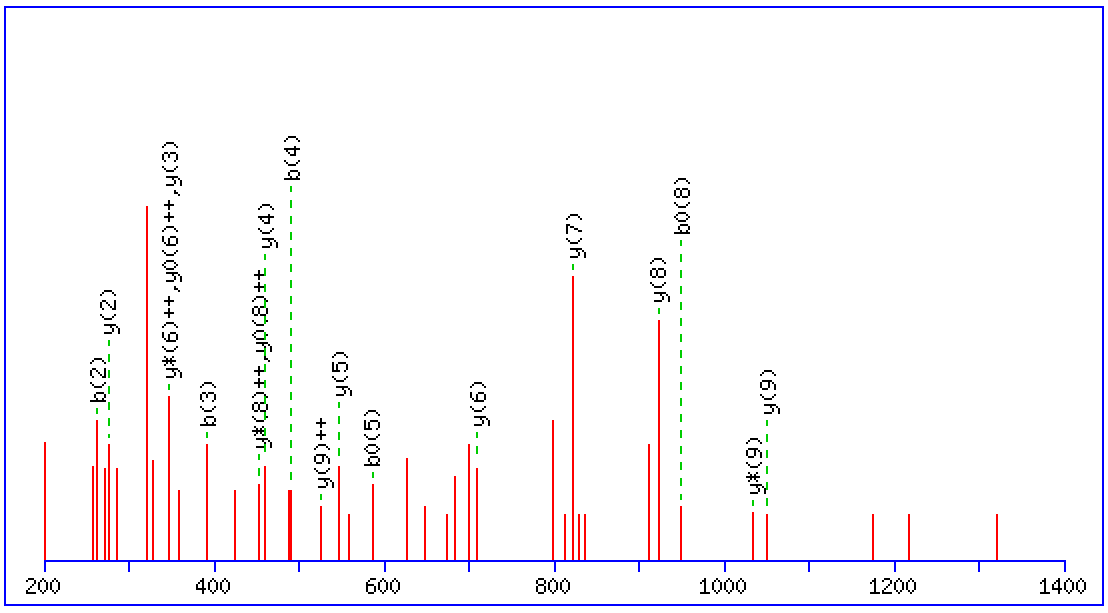
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MDEVLYSIAEK**
Found in **TXN4A_HUMAN**, Thioredoxin-like protein 4A OS=Homo sapiens GN=TXNL4A PE=1 SV=1

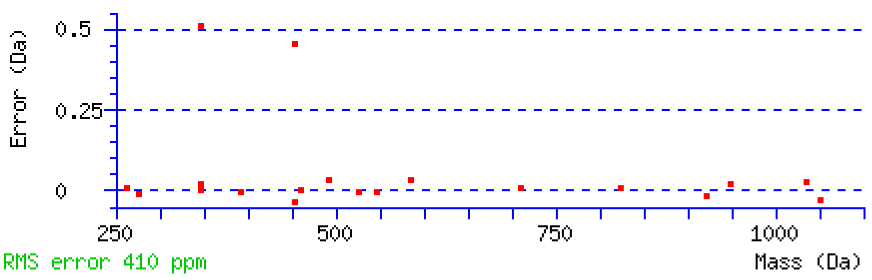
Match to Query 33123: 1312.619628 from(657.317090,2+) rtinseconds(2478) index(23402)
Title: Locus:1.1.1.2401.39
Data file 2011-11-10 - TFD - EP 4-7.mgf

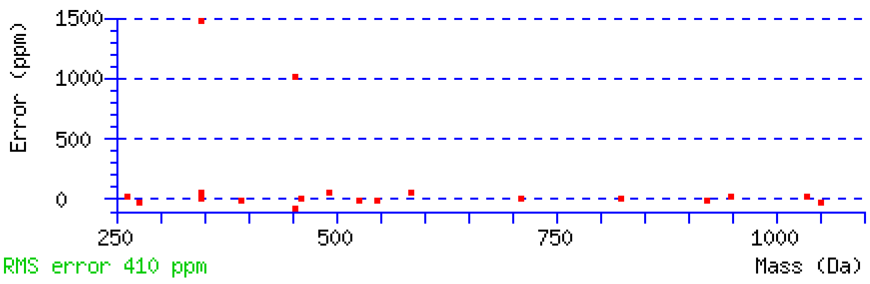
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [1400] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1312.622040
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 53 **Expect:** 1.1e-005
Matches : 19/134 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.042676	74.524976			**M**							**11**
2	**263.069619**	132.038447	245.059054	123.033165	**D**	1166.593946	583.800611	1149.567397	575.287337	1148.583381	574.795328	**10**
3	**392.112212**	196.559744	374.101647	187.554462	**E**	***1051.567003***	526.287139	1034.540454	517.773865	1033.556438	517.281857	**9**
4	**491.180626**	246.093951	473.170061	237.088669	**V**	***922.524410***	461.765843	905.497861	453.252569	904.513845	452.760561	**8**
5	604.264690	302.635983	586.254125	293.630701	**L**	***823.455996***	412.231636	806.429447	403.718361	805.445431	403.226353	**7**
6	767.328019	384.167648	749.317454	375.162365	**Y**	***710.371932***	355.689604	693.345383	347.176329	692.361367	346.684321	**6**
7	854.360047	427.683662	836.349482	418.678379	**S**	***547.308603***	274.157940	530.282054	265.644665	529.298038	265.152657	**5**
8	967.444111	484.225694	949.433546	475.220411	**I**	***460.276575***	230.641925	443.250026	222.128651	442.266010	221.636643	**4**
9	1038.481225	519.744251	1020.470660	510.738968	**A**	***347.192511***	174.099893	330.165962	165.586619	329.181946	165.094611	**3**
10	1167.523818	584.265547	1149.513253	575.260264	**E**	***276.155397***	138.581336	259.128848	130.068062	258.144832	129.576054	**2**
11					**K**	147.112804	74.060040	130.086255	65.546765			**1**





NCBI **BLAST** search of MDEVLYSIAEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.8	1312.622040	-0.002412	MDEVLYSIAEK
0.1	1312.616013	0.003615	FDKLSHASSGAGH

Mascot: http://www.matrixscience.com/

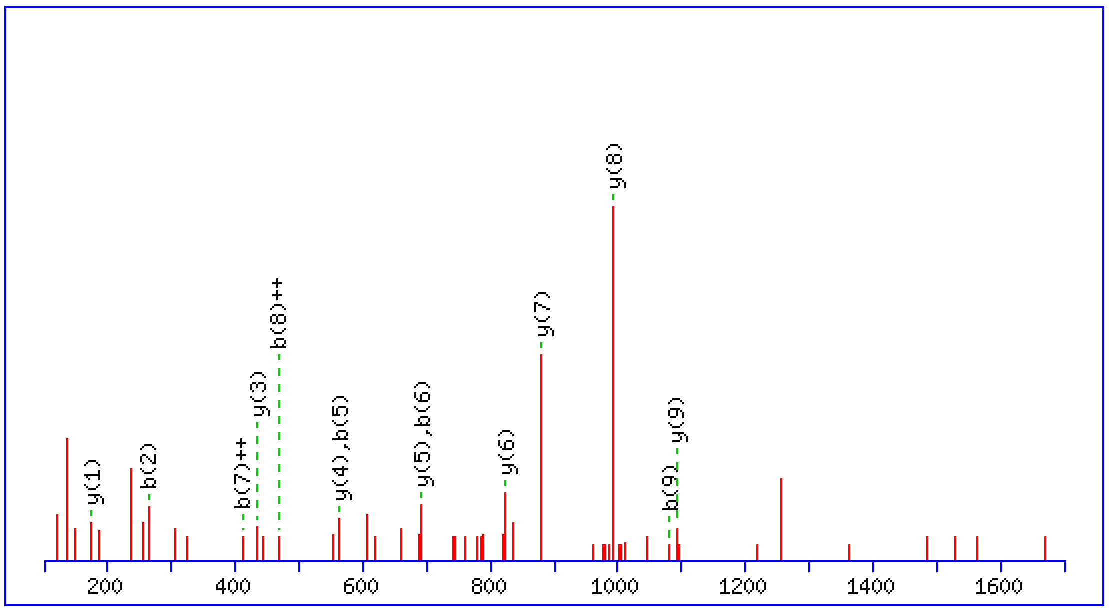
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YVLGMQELFR**
Found in **THOC3_HUMAN**, THO complex subunit 3 OS=Homo sapiens GN=THOC3 PE=1 SV=1

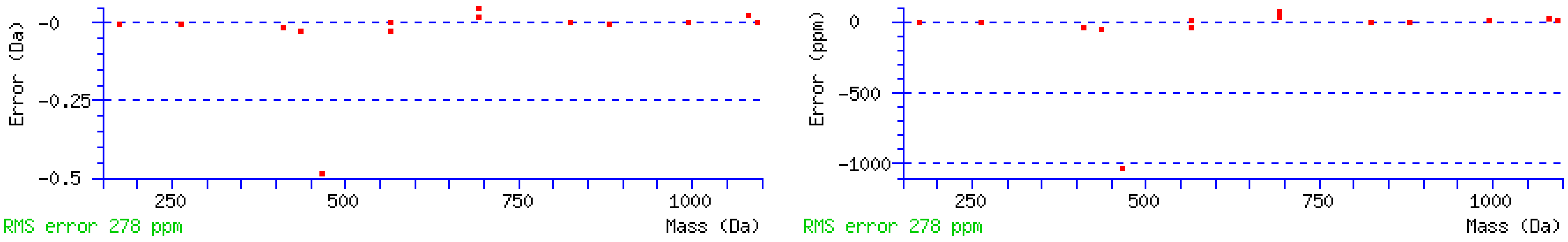
Match to Query 34651: 1254.633848 from(628.324200,2+) rtinseconds(3508) index(51145)
Title: Locus:1.1.1.2717.22
Data file 2011-11-14 - TFD - EP 8-4.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1700] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1254.643066
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 43 **Expect:** 0.00033
Matches : 14/80 fragment ions using 30 most intense peaks (help)

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	164.070605	82.538940					Y							10
2	**263.139019**	132.073148					V	***1092.587028***	546.797152	1075.560479	538.283878	1074.576463	537.791869	9
3	376.223083	188.615180					L	***993.518614***	497.262945	976.492065	488.749670	975.508049	488.257662	8
4	433.244547	217.125912					G	***880.434550***	440.720913	863.408001	432.207638	862.423985	431.715630	7
5	**564.285032**	282.646154					M	***823.413086***	412.210181	806.386537	403.696907	805.402521	403.204899	6
6	**692.343610**	346.675443	675.317061	338.162169			Q	***692.372601***	346.689939	675.346052	338.176664	674.362036	337.684656	5
7	821.386203	**411.196740**	804.359654	402.683465	803.375638	402.191457	E	***564.314023***	282.660650	547.287474	274.147375	546.303458	273.655367	4
8	934.470267	**467.738772**	917.443718	459.225497	916.459702	458.733489	L	***435.271430***	218.139353	418.244881	209.626078			3
9	**1081.538681**	541.272979	1064.512132	532.759704	1063.528116	532.267696	F	322.187366	161.597321	305.160817	153.084046			2
10							R	***175.118952***	88.063114	158.092403	79.549839			1



NCBI **BLAST** search of YVLGMQELFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
43.0	1254.643066	-0.009218	YVLGMQELFR
3.7	1254.635681	-0.001833	HLTDPSYGIPR
2.6	1254.634323	-0.000475	YVSSLTEEISK

Mascot: http://www.matrixscience.com/

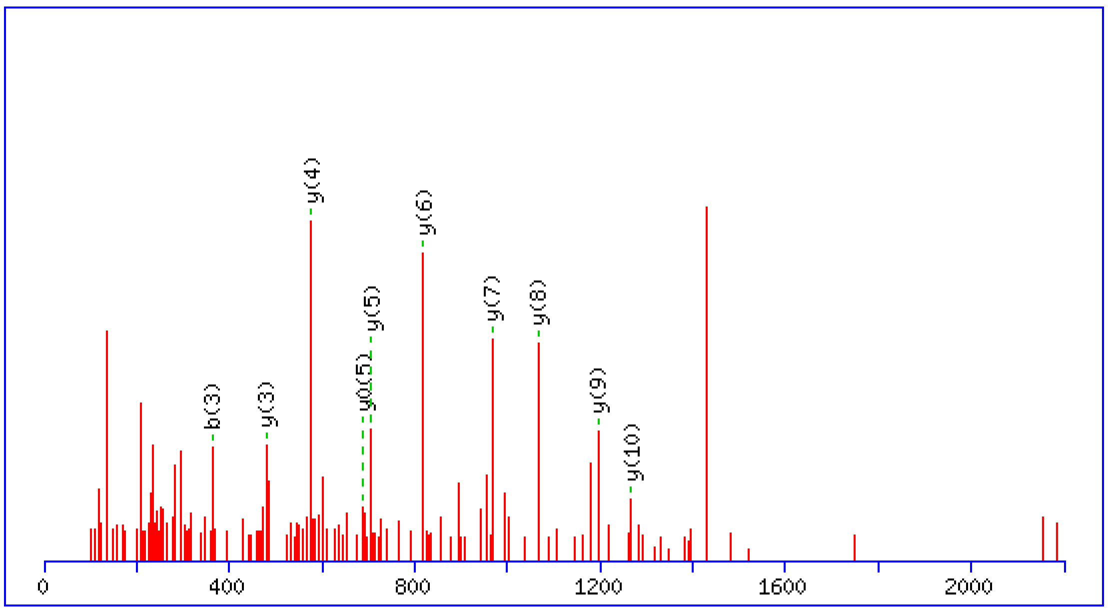
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YAETFLEPWFK**
Found in **THUM1_HUMAN**, THUMP domain-containing protein 1 OS=Homo sapiens GN=THUMPD1 PE=1 SV=2

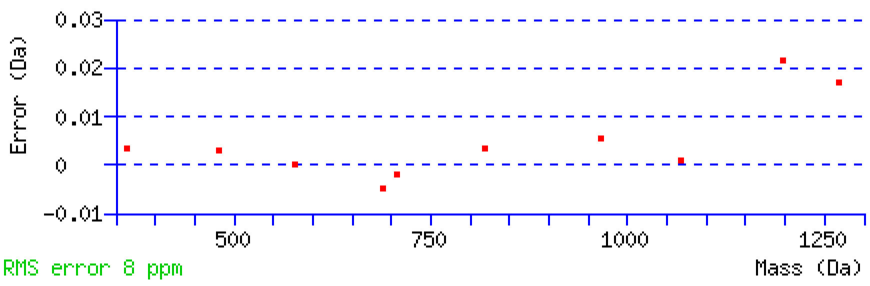
Match to Query 36064: 1429.700328 from(715.857440,2+) rtinseconds(3753) index(55457)
Title: Locus:1.1.1.2942.20
Data file 2011-11-12 - TFD - EP 5-3.mgf

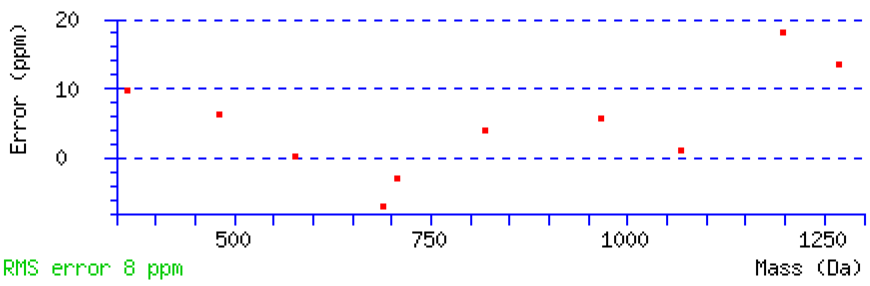
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1429.691788
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 64  Expect: 1.5e-006
Matches : 10/88 fragment ions using 13 most intense peaks   (help)
```

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	164.070605	82.538940			Y							11
2	235.107719	118.057498			A	***1267.635752***	634.321514	1250.609203	625.808240	1249.625187	625.316232	10
3	364.150312	182.578794	346.139747	173.573512	E	***1196.598638***	598.802957	1179.572089	590.289683	1178.588073	589.797675	9
4	465.197991	233.102634	447.187426	224.097351	T	***1067.556045***	534.281661	1050.529496	525.768386	1049.545480	525.276378	8
5	612.266405	306.636841	594.255840	297.631558	F	***966.508366***	483.757821	949.481817	475.244547	948.497801	474.752539	7
6	725.350469	363.178873	707.339904	354.173590	L	***819.439952***	410.223614	802.413403	401.710340	801.429387	401.218332	6
7	854.393062	427.700169	836.382497	418.694887	E	***706.355888***	353.681582	689.329339	345.168308	688.345323	344.676300	5
8	951.445826	476.226551	933.435261	467.221269	P	***577.313295***	289.160286	560.286746	280.647011			4
9	1137.525139	569.266208	1119.514574	560.260925	W	***480.260531***	240.633904	463.233982	232.120629			3
10	1284.593553	642.800415	1266.582988	633.795132	F	294.181218	147.594247	277.154669	139.080973			2
11					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of YAETFLEPWFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
63.9	1429.691788	0.008540	YAETFLEPWFK
1.7	1429.688477	0.011851	VLPCGPSPQHHR
1.7	1429.688477	0.011851	VLPCGPSPQHHR

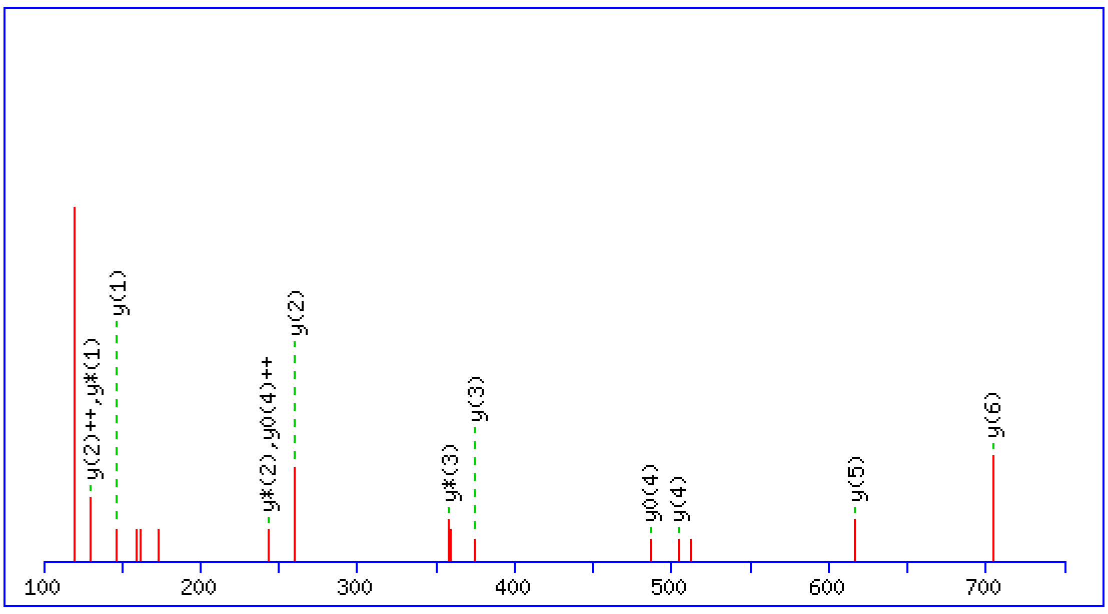
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FSIEDLK**
Found in **THYN1_HUMAN**, Thymocyte nuclear protein 1 OS=Homo sapiens GN=THYN1 PE=1 SV=1

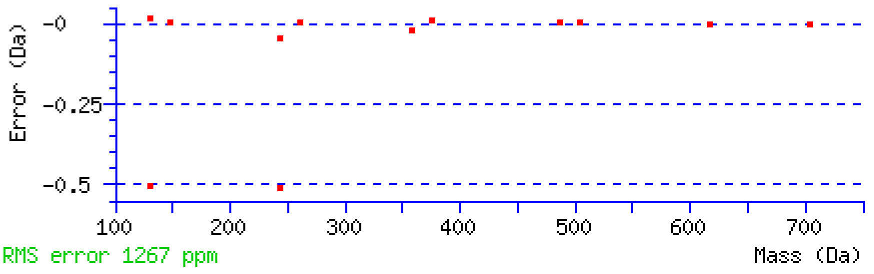
Match to Query 4017: 850.448068 from(426.231310,2+) rtinseconds(2669) index(33133)
Title: Locus:1.1.1.2434.4
Data file 2011-11-13 - TFD - EP 7-5.mgf

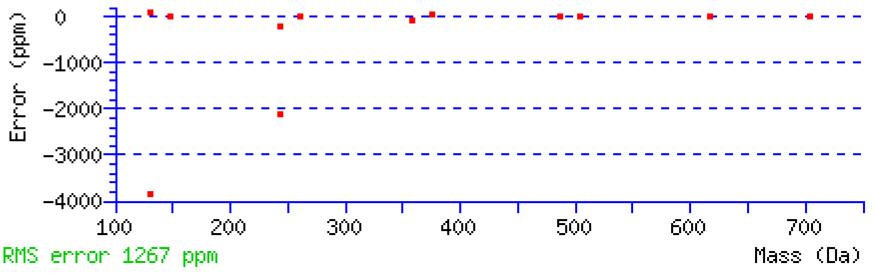
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [750] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 850.443619
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 55  Expect: 3.5e-005
Matches : 12/54 fragment ions using 13 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.075690	74.541483			F							7
2	235.107718	118.057497	217.097153	109.052214	S	***704.382496***	352.694886	687.355947	344.181612	686.371931	343.689604	6
3	348.191782	174.599529	330.181217	165.594247	I	***617.350468***	309.178872	600.323919	300.665598	599.339903	300.173590	5
4	477.234375	239.120826	459.223810	230.115543	E	***504.266404***	252.636840	487.239855	244.123566	486.255839	243.631558	4
5	592.261318	296.634297	574.250753	287.629015	D	***375.223811***	188.115544	358.197262	179.602269	357.213246	179.110261	3
6	705.345382	353.176329	687.334817	344.171047	L	***260.196868***	130.602072	243.170319	122.088798			2
7					K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of FSIEDLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.7	850.443619	0.004449	FSIEDLK
38.0	850.443604	0.004464	AYIEDLK
38.0	850.443604	0.004464	YAIEDLK
21.9	850.443619	0.004449	SFLDELK
11.1	850.443619	0.004449	DYSPLLK
10.4	850.454849	-0.006781	FAANSTLK
9.4	850.443619	0.004449	SFEVELK
9.3	850.443634	0.004434	YTDLVPK
9.2	850.443619	0.004449	ELVSYPK
9.1	850.454865	-0.006797	DLHPLPK

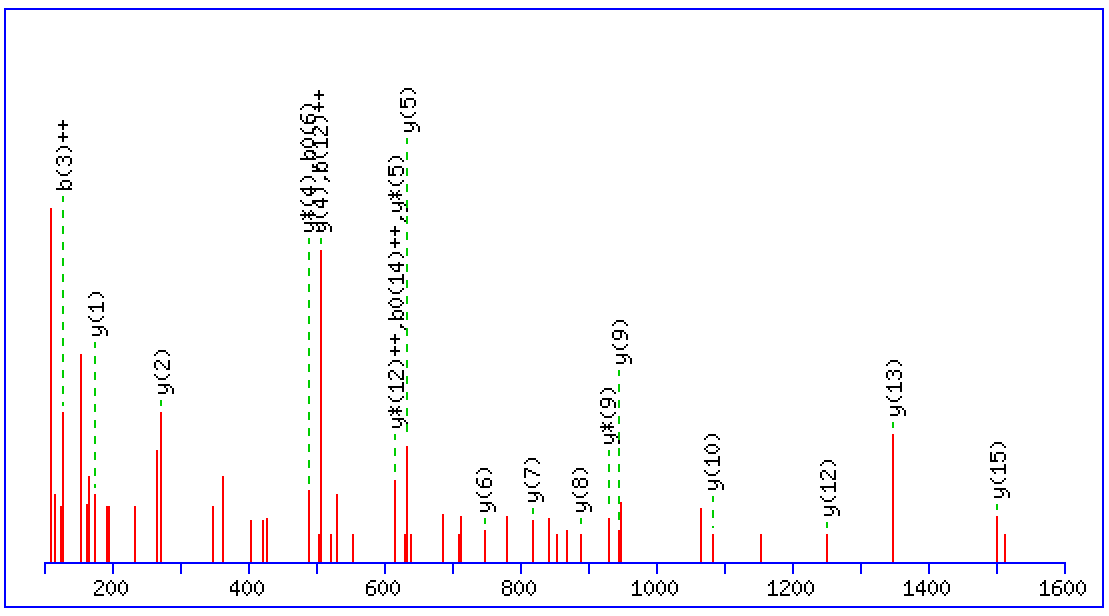
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GTPGPPPAHGAALQPHPR**
Found in **TRIP6_HUMAN**, Thyroid receptor-interacting protein 6 OS=Homo sapiens GN=TRIP6 PE=1 SV=3

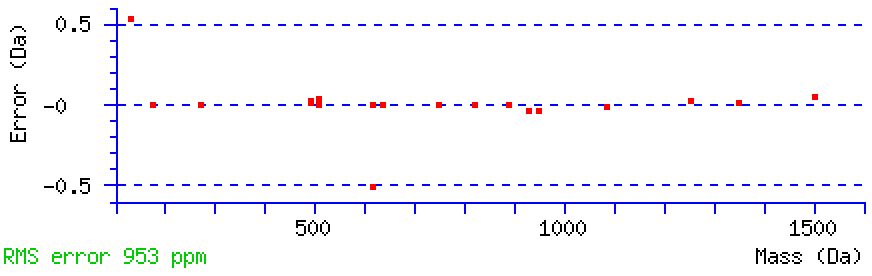
Match to Query 4048: 1756.905216 from(440.233580,4+) rtinseconds(1110) index(5053)
Title: Locus:1.1.1.1934.15
Data file 2011-11-12 - TFD - EP 5-3.mgf

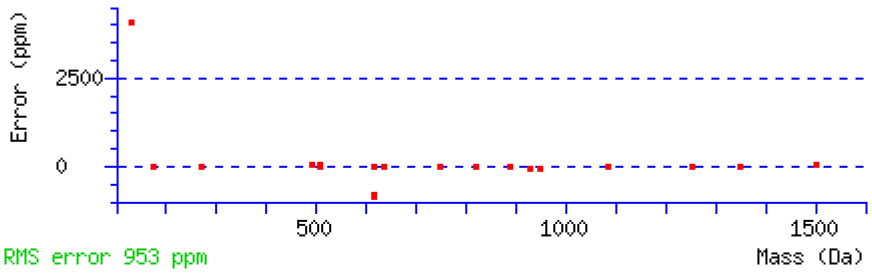
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1756.912140
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 60  Expect: 5.9e-006
Matches : 20/144 fragment ions using 44 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							18
2	159.076419	80.041847			141.065854	71.036565	T	1700.897951	850.952614	1683.871402	842.439339	1682.887386	841.947331	17
3	256.129183	128.568230			238.118618	119.562947	P	1599.850272	800.428774	1582.823723	791.915500			16
4	313.150647	157.078961			295.140082	148.073679	G	***1502.797508***	751.902392	1485.770959	743.389118			15
5	410.203411	205.605344			392.192846	196.600061	P	1445.776044	723.391660	1428.749495	714.878386			14
6	507.256175	254.131726			489.245610	245.126443	P	***1348.723280***	674.865278	1331.696731	666.352004			13
7	604.308939	302.658108			586.298374	293.652825	P	***1251.670516***	626.338896	1234.643967	617.825622			12
8	675.346053	338.176665			657.335488	329.171382	A	1154.617752	577.812514	1137.591203	569.299240			11
9	812.404965	406.706121			794.394400	397.700838	H	***1083.580638***	542.293957	1066.554089	533.780683			10
10	869.426429	435.216853			851.415864	426.211570	G	***946.521726***	473.764501	929.495177	465.251227			9
11	940.463543	470.735410			922.452978	461.730127	A	***889.500262***	445.253769	872.473713	436.740495			8
12	1011.500657	506.253967			993.490092	497.248684	A	***818.463148***	409.735212	801.436599	401.221938			7
13	1124.584721	562.795999			1106.574156	553.790716	L	***747.426034***	374.216655	730.399485	365.703381			6
14	1252.643299	626.825288	1235.616750	618.312013	1234.632734	617.820005	Q	***634.341970***	317.674623	617.315421	309.161349			5
15	1349.696063	675.351670	1332.669514	666.838395	1331.685498	666.346387	P	***506.283392***	253.645334	489.256843	245.132059			4
16	1486.754975	743.881126	1469.728426	735.367851	1468.744410	734.875843	H	409.230628	205.118952	392.204079	196.605677			3
17	1583.807739	792.407508	1566.781190	783.894233	1565.797174	783.402225	P	***272.171716***	136.589496	255.145167	128.076221			2
18							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of GTPGPPPAHGAALQPHPR
(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	1756.912140	-0.006924	GTPGPPPAHGAALQPHPR
2.9	1756.922012	-0.016796	HATAYRVVIESLQDR

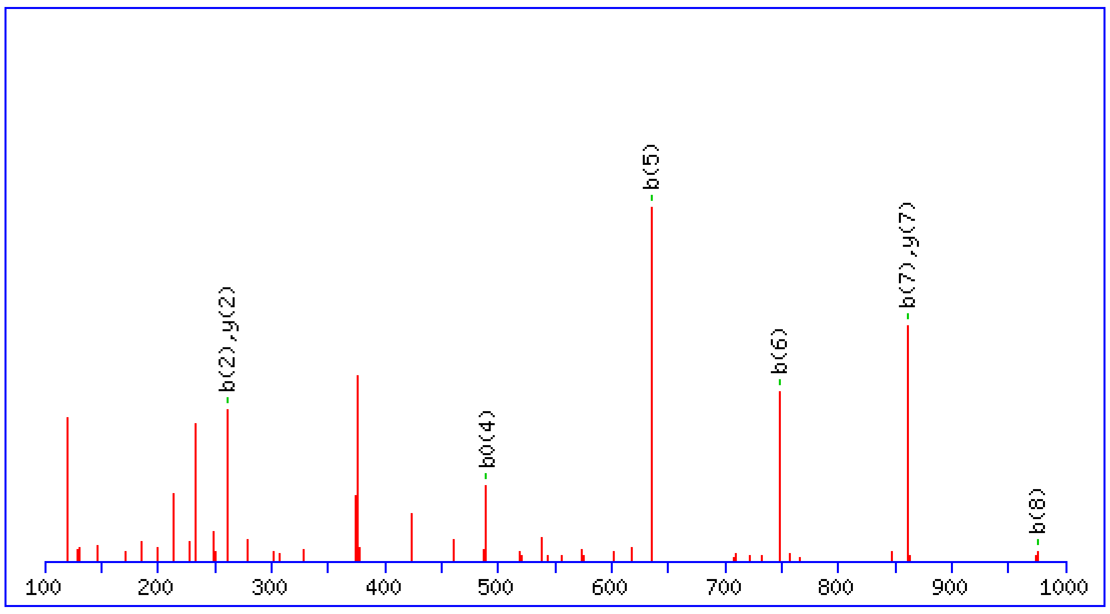
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MEVFKILNK**
Found in **TAP26_HUMAN**, Thyroid transcription factor 1-associated protein 26 OS=Homo sapiens GN=CCDC59 PE=1 SV=2

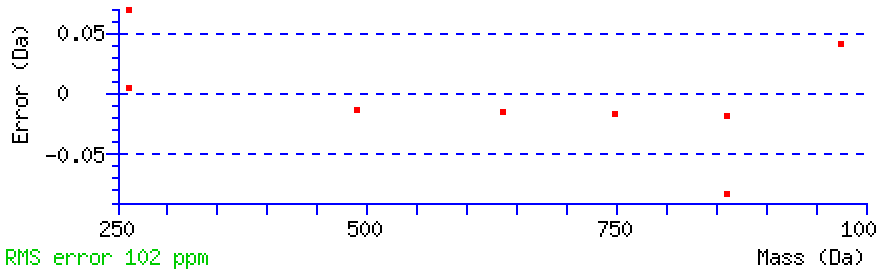
Match to Query 22899: 1120.622268 from(561.318410,2+) rtinseconds(3350) index(37258)
Title: Locus:1.1.1.2635.7
Data file 2011-11-14 - TFD - EP 8-7.mgf

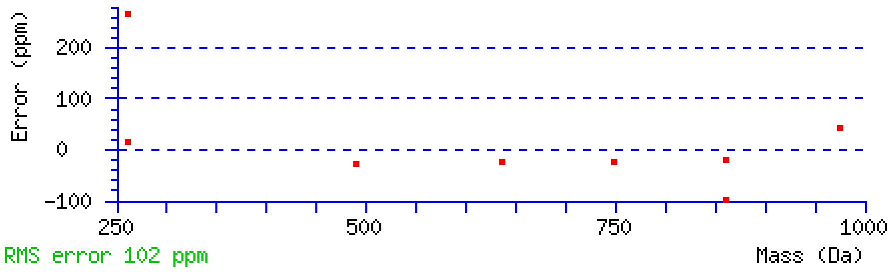
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1120.631424
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.0017
Matches : 8/72 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	132.047761	66.527518					M							9
2	***261.090354***	131.048815			243.079789	122.043533	E	990.598243	495.802760	973.571694	487.289485	972.587678	486.797477	8
3	360.158768	180.583022			342.148203	171.577740	V	**861.555650**	431.281463	844.529101	422.768189			7
4	507.227182	254.117229			489.216617	245.111947	F	762.487236	381.747256	745.460687	373.233982			6
5	***635.322145***	318.164711	618.295596	309.651436	617.311580	309.159428	K	615.418822	308.213049	598.392273	299.699775			5
6	***748.406209***	374.706743	731.379660	366.193468	730.395644	365.701460	I	487.323859	244.165567	470.297310	235.652293			4
7	***861.490273***	431.248775	844.463724	422.735500	843.479708	422.243492	L	374.239795	187.623535	357.213246	179.110261			3
8	***975.533200***	488.270238	958.506651	479.756964	957.522635	479.264956	N	**261.155731**	131.081503	244.129182	122.568229			2
9							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of MEVFKILNK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.4	1120.631424	-0.009156	MEVFKILNK
19.9	1120.620209	0.002059	FLILPDMLK
17.1	1120.631424	-0.009156	MLLLFELAR
7.0	1120.612823	0.009445	LVSAVVEYGGK
6.9	1120.624023	-0.001755	LVELYRSNK
6.8	1120.624023	-0.001755	FLAREASSLK
5.4	1120.612808	0.009460	FIEELKGGTK
5.4	1120.631439	-0.009171	FQLMTAGIIK
2.1	1120.612793	0.009475	ITKFIEENK
1.0	1120.628067	-0.005799	LFSFPAAKPK

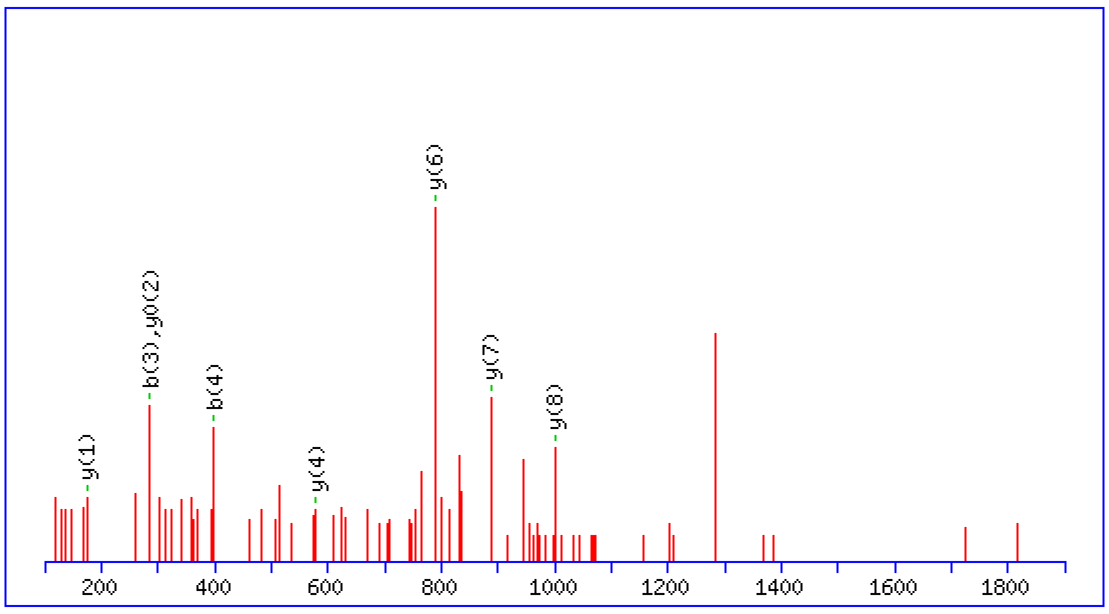
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DGLIVPIFQER**
Found in **FUCO_HUMAN**, Tissue alpha-L-fucosidase OS=Homo sapiens GN=FUCA1 PE=1 SV=4

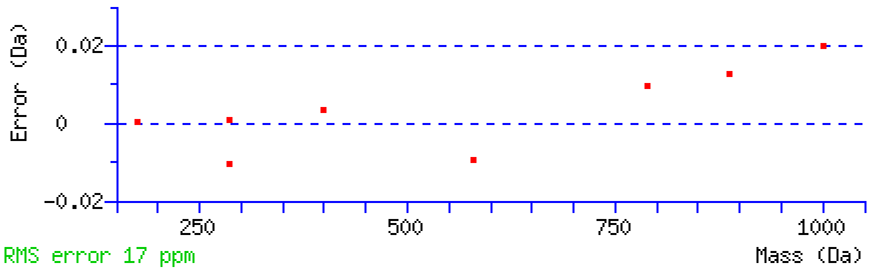
Match to Query 31796: 1285.697588 from(643.856070,2+) rtinseconds(3477) index(50995)
Title: Locus:1.1.1.2873.14
Data file 2011-11-13 - TFD - EP 7-3.mgf

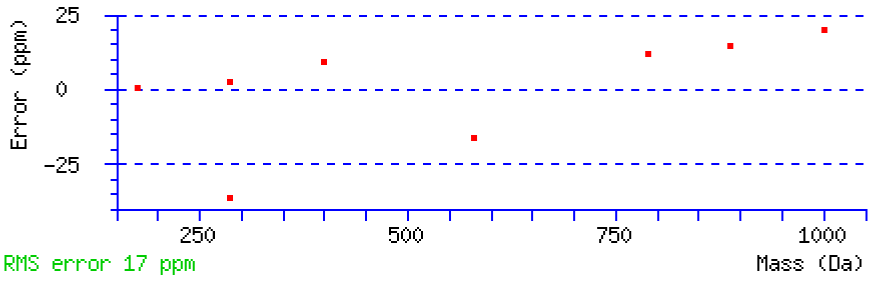
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1285.703033
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 34 **Expect:** 0.0051
Matches : 8/102 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	116.034219	58.520748			98.023654	49.515465	D							11
2	173.055683	87.031479			155.045118	78.026197	G	1171.683371	586.345324	1154.656822	577.832049	1153.672806	577.340041	10
3	**286.139747**	143.573512			268.129182	134.568229	L	1114.661907	557.834592	1097.635358	549.321317	1096.651342	548.829309	9
4	**399.223811**	200.115544			381.213246	191.110261	I	***1001.577843***	501.292560	984.551294	492.779285	983.567278	492.287277	8
5	498.292225	249.649751			480.281660	240.644468	V	***888.493779***	444.750528	871.467230	436.237253	870.483214	435.745245	7
6	595.344989	298.176133			577.334424	289.170850	P	***789.425365***	395.216321	772.398816	386.703046	771.414800	386.211038	6
7	708.429053	354.718165			690.418488	345.712882	I	692.372601	346.689939	675.346052	338.176664	674.362036	337.684656	5
8	855.497467	428.252372			837.486902	419.247089	F	***579.288537***	290.147907	562.261988	281.634632	561.277972	281.142624	4
9	983.556045	492.281661	966.529496	483.768386	965.545480	483.276378	Q	432.220123	216.613700	415.193574	208.100425	414.209558	207.608417	3
10	1112.598638	556.802957	1095.572089	548.289683	1094.588073	547.797675	E	304.161545	152.584411	287.134996	144.071136	286.150980	143.579128	2
11							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of DGLIVPIFQER
(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	1285.703033	-0.005445	DGLIVPIFQER
11.3	1285.703033	-0.005445	WVLVGAPKADSK
9.5	1285.687759	0.009829	DAVLKVVEEER
0.8	1285.703018	-0.005430	AITPPQQPYKK
0.8	1285.703033	-0.005445	WVINPSGGLISK

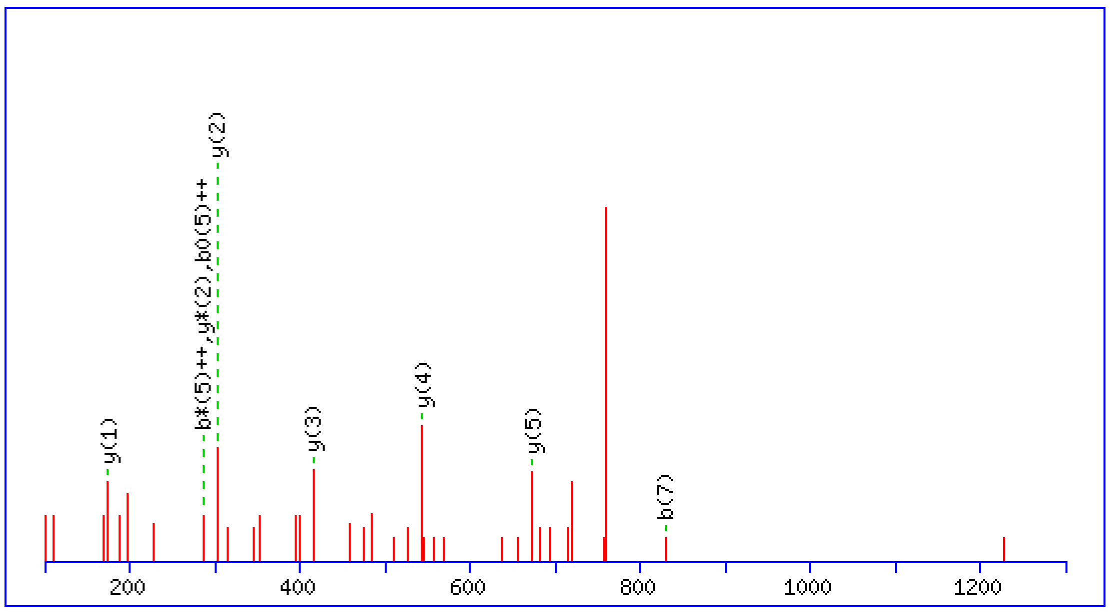
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TTQEQLKR**
Found in **TLR10_HUMAN**, Toll-like receptor 10 OS=Homo sapiens GN=TLR10 PE=1 SV=2

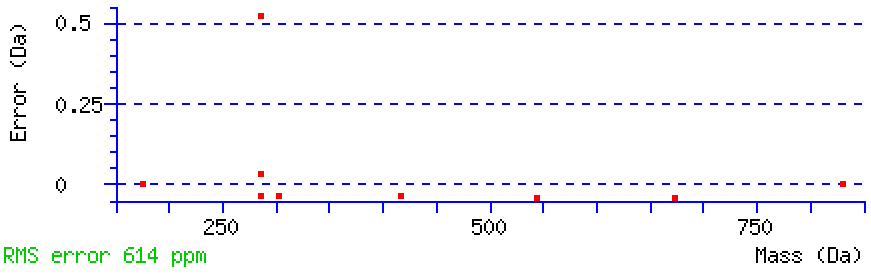
Match to Query 15641: 1002.546528 from(502.280540,2+) rtinseconds(1310) index(6079)
Title: Locus:1.1.1.2144.31
Data file 2011-11-12 - TFD - EP 5-2.mgf

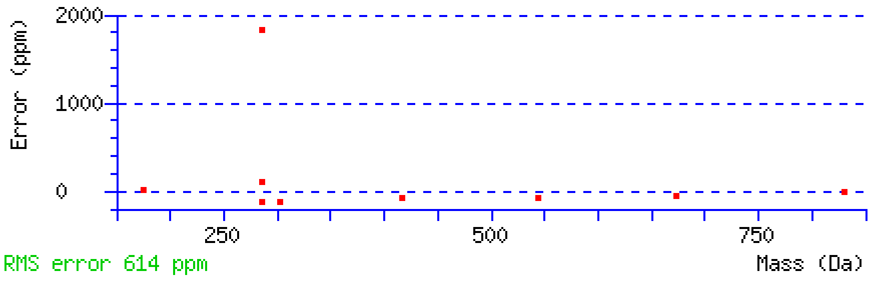
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1002.545792
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.0014
Matches : 9/72 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							8
2	203.102634	102.054955			185.092069	93.049672	T	902.505407	451.756342	885.478858	443.243067	884.494842	442.751059	7
3	331.161212	166.084244	314.134663	157.570970	313.150647	157.078962	Q	801.457728	401.232502	784.431179	392.719228	783.447163	392.227220	6
4	460.203805	230.605541	443.177256	222.092266	442.193240	221.600258	E	*673.399150*	337.203213	656.372601	328.689939	655.388585	328.197931	5
5	588.262383	294.634830	571.235834	286.121555	570.251818	285.629547	Q	*544.356557*	272.681917	527.330008	264.168642			4
6	701.346447	351.176862	684.319898	342.663587	683.335882	342.171579	L	*416.297979*	208.652627	399.271430	200.139353			3
7	829.441410	415.224343	812.414861	406.711069	811.430845	406.219061	K	*303.213915*	152.110595	286.187366	143.597321			2
8							R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of TTQEQLKR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.6	1002.545792	0.000736	TTQEQLKR
37.7	1002.545792	0.000736	SSALGKEVGR
13.1	1002.545792	0.000736	NSTGVEIKR
9.6	1002.549820	-0.003292	IPPTYQIR
9.1	1002.545792	0.000736	ADKTLATQR
8.0	1002.553192	-0.006664	IIDIVMQR
8.0	1002.553192	-0.006664	LPMILTQR
7.1	1002.549835	-0.003307	AITLFPPGR
6.7	1002.545792	0.000736	TVLENSGKR
2.9	1002.543274	0.003254	HILYCKR

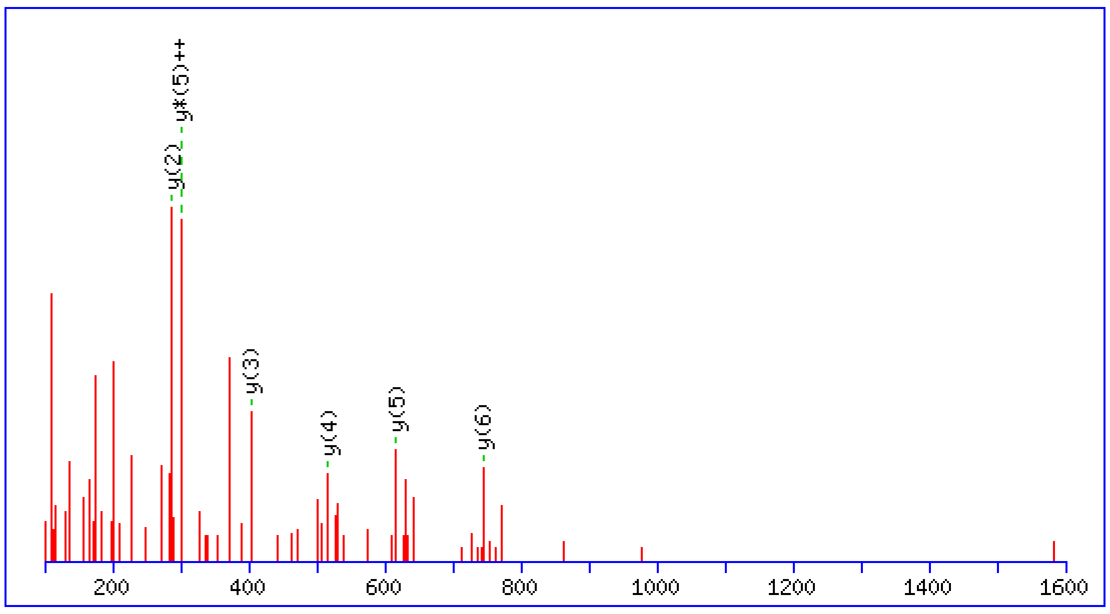
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LQTLDLR**
Found in **TLR5_HUMAN**, Toll-like receptor 5 OS=Homo sapiens GN=TLR5 PE=1 SV=4

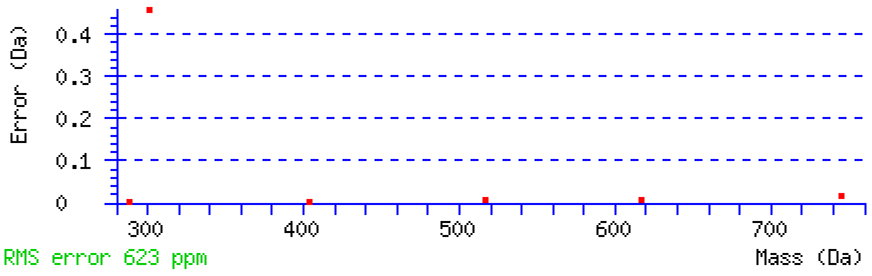
Match to Query 4403: 857.496708 from(429.755630,2+) rtinseconds(1902) index(20116)
Title: Locus:1.1.1.2154.7
Data file 2011-11-10 - TFD - EP 3-1.mgf

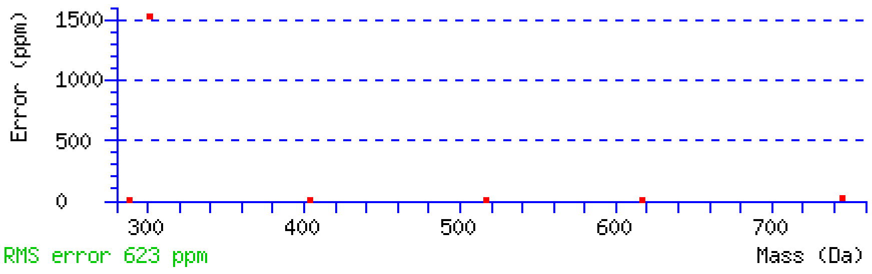
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1600] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 857.497055
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 45  Expect: 0.00042
Matches : 6/62 fragment ions using 7 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							7
2	242.149918	121.578597	225.123369	113.065323			Q	***745.420280***	373.213778	728.393731	364.700504	727.409715	364.208496	6
3	343.197597	172.102437	326.171048	163.589162	325.187032	163.097154	T	***617.361702***	309.184489	600.335153	300.671215	599.351137	300.179207	5
4	456.281661	228.644469	439.255112	220.131194	438.271096	219.639186	L	***516.314023***	258.660650	499.287474	250.147375	498.303458	249.655367	4
5	571.308604	286.157940	554.282055	277.644666	553.298039	277.152658	D	***403.229959***	202.118618	386.203410	193.605343	385.219394	193.113335	3
6	684.392668	342.699972	667.366119	334.186698	666.382103	333.694690	L	***288.203016***	144.605146	271.176467	136.091872			2
7							R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of LQTLDLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.4	857.497055	-0.000347	LQTLDLR
30.6	857.497055	-0.000347	LKDPTLR
30.6	857.497055	-0.000347	LQDLTLR
27.5	857.497055	-0.000347	LGATILDR
18.7	857.497025	-0.000317	LKAEEIR
17.6	857.497055	-0.000347	IQDILTR
15.1	857.497055	-0.000347	VEQLTLR
14.6	857.497055	-0.000347	LKDEVVR
13.6	857.497055	-0.000347	QLTLQQK
13.6	857.497055	-0.000347	DITQLLR

Mascot: http://www.matrixscience.com/

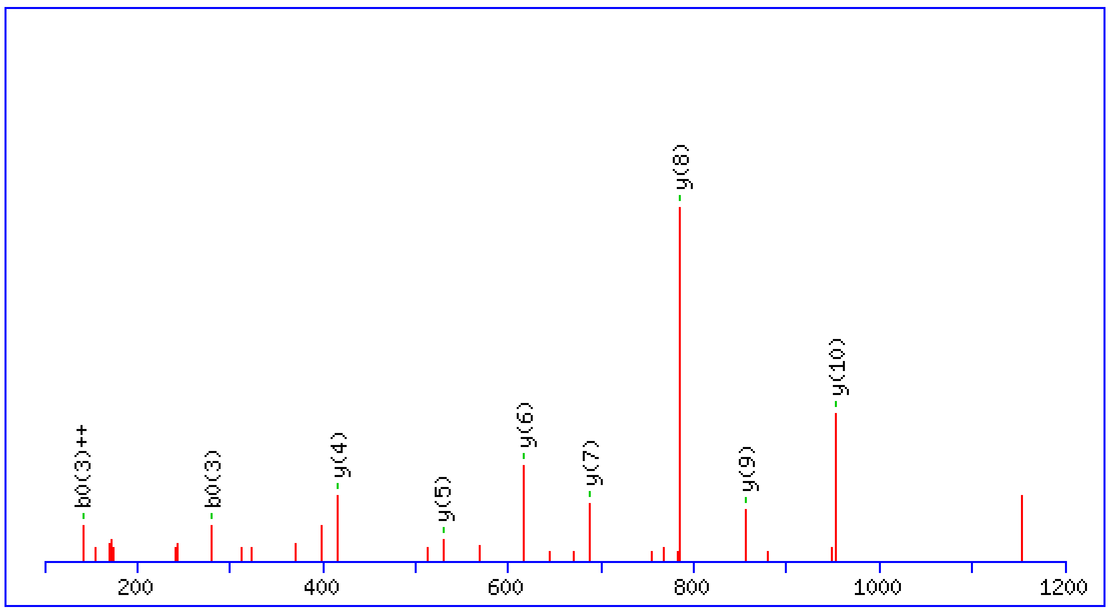
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EAPAPASNPSGR**
Found in **TM1L2_HUMAN**, TOM1-like protein 2 OS=Homo sapiens GN=TOM1L2 PE=1 SV=1

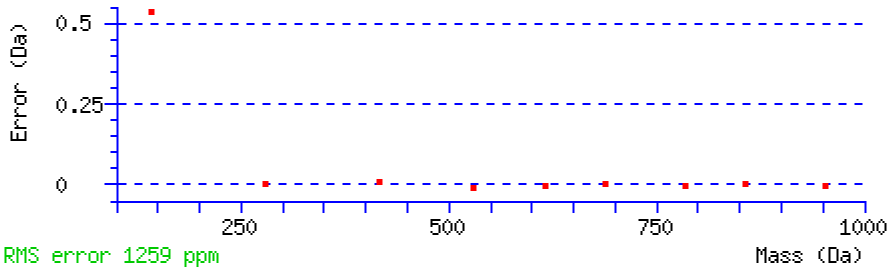
Match to Query 462155: 1152.552708 from(577.283630,2+) rtinseconds(838) index(240773)
Title: Locus:1.1.1.758.28
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

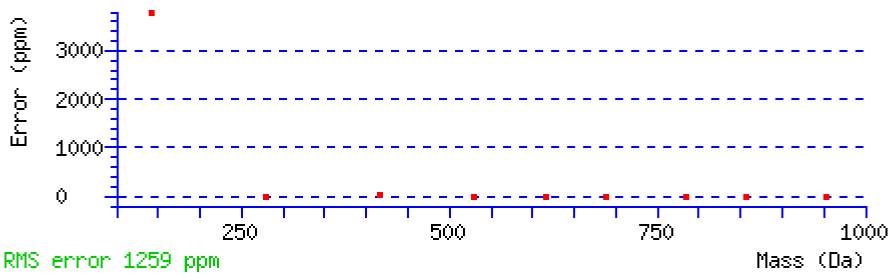
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1200] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1152.552322
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 64  Expect: 6e-006
Matches : 9/114 fragment ions using 9 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	E							12
2	201.086983	101.047130			183.076418	92.041847	A	1024.517033	512.762154	1007.490484	504.248880	1006.506468	503.756872	11
3	298.139747	149.573512			280.129182	140.568229	P	***953.479919***	477.243598	936.453370	468.730323	935.469354	468.238315	10
4	369.176861	185.092068			351.166296	176.086786	A	***856.427155***	428.717216	839.400606	420.203941	838.416590	419.711933	9
5	466.229625	233.618450			448.219060	224.613168	P	***785.390041***	393.198659	768.363492	384.685384	767.379476	384.193376	8
6	537.266739	269.137008			519.256174	260.131725	A	***688.337277***	344.672277	671.310728	336.159002	670.326712	335.666994	7
7	624.298767	312.653022			606.288202	303.647739	S	***617.300163***	309.153720	600.273614	300.640445	599.289598	300.148437	6
8	738.341694	369.674485	721.315145	361.161210	720.331129	360.669202	N	***530.268135***	265.637706	513.241586	257.124431	512.257570	256.632423	5
9	835.394458	418.200867	818.367909	409.687592	817.383893	409.195585	P	***416.225208***	208.616242	399.198659	200.102967	398.214643	199.610959	4
10	922.426486	461.716881	905.399937	453.203606	904.415921	452.711598	S	319.172444	160.089860	302.145895	151.576585	301.161879	151.084577	3
11	979.447950	490.227613	962.421401	481.714339	961.437385	481.222331	G	232.140416	116.573846	215.113867	108.060571			2
12							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of EAPAPASNPSGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
63.7	1152.552322	0.000386	EAPAPASNPSGR
11.2	1152.563568	-0.010860	ERPAPGNAGPR
5.5	1152.563568	-0.010860	ERPAPGNAGPR

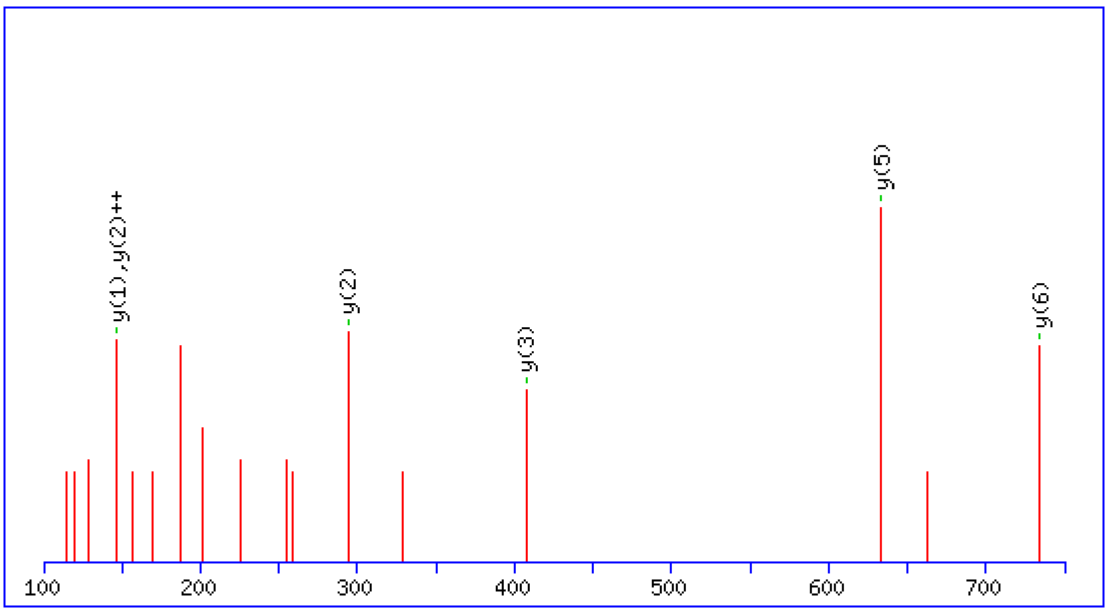
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VTLLLFK**
Found in **TPRKB_HUMAN**, TP53RK-binding protein OS=Homo sapiens GN=TPRKB PE=1 SV=1

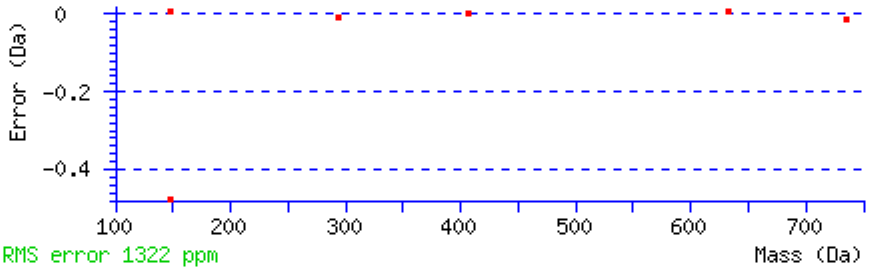
Match to Query 3454: 832.545988 from(417.280270,2+) rtinseconds(3220) index(38521)
Title: Locus:1.1.1.2493.3
Data file 2011-11-10 - TFD - EP 3-6.mgf

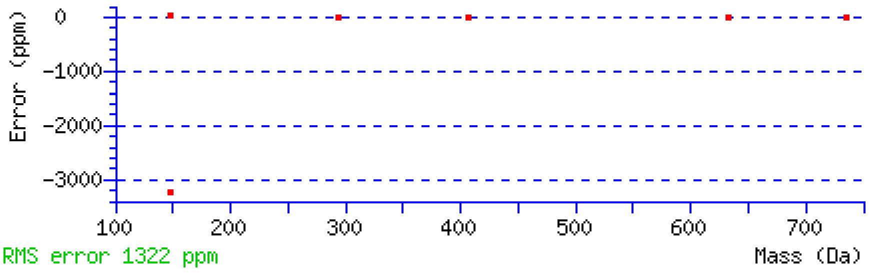
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 832.542221
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 53 **Expect:** 5e-006
Matches : 6/48 fragment ions using 5 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483			**V**							7
2	201.123369	101.065322	183.112804	92.060040	**T**	***734.481089***	367.744183	717.454540	359.230908	716.470524	358.738900	6
3	314.207433	157.607354	296.196868	148.602072	**L**	***633.433410***	317.220343	616.406861	308.707069			5
4	427.291497	214.149386	409.280932	205.144104	**L**	520.349346	260.678311	503.322797	252.165037			4
5	540.375561	270.691419	522.364996	261.686136	**L**	***407.265282***	204.136279	390.238733	195.623004			3
6	687.443975	344.225626	669.433410	335.220343	**F**	***294.181218***	147.594247	277.154669	139.080972			2
7					**K**	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of VTLLLFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
53.0	832.542221	0.003767	VTLLLFK
1.9	832.542206	0.003782	SLFLIIK
0.3	832.542221	0.003767	LTVLFLK

Mascot: http://www.matrixscience.com/

{MATRIX SCIENCE}

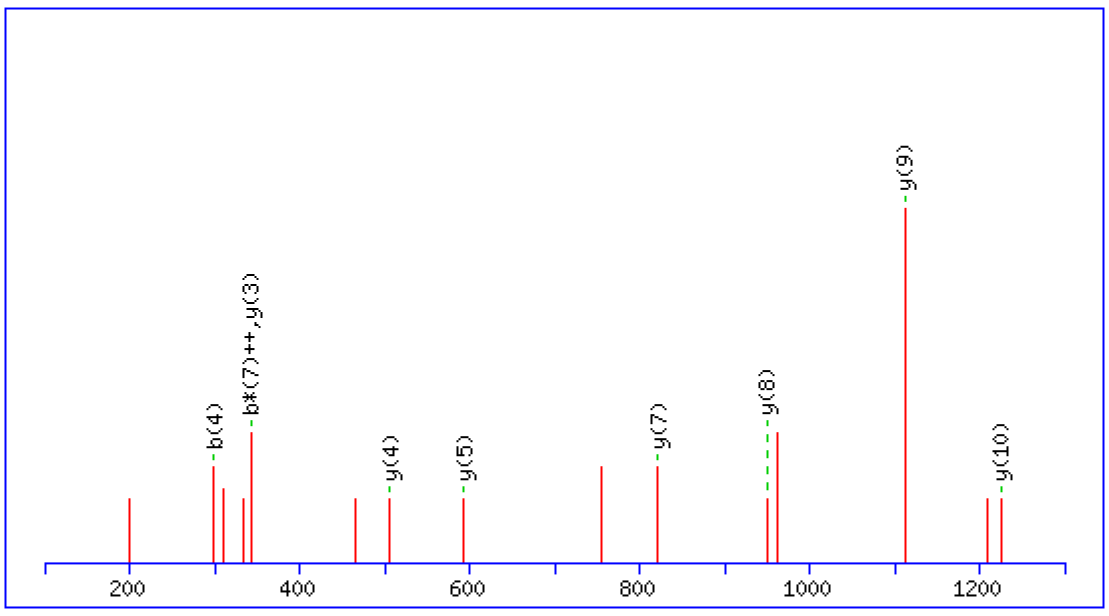
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AGGLIYQLDSYAPR**
Found in **TPPC4_HUMAN**, Trafficking protein particle complex subunit 4 OS=Homo sapiens GN=TRAPPC4 PE=1 SV=1

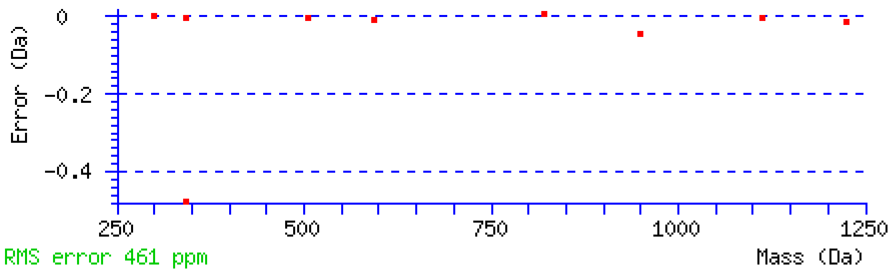
Match to Query 45460: 1522.767788 from(762.391170,2+) rtinseconds(3276) index(44871)
Title: Locus:1.1.1.2561.47
Data file 2011-11-10 - TFD - EP 4-5.mgf

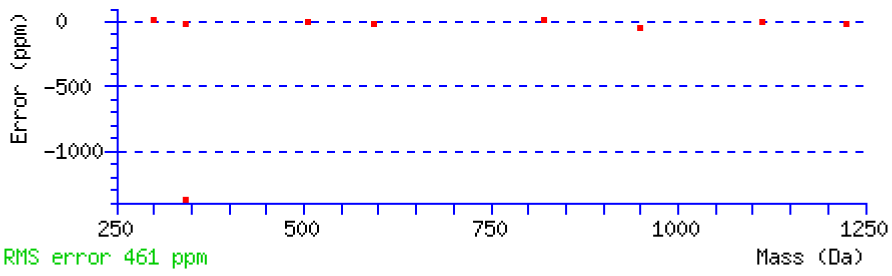
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1522.777969
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 42  Expect: 0.00021
Matches : 9/120 fragment ions using 15 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							14
2	129.065854	65.036565					G	1452.748157	726.877717	1435.721608	718.364442	1434.737592	717.872434	13
3	186.087318	93.547297					G	1395.726693	698.366984	1378.700144	689.853710	1377.716128	689.361702	12
4	299.171382	150.089329					L	1338.705229	669.856252	1321.678680	661.342978	1320.694664	660.850970	11
5	412.255446	206.631361					I	***1225.621165***	613.314221	1208.594616	604.800946	1207.610600	604.308938	10
6	575.318775	288.163026					Y	***1112.537101***	556.772188	1095.510552	548.258914	1094.526536	547.766906	9
7	703.377353	352.192315	686.350804	343.679040			Q	***949.473772***	475.240524	932.447223	466.727249	931.463207	466.235241	8
8	816.461417	408.734347	799.434868	400.221072			L	***821.415194***	411.211235	804.388645	402.697960	803.404629	402.205952	7
9	931.488360	466.247818	914.461811	457.734544	913.477795	457.242536	D	708.331130	354.669203	691.304581	346.155928	690.320565	345.663920	6
10	1018.520388	509.763832	1001.493839	501.250558	1000.509823	500.758550	S	***593.304187***	297.155732	576.277638	288.642457	575.293622	288.150449	5
11	1181.583717	591.295497	1164.557168	582.782222	1163.573152	582.290214	Y	***506.272159***	253.639717	489.245610	245.126443			4
12	1252.620831	626.814054	1235.594282	618.300779	1234.610266	617.808771	A	***343.208830***	172.108053	326.182281	163.594778			3
13	1349.673595	675.340436	1332.647046	666.827161	1331.663030	666.335153	P	272.171716	136.589496	255.145167	128.076221			2
14							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of AGGLIYQLDSYAPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.3	1522.777969	-0.010181	AGGLIYQLDSYAPR
2.9	1522.766083	0.001705	QLGISATMLNASSSK
1.2	1522.764038	0.003750	HQKTHAEERPYK
0.3	1522.762711	0.005077	QAPVENISPEAPAGK
0.3	1522.781342	-0.013554	ALNILQSTNMAFGK
0.0	1522.760193	0.007595	WYRAPEIMLNSK

Mascot: http://www.matrixscience.com/

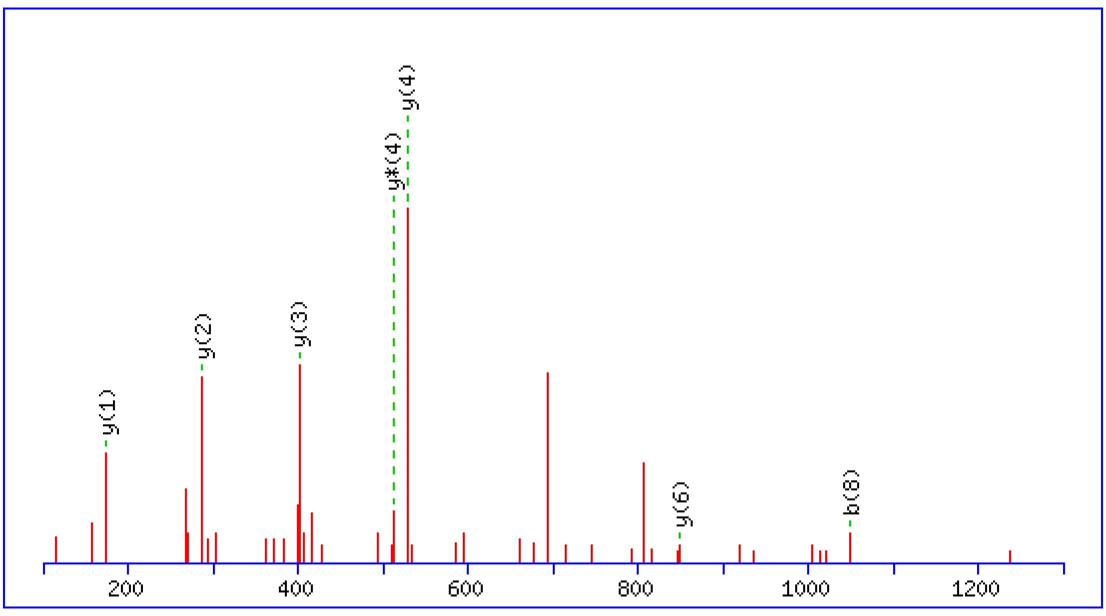
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MLPCFQLLR**
Found in **TCF19_HUMAN**, Transcription factor 19 OS=Homo sapiens GN=TCF19 PE=1 SV=2

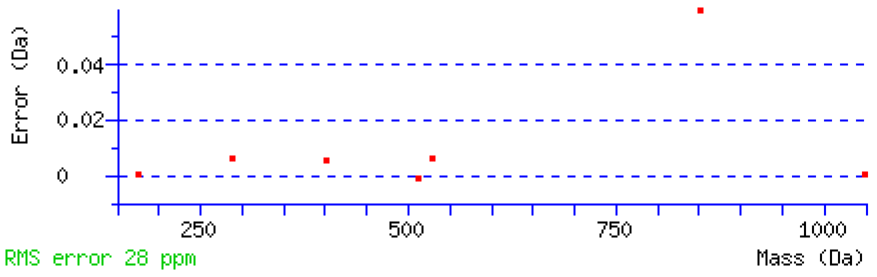
Match to Query 30194: 1222.624608 from(612.319580,2+) rtinseconds(4433) index(57105)
Title: Locus:1.1.1.3097.6
Data file 2011-11-13 - TFD - EP 7-5.mgf

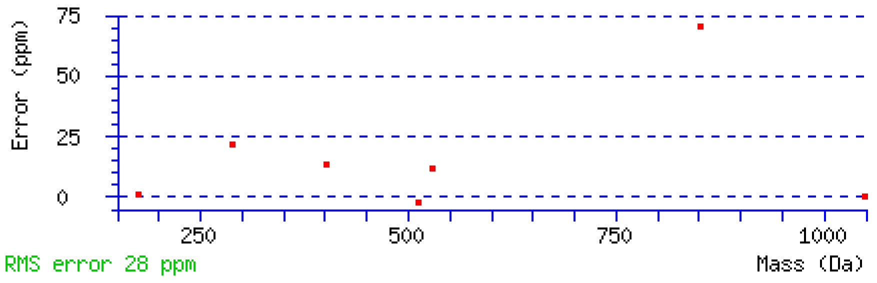
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1222.620224
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
P3 : Oxidation (P)
Ions Score: 32 **Expect:** 0.0083
Matches : 7/76 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	148.042676	74.524976			M					9
2	261.126740	131.067008			L	1076.592114	538.799695	1059.565565	530.286421	8
3	374.174419	187.590848			P	963.508050	482.257663	946.481501	473.744389	7
4	548.220718	274.613997			C	*850.460371*	425.733824	833.433822	417.220549	6
5	695.289132	348.148204			F	676.414072	338.710674	659.387523	330.197400	5
6	823.347710	412.177493	806.321161	403.664219	Q	*529.345658*	265.176467	512.319109	256.663193	4
7	936.431774	468.719525	919.405225	460.206251	L	*401.287080*	201.147178	384.260531	192.633903	3
8	1049.515838	525.261557	1032.489289	516.748283	L	*288.203016*	144.605146	271.176467	136.091871	2
9					R	*175.118952*	88.063114	158.092403	79.549839	1





NCBI **BLAST** search of MLPCFQLLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.2	1222.620224	0.004384	MLPCFQLLR
21.3	1222.630569	-0.005961	EQHVLAELER
18.1	1222.616653	0.007955	DHERRPIER
14.2	1222.620682	0.003926	AHGYGAHLELR
13.6	1222.624069	0.000539	VTLSCHSHLR
9.9	1222.630600	-0.005992	GLDDLSHTPLR
9.6	1222.634613	-0.010005	LGIDNFEFIR
7.6	1222.612823	0.011785	ERLFEQVMR
5.2	1222.616196	0.008412	TMADRILTMR
4.3	1222.630585	-0.005977	DEEVLNHVLR

Mascot: http://www.matrixscience.com/

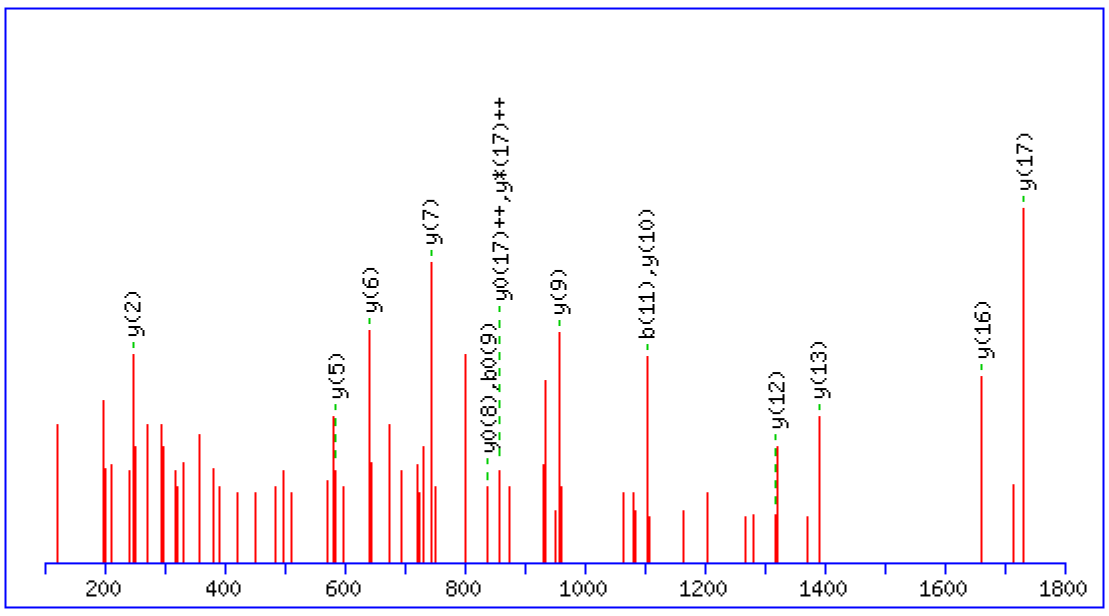
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VQASLAANTFTITGHAETK**
Found in **BTF3_HUMAN**, Transcription factor BTF3 OS=Homo sapiens GN=BTF3 PE=1 SV=1

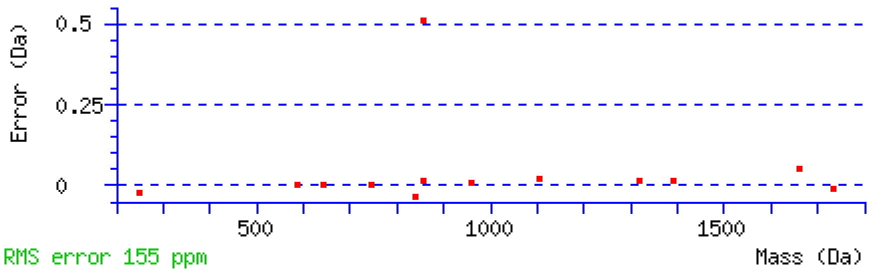
Match to Query 56193: 1959.002352 from(654.008060,3+) rtinseconds(2394) index(28571)
Title: Locus:1.1.1.2063.43
Data file 2011-11-12 - TFD - EP 6-6.mgf

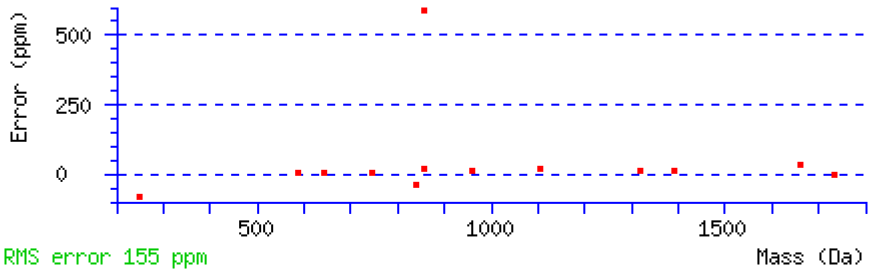
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1959.006149
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 50  Expect: 5e-005
Matches : 15/206 fragment ions using 29 most intense peaks    (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							19
2	228.134268	114.570772	211.107719	106.057498			Q	1860.945020	930.976148	1843.918471	922.462874	1842.934455	921.970865	18
3	299.171382	150.089329	282.144833	141.576055			A	***1732.886442***	866.946859	1715.859893	858.433585	1714.875877	857.941577	17
4	386.203410	193.605343	369.176861	185.092069	368.192845	184.600061	S	***1661.849328***	831.428302	1644.822779	822.915028	1643.838763	822.423020	16
5	499.287474	250.147375	482.260925	241.634101	481.276909	241.142093	L	1574.817300	787.912288	1557.790751	779.399014	1556.806735	778.907005	15
6	570.324588	285.665932	553.298039	277.152658	552.314023	276.660650	A	1461.733236	731.370256	1444.706687	722.856981	1443.722671	722.364973	14
7	641.361702	321.184489	624.335153	312.671215	623.351137	312.179207	A	***1390.696122***	695.851699	1373.669573	687.338425	1372.685557	686.846417	13
8	755.404629	378.205953	738.378080	369.692678	737.394064	369.200670	N	***1319.659008***	660.333142	1302.632459	651.819867	1301.648443	651.327859	12
9	856.452308	428.729792	839.425759	420.216518	838.441743	419.724510	T	1205.616081	603.311678	1188.589532	594.798404	1187.605516	594.306396	11
10	1003.520722	502.263999	986.494173	493.750724	985.510157	493.258716	F	***1104.568402***	552.787839	1087.541853	544.274565	1086.557837	543.782557	10
11	1104.568401	552.787839	1087.541852	544.274564	1086.557836	543.782556	T	***957.499988***	479.253632	940.473439	470.740358	939.489423	470.248350	9
12	1217.652465	609.329870	1200.625916	600.816596	1199.641900	600.324588	I	856.452309	428.729793	839.425760	420.216518	838.441744	419.724510	8
13	1318.700144	659.853710	1301.673595	651.340436	1300.689579	650.848427	T	***743.368245***	372.187761	726.341696	363.674486	725.357680	363.182478	7
14	1375.721608	688.364442	1358.695059	679.851167	1357.711043	679.359159	G	***642.320566***	321.663921	625.294017	313.150647	624.310001	312.658639	6
15	1512.780520	756.893898	1495.753971	748.380623	1494.769955	747.888615	H	***585.299102***	293.153189	568.272553	284.639915	567.288537	284.147907	5
16	1583.817634	792.412455	1566.791085	783.899180	1565.807069	783.407172	A	448.240190	224.623733	431.213641	216.110459	430.229625	215.618451	4
17	1712.860227	856.933751	1695.833678	848.420477	1694.849662	847.928469	E	377.203076	189.105176	360.176527	180.591902	359.192511	180.099894	3
18	1813.907906	907.457591	1796.881357	898.944317	1795.897341	898.452308	T	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.578597	2
19							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of VQASLAANTFTITGHAETK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
50.1	1959.006149	-0.003797	VQASLAANTFTITGHAETK
4.2	1958.992401	0.009951	LPIAVSCYWLQHTETK

Mascot: http://www.matrixscience.com/

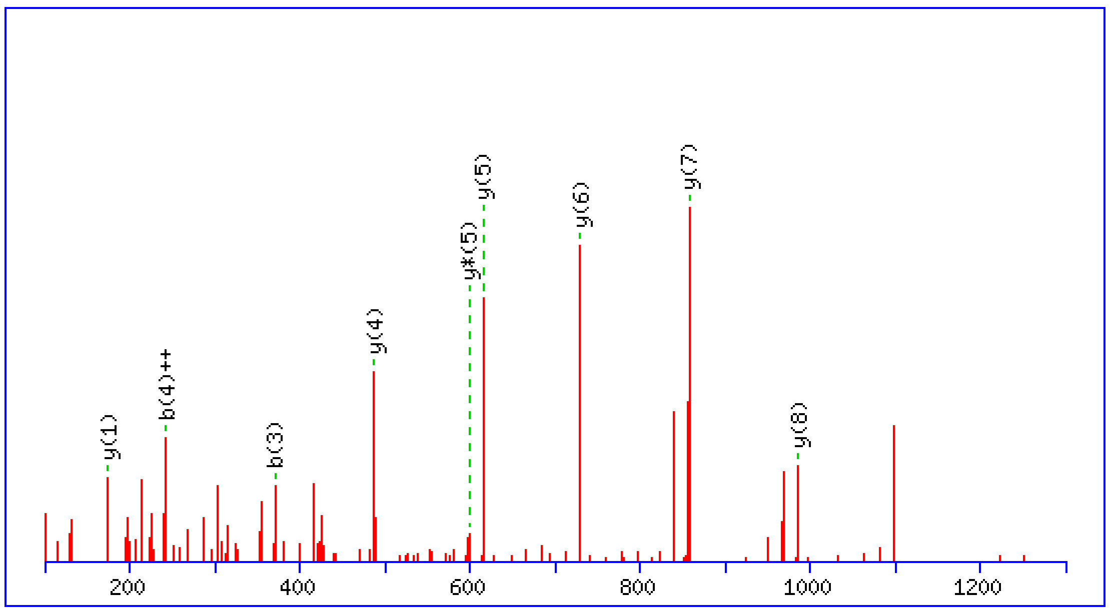
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IQELEIQAR**
Found in **TFEC_HUMAN**, Transcription factor EC OS=Homo sapiens GN=TFEC PE=1 SV=1

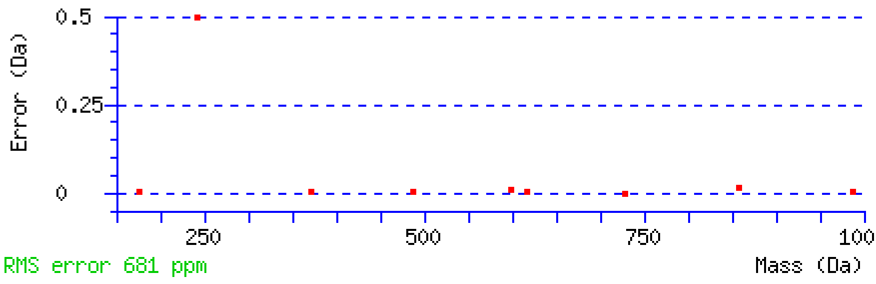
Match to Query 16353: 1098.611368 from(550.312960,2+) rtinseconds(1959) index(21990)
Title: Locus:1.1.1.2234.24
Data file 2011-11-10 - TFD - EP 4-3.mgf

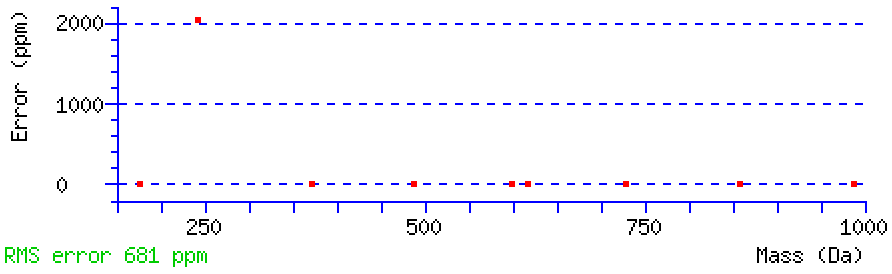
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1098.603287
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 53  Expect: 6.2e-005
Matches : 9/82 fragment ions using 10 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					I							9
2	242.149918	121.578597	225.123369	113.065323			Q	***986.526536***	493.766906	969.499987	485.253632	968.515971	484.761624	8
3	371.192511	186.099894	354.165962	177.586619	353.181946	177.094611	E	***858.467958***	429.737617	841.441409	421.224343	840.457393	420.732335	7
4	484.276575	242.641926	467.250026	234.128651	466.266010	233.636643	L	***729.425365***	365.216321	712.398816	356.703046	711.414800	356.211038	6
5	613.319168	307.163222	596.292619	298.649948	595.308603	298.157940	E	***616.341301***	308.674289	599.314752	300.161014	598.330736	299.669006	5
6	726.403232	363.705254	709.376683	355.191980	708.392667	354.699972	I	***487.298708***	244.152992	470.272159	235.639718			4
7	854.461810	427.734543	837.435261	419.221269	836.451245	418.729261	Q	374.214644	187.610960	357.188095	179.097686			3
8	925.498924	463.253100	908.472375	454.739826	907.488359	454.247818	A	246.156066	123.581671	229.129517	115.068397			2
9							R	***175.118952***	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of IQELEIQAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.8	1098.603287	0.008081	IQELEIQAR
19.2	1098.614532	-0.003164	LRTELPAGAR
13.4	1098.614532	-0.003164	VRDLLAEQR
13.1	1098.614548	-0.003180	GPLSPARTLR
12.1	1098.614517	-0.003149	LQNAKEQLR
11.9	1098.614532	-0.003164	LLEQARDVR
11.3	1098.603302	0.008066	VLSAPPKESR
10.5	1098.603317	0.008051	VPAPSSILQR
9.2	1098.614517	-0.003149	IQQAKNEIR
8.2	1098.607330	0.004038	EIQPPFKPK

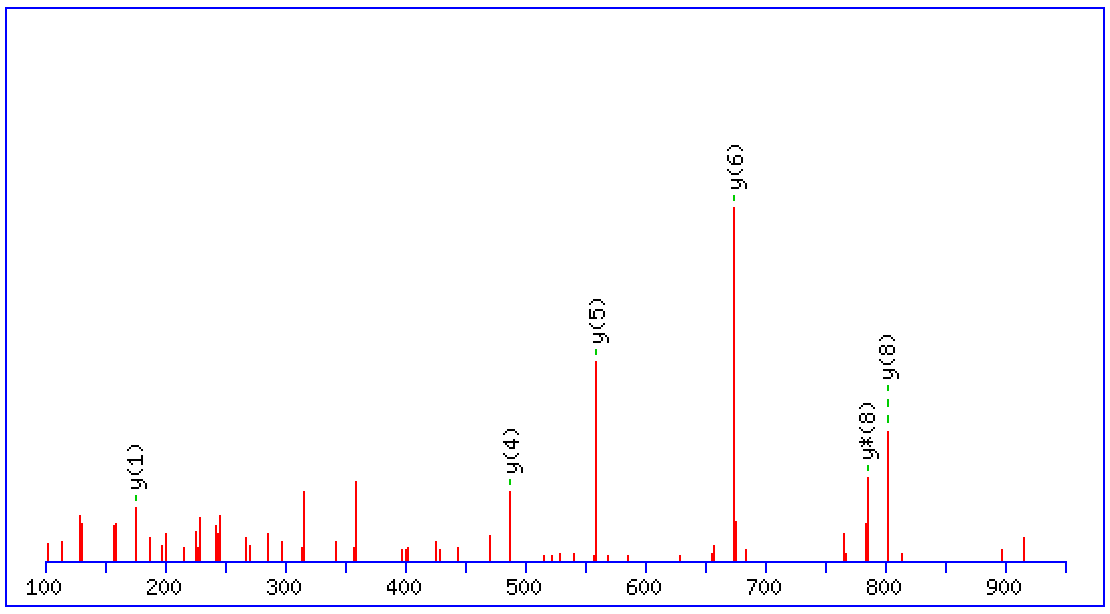
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **RAGDAAELR**
Found in **HES2_HUMAN**, Transcription factor HES-2 OS=Homo sapiens GN=HES2 PE=2 SV=1

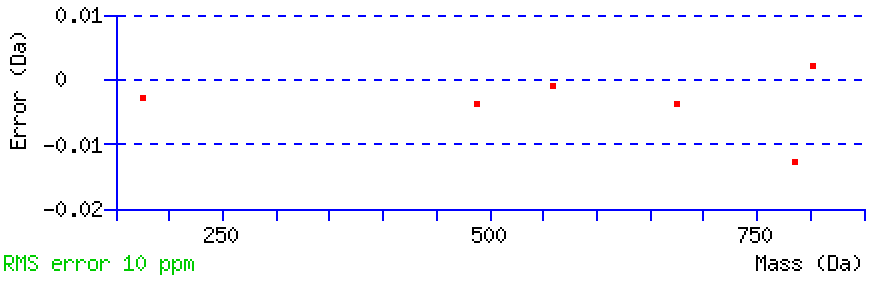
Match to Query 204428: 957.491328 from(479.752940,2+) rtinseconds(2181) index(266020)
Title: Locus:1.1.1.1280.9
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

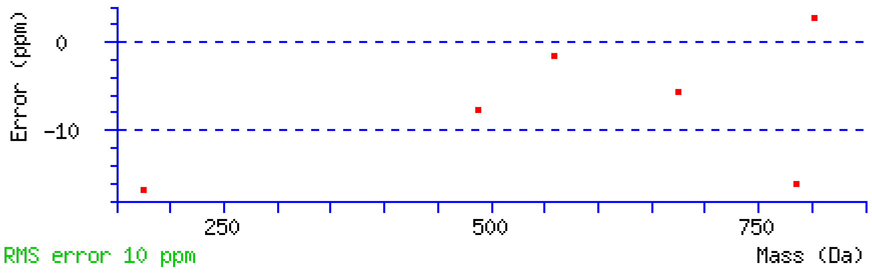
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 957.499161
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 38   Expect: 0.0025
Matches : 6/86 fragment ions using 9 most intense peaks    (help)
```

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	157.108387	79.057831	140.081838	70.544557			R							9
2	228.145501	114.576388	211.118952	106.063114			A	***802.405358***	401.706317	785.378809	393.193043	784.394793	392.701035	8
3	285.166965	143.087121	268.140416	134.573846			G	731.368244	366.187760	714.341695	357.674486	713.357679	357.182478	7
4	400.193908	200.600592	383.167359	192.087318	382.183343	191.595310	D	***674.346780***	337.677028	657.320231	329.163754	656.336215	328.671746	6
5	471.231022	236.119149	454.204473	227.605875	453.220457	227.113867	A	***559.319837***	280.163557	542.293288	271.650282	541.309272	271.158274	5
6	542.268136	271.637706	525.241587	263.124432	524.257571	262.632424	A	***488.282723***	244.645000	471.256174	236.131725	470.272158	235.639717	4
7	671.310729	336.159003	654.284180	327.645728	653.300164	327.153720	E	417.245609	209.126443	400.219060	200.613168	399.235044	200.121160	3
8	784.394793	392.701035	767.368244	384.187760	766.384228	383.695752	L	288.203016	144.605146	271.176467	136.091872			2
9							R	***175.118952***	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of RAGDAAELR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.5	957.499161	-0.007833	RAGDAAELR
23.8	957.499176	-0.007848	RQEVSSPR
20.7	957.487946	0.003382	QGVDIEAAR
18.3	957.487946	0.003382	NSTPPSLAR
12.8	957.499161	-0.007833	GEEQLRAR
12.2	957.499161	-0.007833	RQEELQR
12.2	957.499176	-0.007848	RQSDPSIR
11.0	957.489288	0.002040	RGWRPDR
10.4	957.499176	-0.007848	SDGAAIPRR
10.1	957.499176	-0.007848	TPASRPSAR

Mascot: http://www.matrixscience.com/

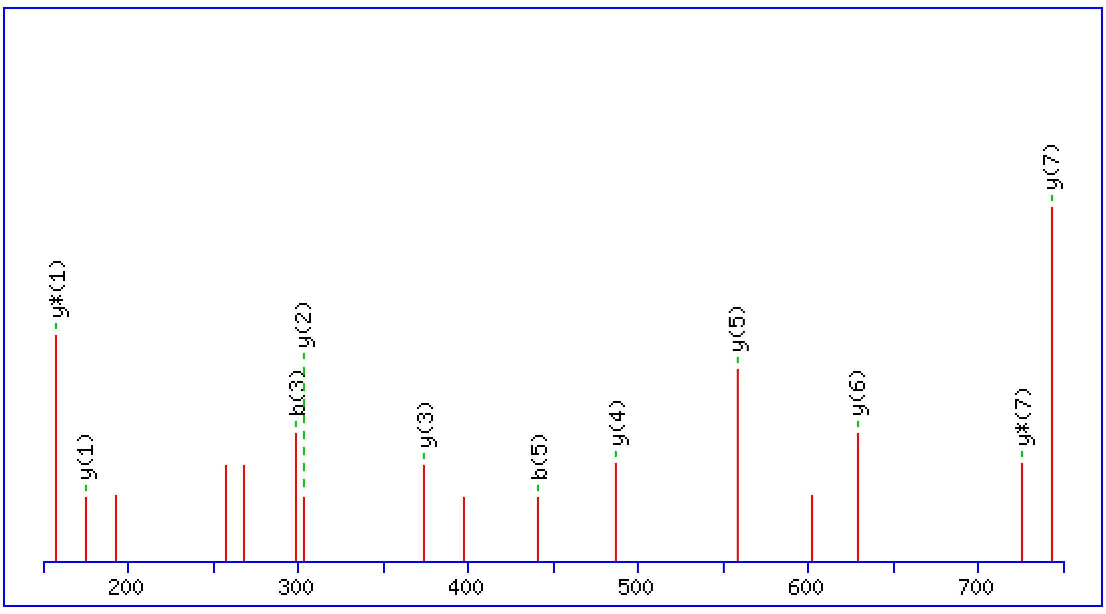
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AINAALAQR**
Found in **T2AG_HUMAN**, Transcription initiation factor IIA subunit 2 OS=Homo sapiens GN=GTF2A2 PE=1 SV=1

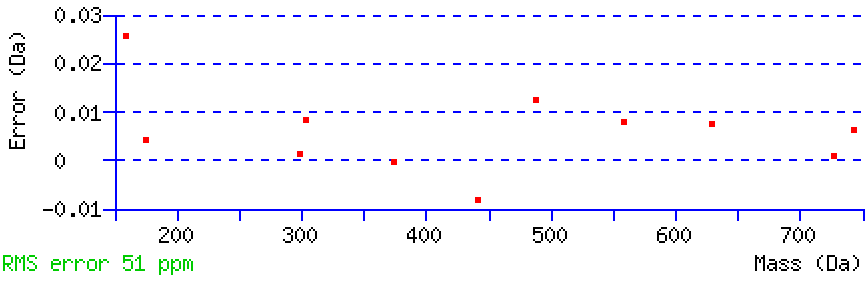
Match to Query 10047: 926.533408 from(464.273980,2+) rtinseconds(1464) index(7277)
Title: Locus:1.1.1.1964.20
Data file 2011-11-10 - TFD - EP 3-7.mgf

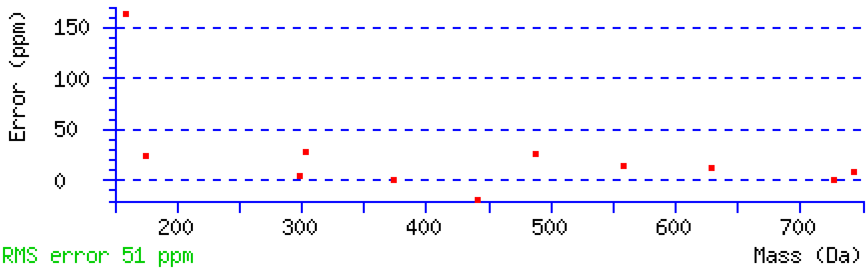
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 926.529724
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 59  Expect: 6.8e-006
Matches : 11/60 fragment ions using 17 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	72.044390	36.525833			A					9
2	185.128454	93.067865			I	856.499927	428.753602	839.473378	420.240327	8
3	**299.171381**	150.089328	282.144832	141.576054	N	***743.415863***	372.211570	726.389314	363.698295	7
4	370.208495	185.607886	353.181946	177.094611	A	***629.372936***	315.190106	612.346387	306.676831	6
5	**441.245609**	221.126443	424.219060	212.613168	A	***558.335822***	279.671549	541.309273	271.158275	5
6	554.329673	277.668475	537.303124	269.155200	L	***487.298708***	244.152992	470.272159	235.639717	4
7	625.366787	313.187032	608.340238	304.673757	A	***374.214644***	187.610960	357.188095	179.097685	3
8	753.425365	377.216321	736.398816	368.703046	Q	***303.177530***	152.092403	286.150981	143.579128	2
9					R	***175.118952***	88.063114	158.092403	79.549839	1





NCBI **BLAST** search of AINAALAQR
(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	926.529724	0.003684	AINAALAQR
13.6	926.529755	0.003653	NQVVIAAGR
6.6	926.529739	0.003669	NALNVLQR
4.5	926.529739	0.003669	LQQAQALR
3.0	926.529755	0.003653	IGVNQPKR
1.3	926.529739	0.003669	SPGLLERR
0.5	926.529739	0.003669	LADPRLSR

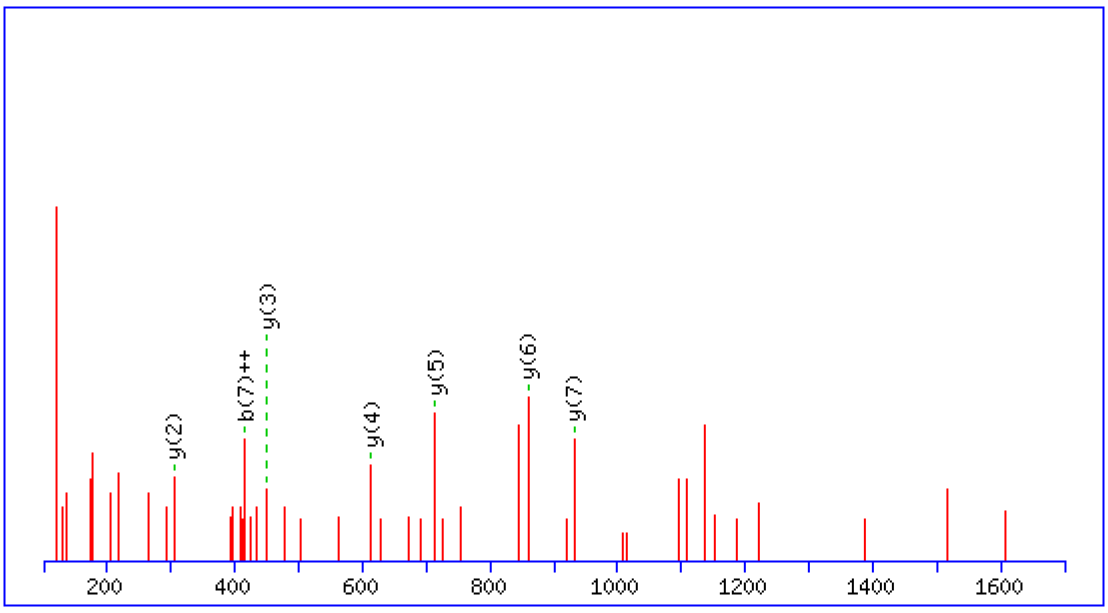
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GFAFVYFER**
Found in **TRA2A_HUMAN**, Transformer-2 protein homolog alpha OS=Homo sapiens GN=TRA2A PE=1 SV=1

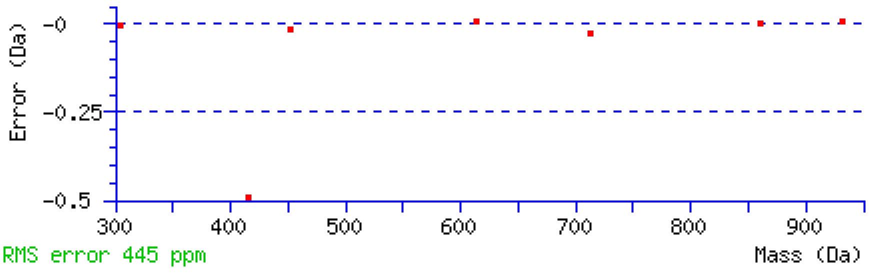
Match to Query 24668: 1134.551188 from(568.282870,2+) rtinseconds(3437) index(50134)
Title: Locus:1.1.1.2632.5
Data file 2011-11-10 - TFD - EP 4-4.mgf

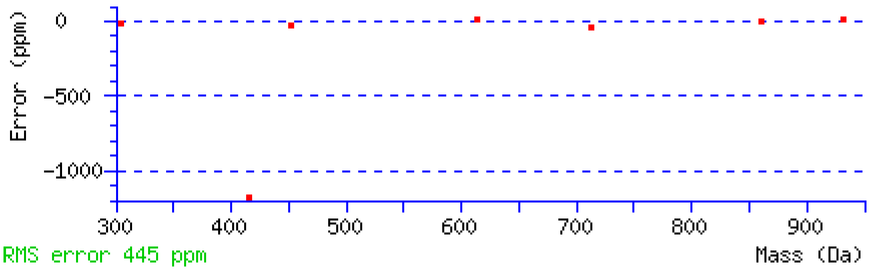
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1134.549835
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 42 **Expect:** 0.00065
Matches : 7/64 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008			G							9
2	205.097154	103.052215			F	1078.535644	539.771460	1061.509095	531.258186	1060.525079	530.766178	8
3	276.134268	138.570772			A	***931.467230***	466.237253	914.440681	457.723978	913.456665	457.231970	7
4	423.202682	212.104979			F	***860.430116***	430.718696	843.403567	422.205422	842.419551	421.713414	6
5	522.271096	261.639186			V	***713.361702***	357.184489	696.335153	348.671215	695.351137	348.179207	5
6	685.334425	343.170851			Y	***614.293288***	307.650282	597.266739	299.137008	596.282723	298.645000	4
7	832.402839	416.705058			F	***451.229959***	226.118617	434.203410	217.605343	433.219394	217.113335	3
8	961.445432	481.226354	943.434867	472.221071	E	***304.161545***	152.584410	287.134996	144.071136	286.150980	143.579128	2
9					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of GFAFVYFER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.8	1134.549835	0.001353	GFAFVYFER
7.8	1134.545822	0.005366	THYPDVFTR
6.1	1134.559082	-0.007894	MGADGETVVLK

Mascot: http://www.matrixscience.com/

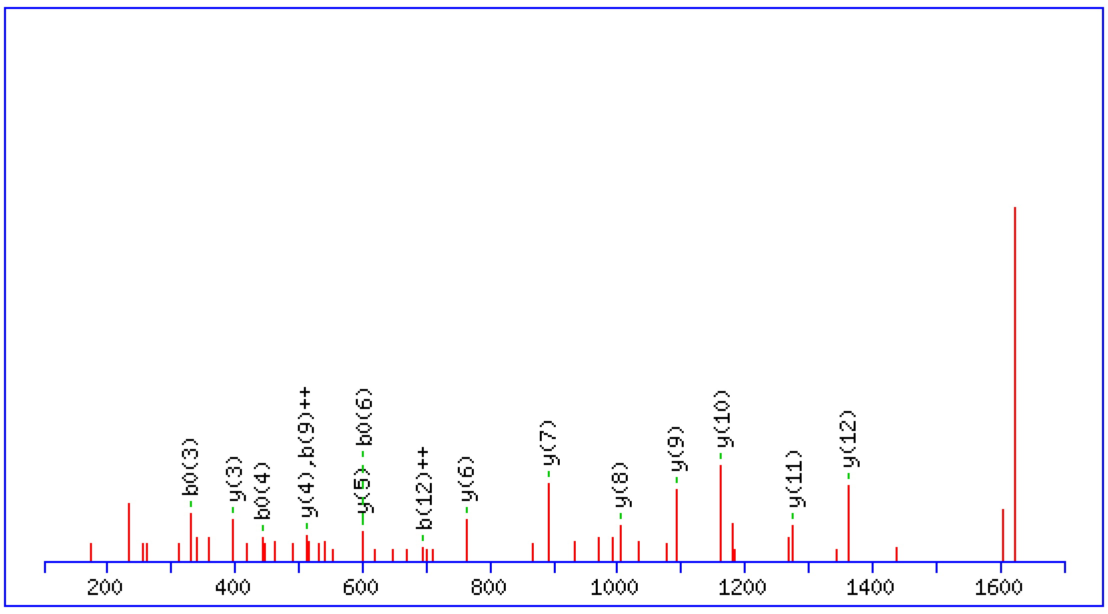
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FISLASLEYSDYSK**
Found in **EI2BA_HUMAN**, Translation initiation factor eIF-2B subunit alpha OS=Homo sapiens GN=EIF2B1 PE=1 SV=1

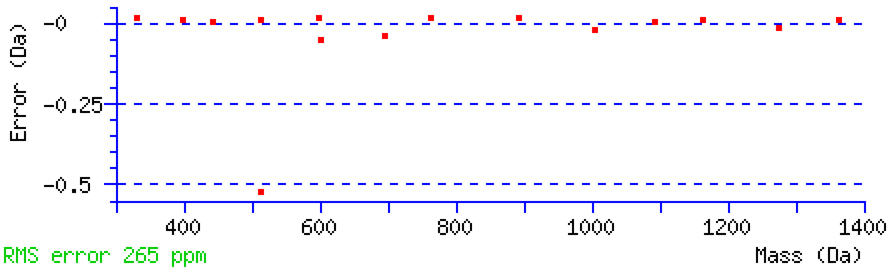
Match to Query 47321: 1621.791588 from(811.903070,2+) rtinseconds(3377) index(44337)
Title: Locus:1.1.1.2870.49
Data file 2011-11-12 - TFD - EP 5-5.mgf

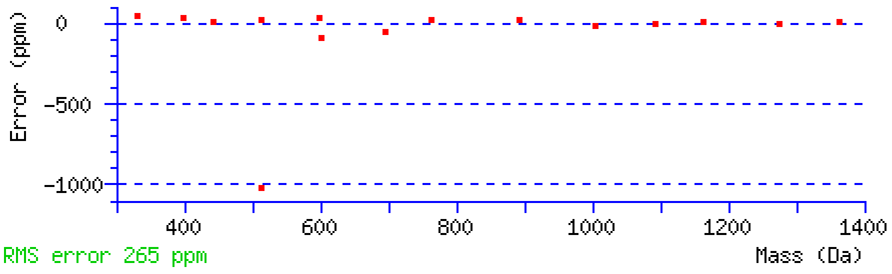
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1621.787521
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 65 **Expect:** 1.1e-006
Matches : 15/124 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.075690	74.541483			F							14
2	261.159754	131.083515			I	1475.726416	738.366846	1458.699867	729.853572	1457.715851	729.361564	13
3	348.191782	174.599529	330.181217	165.594246	S	***1362.642352***	681.824814	1345.615803	673.311540	1344.631787	672.819532	12
4	461.275846	231.141561	443.265281	222.136278	L	***1275.610324***	638.308800	1258.583775	629.795526	1257.599759	629.303518	11
5	532.312960	266.660118	514.302395	257.654835	A	***1162.526260***	581.766768	1145.499711	573.253494	1144.515695	572.761486	10
6	619.344988	310.176132	601.334423	301.170849	S	***1091.489146***	546.248211	1074.462597	537.734937	1073.478581	537.242929	9
7	732.429052	366.718164	714.418487	357.712881	L	***1004.457118***	502.732197	987.430569	494.218923	986.446553	493.726915	8
8	861.471645	431.239461	843.461080	422.234178	E	***891.373054***	446.190165	874.346505	437.676891	873.362489	437.184883	7
9	1024.534974	**512.771125**	1006.524409	503.765842	Y	***762.330461***	381.668869	745.303912	373.155594	744.319896	372.663586	6
10	1111.567002	556.287139	1093.556437	547.281857	S	***599.267132***	300.137204	582.240583	291.623930	581.256567	291.131922	5
11	1226.593945	613.800611	1208.583380	604.795328	D	***512.235104***	256.621190	495.208555	248.107916	494.224539	247.615908	4
12	1389.657274	**695.332275**	1371.646709	686.326993	Y	***397.208161***	199.107719	380.181612	190.594444	379.197596	190.102436	3
13	1476.689302	738.848289	1458.678737	729.843007	S	234.144832	117.576054	217.118283	109.062780	216.134267	108.570772	2
14					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of FISLASLEYSDYSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
65.3	1621.787521	0.004067	FISLASLEYSDYSK
1.6	1621.777008	0.014580	MFAVGVGNAVEDELR

Mascot: http://www.matrixscience.com/

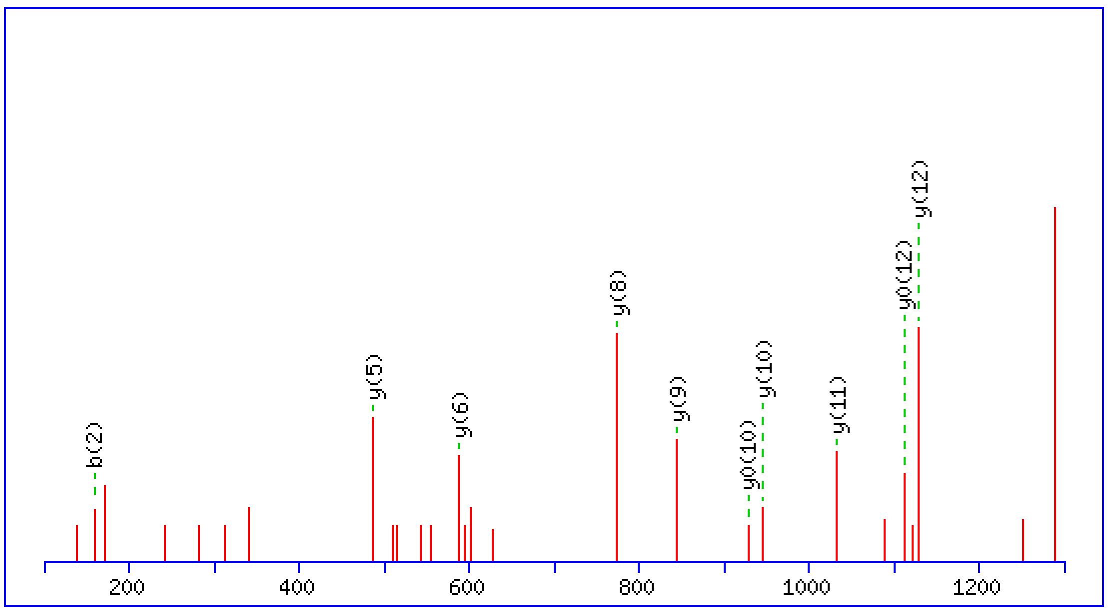
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ASPSTAGETPSGVK**
Found in **EI2BD_HUMAN**, Translation initiation factor eIF-2B subunit delta OS=Homo sapiens GN=EIF2B4 PE=1 SV=2

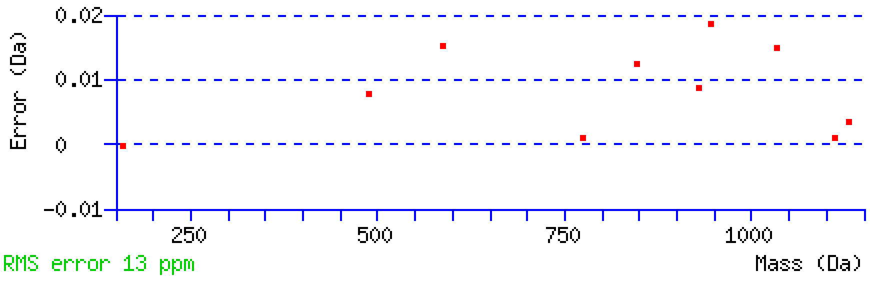
Match to Query 626464: 1287.634708 from(644.824630,2+) rtinseconds(1081) index(159399)
Title: Locus:1.1.1.1096.25
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

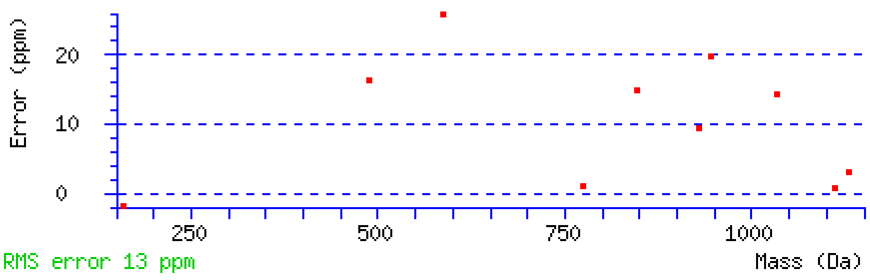
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1287.630661
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 45 **Expect:** 7e-005
Matches : 10/122 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			**A**							**14**
2	159.076418	80.041847	141.065853	71.036564	**S**	1217.600823	609.304050	1200.574274	600.790775	1199.590258	600.298767	**13**
3	256.129182	128.568229	238.118617	119.562947	**P**	***1130.568795***	565.788036	1113.542246	557.274761	1112.558230	556.782753	**12**
4	343.161210	172.084243	325.150645	163.078960	**S**	***1033.516031***	517.261654	1016.489482	508.748379	1015.505466	508.256371	**11**
5	444.208889	222.608082	426.198324	213.602800	**T**	***946.484003***	473.745640	929.457454	465.232365	928.473438	464.740357	**10**
6	515.246003	258.126640	497.235438	249.121357	**A**	***845.436324***	423.221800	828.409775	414.708526	827.425759	414.216518	**9**
7	572.267467	286.637372	554.256902	277.632089	**G**	***774.399210***	387.703243	757.372661	379.189969	756.388645	378.697961	**8**
8	701.310060	351.158668	683.299495	342.153386	**E**	717.377746	359.192511	700.351197	350.679237	699.367181	350.187229	**7**
9	802.357739	401.682508	784.347174	392.677225	**T**	***588.335153***	294.671215	571.308604	286.157940	570.324588	285.665932	**6**
10	899.410503	450.208890	881.399938	441.203607	**P**	***487.287474***	244.147375	470.260925	235.634100	469.276909	235.142092	**5**
11	986.442531	493.724904	968.431966	484.719621	**S**	390.234710	195.620993	373.208161	187.107718	372.224145	186.615710	**4**
12	1043.463995	522.235636	1025.453430	513.230353	**G**	303.202682	152.104979	286.176133	143.591704			**3**
13	1142.532409	571.769843	1124.521844	562.764560	**V**	246.181218	123.594247	229.154669	115.080973			**2**
14					**K**	147.112804	74.060040	130.086255	65.546765			**1**





NCBI **BLAST** search of ASPSTAGETPSGVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.7	1287.630661	0.004047	ASPSTAGETPSGVK
0.4	1287.628143	0.006565	HPLAMYPNLGK

Mascot: http://www.matrixscience.com/

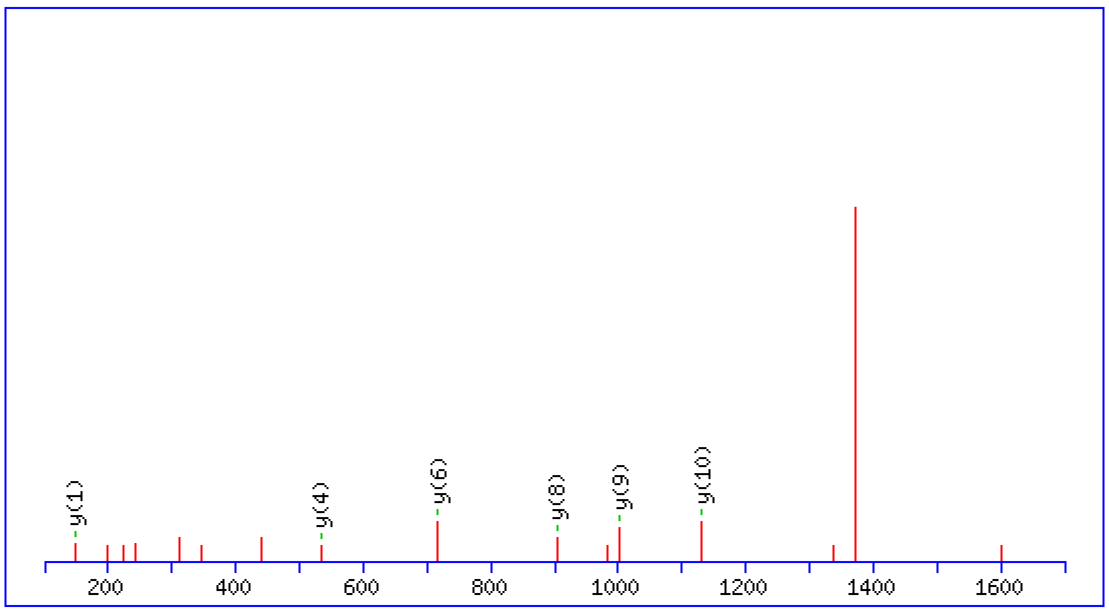
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IQEVGEPSKEEK**
Found in **SEC62_HUMAN**, Translocation protein SEC62 OS=Homo sapiens GN=SEC62 PE=1 SV=1

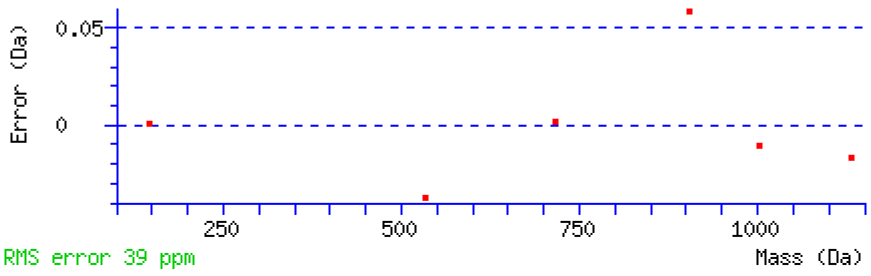
Match to Query 719267: 1371.691208 from(686.852880,2+) rtinseconds(942) index(327727)
Title: Locus:1.1.1.690.47
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

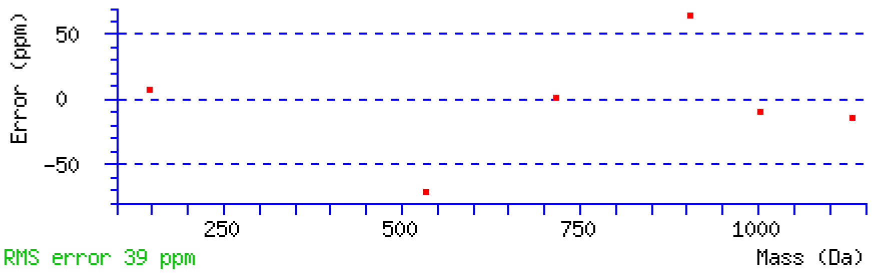
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1371.688141
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 45  Expect: 0.00038
Matches : 6/124 fragment ions using 9 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					I							12
2	242.149918	121.578597	225.123369	113.065323			Q	1259.611387	630.309332	1242.584838	621.796057	1241.600822	621.304049	11
3	371.192511	186.099894	354.165962	177.586619	353.181946	177.094611	E	***1131.552809***	566.280043	1114.526260	557.766768	1113.542244	557.274760	10
4	470.260925	235.634101	453.234376	227.120826	452.250360	226.628818	V	***1002.510216***	501.758746	985.483667	493.245472	984.499651	492.753464	9
5	527.282389	264.144833	510.255840	255.631558	509.271824	255.139550	G	***903.441802***	452.224539	886.415253	443.711265	885.431237	443.219257	8
6	656.324982	328.666129	639.298433	320.152855	638.314417	319.660847	E	846.420338	423.713807	829.393789	415.200533	828.409773	414.708525	7
7	753.377746	377.192511	736.351197	368.679237	735.367181	368.187229	P	***717.377745***	359.192511	700.351196	350.679236	699.367180	350.187228	6
8	840.409774	420.708525	823.383225	412.195251	822.399209	411.703243	S	620.324981	310.666129	603.298432	302.152854	602.314416	301.660846	5
9	968.504737	484.756007	951.478188	476.242732	950.494172	475.750724	K	***533.292953***	267.150115	516.266404	258.636840	515.282388	258.144832	4
10	1097.547330	549.277303	1080.520781	540.764029	1079.536765	540.272021	E	405.197990	203.102633	388.171441	194.589359	387.187425	194.097351	3
11	1226.589923	613.798600	1209.563374	605.285325	1208.579358	604.793317	E	276.155397	138.581337	259.128848	130.068062	258.144832	129.576054	2
12							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of IQEVGEPSKEEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.3	1371.688141	0.003067	IQEVGEPSKEEK
8.5	1371.688141	0.003067	QLEDELQDLAAK
7.6	1371.699387	-0.008179	ELQVNISQQGEK
7.1	1371.699387	-0.008179	RDVKPDEDLASK
5.3	1371.699371	-0.008163	KPSASERLPDEK
3.3	1371.678253	0.012955	LYNTESQSFRK

Mascot: http://www.matrixscience.com/

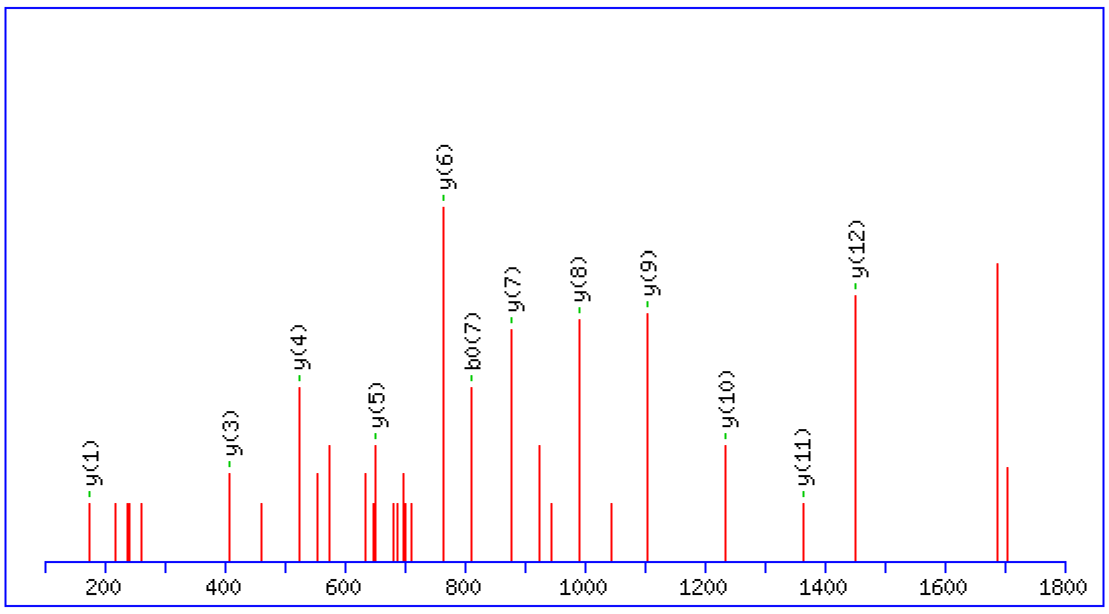
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QQSEEDLLLQDFSR**
Found in **SSRG_HUMAN**, Translocon-associated protein subunit gamma OS=Homo sapiens GN=SSR3 PE=1 SV=1

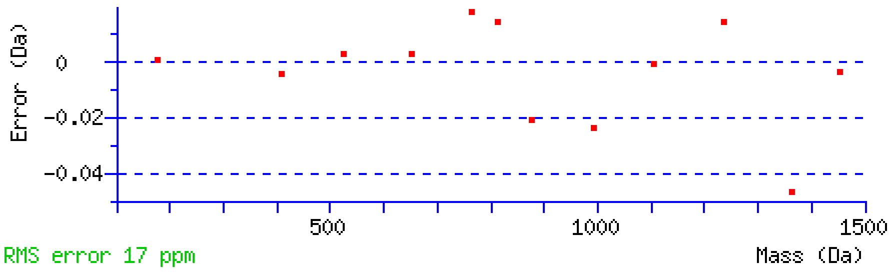
Match to Query 51920: 1706.812808 from(854.413680,2+) rtinseconds(3422) index(47627)
Title: Locus:1.1.1.2453.43
Data file 2011-11-12 - TFD - EP 6-6.mgf

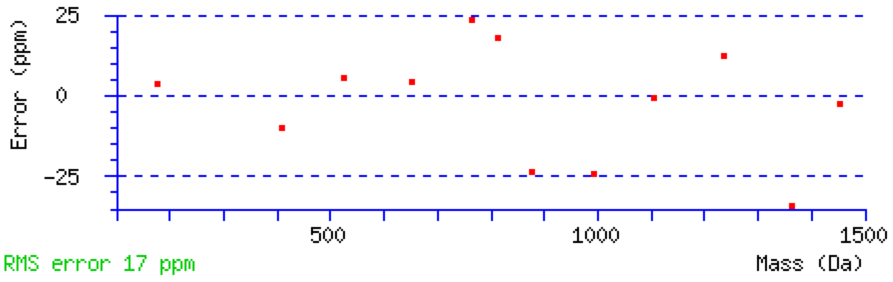
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1706.811127
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 115 **Expect:** 3.2e-011
Matches : 12/150 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	129.065854	65.036565	112.039305	56.523291			Q							14
2	257.124432	129.065854	240.097883	120.552580			Q	1579.759842	790.383559	1562.733293	781.870285	1561.749277	781.378277	13
3	344.156460	172.581868	327.129911	164.068593	326.145895	163.576585	S	***1451.701264***	726.354270	1434.674715	717.840996	1433.690699	717.348988	12
4	473.199053	237.103164	456.172504	228.589890	455.188488	228.097882	E	***1364.669236***	682.838256	1347.642687	674.324982	1346.658671	673.832974	11
5	602.241646	301.624461	585.215097	293.111187	584.231081	292.619179	E	***1235.626643***	618.316960	1218.600094	609.803685	1217.616078	609.311677	10
6	717.268589	359.137933	700.242040	350.624658	699.258024	350.132650	D	***1106.584050***	553.795663	1089.557501	545.282389	1088.573485	544.790381	9
7	830.352653	415.679965	813.326104	407.166690	812.342088	406.674682	L	***991.557107***	496.282192	974.530558	487.768917	973.546542	487.276909	8
8	943.436717	472.221997	926.410168	463.708722	925.426152	463.216714	L	***878.473043***	439.740160	861.446494	431.226885	860.462478	430.734877	7
9	1056.520781	528.764028	1039.494232	520.250754	1038.510216	519.758746	L	***765.388979***	383.198128	748.362430	374.684853	747.378414	374.192845	6
10	1184.579359	592.793318	1167.552810	584.280043	1166.568794	583.788035	Q	***652.304915***	326.656096	635.278366	318.142821	634.294350	317.650813	5
11	1299.606302	650.306789	1282.579753	641.793515	1281.595737	641.301507	D	***524.246337***	262.626807	507.219788	254.113532	506.235772	253.621524	4
12	1446.674716	723.840996	1429.648167	715.327722	1428.664151	714.835714	F	***409.219394***	205.113335	392.192845	196.600061	391.208829	196.108053	3
13	1533.706744	767.357010	1516.680195	758.843736	1515.696179	758.351728	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
14							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of QQSEEDLLLQDFSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
114.9	1706.811127	0.001681	QQSEEDLLLQDFSR
2.8	1706.829788	-0.016980	VLLMEFVDGGQVNDR
2.0	1706.819366	-0.006558	MCSLPMARYYIIK
0.5	1706.814514	-0.001706	ATDKGSPPMSEITSVR
0.2	1706.827286	-0.014478	VPHFFCDIRPVMK

Mascot: http://www.matrixscience.com/

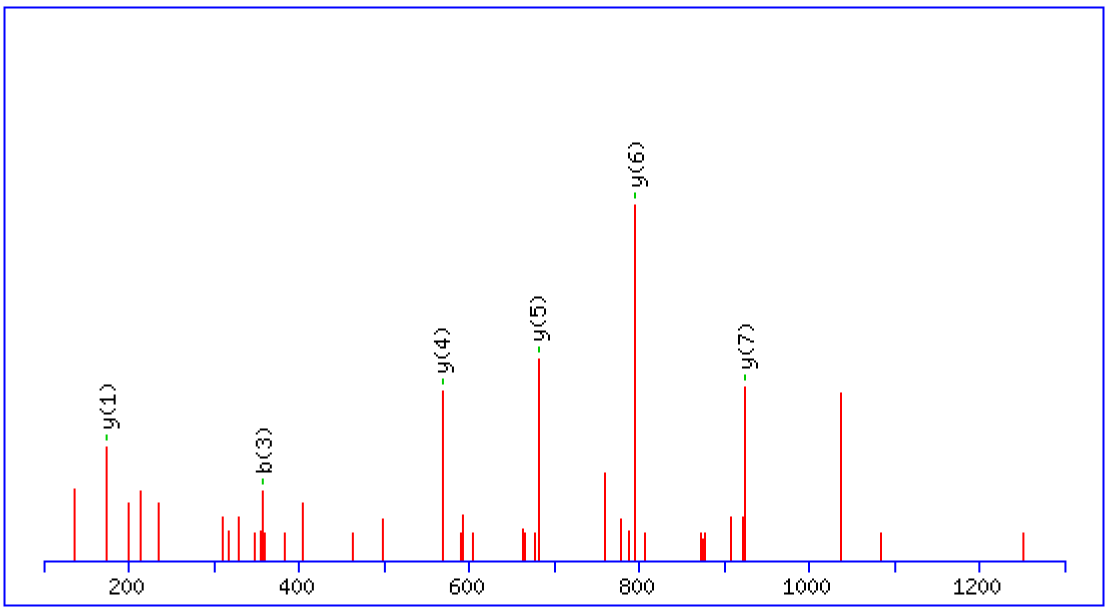
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IEDLYTER**
Found in **TM9S3_HUMAN**, Transmembrane 9 superfamily member 3 OS=Homo sapiens GN=TM9SF3 PE=1 SV=2

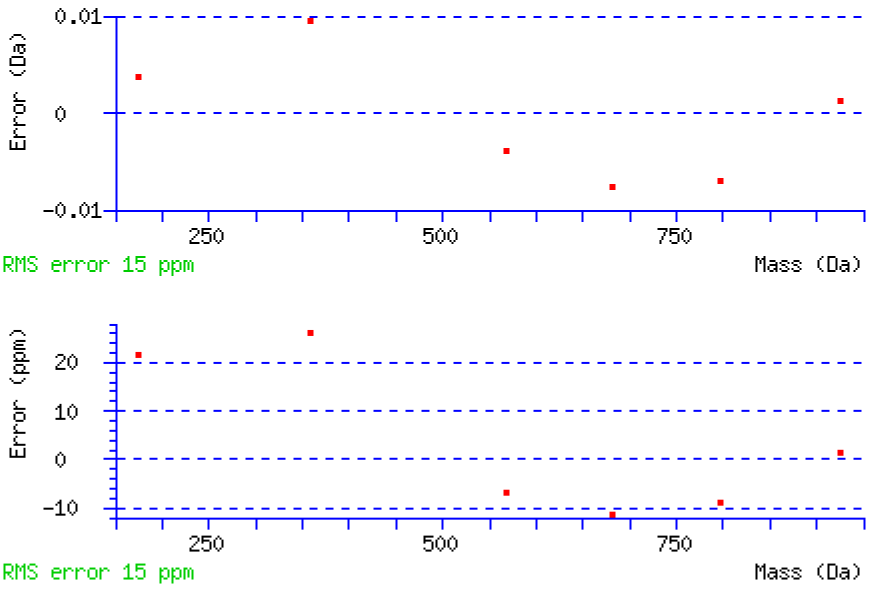
Match to Query 313189: 1037.505668 from(519.760110,2+) rtinseconds(1747) index(590253)
Title: Locus:1.1.1.987.24
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1300] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1037.502914
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 37  Expect: 0.00084
Matches : 6/66 fragment ions using 8 most intense peaks  (help)
```

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308			I							8
2	243.133933	122.070605	225.123368	113.065322	E	*925.426153*	463.216715	908.399604	454.703440	907.415588	454.211432	7
3	358.160876	179.584076	340.150311	170.578794	D	*796.383560*	398.695418	779.357011	390.182144	778.372995	389.690136	6
4	471.244940	236.126108	453.234375	227.120826	L	*681.356617*	341.181947	664.330068	332.668672	663.346052	332.176664	5
5	634.308269	317.657773	616.297704	308.652490	Y	*568.272553*	284.639915	551.246004	276.126640	550.261988	275.634632	4
6	735.355948	368.181612	717.345383	359.176330	T	405.209224	203.108250	388.182675	194.594976	387.198659	194.102968	3
7	864.398541	432.702909	846.387976	423.697626	E	304.161545	152.584411	287.134996	144.071136	286.150980	143.579128	2
8					R	*175.118952*	88.063114	158.092403	79.549840			1



NCBI **BLAST** search of IEDLYTER
(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	1037.502914	0.002754	IEDLYTER
3.8	1037.511673	-0.006005	LHFGHPAIM
3.1	1037.496414	0.009254	LADFGSCLR
1.5	1037.514160	-0.008492	ELPSGPGPER

Mascot: http://www.matrixscience.com/

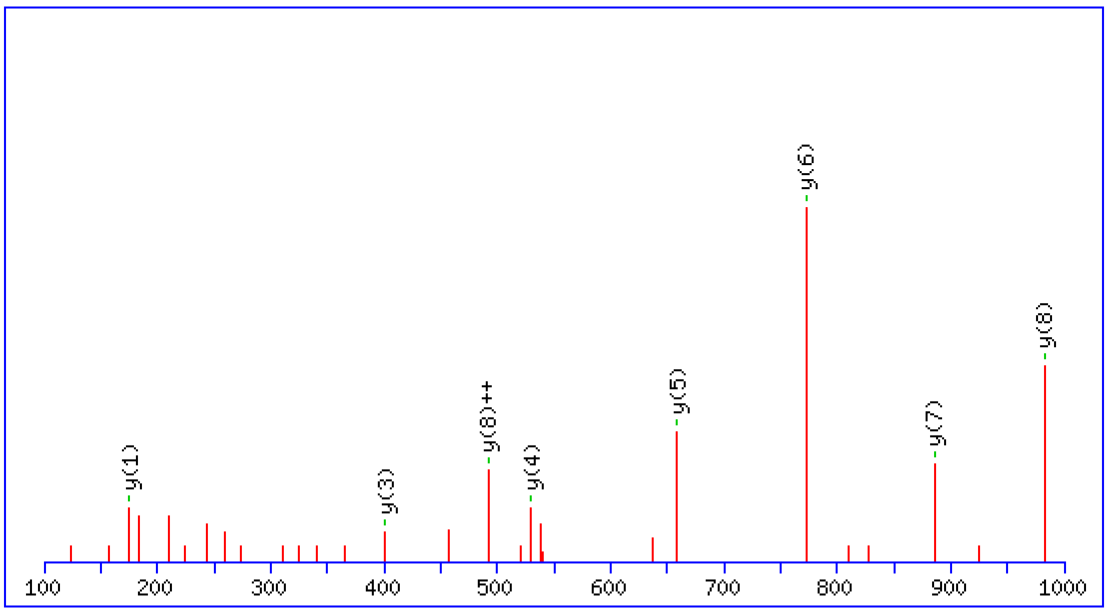
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALPILEELLR**
Found in **TMTC3_HUMAN**, Transmembrane and TPR repeat-containing protein 3 OS=Homo sapiens GN=TMTC3 PE=1 SV=2

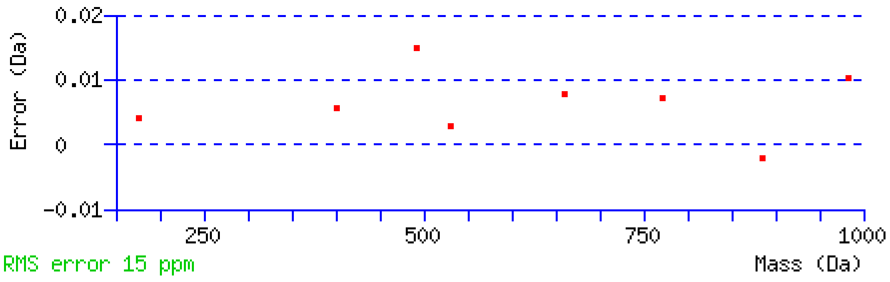
Match to Query 27188: 1165.710428 from(583.862490,2+) rtinseconds(4339) index(66294)
Title: Locus:1.1.1.2947.10
Data file 2011-11-12 - TFD - EP 6-1.mgf

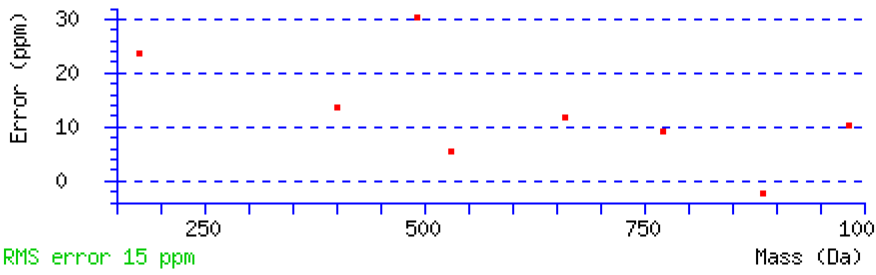
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1165.707016
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 65 **Expect:** 3.8e-007
Matches : 8/74 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			A							10
2	185.128454	93.067865			L	1095.677222	548.342249	1078.650673	539.828975	1077.666657	539.336967	9
3	282.181218	141.594247			P	***982.593158***	491.800217	965.566609	483.286943	964.582593	482.794935	8
4	395.265282	198.136279			I	***885.540394***	443.273835	868.513845	434.760561	867.529829	434.268553	7
5	508.349346	254.678311			L	***772.456330***	386.731803	755.429781	378.218529	754.445765	377.726521	6
6	637.391939	319.199608	619.381374	310.194325	E	***659.372266***	330.189771	642.345717	321.676497	641.361701	321.184489	5
7	766.434532	383.720904	748.423967	374.715622	E	***530.329673***	265.668475	513.303124	257.155200	512.319108	256.663192	4
8	879.518596	440.262936	861.508031	431.257654	L	***401.287080***	201.147178	384.260531	192.633904			3
9	992.602660	496.804968	974.592095	487.799686	L	288.203016	144.605146	271.176467	136.091872			2
10					R	***175.118952***	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of ALPILEELLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
65.4	1165.707016	0.003412	ALPILEELLR

Mascot: http://www.matrixscience.com/

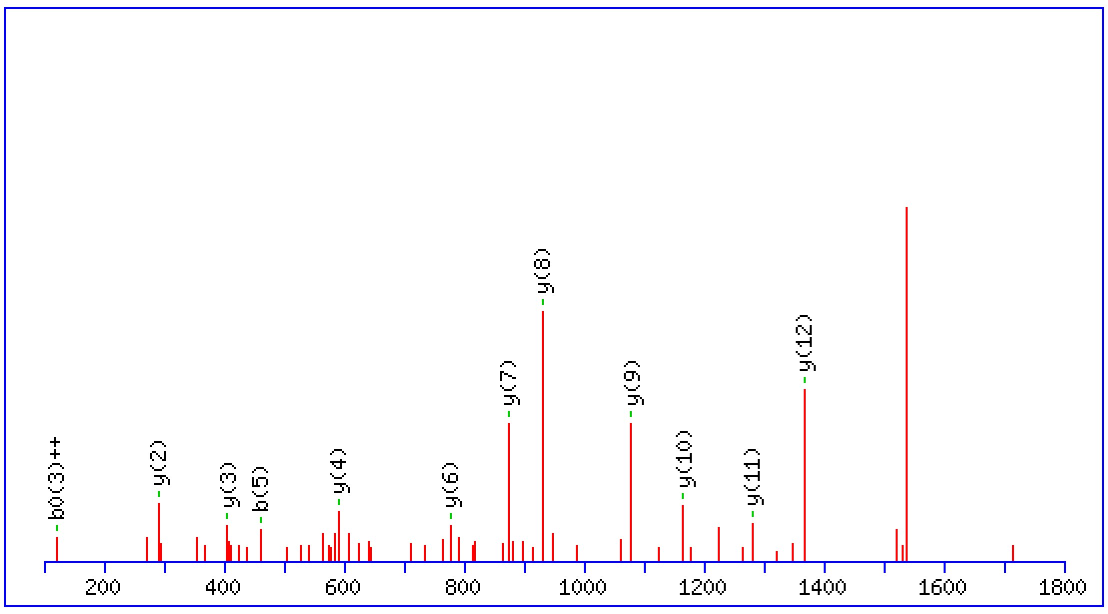
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AVSDSFGPGEWDDR**
Found in **TMBI1_HUMAN**, Transmembrane BAX inhibitor motif-containing protein 1 OS=Homo sapiens GN=TMBIM1 PE=1 SV=2

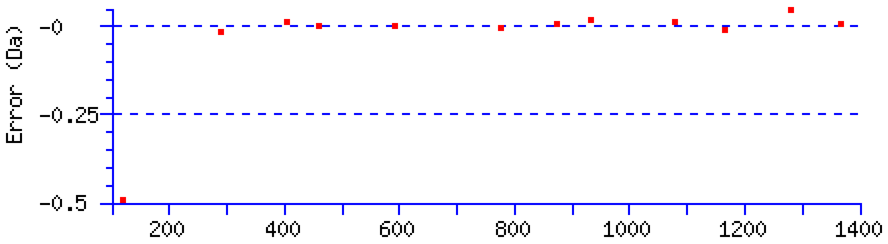
Match to Query 47756: 1536.655828 from(769.335190,2+) rtinseconds(2551) index(32142)
Title: Locus:1.1.1.2316.47
Data file 2011-11-10 - TFD - EP 4-1.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●

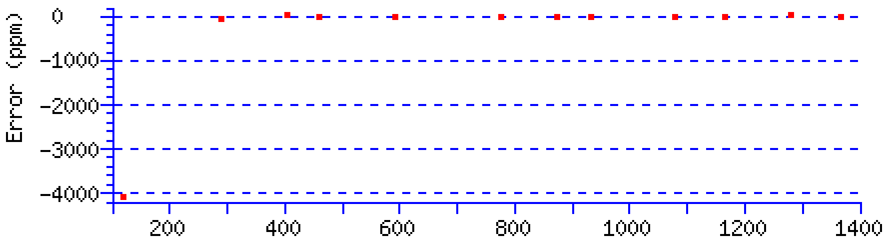


Monoisotopic mass of neutral peptide Mr(calc): 1536.648117
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 95 **Expect:** 9.9e-010
Matches : 12/124 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			A							14
2	171.112804	86.060040			V	1466.618263	733.812770	1449.591714	725.299495	1448.607698	724.807487	13
3	258.144832	129.576054	240.134267	120.570772	S	***1367.549849***	684.278563	1350.523300	675.765288	1349.539284	675.273280	12
4	373.171775	187.089526	355.161210	178.084243	D	***1280.517821***	640.762549	1263.491272	632.249274	1262.507256	631.757266	11
5	460.203803	230.605540	442.193238	221.600257	S	***1165.490878***	583.249077	1148.464329	574.735803	1147.480313	574.243795	10
6	607.272217	304.139747	589.261652	295.134464	F	***1078.458850***	539.733063	1061.432301	531.219789	1060.448285	530.727781	9
7	664.293681	332.650479	646.283116	323.645196	G	***931.390436***	466.198856	914.363887	457.685582	913.379871	457.193574	8
8	761.346445	381.176861	743.335880	372.171578	P	***874.368972***	437.688124	857.342423	429.174850	856.358407	428.682842	7
9	818.367909	409.687593	800.357344	400.682310	G	***777.316208***	389.161742	760.289659	380.648468	759.305643	380.156460	6
10	947.410502	474.208889	929.399937	465.203607	E	720.294744	360.651010	703.268195	352.137736	702.284179	351.645728	5
11	1133.489815	567.248546	1115.479250	558.243263	W	***591.252151***	296.129714	574.225602	287.616439	573.241586	287.124431	4
12	1248.516758	624.762017	1230.506193	615.756735	D	***405.172838***	203.090057	388.146289	194.576783	387.162273	194.084775	3
13	1363.543701	682.275489	1345.533136	673.270206	D	***290.145895***	145.576585	273.119346	137.063311	272.135330	136.571303	2
14					R	175.118952	88.063114	158.092403	79.549839			1



RMS error 1178 ppm



RMS error 1178 ppm

NCBI **BLAST** search of AVSDSFGPGEWDDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
95.2	1536.648117	0.007711	AVSDSFGPGEWDDR

Mascot: http://www.matrixscience.com/

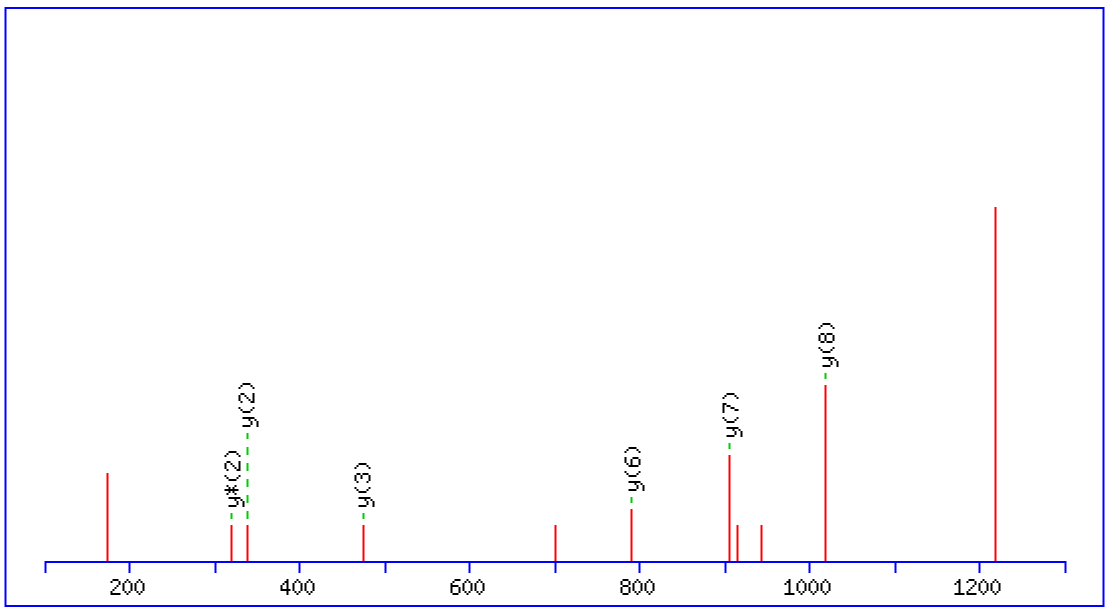
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TVIDSQTHYR**
Found in **TMED3_HUMAN**, Transmembrane emp24 domain-containing protein 3 OS=Homo sapiens GN=TMED3 PE=2 SV=1

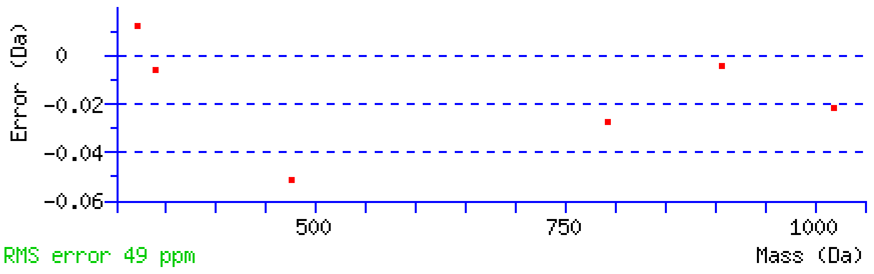
Match to Query 543146: 1218.596448 from(610.305500,2+) rtinseconds(1247) index(741974)
Title: Locus:1.1.1.815.39
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

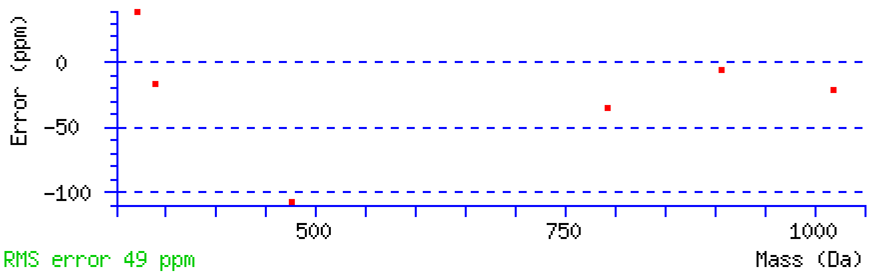
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1218.599304
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 38  Expect: 0.0025
Matches : 6/92 fragment ions using 9 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							10
2	201.123369	101.065322			183.112804	92.060040	V	1118.558899	559.783088	1101.532350	551.269813	1100.548334	550.777805	9
3	314.207433	157.607354			296.196868	148.602072	I	***1019.490485***	510.248881	1002.463936	501.735606	1001.479920	501.243598	8
4	429.234376	215.120826			411.223811	206.115544	D	***906.406421***	453.706849	889.379872	445.193574	888.395856	444.701566	7
5	516.266404	258.636840			498.255839	249.631558	S	***791.379478***	396.193377	774.352929	387.680103	773.368913	387.188095	6
6	644.324982	322.666129	627.298433	314.152855	626.314417	313.660847	Q	704.347450	352.677363	687.320901	344.164089	686.336885	343.672081	5
7	745.372661	373.189969	728.346112	364.676694	727.362096	364.184686	T	576.288872	288.648074	559.262323	280.134800	558.278307	279.642792	4
8	882.431573	441.719425	865.405024	433.206150	864.421008	432.714142	H	***475.241193***	238.124234	458.214644	229.610960			3
9	1045.494902	523.251089	1028.468353	514.737815	1027.484337	514.245807	Y	***338.182281***	169.594778	321.155732	161.081504			2
10							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of TVIDSQTHYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.9	1218.599304	-0.002856	TVIDSQTHYR
10.7	1218.595459	0.000989	SSPPPPPALPPM
5.7	1218.599304	-0.002856	SPPPGPDGHAKK
5.2	1218.591431	0.005017	SLPQGEKVQAM
3.9	1218.588074	0.008374	SPDPFGAVAAQK
3.4	1218.588074	0.008374	LSPFSPPSPAR
3.4	1218.591431	0.005017	SPIERAVAPTM
1.2	1218.602661	-0.006213	SLRQKPGDSTM

Mascot: http://www.matrixscience.com/

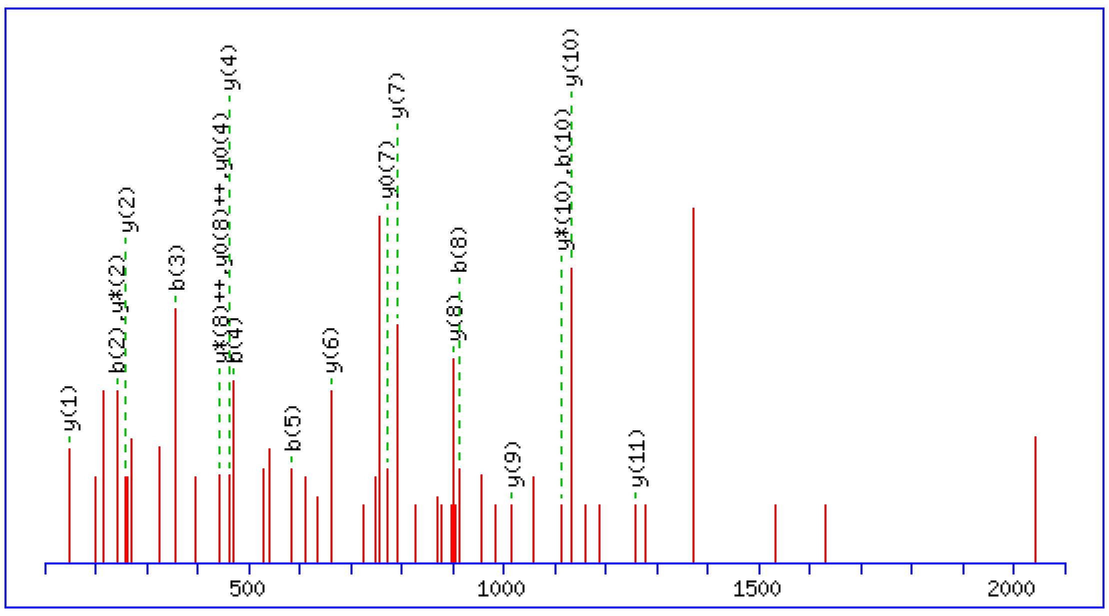
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LEDILESINSIK**
Found in **TMED5_HUMAN**, Transmembrane emp24 domain-containing protein 5 OS=Homo sapiens GN=TMED5 PE=1 SV=1

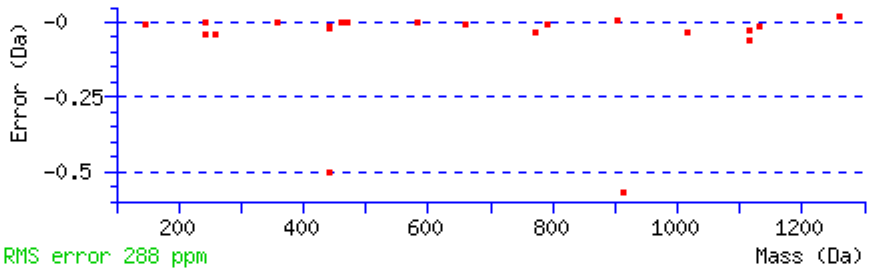
Match to Query 39362: 1372.744108 from(687.379330,2+) rtinseconds(3479) index(49032)
Title: Locus:1.1.1.2614.31
Data file 2011-11-12 - TFD - EP 6-5.mgf

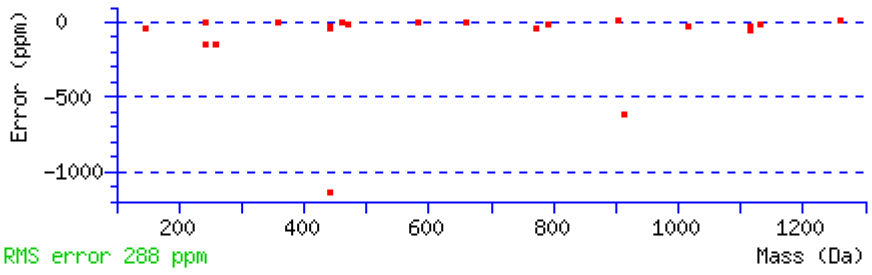
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1372.744919
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 45  Expect: 0.00037
Matches : 21/110 fragment ions using 43 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							12
2	**243.133933**	122.070605			225.123368	113.065322	E	***1260.668172***	630.837724	1243.641623	622.324450	1242.657607	621.832442	11
3	**358.160876**	179.584076			340.150311	170.578794	D	***1131.625579***	566.316428	1114.599030	557.803153	1113.615014	557.311145	10
4	**471.244940**	236.126108			453.234375	227.120826	I	***1016.598636***	508.802956	999.572087	500.289681	998.588071	499.797673	9
5	**584.329004**	292.668140			566.318439	283.662858	L	***903.514572***	452.260924	886.488023	443.747650	885.504007	443.255642	8
6	713.371597	357.189437			695.361032	348.184154	E	***790.430508***	395.718892	773.403959	387.205618	772.419943	386.713610	7
7	800.403625	400.705451			782.393060	391.700168	S	***661.387915***	331.197596	644.361366	322.684321	643.377350	322.192313	6
8	**913.487689**	457.247483			895.477124	448.242200	I	574.355887	287.681582	557.329338	279.168307	556.345322	278.676299	5
9	1027.530616	514.268946	1010.504067	505.755672	1009.520051	505.263664	N	***461.271823***	231.139549	444.245274	222.626275	443.261258	222.134267	4
10	**1114.562644**	557.784960	1097.536095	549.271686	1096.552079	548.779678	S	347.228896	174.118086	330.202347	165.604811	329.218331	165.112803	3
11	1227.646708	614.326992	1210.620159	605.813718	1209.636143	605.321710	I	***260.196868***	130.602072	243.170319	122.088797			2
12							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of LEDILESINSIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.5	1372.744919	-0.000811	LEDILESINSIK
13.5	1372.735062	0.009046	EIDPPFRPKVK
7.9	1372.735031	0.009077	LEDLNFPEIKR
6.4	1372.738419	0.005689	GSDGGSMLKALPLK
4.8	1372.735046	0.009062	GQEGVKWSELIK
4.8	1372.756195	-0.012087	LTQQDTSVLQLK
4.2	1372.746307	-0.002199	HGAIPGGLSIGPPGK
4.1	1372.746292	-0.002184	KGASFQTVASLHK
3.7	1372.738403	0.005705	LECSKLQPSAVK
3.1	1372.756180	-0.012072	TQQSLAAIVDSLK

Mascot: http://www.matrixscience.com/

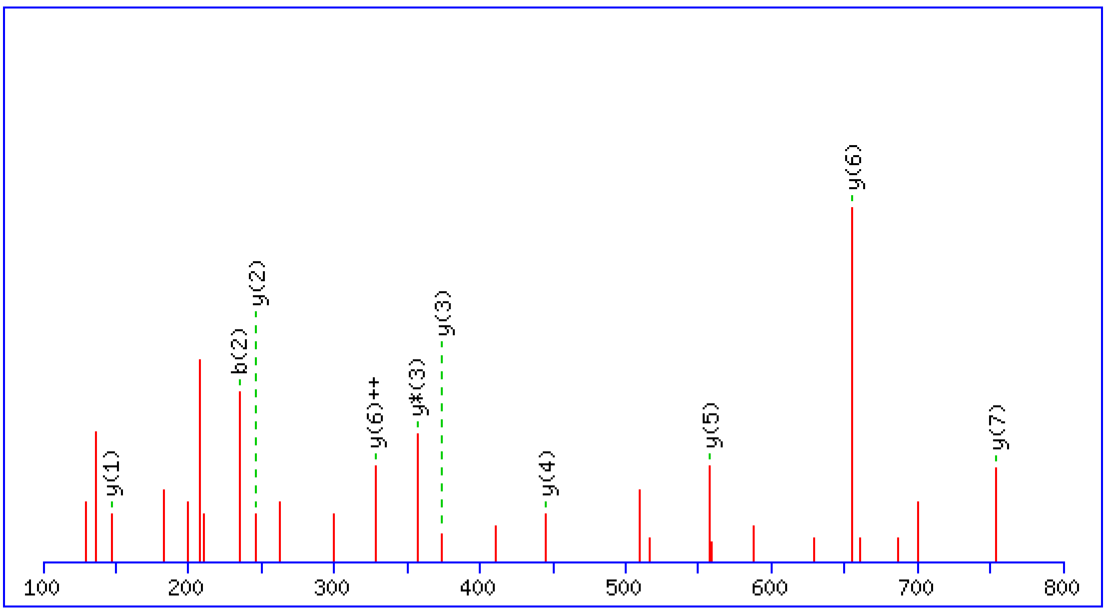
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AYVPIAQVK**
Found in **GPNMB_HUMAN**, Transmembrane glycoprotein NMB OS=Homo sapiens GN=GPNMB PE=1 SV=2

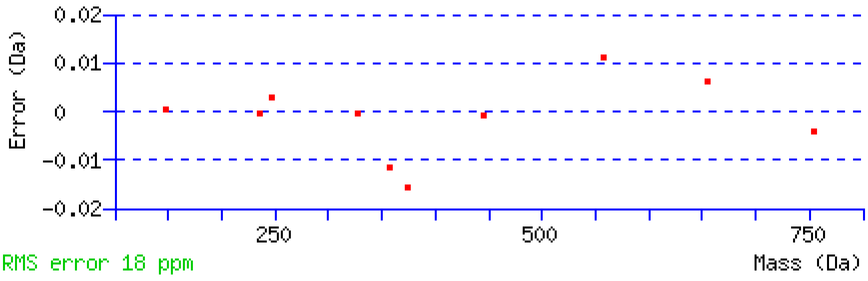
Match to Query 15003: 987.575988 from(494.795270,2+) rtinseconds(1928) index(16349)
Title: Locus:1.1.1.2090.22
Data file 2011-11-14 - TFD - EP 8-7.mgf

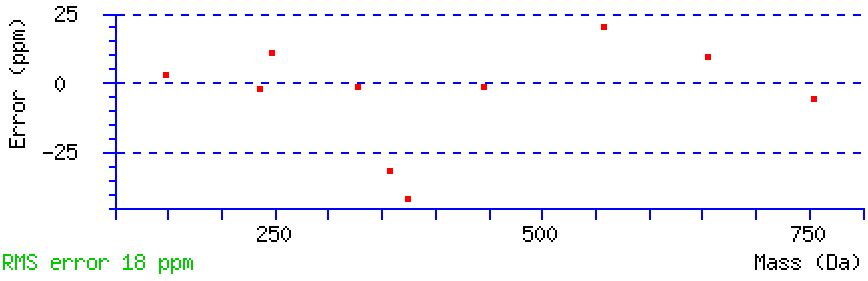
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 987.575302
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 35  Expect: 0.0016
Matches : 10/52 fragment ions using 27 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	72.044390	36.525833			A					9
2	235.107719	118.057498			Y	917.545481	459.276379	900.518932	450.763104	8
3	334.176133	167.591704			V	***754.482152***	377.744714	737.455603	369.231440	7
4	431.228897	216.118087			P	***655.413738***	328.210507	638.387189	319.697233	6
5	544.312961	272.660119			I	***558.360974***	279.684125	541.334425	271.170851	5
6	615.350075	308.178676			A	***445.276910***	223.142093	428.250361	214.628818	4
7	743.408653	372.207965	726.382104	363.694690	Q	***374.239796***	187.623536	357.213247	179.110261	3
8	842.477067	421.742172	825.450518	413.228897	V	***246.181218***	123.594247	229.154669	115.080972	2
9					K	***147.112804***	74.060040	130.086255	65.546765	1





NCBI **BLAST** search of AYVPIAQVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.2	987.575302	0.000686	AYVPIAQVK

Mascot: http://www.matrixscience.com/

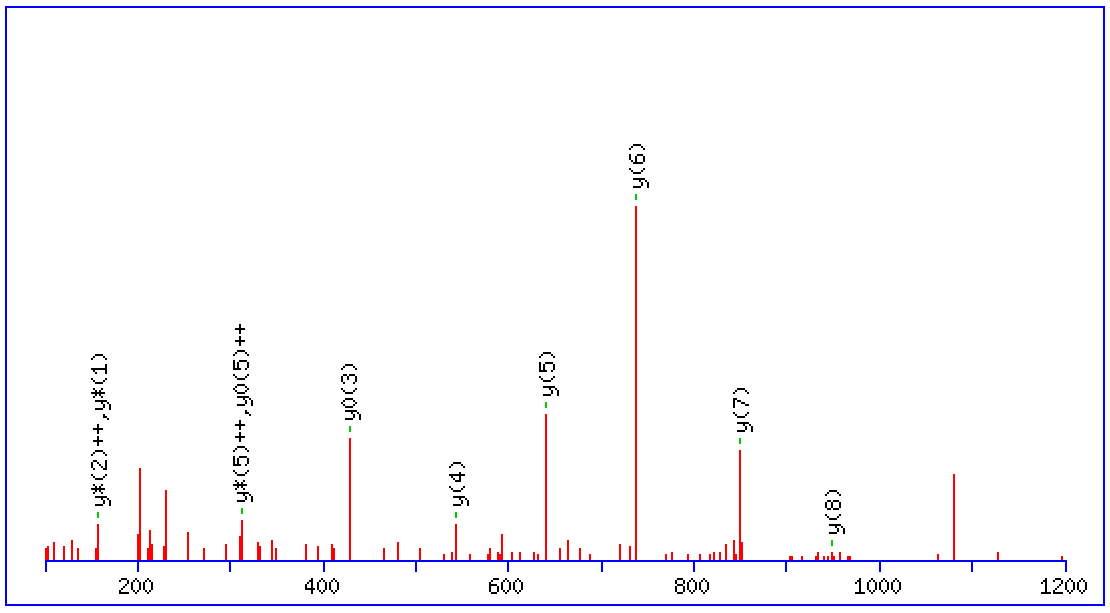
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVLPPPDRR**
Found in **TM121_HUMAN**, Transmembrane protein 121 OS=Homo sapiens GN=TMEM121 PE=2 SV=1

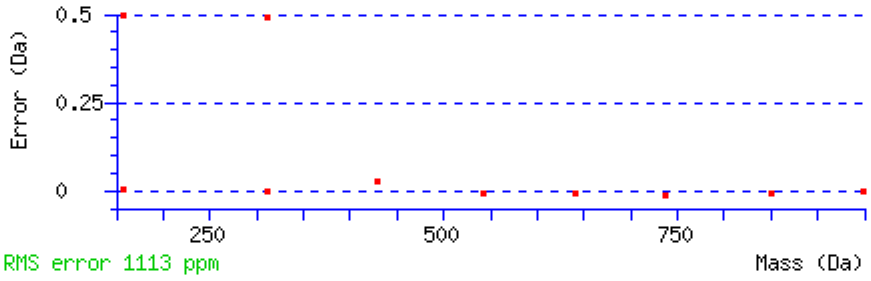
Match to Query 20956: 1079.586308 from(540.800430,2+) rtinseconds(2253) index(26681)
Title: Locus:1.1.1.2285.22
Data file 2011-11-10 - TFD - EP 3-1.mgf

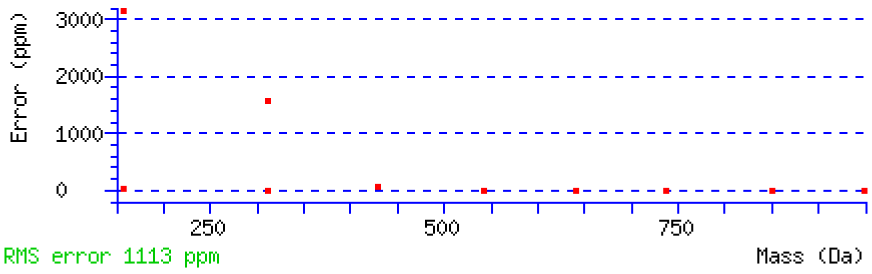
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1200] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1079.590973
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 45 **Expect:** 0.00022
Matches : 10/66 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^0	y^{0++}	#
1	132.047761	66.527518					M							9
2	231.116175	116.061725					V	***949.557776***	475.282526	932.531227	466.769252	931.547211	466.277244	8
3	344.200239	172.603758					L	***850.489362***	425.748319	833.462813	417.235045	832.478797	416.743037	7
4	441.253003	221.130139					P	***737.405298***	369.206287	720.378749	360.693013	719.394733	360.201005	6
5	538.305767	269.656522					P	***640.352534***	320.679905	623.325985	312.166631	622.341969	311.674623	5
6	635.358531	318.182904					P	***543.299770***	272.153523	526.273221	263.640249	525.289205	263.148241	4
7	750.385474	375.696375			732.374909	366.691093	D	446.247006	223.627141	429.220457	215.113866	428.236441	214.621858	3
8	906.486585	453.746931	889.460036	445.233656	888.476020	444.741648	R	331.220063	166.113669	314.193514	157.600395			2
9							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of MVLPPPDRR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
57.7	1079.579758	0.006550	MVLPPDVGPR
45.1	1079.590973	-0.004665	MVLPPPDRR

Mascot: http://www.matrixscience.com/

{MATRIX SCIENCE}

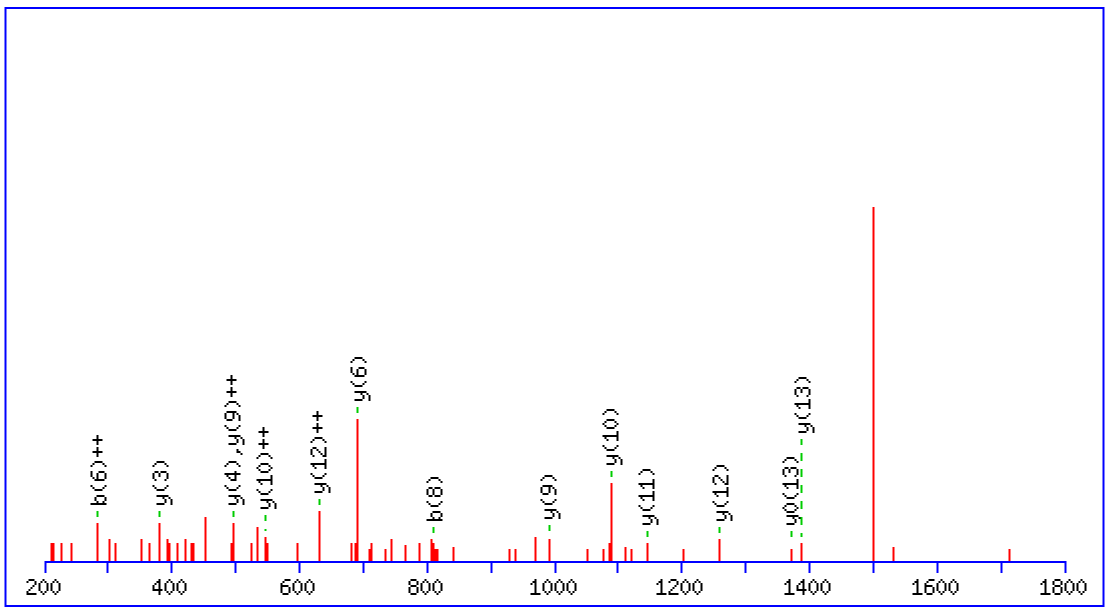
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IENGPGEIPVDFSK**
Found in **TMM19_HUMAN**, Transmembrane protein 19 OS=Homo sapiens GN=TMEM19 PE=2 SV=1

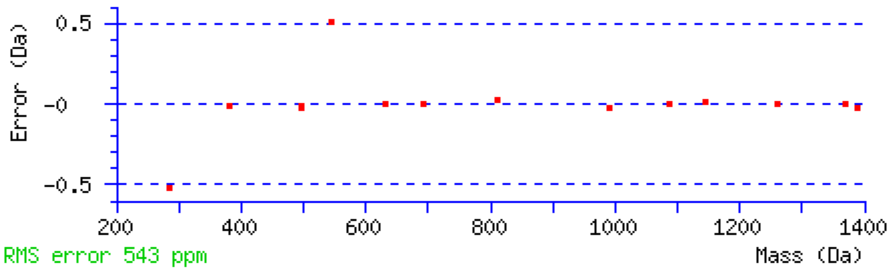
Match to Query 838337: 1500.744468 from(751.379510,2+) rtinseconds(2567) index(605688)
Title: Locus:1.1.1.1303.46
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

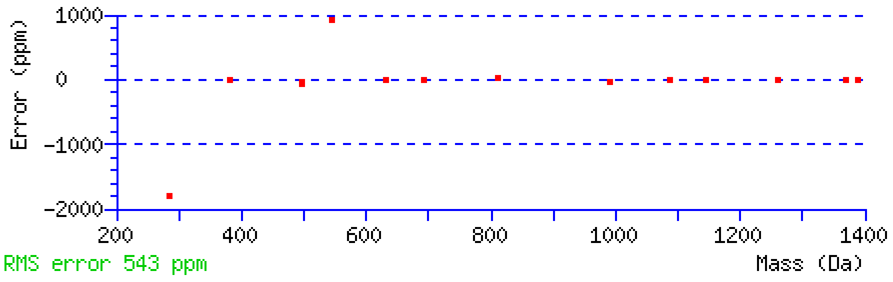
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1500.746017
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 49 **Expect:** 8e-005
Matches : 14/148 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					I							14
2	243.133933	122.070605			225.123368	113.065322	E	***1388.669236***	694.838256	1371.642687	686.324982	1370.658671	685.832974	13
3	357.176860	179.092068	340.150311	170.578794	339.166295	170.086786	N	***1259.626643***	630.316960	1242.600094	621.803685	1241.616078	621.311677	12
4	414.198324	207.602800	397.171775	199.089526	396.187759	198.597518	G	***1145.583716***	573.295496	1128.557167	564.782222	1127.573151	564.290214	11
5	511.251088	256.129182	494.224539	247.615908	493.240523	247.123900	P	***1088.562252***	544.784764	1071.535703	536.271490	1070.551687	535.779482	10
6	568.272552	284.639914	551.246003	276.126640	550.261987	275.634632	G	***991.509488***	496.258382	974.482939	487.745108	973.498923	487.253100	9
7	697.315145	349.161211	680.288596	340.647936	679.304580	340.155928	E	934.488024	467.747650	917.461475	459.234376	916.477459	458.742368	8
8	810.399209	405.703243	793.372660	397.189968	792.388644	396.697960	I	805.445431	403.226354	788.418882	394.713079	787.434866	394.221071	7
9	907.451973	454.229625	890.425424	445.716350	889.441408	445.224342	P	***692.361367***	346.684322	675.334818	338.171047	674.350802	337.679039	6
10	1006.520387	503.763832	989.493838	495.250557	988.509822	494.758549	V	595.308603	298.157940	578.282054	289.644665	577.298038	289.152657	5
11	1121.547330	561.277303	1104.520781	552.764029	1103.536765	552.272021	D	***496.240189***	248.623733	479.213640	240.110458	478.229624	239.618450	4
12	1268.615744	634.811510	1251.589195	626.298236	1250.605179	625.806228	F	***381.213246***	191.110261	364.186697	182.596987	363.202681	182.104979	3
13	1355.647772	678.327524	1338.621223	669.814250	1337.637207	669.322242	S	234.144832	117.576054	217.118283	109.062780	216.134267	108.570772	2
14							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of IENGPGEIPVDFSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.1	1500.746017	-0.001549	IENGPGEIPVDFSK
5.2	1500.749390	-0.004922	GEPGSIIMSSLPGPK
4.9	1500.732101	0.012367	LPGNHSTSQEIFR
2.2	1500.746033	-0.001565	EPGPPGTPFATAISK
0.3	1500.749390	-0.004922	GEPGSIIMSSLPGPK

Mascot: http://www.matrixscience.com/

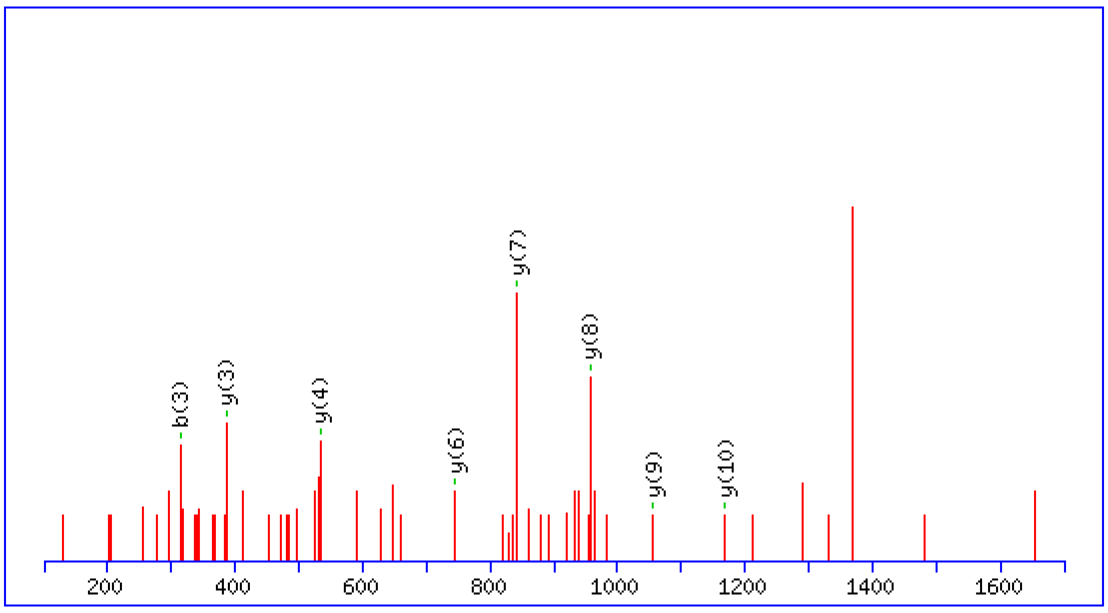
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SLLVNPVLFPNR**
Found in **TMM70_HUMAN**, Transmembrane protein 70, mitochondrial OS=Homo sapiens GN=TMEM70 PE=1 SV=2

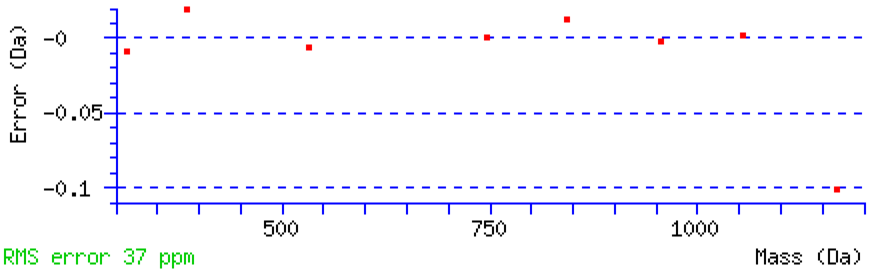
Match to Query 40016: 1367.793488 from(684.904020,2+) rtinseconds(3347) index(46323)
Title: Locus:1.1.1.2425.27
Data file 2011-11-12 - TFD - EP 6-6.mgf

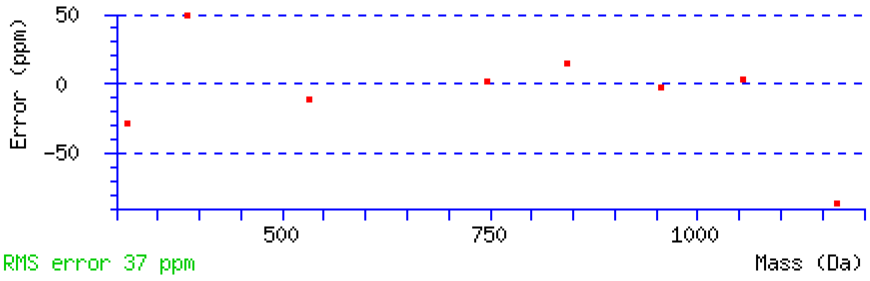
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1700] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1367.792511
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 46  Expect: 0.00011
Matches : 8/102 fragment ions using 13 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	#
1	88.039304	44.523290			70.028739	35.518008	S					12
2	201.123368	101.065322			183.112803	92.060039	L	1281.767768	641.387522	1264.741219	632.874248	11
3	314.207432	157.607354			296.196867	148.602071	L	***1168.683704***	584.845490	1151.657155	576.332216	10
4	413.275846	207.141561			395.265281	198.136279	V	***1055.599640***	528.303458	1038.573091	519.790184	9
5	527.318773	264.163025	510.292224	255.649750	509.308208	255.157742	N	***956.531226***	478.769251	939.504677	470.255977	8
6	624.371537	312.689407	607.344988	304.176132	606.360972	303.684124	P	***842.488299***	421.747788	825.461750	413.234513	7
7	723.439951	362.223614	706.413402	353.710339	705.429386	353.218331	V	***745.435535***	373.221406	728.408986	364.708131	6
8	836.524015	418.765646	819.497466	410.252371	818.513450	409.760363	L	646.367121	323.687199	629.340572	315.173924	5
9	983.592429	492.299853	966.565880	483.786578	965.581864	483.294570	F	***533.283057***	267.145167	516.256508	258.631892	4
10	1080.645193	540.826235	1063.618644	532.312960	1062.634628	531.820952	P	***386.214643***	193.610959	369.188094	185.097685	3
11	1194.688120	597.847698	1177.661571	589.334424	1176.677555	588.842416	N	289.161879	145.084577	272.135330	136.571303	2
12							R	175.118952	88.063114	158.092403	79.549839	1





NCBI **BLAST** search of SLLVNPVLFPNR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.5	1367.792511	0.000977	SLLVNPVLFPNR

Mascot: http://www.matrixscience.com/

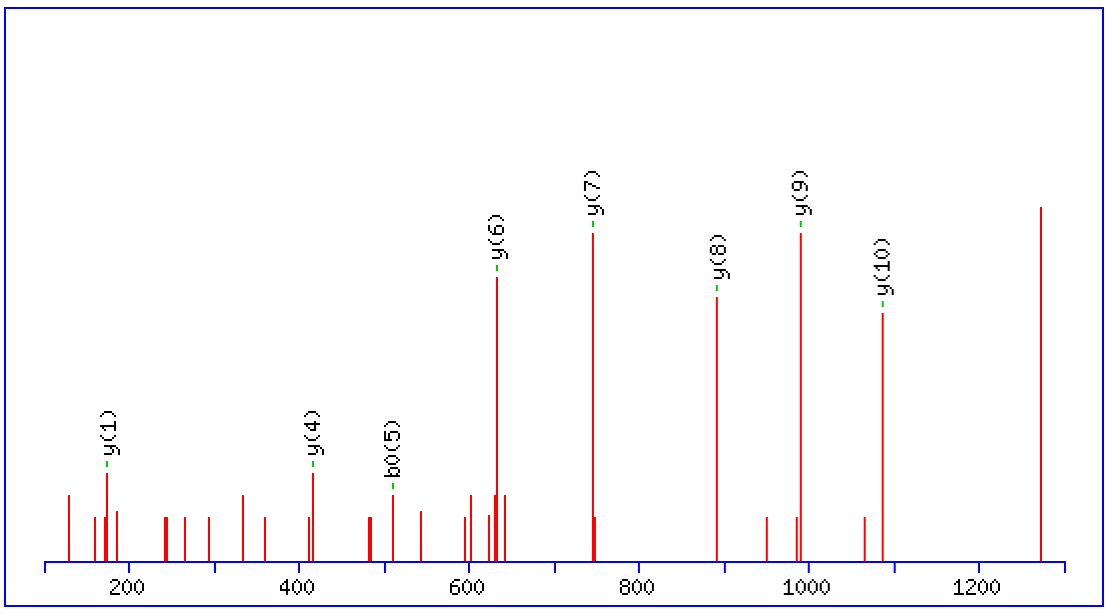
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EGPPFISEAAVR**
Found in **TMM93_HUMAN**, Transmembrane protein 93 OS=Homo sapiens GN=TMEM93 PE=1 SV=1

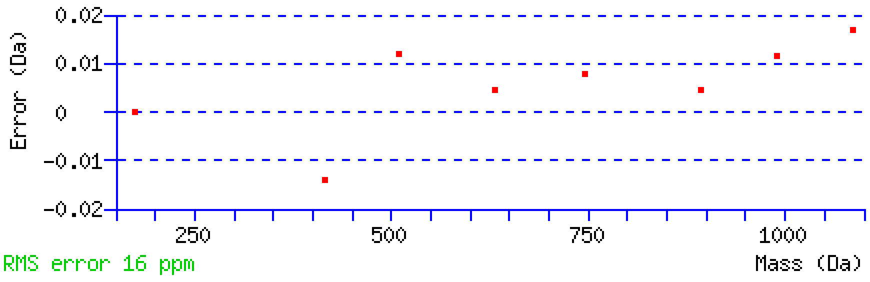
Match to Query 30451: 1271.656248 from(636.835400,2+) rtinseconds(2549) index(27432)
Title: Locus:1.1.1.2328.39
Data file 2011-11-14 - TFD - EP 8-7.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1300] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●

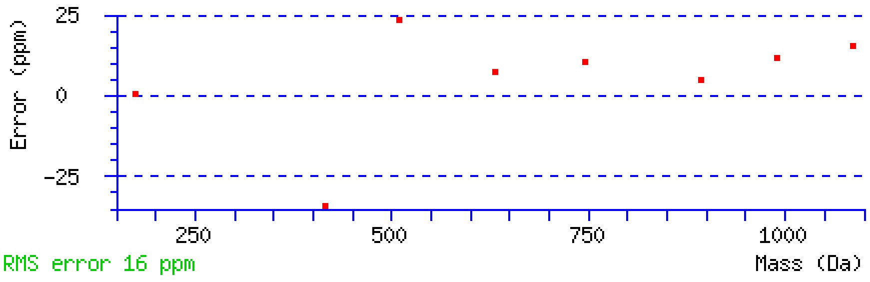


```
Monoisotopic mass of neutral peptide Mr(calc): 1271.650986
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 59  Expect: 4.2e-006
Matches : 8/102 fragment ions using 10 most intense peaks   (help)
```

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	130.049869	65.528572	112.039304	56.523290	**E**							**12**
2	187.071333	94.039305	169.060768	85.034022	**G**	1143.615685	572.311481	1126.589136	563.798206	1125.605120	563.306198	**11**
3	284.124097	142.565687	266.113532	133.560404	**P**	***1086.594221***	543.800748	1069.567672	535.287474	1068.583656	534.795466	**10**
4	381.176861	191.092068	363.166296	182.086786	**P**	***989.541457***	495.274366	972.514908	486.761092	971.530892	486.269084	**9**
5	528.245275	264.626276	510.234710	255.620993	**F**	***892.488693***	446.747984	875.462144	438.234710	874.478128	437.742702	**8**
6	641.329339	321.168308	623.318774	312.163025	**I**	***745.420279***	373.213777	728.393730	364.700503	727.409714	364.208495	**7**
7	728.361367	364.684322	710.350802	355.679039	**S**	***632.336215***	316.671745	615.309666	308.158471	614.325650	307.666463	**6**
8	857.403960	429.205618	839.393395	420.200335	**E**	545.304187	273.155732	528.277638	264.642457	527.293622	264.150449	**5**
9	928.441074	464.724175	910.430509	455.718892	**A**	***416.261594***	208.634435	399.235045	200.121160			**4**
10	999.478188	500.242732	981.467623	491.237449	**A**	345.224480	173.115878	328.197931	164.602603			**3**
11	1098.546602	549.776939	1080.536037	540.771656	**V**	274.187366	137.597321	257.160817	129.084046			**2**
12					**R**	***175.118952***	88.063114	158.092403	79.549839			**1**



RMS error 16 ppm



RMS error 16 ppm

NCBI **BLAST** search of EGPPFISEAAVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.8	1271.650986	0.005262	EGPPFISEAAVR
1.4	1271.651001	0.005247	WALLTDPGDIR
0.6	1271.651001	0.005247	IAVGTEWDIPR

Mascot: http://www.matrixscience.com/

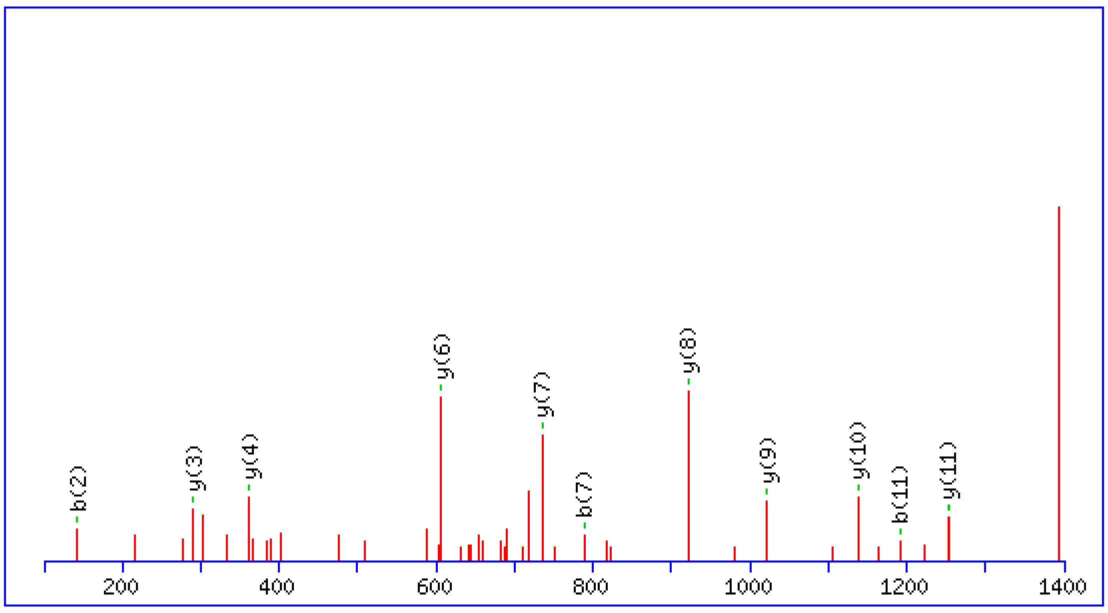
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AADDTWEPFASGK**
Found in **TTHY_HUMAN**, Transthyretin OS=Homo sapiens GN=TTR PE=1 SV=1

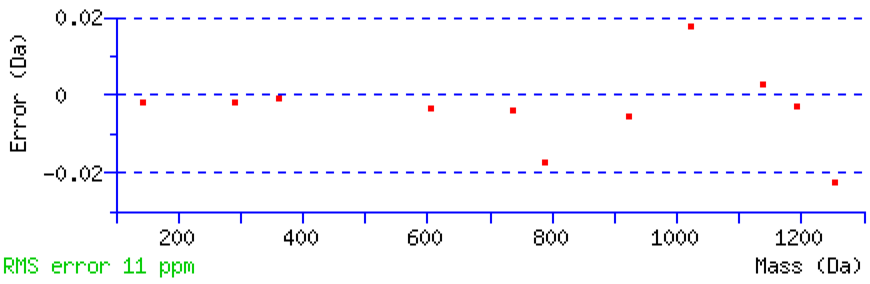
Match to Query 35100: 1393.612828 from(697.813690,2+) rtinseconds(2660) index(27736)
Title: Locus:1.1.1.2343.30
Data file 2011-11-12 - TFD - EP 5-7.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●

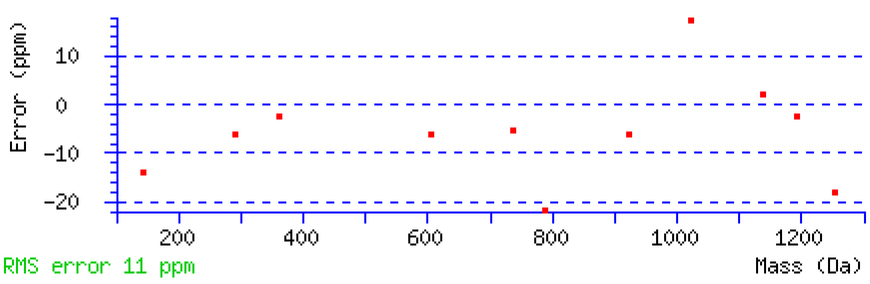


```
Monoisotopic mass of neutral peptide Mr(calc): 1393.615005
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 80  Expect: 4.7e-008
Matches : 11/112 fragment ions using 12 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			A							13
2	**143.081504**	72.044390			A	1323.585173	662.296225	1306.558624	653.782950	1305.574608	653.290942	12
3	258.108447	129.557862	240.097882	120.552579	D	***1252.548059***	626.777668	1235.521510	618.264393	1234.537494	617.772385	11
4	373.135390	187.071333	355.124825	178.066051	D	***1137.521116***	569.264196	1120.494567	560.750922	1119.510551	560.258914	10
5	474.183069	237.595173	456.172504	228.589890	T	***1022.494173***	511.750725	1005.467624	503.237450	1004.483608	502.745442	9
6	660.262382	330.634829	642.251817	321.629547	W	***921.446494***	461.226885	904.419945	452.713611	903.435929	452.221603	8
7	**789.304975**	395.156126	771.294410	386.150843	E	***735.367181***	368.187229	718.340632	359.673954	717.356616	359.181946	7
8	886.357739	443.682508	868.347174	434.677225	P	***606.324588***	303.665932	589.298039	295.152658	588.314023	294.660650	6
9	1033.426153	517.216715	1015.415588	508.211432	F	509.271824	255.139550	492.245275	246.626275	491.261259	246.134267	5
10	1104.463267	552.735272	1086.452702	543.729989	A	***362.203410***	181.605343	345.176861	173.092068	344.192845	172.600060	4
11	**1191.495295**	596.251286	1173.484730	587.246003	S	***291.166296***	146.086786	274.139747	137.573512	273.155731	137.081504	3
12	1248.516759	624.762018	1230.506194	615.756735	G	204.134268	102.570772	187.107719	94.057497			2
13					K	147.112804	74.060040	130.086255	65.546765			1



RMS error 11 ppm



RMS error 11 ppm

NCBI **BLAST** search of AADDTWEPFASGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
79.7	1393.615005	-0.002177	AADDTWEPFASGK

Mascot: http://www.matrixscience.com/

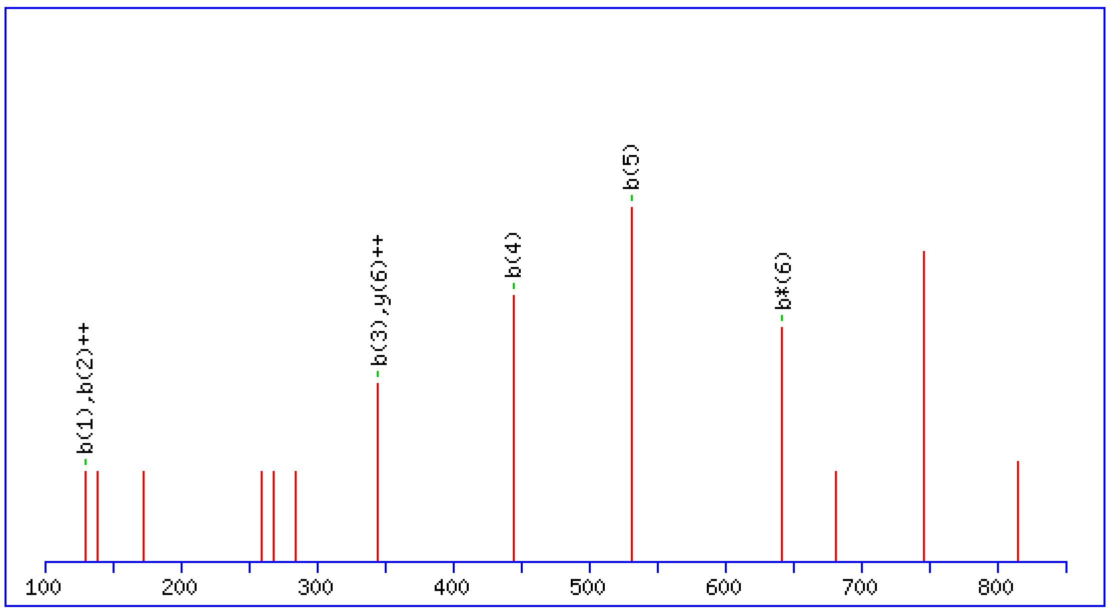
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EQSVSKIR**
Found in **TCHL1_HUMAN**, Trichohyalin-like protein 1 OS=Homo sapiens GN=TCHHL1 PE=2 SV=1

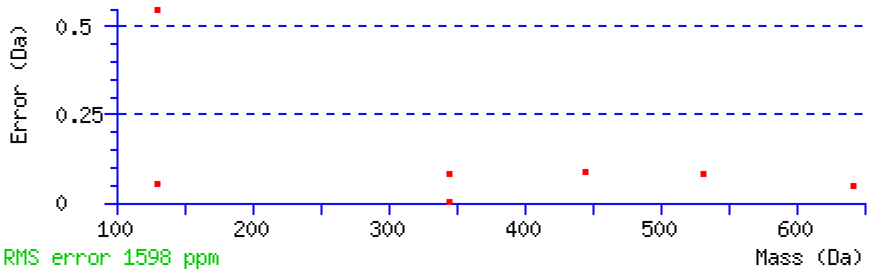
Match to Query 11663: 945.526148 from(473.770350,2+) rtinseconds(1490) index(7772)
Title: Locus:1.1.1.1974.17
Data file 2011-11-10 - TFD - EP 3-7.mgf

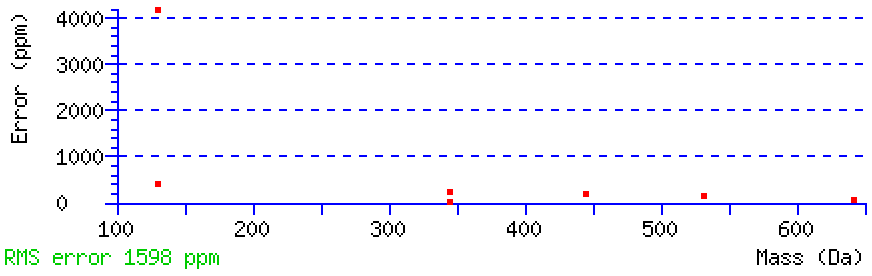
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 945.524323
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.006
Matches : 7/76 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	***130.049869***	65.528572			112.039304	56.523290	**E**							8
2	258.108447	129.557862	241.081898	121.044587	240.097882	120.552579	**Q**	817.489027	409.248152	800.462478	400.734877	799.478462	400.242869	7
3	***345.140475***	173.073875	328.113926	164.560601	327.129910	164.068593	**S**	689.430449	345.218863	672.403900	336.705588	671.419884	336.213580	6
4	***444.208889***	222.608082	427.182340	214.094808	426.198324	213.602800	**V**	602.398421	301.702849	585.371872	293.189574	584.387856	292.697566	5
5	***531.240917***	266.124097	514.214368	257.610822	513.230352	257.118814	**S**	503.330007	252.168642	486.303458	243.655367	485.319442	243.163359	4
6	659.335880	330.171578	642.309331	321.658304	641.325315	321.166296	**K**	416.297979	208.652628	399.271430	200.139353			3
7	772.419944	386.713610	755.393395	378.200336	754.409379	377.708328	**I**	288.203016	144.605146	271.176467	136.091872			2
8							**R**	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of EQSVSKIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.7	945.524323	0.001825	EQSVSKIR
6.6	945.520493	0.005655	LSPPMLLK
3.2	945.524323	0.001825	SEQSVKLR
2.0	945.524323	0.001825	ISQSTALAR
1.6	945.524323	0.001825	SQLDSLKR
1.0	945.528366	-0.002218	EPIFVGLR
0.2	945.524323	0.001825	ETATKPKR
0.2	945.524353	0.001795	QTDVRVTK

Mascot: http://www.matrixscience.com/

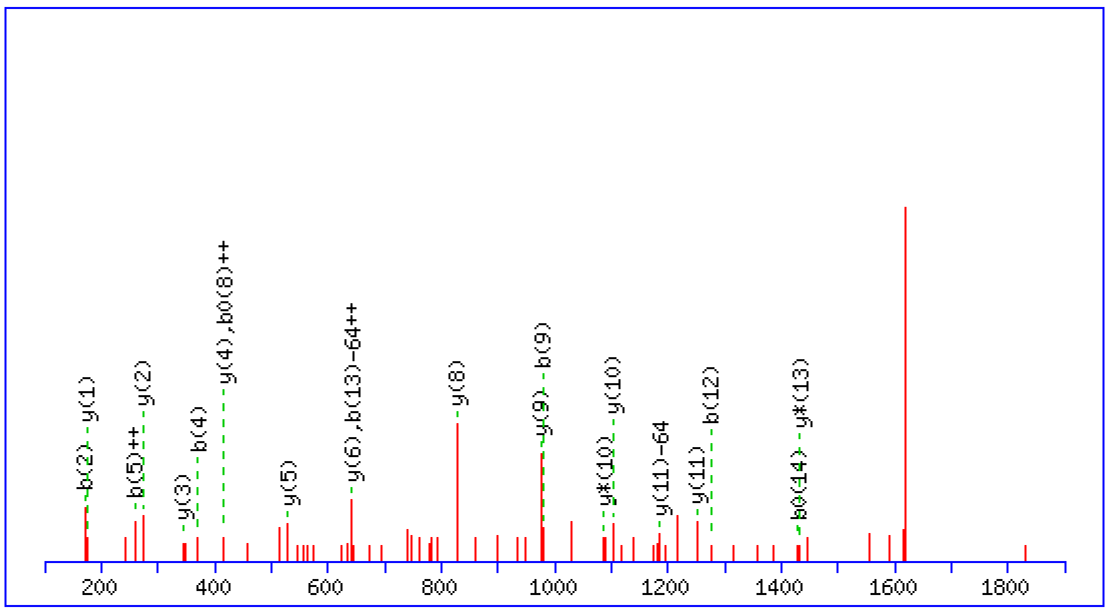
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AVAEMQFGELLAAVR**
Found in **TRI16_HUMAN**, Tripartite motif-containing protein 16 OS=Homo sapiens GN=TRIM16 PE=1 SV=3

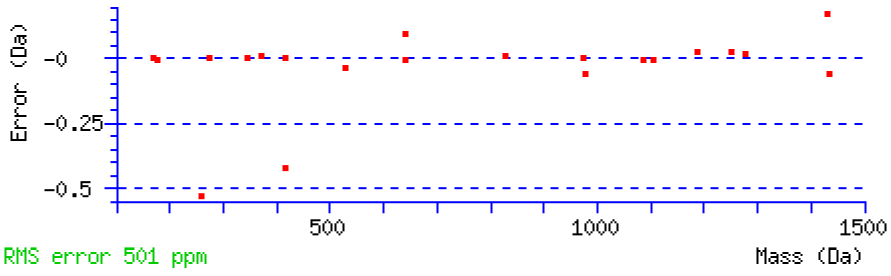
Match to Query 53048: 1619.837588 from(810.926070,2+) rtinseconds(3654) index(52988)
Title: Locus:1.1.1.2807.44
Data file 2011-11-14 - TFD - EP 8-2.mgf

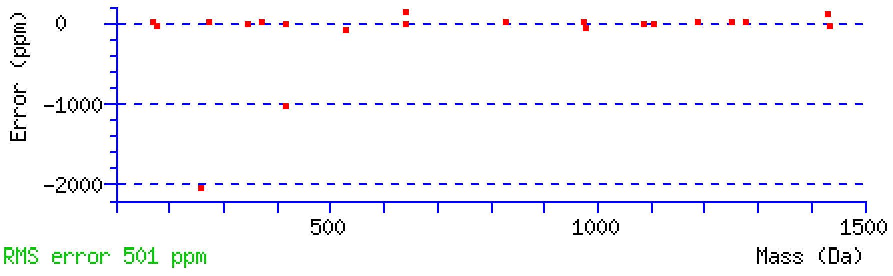
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1619.834106
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M5      : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 55  Expect: 3e-005
Matches : 21/222 fragment ions using 42 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.044390	36.525833					A							15
2	**171.112804**	86.060040					V	1549.804292	775.405784	1532.777743	766.892510	1531.793727	766.400502	14
3	242.149918	121.578597					A	1450.735878	725.871577	1433.709329	717.358303	1432.725313	716.866294	13
4	**371.192511**	186.099894			353.181946	177.094611	E	1379.698764	690.353020	1362.672215	681.839746	1361.688199	681.347737	12
5	518.227911	259.617594			500.217346	250.612311	M	***1250.656171***	625.831723	1233.629622	617.318449	1232.645606	616.826441	11
6	646.286489	323.646883	629.259940	315.133608	628.275924	314.641600	Q	***1103.620771***	552.314024	1086.594222	543.800749	1085.610206	543.308741	10
7	793.354903	397.181090	776.328354	388.667815	775.344338	388.175807	F	***975.562193***	488.284735	958.535644	479.771460	957.551628	479.279452	9
8	850.376367	425.691822	833.349818	417.178547	832.365802	416.686539	G	***828.493779***	414.750528	811.467230	406.237253	810.483214	405.745245	8
9	**979.418960**	490.213118	962.392411	481.699844	961.408395	481.207836	E	771.472315	386.239796	754.445766	377.726521	753.461750	377.234513	7
10	1092.503024	546.755150	1075.476475	538.241876	1074.492459	537.749868	L	***642.429722***	321.718499	625.403173	313.205224			6
11	1205.587088	603.297182	1188.560539	594.783908	1187.576523	594.291900	L	***529.345658***	265.176467	512.319109	256.663192			5
12	**1276.624202**	638.815739	1259.597653	630.302465	1258.613637	629.810456	A	***416.261594***	208.634435	399.235045	200.121160			4
13	1347.661316	674.334296	1330.634767	665.821022	1329.650751	665.329013	A	***345.224480***	173.115878	328.197931	164.602603			3
14	1446.729730	723.868503	1429.703181	715.355229	1428.719165	714.863221	V	***274.187366***	137.597321	257.160817	129.084047			2
15							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of AVAEMQFGELLAAVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.5	1619.834106	0.003482	AVAEMQFGELLAAVR
7.3	1619.837967	-0.000379	RPAGPGSPATSPPASVR

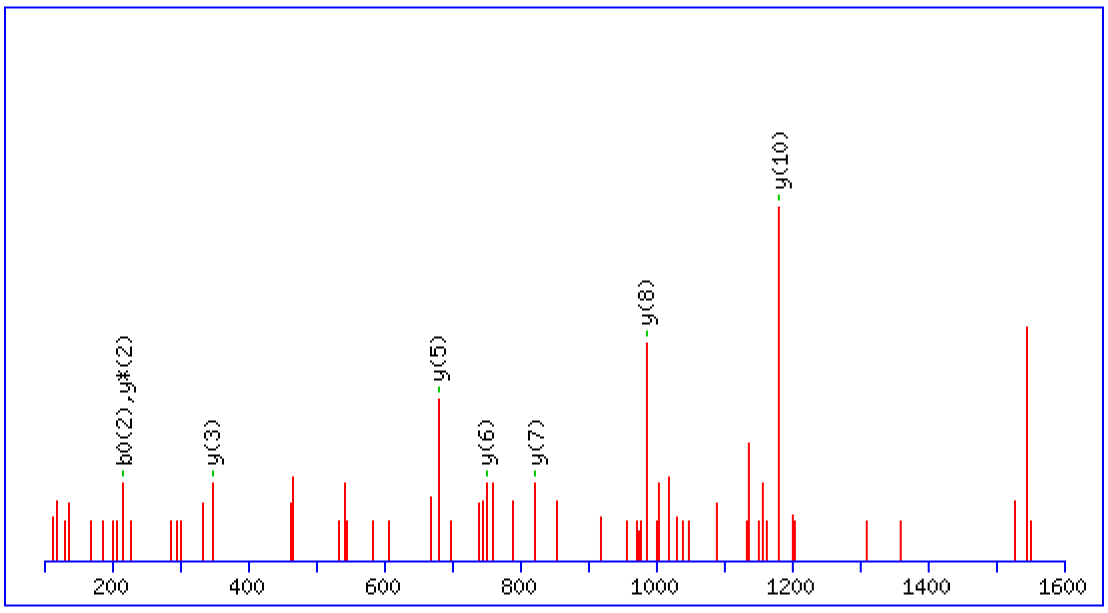
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FSEPVYAAFWLSK**
Found in **TR16L_HUMAN**, Tripartite motif-containing protein 16-like protein OS=Homo sapiens GN=TRIM16L PE=2 SV=3

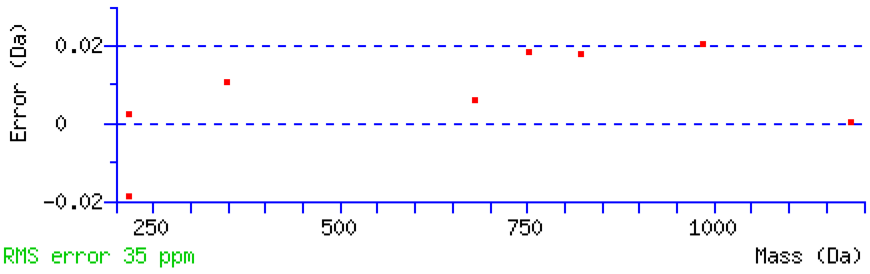
Match to Query 48521: 1543.780948 from(772.897750,2+) rtinseconds(3893) index(57093)
Title: Locus:1.1.1.2961.35
Data file 2011-11-10 - TFD - EP 4-2.mgf

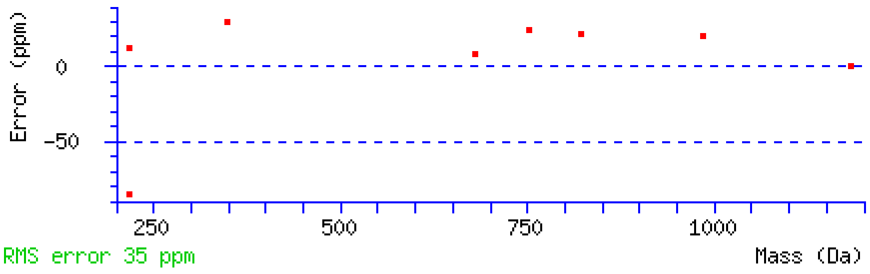
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1543.771103
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 35 **Expect:** 0.0048
Matches : 8/116 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	148.075690	74.541483			F							13
2	235.107718	118.057497	217.097153	109.052214	S	1397.709979	699.358628	1380.683430	690.845353	1379.699414	690.353345	12
3	364.150311	182.578793	346.139746	173.573511	E	1310.677951	655.842614	1293.651402	647.329339	1292.667386	646.837331	11
4	461.203075	231.105175	443.192510	222.099893	P	*1181.635358*	591.321317	1164.608809	582.808043	1163.624793	582.316035	10
5	560.271489	280.639383	542.260924	271.634100	V	1084.582594	542.794935	1067.556045	534.281661	1066.572029	533.789653	9
6	723.334818	362.171047	705.324253	353.165765	Y	*985.514180*	493.260728	968.487631	484.747454	967.503615	484.255446	8
7	794.371932	397.689604	776.361367	388.684322	A	*822.450851*	411.729064	805.424302	403.215789	804.440286	402.723781	7
8	865.409046	433.208161	847.398481	424.202879	A	*751.413737*	376.210507	734.387188	367.697232	733.403172	367.205224	6
9	1012.477460	506.742368	994.466895	497.737085	F	*680.376623*	340.691950	663.350074	332.178675	662.366058	331.686667	5
10	1198.556773	599.782025	1180.546208	590.776742	W	533.308209	267.157743	516.281660	258.644468	515.297644	258.152460	4
11	1311.640837	656.324056	1293.630272	647.318774	L	*347.228896*	174.118086	330.202347	165.604811	329.218331	165.112803	3
12	1398.672865	699.840071	1380.662300	690.834788	S	234.144832	117.576054	217.118283	109.062780	216.134267	108.570772	2
13					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of FSEPVYAAFWLSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.1	1543.771103	0.009845	FSEPVYAAFWLSK

Mascot: http://www.matrixscience.com/

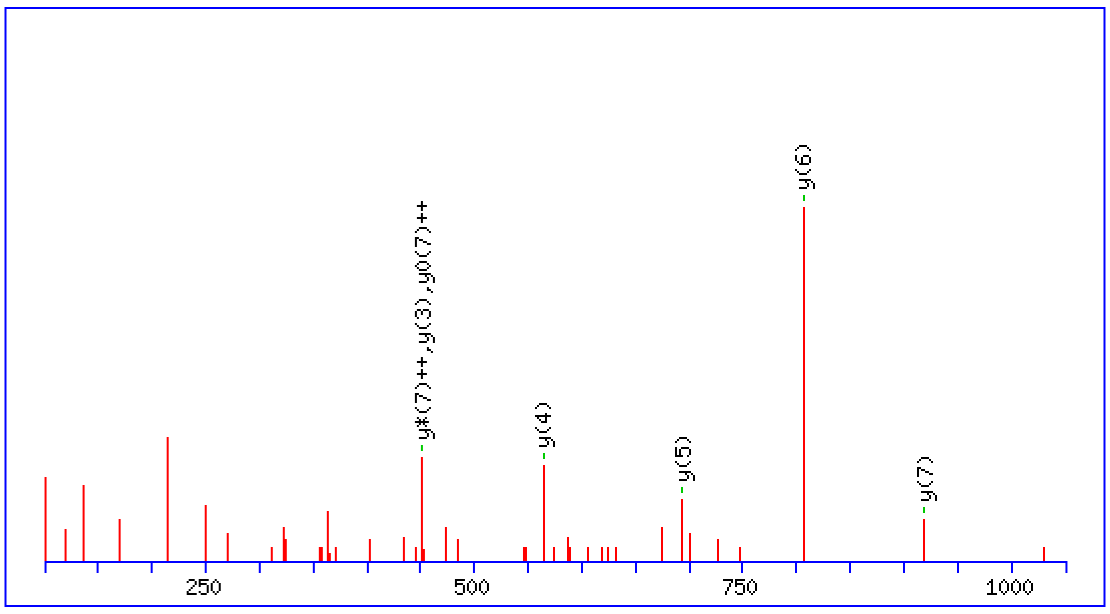
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KPLELREM**
Found in **TRI75_HUMAN**, Tripartite motif-containing protein 75 OS=Homo sapiens GN=TRIM75 PE=2 SV=2

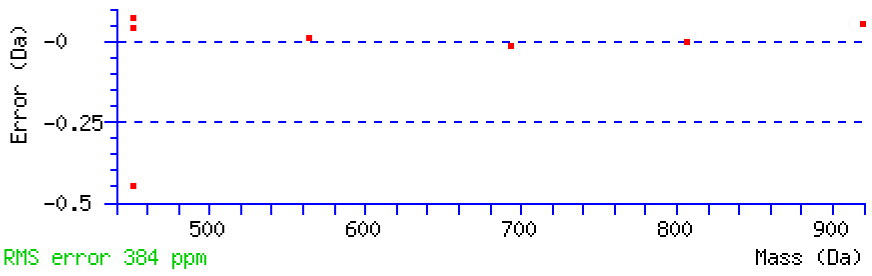
Match to Query 324775: 1046.551548 from(524.283050,2+) rtinseconds(2051) index(837341)
Title: Locus:1.1.1.1327.24
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

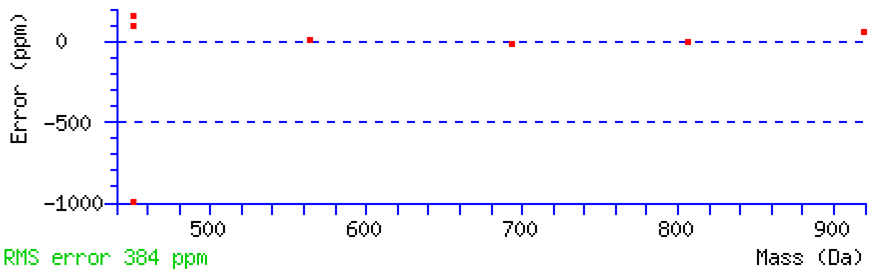
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1046.542999
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
P2 : Oxidation (P)
M8 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 34 **Expect:** 0.0055
Matches : 7/108 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	129.102239	65.054757	112.075690	56.541483			K							8
2	242.149918	121.578597	225.123369	113.065322			P	***919.455345***	460.231311	902.428796	451.718036	901.444780	451.226028	7
3	355.233982	178.120629	338.207433	169.607354			L	***806.407666***	403.707471	789.381117	395.194197	788.397101	394.702189	6
4	484.276575	242.641925	467.250026	234.128651	466.266010	233.636643	E	***693.323602***	347.165439	676.297053	338.652165	675.313037	338.160157	5
5	597.360639	299.183958	580.334090	290.670683	579.350074	290.178675	L	***564.281009***	282.644143	547.254460	274.130868	546.270444	273.638860	4
6	753.461750	377.234513	736.435201	368.721238	735.451185	368.229230	R	***451.196945***	226.102111	434.170396	217.588836	433.186380	217.096828	3
7	882.504343	441.755810	865.477794	433.242535	864.493778	432.750527	E	295.095834	148.051555			277.085269	139.046273	2
8							M	166.053241	83.530259					1





NCBI **BLAST** search of KPLELREM
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.1	1046.542999	0.008549	KPLELREM
12.8	1046.550888	0.000660	QLLSFGNPR
9.5	1046.543030	0.008518	QVQKEVSVM
8.3	1046.550858	0.000690	QLYENKPR
7.8	1046.547028	0.004520	LLKELWDM
3.3	1046.542999	0.008549	LLGAEERIM
1.4	1046.554245	-0.002697	LQEITRCK
1.4	1046.560760	-0.009212	KISTEDINK
1.4	1046.560760	-0.009212	KLENDTISK
0.5	1046.542999	0.008549	LKELGINNM

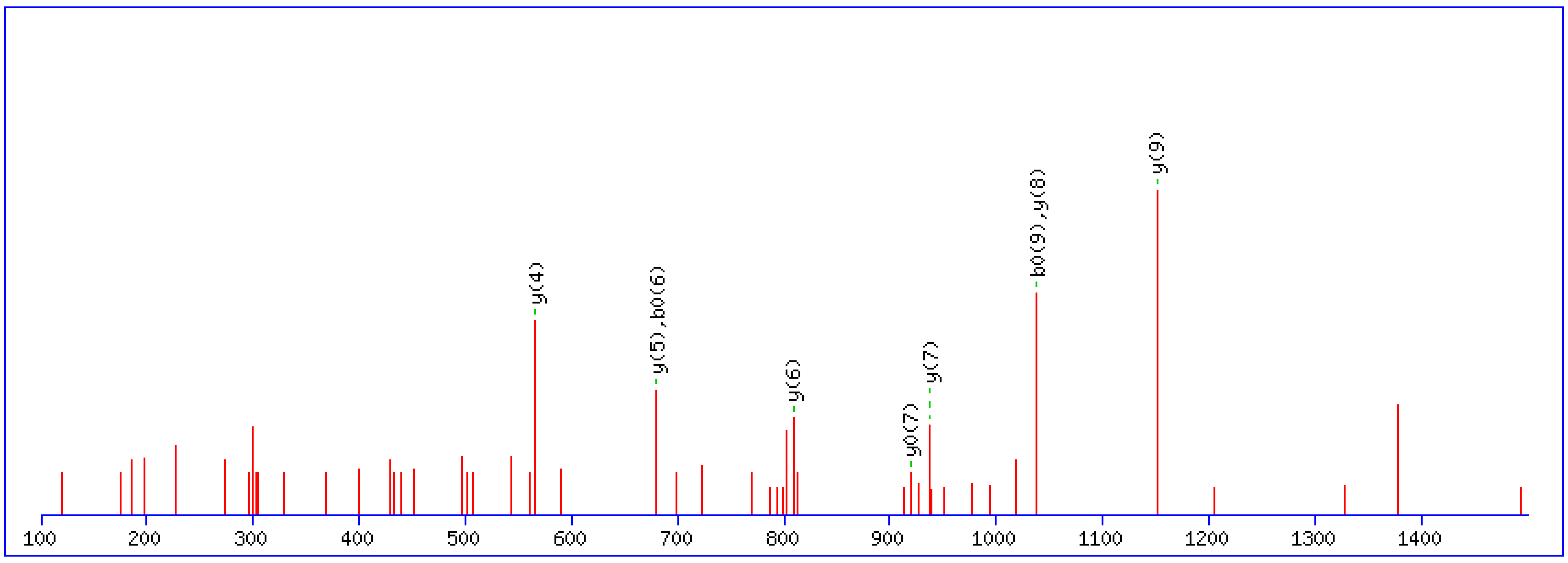
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILLTQENPFFR**
Found in **NSUN2_HUMAN**, tRNA (cytosine(34)-C(5))-methyltransferase OS=Homo sapiens GN=NSUN2 PE=1 SV=2

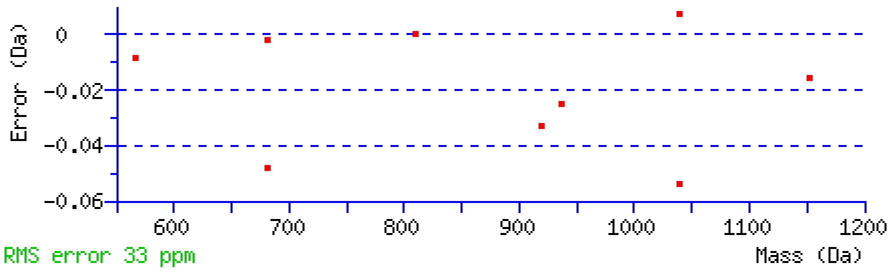
Match to Query 45397: 1376.736968 from(689.375760,2+) rtinseconds(3442) index(50518)
Title: Locus:1.1.1.1697.31
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 1.mgf

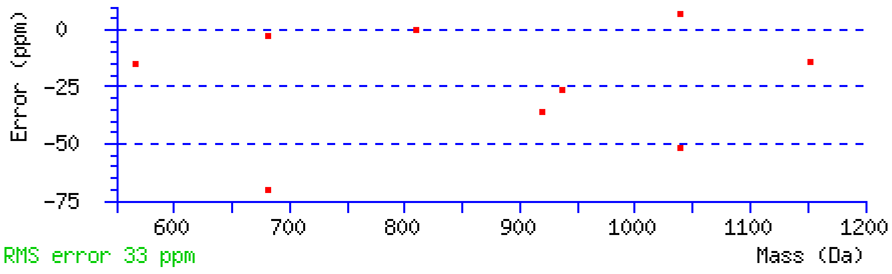
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1376.745224
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.0012
Matches : 9/96 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					I							11
2	227.175404	114.091340					L	1264.668449	632.837863	1247.641900	624.324588	1246.657884	623.832580	10
3	340.259468	170.633372					L	***1151.584385***	576.295831	1134.557836	567.782556	1133.573820	567.290548	9
4	441.307147	221.157211			423.296582	212.151929	T	***1038.500321***	519.753799	1021.473772	511.240524	1020.489756	510.748516	8
5	569.365725	285.186501	552.339176	276.673226	551.355160	276.181218	Q	***937.452642***	469.229959	920.426093	460.716685	919.442077	460.224677	7
6	698.408318	349.707797	681.381769	341.194523	680.397753	340.702515	E	***809.394064***	405.200670	792.367515	396.687396	791.383499	396.195388	6
7	812.451245	406.729261	795.424696	398.215986	794.440680	397.723978	N	***680.351471***	340.679374	663.324922	332.166099			5
8	909.504009	455.255643	892.477460	446.742368	891.493444	446.250360	P	***566.308544***	283.657910	549.281995	275.144636			4
9	1056.572423	528.789850	1039.545874	520.276575	1038.561858	519.784567	F	469.255780	235.131528	452.229231	226.618253			3
10	1203.640837	602.324057	1186.614288	593.810782	1185.630272	593.318774	F	322.187366	161.597321	305.160817	153.084047			2
11							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of ILLTQENPFFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.7	1376.745224	-0.008256	ILLTQENPFFR
7.0	1376.745239	-0.008271	LPPTWKPLPHK
6.7	1376.723465	0.013503	IPPVGPSILHCR
0.1	1376.737366	-0.000398	LLLPLFREVDM

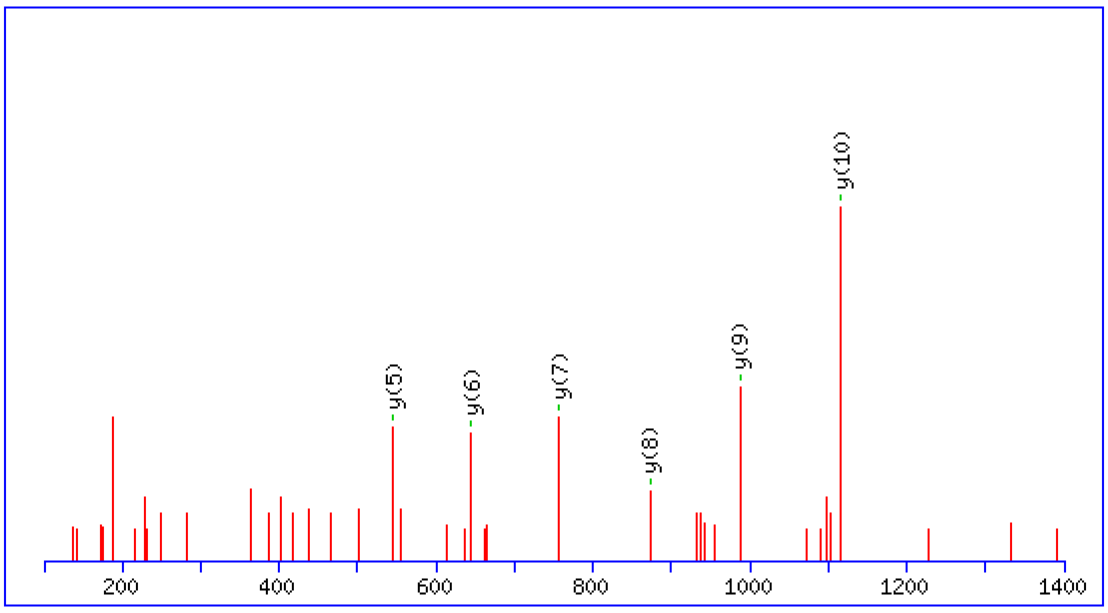
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TIEDDLVSALVR**
Found in **TRUA_HUMAN**, tRNA pseudouridine synthase A, mitochondrial OS=Homo sapiens GN=PUS1 PE=1 SV=3

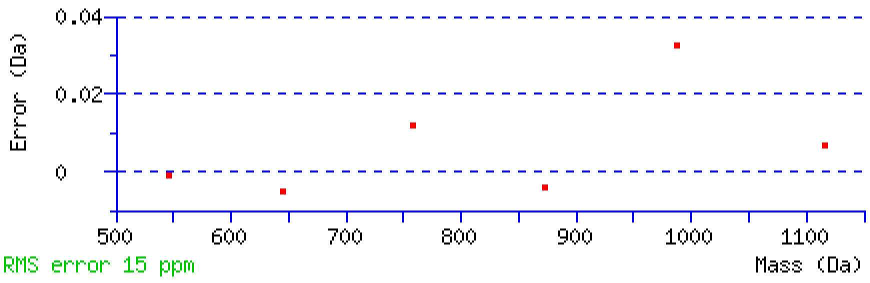
Match to Query 37940: 1329.723488 from(665.869020,2+) rtinseconds(3772) index(55947)
Title: Locus:1.1.1.2772.29
Data file 2011-11-10 - TFD - EP 3-4.mgf

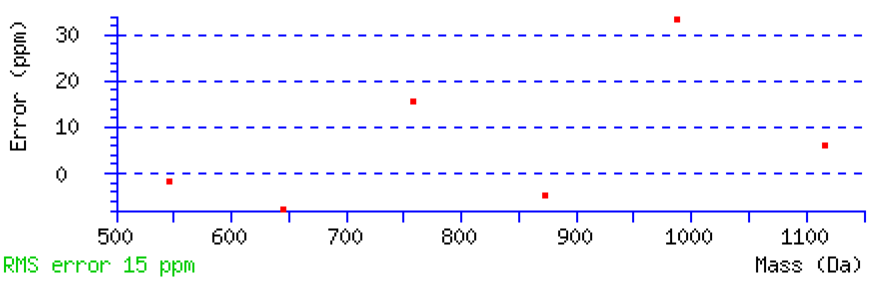
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1329.713989
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.00022
Matches : 6/102 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116	84.044390	42.525833	T							12
2	215.139019	108.073147	197.128454	99.067865	I	1229.673593	615.340435	1212.647044	606.827160	1211.663028	606.335152	11
3	344.181612	172.594444	326.171047	163.589162	E	***1116.589529***	558.798403	1099.562980	550.285128	1098.578964	549.793120	10
4	459.208555	230.107916	441.197990	221.102633	D	***987.546936***	494.277106	970.520387	485.763831	969.536371	485.271823	9
5	574.235498	287.621387	556.224933	278.616105	D	***872.519993***	436.763634	855.493444	428.250360	854.509428	427.758352	8
6	687.319562	344.163419	669.308997	335.158137	L	***757.493050***	379.250163	740.466501	370.736888	739.482485	370.244880	7
7	786.387976	393.697626	768.377411	384.692344	V	***644.408986***	322.708131	627.382437	314.194856	626.398421	313.702848	6
8	873.420004	437.213640	855.409439	428.208358	S	***545.340572***	273.173924	528.314023	264.660649	527.330007	264.168641	5
9	944.457118	472.732197	926.446553	463.726915	A	458.308544	229.657910	441.281995	221.144635			4
10	1057.541182	529.274229	1039.530617	520.268946	L	387.271430	194.139353	370.244881	185.626078			3
11	1156.609596	578.808436	1138.599031	569.803154	V	274.187366	137.597321	257.160817	129.084047			2
12					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of TIEDDLVSALVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.4	1329.713989	0.009499	TIEDDLVSALVR
0.5	1329.732605	-0.009117	TLMLPLTEGSLR

Mascot: http://www.matrixscience.com/

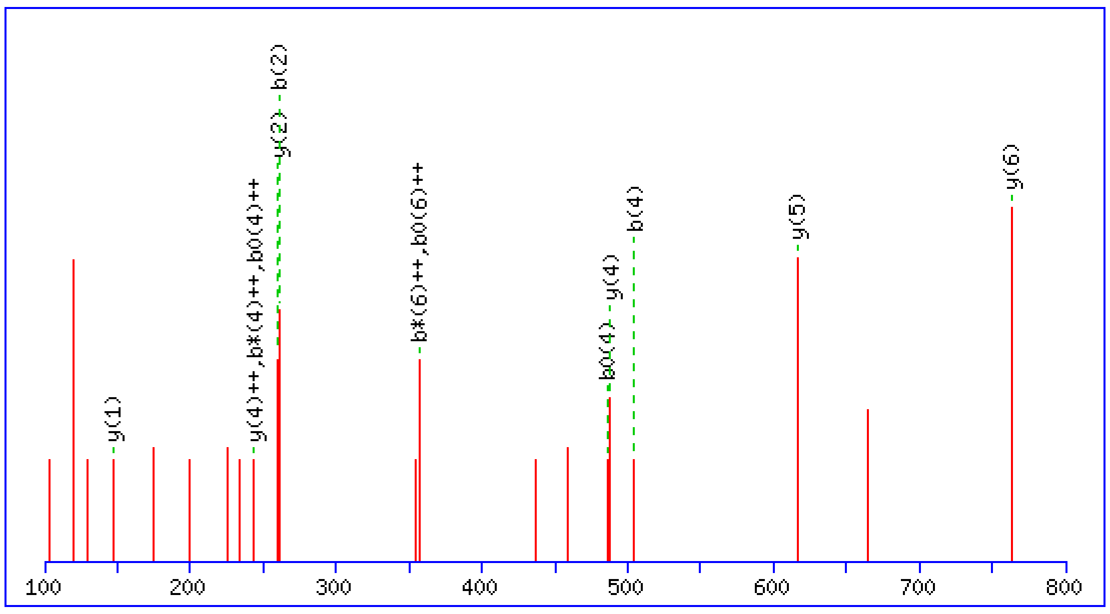
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IMKDLIK**
Found in **TP8L3_HUMAN**, Tumor necrosis factor alpha-induced protein 8-like protein 3 OS=Homo sapiens GN=TNFAIP8L3 PE=2 SV=1

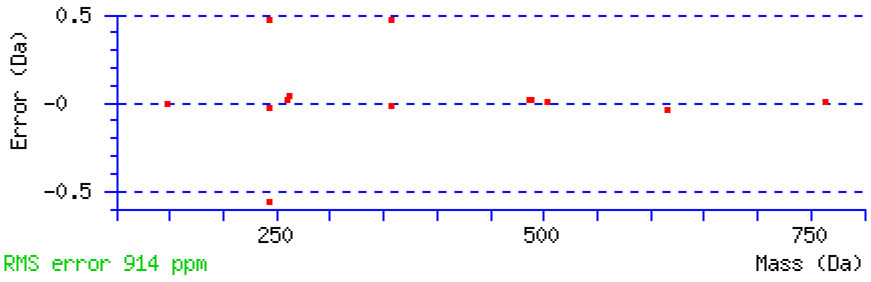
Match to Query 6851: 875.514588 from(438.764570,2+) rtinseconds(3023) index(37352)
Title: Locus:1.1.1.2419.5
Data file 2011-11-10 - TFD - EP 3-6.mgf

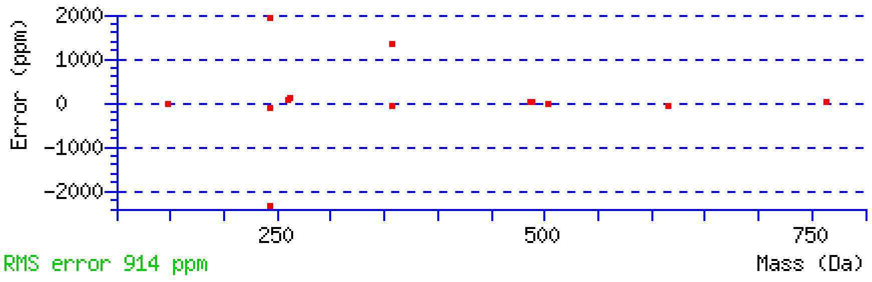
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 875.514999
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M2      : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 30  Expect: 0.0075
Matches : 13/86 fragment ions using 20 most intense peaks   (help)
```

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					**I**							7
2	**261.126740**	131.067008					**M**	***763.438238***	382.222757	746.411689	373.709483	745.427673	373.217475	6
3	389.221703	195.114489	372.195154	186.601215			**K**	***616.402838***	308.705057	599.376289	300.191783	598.392273	299.699775	5
4	**504.248646**	252.627961	487.222097	244.114687	486.238081	243.622679	**D**	***488.307875***	244.657575	471.281326	236.144301	470.297310	235.652293	4
5	617.332710	309.169993	600.306161	300.656719	599.322145	300.164711	**L**	373.280932	187.144104	356.254383	178.630829			3
6	730.416774	365.712025	713.390225	357.198751	712.406209	356.706743	**I**	***260.196868***	130.602072	243.170319	122.088798			2
7							**K**	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of IMKDLIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.3	875.514999	-0.000411	IMKDLIK
19.3	875.511658	0.002930	LFVGSIPK
16.2	875.511642	0.002946	IFLQDIK
15.7	875.522873	-0.008285	FLKGLGNK
14.1	875.522873	-0.008285	IFIRSPK
12.7	875.522873	-0.008285	ISRFPLK
11.5	875.511642	0.002946	LKFIDPK
11.0	875.522873	-0.008285	VLQFKNK
10.7	875.511627	0.002961	FLNELIK
10.7	875.522873	-0.008285	FLRSPLK

Mascot: http://www.matrixscience.com/

{MATRIX SCIENCE}

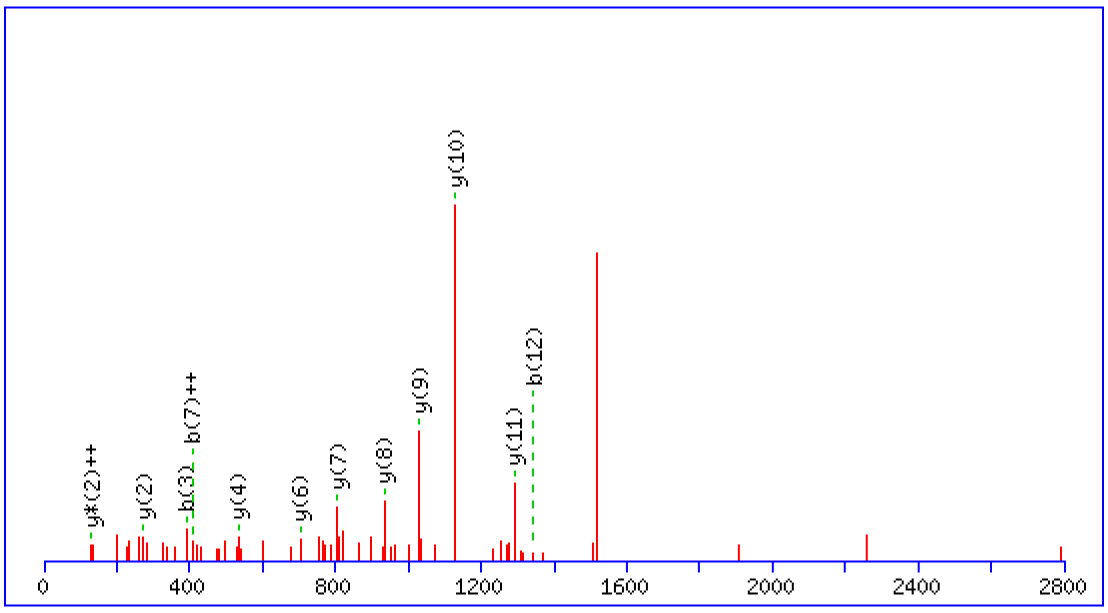
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLYPPETGLFLVR**
Found in **CSK_HUMAN**, Tyrosine-protein kinase CSK OS=Homo sapiens GN=CSK PE=1 SV=1

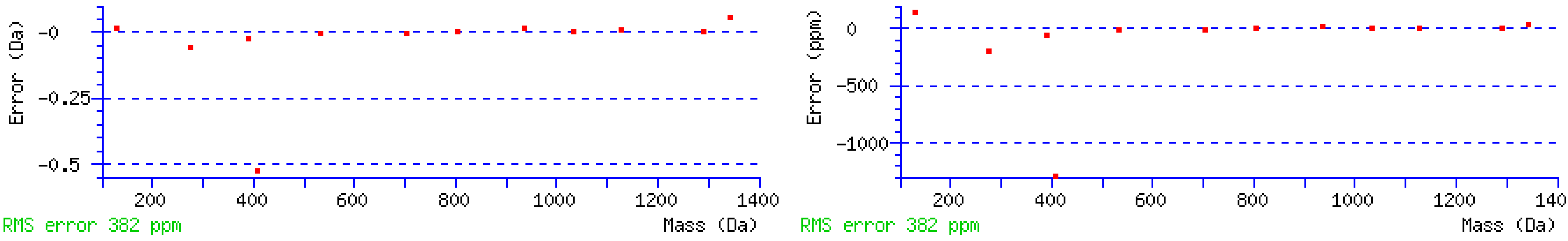
Match to Query 46675: 1516.872648 from(759.443600,2+) rtinseconds(3742) index(56346)
Title: Locus:1.1.1.2842.30
Data file 2011-11-10 - TFD - EP 3-3.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1516.865341
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 43 **Expect:** 0.00018
Matches : 12/98 fragment ions using 26 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							13
2	227.175404	114.091340			L	1404.788565	702.897921	1387.762016	694.384646	1386.778000	693.892638	12
3	**390.238733**	195.623004			Y	*1291.704501*	646.355889	1274.677952	637.842614	1273.693936	637.350606	11
4	487.291497	244.149386			P	*1128.641172*	564.824224	1111.614623	556.310950	1110.630607	555.818942	10
5	584.344261	292.675769			P	*1031.588408*	516.297842	1014.561859	507.784568	1013.577843	507.292560	9
6	713.386854	357.197065	695.376289	348.191783	E	*934.535644*	467.771460	917.509095	459.258186	916.525079	458.766178	8
7	814.434533	407.720905	796.423968	398.715622	T	*805.493051*	403.250164	788.466502	394.736889	787.482486	394.244881	7
8	871.455997	436.231637	853.445432	427.226354	G	*704.445372*	352.726324	687.418823	344.213050			6
9	984.540061	492.773669	966.529496	483.768386	L	647.423908	324.215592	630.397359	315.702318			5
10	1131.608475	566.307876	1113.597910	557.302593	F	*534.339844*	267.673560	517.313295	259.160286			4
11	1244.692539	622.849908	1226.681974	613.844625	L	387.271430	194.139353	370.244881	185.626078			3
12	**1343.760953**	672.384115	1325.750388	663.378832	V	*274.187366*	137.597321	257.160817	129.084047			2
13					R	175.118952	88.063114	158.092403	79.549839			1



NCBI **BLAST** search of LLYPPETGLFLVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
43.2	1516.865341	0.007307	LLYPPETGLFLVR

Mascot: http://www.matrixscience.com/

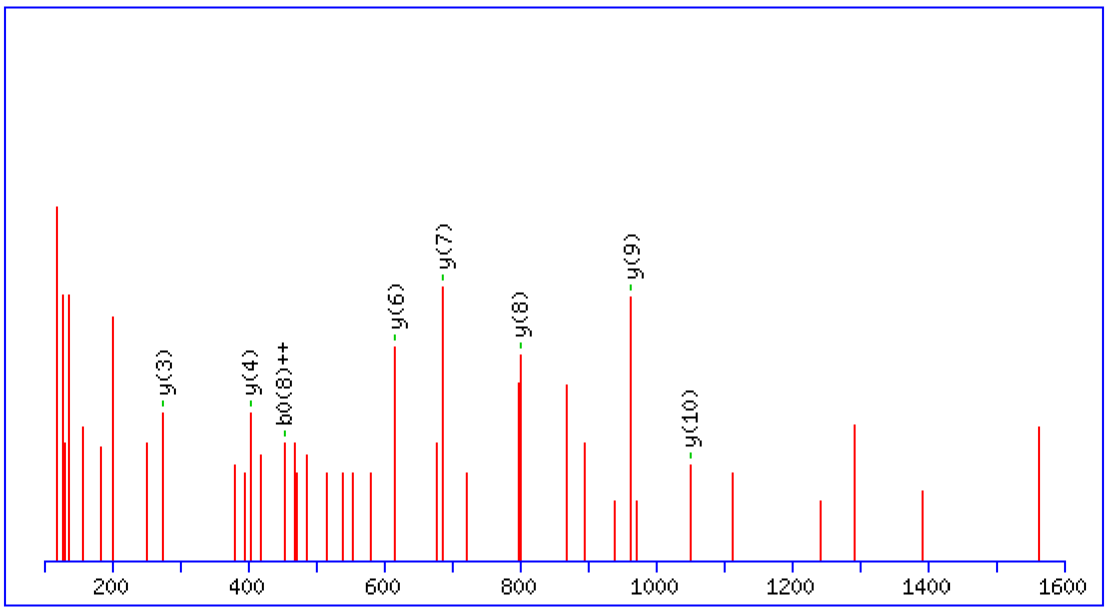
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FSYLAVIEGAK**
Found in **PTN1_HUMAN**, Tyrosine-protein phosphatase non-receptor type 1 OS=Homo sapiens GN=PTPN1 PE=1 SV=1

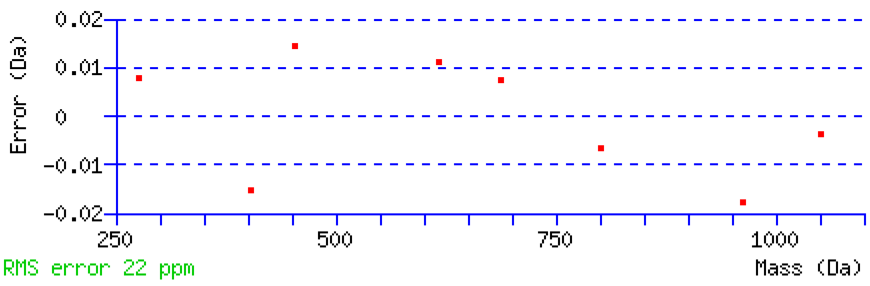
Match to Query 29138: 1196.637888 from(599.326220,2+) rtinseconds(3357) index(47644)
Title: Locus:1.1.1.2691.8
Data file 2011-11-12 - TFD - EP 5-4.mgf

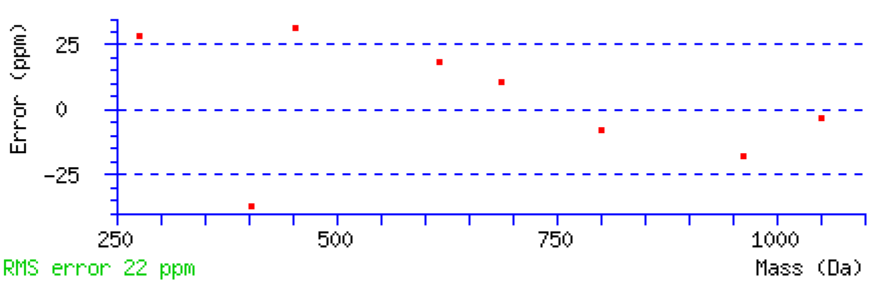
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1196.644104
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 57 **Expect:** 1.5e-005
Matches : 8/92 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.075690	74.541483			F							11
2	235.107718	118.057497	217.097153	109.052214	S	***1050.582988***	525.795132	1033.556439	517.281858	1032.572423	516.789850	10
3	398.171047	199.589161	380.160482	190.583879	Y	***963.550960***	482.279118	946.524411	473.765844	945.540395	473.273836	9
4	511.255111	256.131193	493.244546	247.125911	L	***800.487631***	400.747454	783.461082	392.234179	782.477066	391.742171	8
5	582.292225	291.649751	564.281660	282.644468	A	***687.403567***	344.205422	670.377018	335.692147	669.393002	335.200139	7
6	681.360639	341.183958	663.350074	332.178675	V	***616.366453***	308.686865	599.339904	300.173590	598.355888	299.681582	6
7	794.444703	397.725990	776.434138	388.720707	I	517.298039	259.152658	500.271490	250.639383	499.287474	250.147375	5
8	923.487296	462.247286	905.476731	453.242004	E	***404.213975***	202.610626	387.187426	194.097351	386.203410	193.605343	4
9	980.508760	490.758018	962.498195	481.752736	G	***275.171382***	138.089329	258.144833	129.576055			3
10	1051.545874	526.276575	1033.535309	517.271293	A	218.149918	109.578597	201.123369	101.065323			2
11					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of FSYLAVIEGAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
57.0	1196.644104	-0.006216	FSYLAVIEGAK

Mascot: http://www.matrixscience.com/

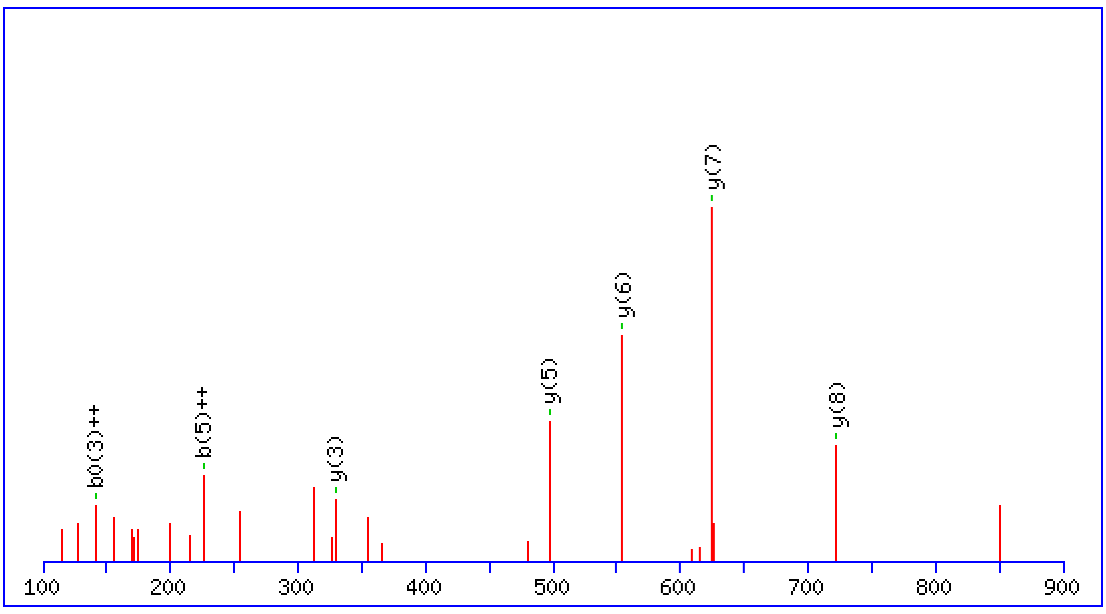
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EPAGPAPGR**
Found in **SHPS1_HUMAN**, Tyrosine-protein phosphatase non-receptor type substrate 1 OS=Homo sapiens GN=SIRPA PE=1 SV=2

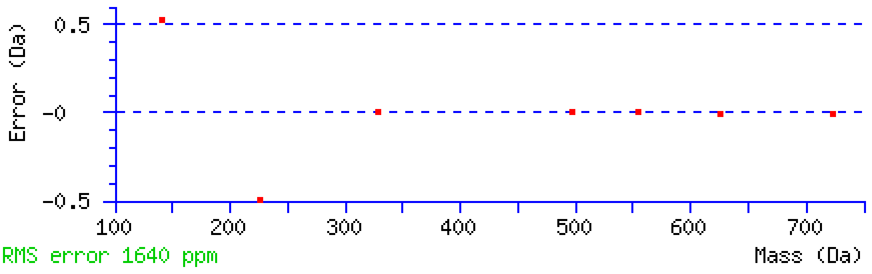
Match to Query 64000: 850.436968 from(426.225760,2+) rtinseconds(863) index(241223)
Title: Locus:1.1.1.768.3
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

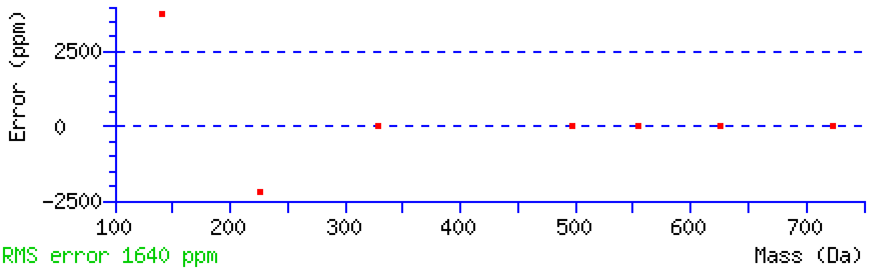
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 850.429703
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 43 **Expect:** 0.00043
Matches : 7/64 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	130.049869	65.528572	112.039304	56.523290	E					9
2	227.102633	114.054954	209.092068	105.049672	P	*722.394400*	361.700838	705.367851	353.187564	8
3	298.139747	149.573512	280.129182	140.568229	A	*625.341636*	313.174456	608.315087	304.661182	7
4	355.161211	178.084243	337.150646	169.078961	G	*554.304522*	277.655899	537.277973	269.142625	6
5	452.213975	226.610625	434.203410	217.605343	P	*497.283058*	249.145167	480.256509	240.631892	5
6	523.251089	262.129183	505.240524	253.123900	A	400.230294	200.618785	383.203745	192.105510	4
7	620.303853	310.655565	602.293288	301.650282	P	*329.193180*	165.100228	312.166631	156.586953	3
8	677.325317	339.166297	659.314752	330.161014	G	232.140416	116.573846	215.113867	108.060571	2
9					R	175.118952	88.063114	158.092403	79.549839	1





NCBI **BLAST** search of EPAGPAPGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.6	850.429703	0.007265	EPAGPAPGR
6.3	850.429703	0.007265	PEPQAPGR
4.4	850.429688	0.007280	ELEAPHR
3.4	850.440918	-0.003950	KEPNAHR
2.5	850.443604	-0.006636	ILAYDEK
1.8	850.437103	-0.000135	YPVVMAR
1.6	850.440918	-0.003950	EPNAHRK

Mascot: http://www.matrixscience.com/

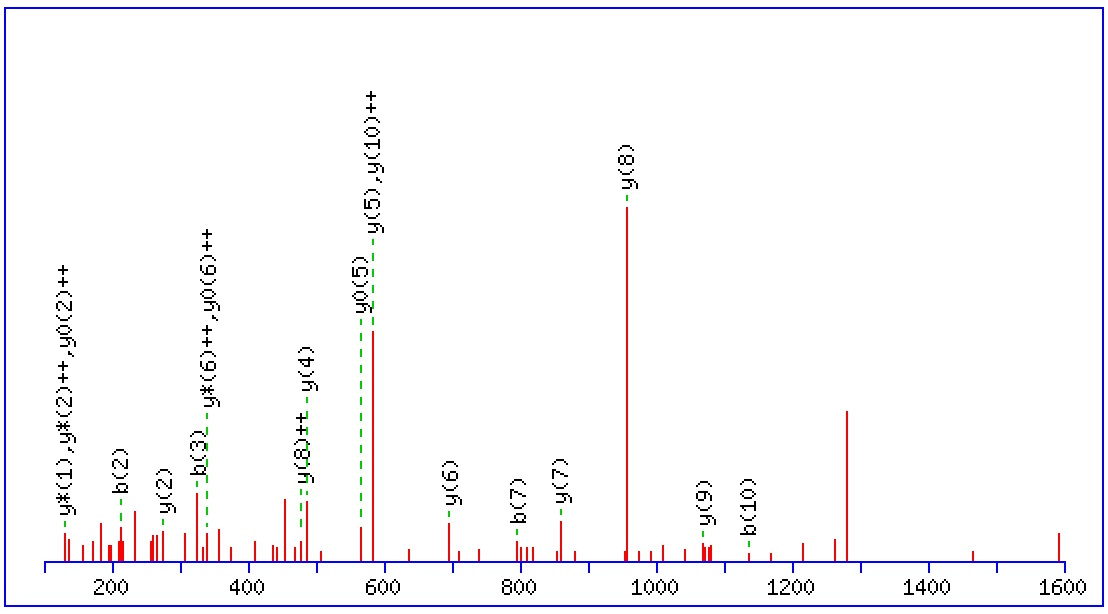
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DPIPYLPPLEK**
Found in **RU17_HUMAN**, U1 small nuclear ribonucleoprotein 70 kDa OS=Homo sapiens GN=SNRNP70 PE=1 SV=2

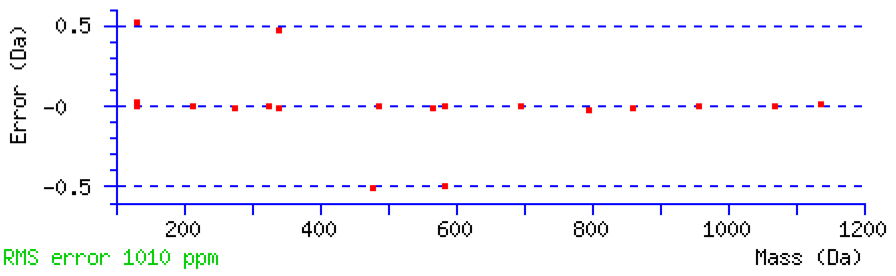
Match to Query 32129: 1280.705248 from(641.359900,2+) rtinseconds(3084) index(43865)
Title: Locus:1.1.1.2592.20
Data file 2011-11-10 - TFD - EP 3-3.mgf

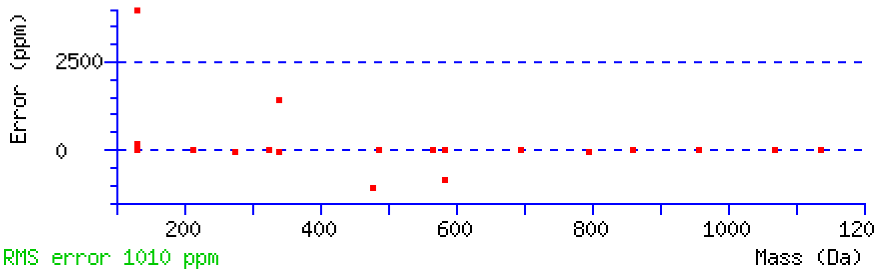
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1600] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1280.701614
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 38 **Expect:** 0.00074
Matches : 19/98 fragment ions using 33 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.034219	58.520748	98.023654	49.515465	D							11
2	**213.086983**	107.047129	195.076418	98.041847	P	1166.681974	583.844625	1149.655425	575.331351	1148.671409	574.839343	10
3	**326.171047**	163.589161	308.160482	154.583879	I	***1069.629210***	535.318243	1052.602661	526.804969	1051.618645	526.312961	9
4	423.223811	212.115544	405.213246	203.110261	P	***956.545146***	478.776211	939.518597	470.262937	938.534581	469.770929	8
5	586.287140	293.647208	568.276575	284.641926	Y	***859.492382***	430.249829	842.465833	421.736555	841.481817	421.244547	7
6	699.371204	350.189240	681.360639	341.183958	L	***696.429053***	348.718165	679.402504	340.204890	678.418488	339.712882	6
7	**796.423968**	398.715622	778.413403	389.710340	P	***583.344989***	292.176133	566.318440	283.662858	565.334424	283.170850	5
8	893.476732	447.242004	875.466167	438.236722	P	***486.292225***	243.649750	469.265676	235.136476	468.281660	234.644468	4
9	1006.560796	503.784036	988.550231	494.778754	L	389.239461	195.123368	372.212912	186.610094	371.228896	186.118086	3
10	**1135.603389**	568.305333	1117.592824	559.300050	E	***276.155397***	138.581336	259.128848	130.068062	258.144832	129.576054	2
11					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of DPIPYLPPLEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.0	1280.701614	0.003634	DPIPYLPPLEK
4.4	1280.697601	0.007647	DPINVEGLLPSK
1.6	1280.697617	0.007631	DLPLAPVPTSGAK
1.6	1280.697617	0.007631	DLPLAPVPTSGAK
1.3	1280.708832	-0.003584	EDINSHVIKVK

Mascot: http://www.matrixscience.com/

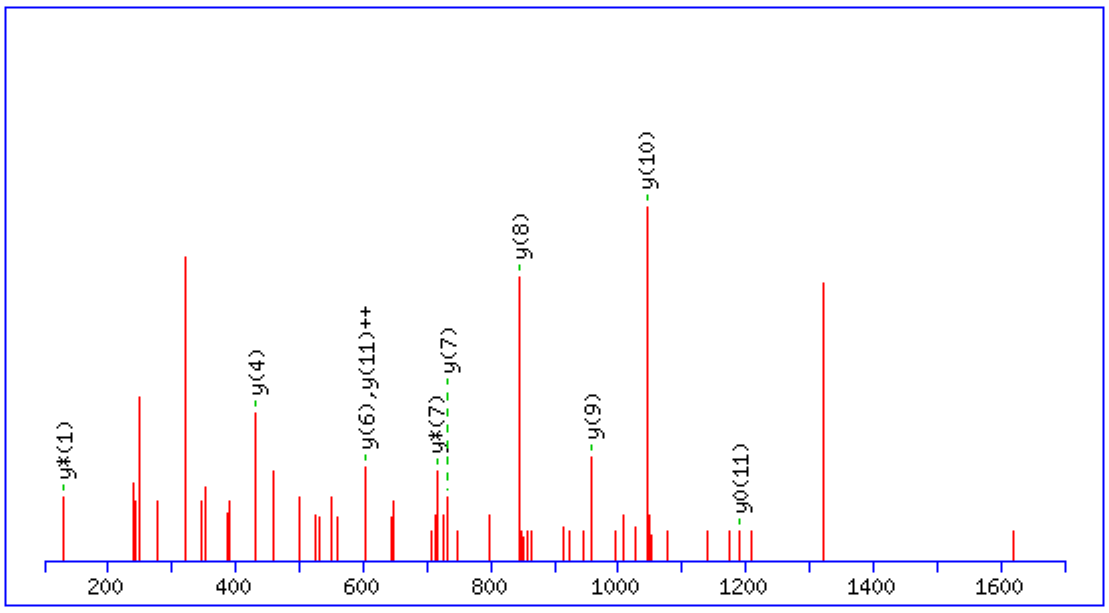
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LYSILQGDSPTK**
Found in **SR140_HUMAN**, U2 snRNP-associated SURP motif-containing protein OS=Homo sapiens GN=U2SURP PE=1 SV=2

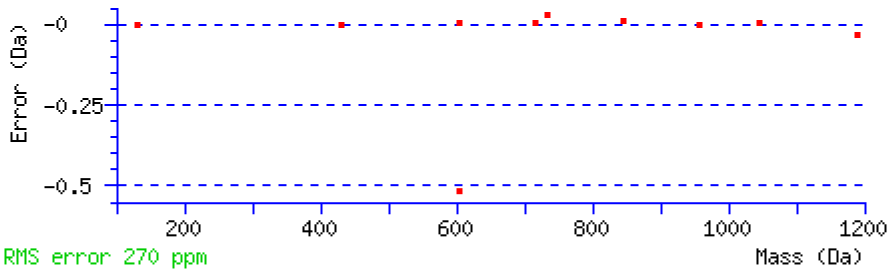
Match to Query 35578: 1320.685748 from(661.350150,2+) rtinseconds(2411) index(29299)
Title: Locus:1.1.1.2356.40
Data file 2011-11-14 - TFD - EP 7-1.mgf

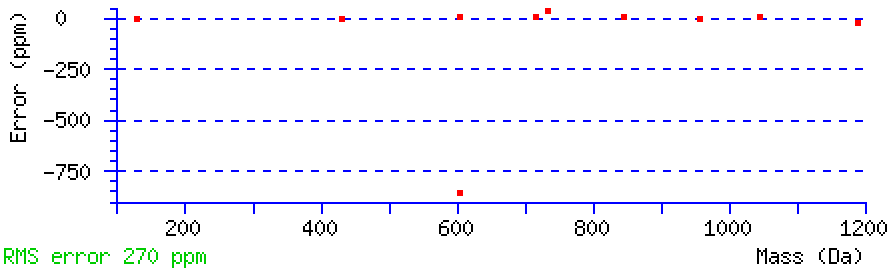
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1320.692520
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 49  Expect: 3.2e-005
Matches : 10/116 fragment ions using 11 most intense peaks    (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							12
2	277.154669	139.080973					Y	1208.615745	604.811511	1191.589196	596.298236	1190.605180	595.806228	11
3	364.186697	182.596987			346.176132	173.591704	S	***1045.552416***	523.279846	1028.525867	514.766572	1027.541851	514.274564	10
4	477.270761	239.139019			459.260196	230.133736	I	***958.520388***	479.763832	941.493839	471.250558	940.509823	470.758550	9
5	590.354825	295.681051			572.344260	286.675768	L	***845.436324***	423.221800	828.409775	414.708526	827.425759	414.216518	8
6	718.413403	359.710340	701.386854	351.197065	700.402838	350.705057	Q	***732.352260***	366.679768	715.325711	358.166494	714.341695	357.674486	7
7	775.434867	388.221072	758.408318	379.707797	757.424302	379.215789	G	***604.293682***	302.650479	587.267133	294.137205	586.283117	293.645197	6
8	890.461810	445.734543	873.435261	437.221269	872.451245	436.729261	D	547.272218	274.139747	530.245669	265.626473	529.261653	265.134465	5
9	977.493838	489.250557	960.467289	480.737283	959.483273	480.245275	S	***432.245275***	216.626275	415.218726	208.113001	414.234710	207.620993	4
10	1074.546602	537.776939	1057.520053	529.263665	1056.536037	528.771657	P	345.213247	173.110262	328.186698	164.596987	327.202682	164.104979	3
11	1175.594281	588.300779	1158.567732	579.787504	1157.583716	579.295496	T	248.160483	124.583879	231.133934	116.070605	230.149918	115.578597	2
12							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of LYSILQGDSPTK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.5	1320.692520	-0.006772	LYSILQGDSPTK
1.6	1320.674591	0.011157	SSARSTQGTTGIR

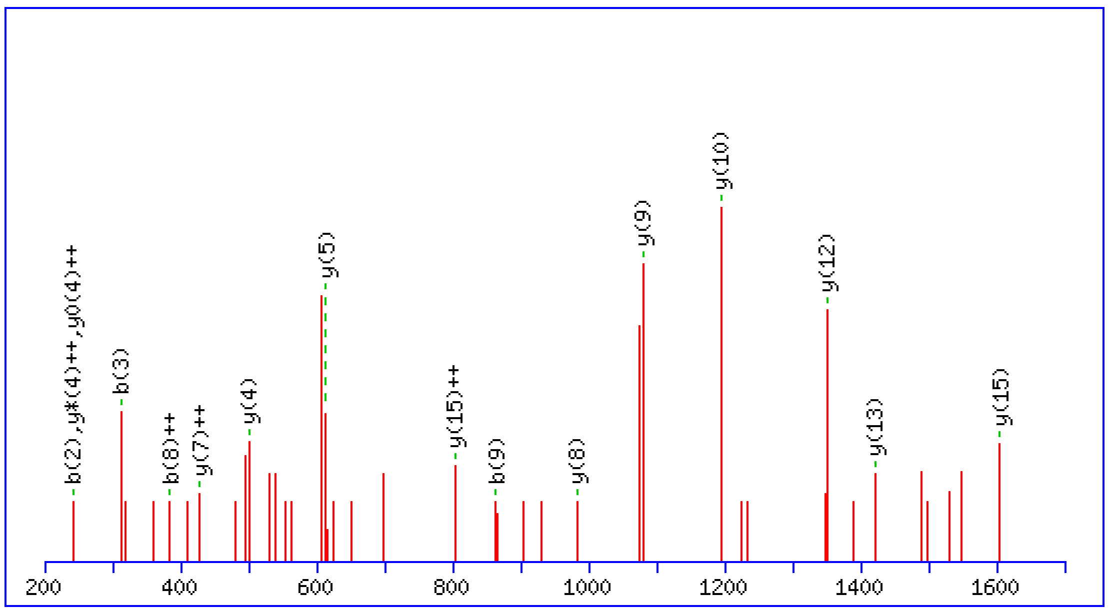
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LQALAGVNPQLQNPEVR**
Found in **UBQL1_HUMAN**, Ubiquilin-1 OS=Homo sapiens GN=UBQLN1 PE=1 SV=2

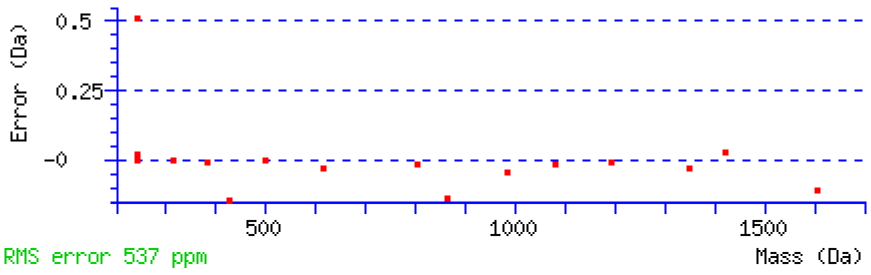
Match to Query 997929: 1845.989948 from(924.002250,2+) rtinseconds(2563) index(522673)
Title: Locus:1.1.1.1310.48
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●

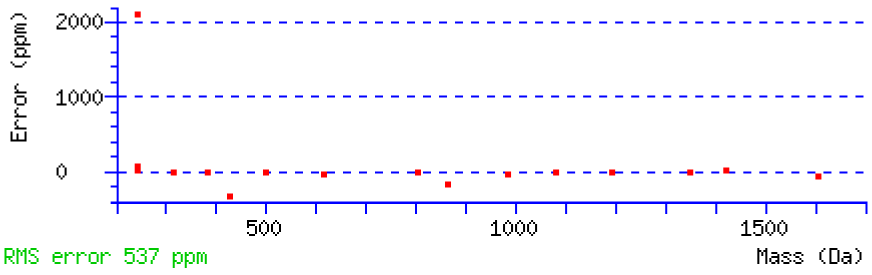


Monoisotopic mass of neutral peptide Mr(calc): 1846.006073
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 46 **Expect:** 0.00017
Matches : 16/158 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							17
2	**242.149918**	121.578597	225.123369	113.065323			Q	1733.929309	867.468293	1716.902760	858.955018	1715.918744	858.463010	16
3	**313.187032**	157.097154	296.160483	148.583879			A	***1605.870731***	803.439004	1588.844182	794.925729	1587.860166	794.433721	15
4	426.271096	213.639186	409.244547	205.125912			L	1534.833617	767.920447	1517.807068	759.407172	1516.823052	758.915164	14
5	497.308210	249.157743	480.281661	240.644468			A	***1421.749553***	711.378415	1404.723004	702.865140	1403.738988	702.373132	13
6	554.329674	277.668475	537.303125	269.155201			G	***1350.712439***	675.859858	1333.685890	667.346583	1332.701874	666.854575	12
7	653.398088	327.202682	636.371539	318.689408			V	1293.690975	647.349126	1276.664426	638.835851	1275.680410	638.343843	11
8	767.441015	384.224146	750.414466	375.710871			N	***1194.622561***	597.814919	1177.596012	589.301644	1176.611996	588.809636	10
9	**864.493779**	432.750528	847.467230	424.237253			P	***1080.579634***	540.793455	1063.553085	532.280181	1062.569069	531.788173	9
10	992.552357	496.779817	975.525808	488.266542			Q	***983.526870***	492.267073	966.500321	483.753799	965.516305	483.261791	8
11	1105.636421	553.321848	1088.609872	544.808574			L	855.468292	428.237784	838.441743	419.724510	837.457727	419.232502	7
12	1233.694999	617.351138	1216.668450	608.837863			Q	742.384228	371.695752	725.357679	363.182478	724.373663	362.690470	6
13	1347.737926	674.372601	1330.711377	665.859327			N	***614.325650***	307.666463	597.299101	299.153189	596.315085	298.661181	5
14	1444.790690	722.898983	1427.764141	714.385709			P	***500.282723***	250.645000	483.256174	242.131725	482.272158	241.639717	4
15	1573.833283	787.420280	1556.806734	778.907005	1555.822718	778.414997	E	403.229959	202.118618	386.203410	193.605343	385.219394	193.113335	3
16	1672.901697	836.954487	1655.875148	828.441212	1654.891132	827.949204	V	274.187366	137.597321	257.160817	129.084047			2
17							R	175.118952	88.063114	158.092403	79.549839			1



RMS error 537 ppm



RMS error 537 ppm

NCBI **BLAST** search of LQALAGVNPQLQNPEVR
(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	1846.006073	-0.016125	LQALAGVNPQLQNPEVR

Mascot: http://www.matrixscience.com/

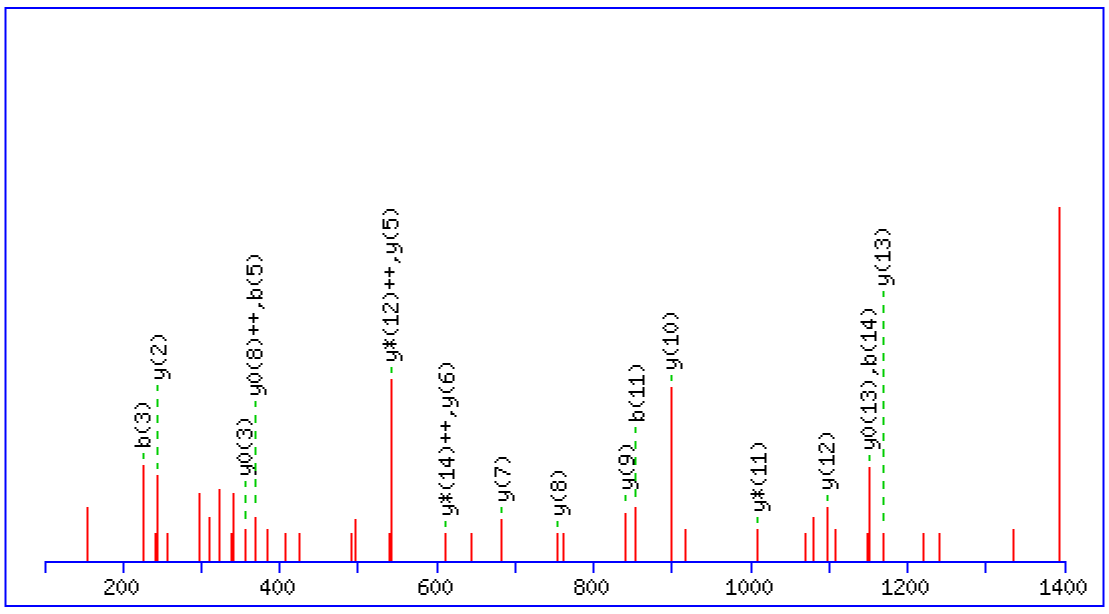
{MATRIX}{SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GPAAAQGSAAAPAEPK**
Found in **UBQL2_HUMAN**, Ubiquilin-2 OS=Homo sapiens GN=UBQLN2 PE=1 SV=2

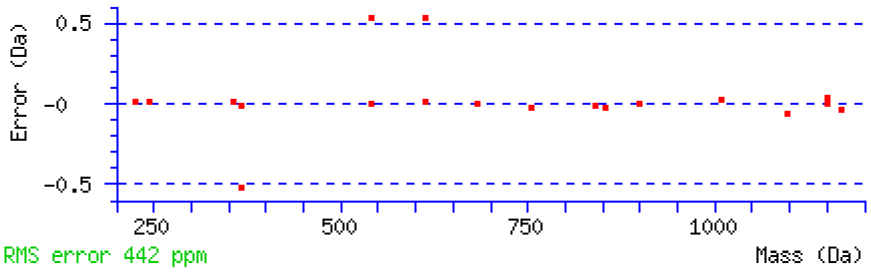
Match to Query 39409: 1392.701148 from(697.357850,2+) rtinseconds(1066) index(1504)
Title: Locus:1.1.1.2052.42
Data file 2011-11-12 - TFD - EP 5-2.mgf

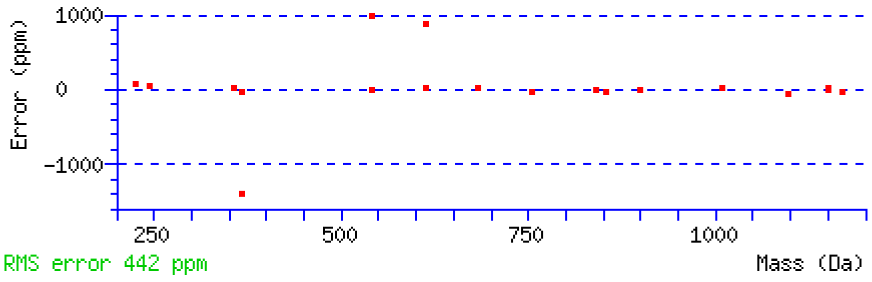
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1392.699707
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 67 **Expect:** 5.9e-007
Matches : 19/152 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							16
2	155.081504	78.044390					P	1336.685557	668.846417	1319.659008	660.333142	1318.674992	659.841134	15
3	**226.118618**	113.562947					A	1239.632793	620.320035	1222.606244	611.806760	1221.622228	611.314752	14
4	297.155732	149.081504					A	***1168.595679***	584.801478	1151.569130	576.288203	1150.585114	575.796195	13
5	**368.192846**	184.600061					A	***1097.558565***	549.282921	1080.532016	540.769646	1079.548000	540.277638	12
6	496.251424	248.629350	479.224875	240.116075			Q	1026.521451	513.764364	1009.494902	505.251089	1008.510886	504.759081	11
7	553.272888	277.140082	536.246339	268.626808			G	***898.462873***	449.735075	881.436324	441.221800	880.452308	440.729792	10
8	640.304916	320.656096	623.278367	312.142822	622.294351	311.650814	S	***841.441409***	421.224342	824.414860	412.711068	823.430844	412.219060	9
9	711.342030	356.174653	694.315481	347.661379	693.331465	347.169371	A	***754.409381***	377.708328	737.382832	369.195054	736.398816	368.703046	8
10	782.379144	391.693210	765.352595	383.179936	764.368579	382.687928	A	***683.372267***	342.189772	666.345718	333.676497	665.361702	333.184489	7
11	**853.416258**	427.211767	836.389709	418.698492	835.405693	418.206484	A	***612.335153***	306.671215	595.308604	298.157940	594.324588	297.665932	6
12	950.469022	475.738149	933.442473	467.224875	932.458457	466.732867	P	***541.298039***	271.152658	524.271490	262.639383	523.287474	262.147375	5
13	1021.506136	511.256706	1004.479587	502.743431	1003.495571	502.251423	A	444.245275	222.626275	427.218726	214.113001	426.234710	213.620993	4
14	**1150.548729**	575.778002	1133.522180	567.264728	1132.538164	566.772720	E	373.208161	187.107718	356.181612	178.594444	355.197596	178.102436	3
15	1247.601493	624.304384	1230.574944	615.791110	1229.590928	615.299102	P	***244.165568***	122.586422	227.139019	114.073148			2
16							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of GPAAAQGSAAAPAEPK
(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	1392.699707	0.001441	GPAAAQGSAAAPAEPK
0.6	1392.688507	0.012641	LPSLSGSDGIPYR

Mascot: http://www.matrixscience.com/

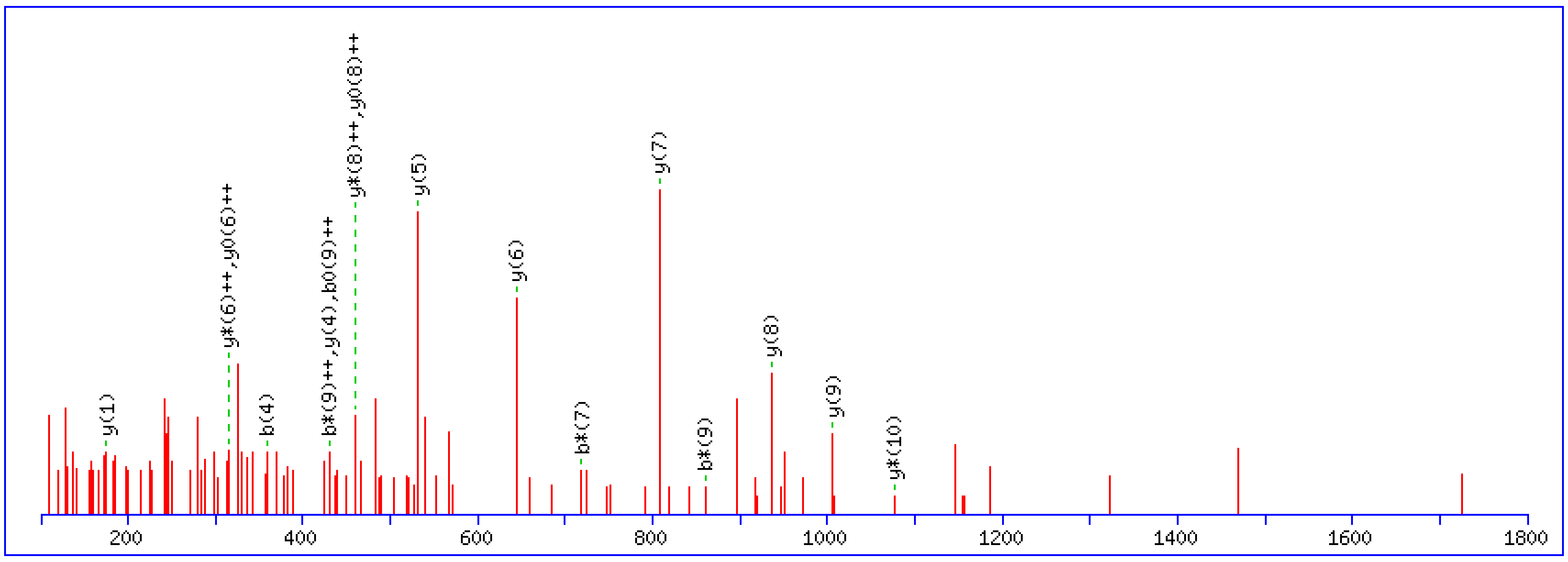
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ASAQYITAALR**
Found in **UBP14_HUMAN**, Ubiquitin carboxyl-terminal hydrolase 14 OS=Homo sapiens GN=USP14 PE=1 SV=3

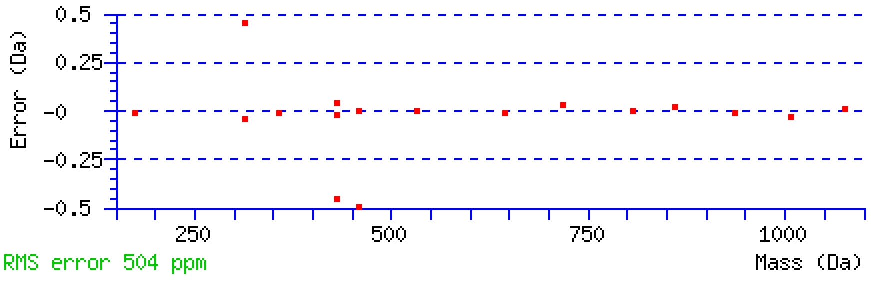
Match to Query 19356: 1163.626128 from(582.820340,2+) rtinseconds(2131) index(25180)
Title: Locus:1.1.1.1193.21
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 2.mgf

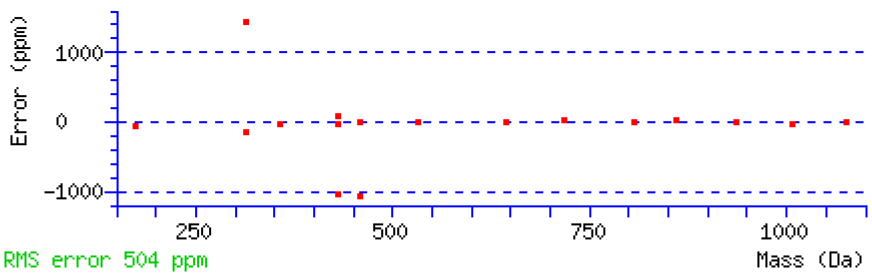
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1163.629837
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31  Expect: 0.0053
Matches : 17/104 fragment ions using 31 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.044390	36.525833					A							11
2	159.076418	80.041847			141.065853	71.036564	S	1093.600036	547.303656	1076.573487	538.790382	1075.589471	538.298374	10
3	230.113532	115.560404			212.102967	106.555121	A	***1006.568008***	503.787642	989.541459	495.274367	988.557443	494.782359	9
4	358.172110	179.589693	341.145561	171.076419	340.161545	170.584411	Q	***935.530894***	468.269085	918.504345	459.755811	917.520329	459.263803	8
5	521.235439	261.121358	504.208890	252.608083	503.224874	252.116075	Y	***807.472316***	404.239796	790.445767	395.726521	789.461751	395.234513	7
6	634.319503	317.663390	617.292954	309.150115	616.308938	308.658107	I	***644.408987***	322.708132	627.382438	314.194857	626.398422	313.702849	6
7	735.367182	368.187229	718.340633	359.673955	717.356617	359.181947	T	***531.324923***	266.166100	514.298374	257.652825	513.314358	257.160817	5
8	806.404296	403.705786	789.377747	395.192512	788.393731	394.700504	A	***430.277244***	215.642260	413.250695	207.128985			4
9	877.441410	439.224343	860.414861	430.711069	859.430845	430.219061	A	359.240130	180.123703	342.213581	171.610428			3
10	990.525474	495.766375	973.498925	487.253101	972.514909	486.761093	L	288.203016	144.605146	271.176467	136.091871			2
11							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of ASAQYITAALR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.9	1163.629837	-0.003709	ASAQYITAALR
6.3	1163.619995	0.006133	VWQVGPHVAR
0.8	1163.629868	-0.003740	GLSSLQPPPPR

Mascot: http://www.matrixscience.com/

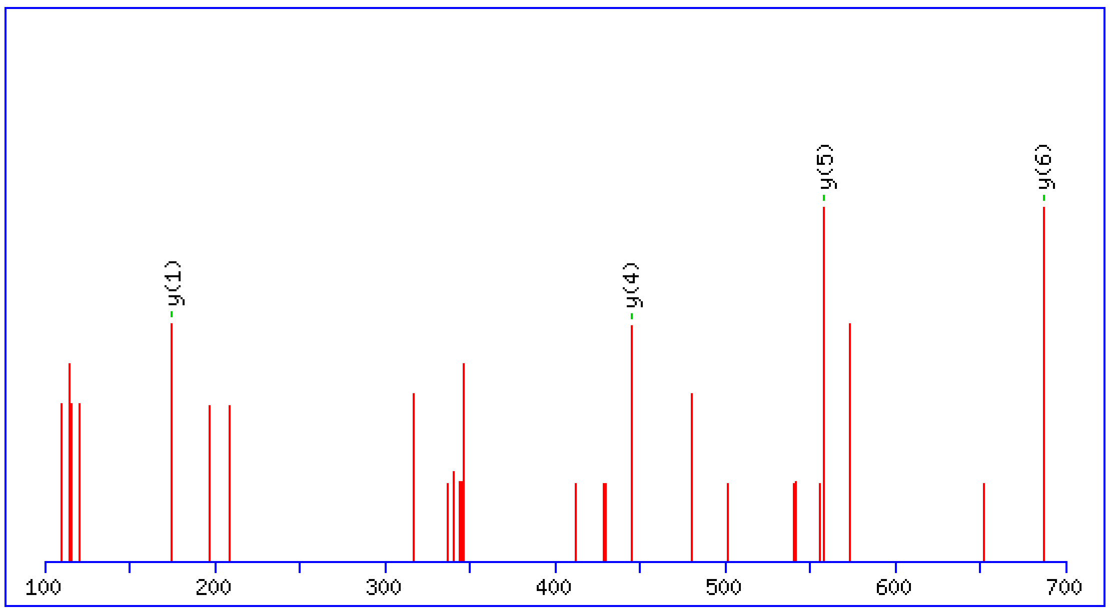
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LELGRGR**
Found in **UBP21_HUMAN**, Ubiquitin carboxyl-terminal hydrolase 21 OS=Homo sapiens GN=USP21 PE=1 SV=1

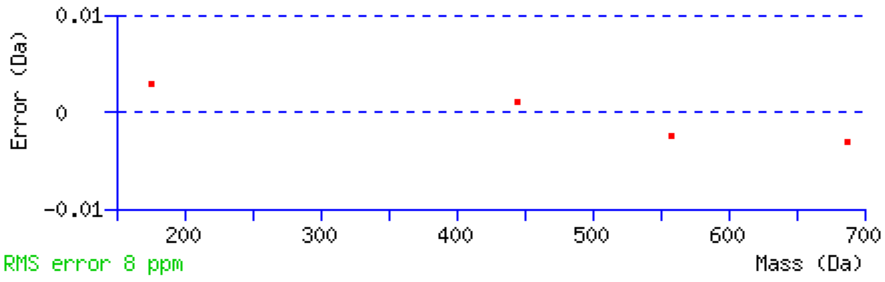
Match to Query 143: 799.458448 from(400.736500,2+) rtinseconds(1177) index(6511)
Title: Locus:1.1.1.1882.2
Data file 2011-11-10 - TFD - EP 3-1.mgf

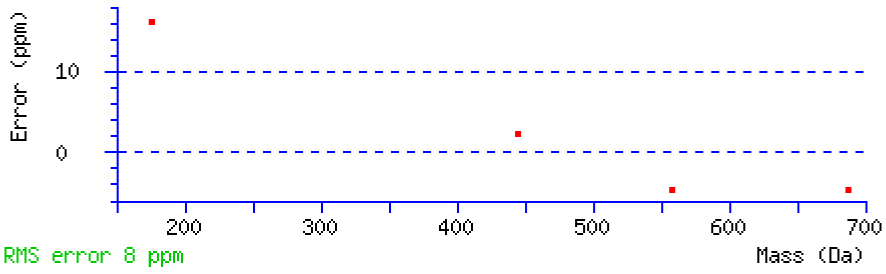
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 799.466415
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 33  Expect: 0.011
Matches : 4/52 fragment ions using 5 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							7
2	243.133933	122.070605			225.123368	113.065322	E	*687.389648*	344.198462	670.363099	335.685188	669.379083	335.193180	6
3	356.217997	178.612637			338.207432	169.607354	L	*558.347055*	279.677166	541.320506	271.163891			5
4	413.239461	207.123369			395.228896	198.118086	G	*445.262991*	223.135134	428.236442	214.621859			4
5	569.340572	285.173924	552.314023	276.660650	551.330007	276.168642	R	388.241527	194.624402	371.214978	186.111127			3
6	626.362036	313.684656	609.335487	305.171382	608.351471	304.679374	G	232.140416	116.573846	215.113867	108.060572			2
7							R	*175.118952*	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of LELGRGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.5	799.466415	-0.007967	LELGRGR
31.9	799.455185	0.003263	IIEVNGR
31.9	799.455185	0.003263	ILEVNGR
22.7	799.455170	0.003278	LEQLAAR
16.7	799.466400	-0.007952	IENIRR
16.7	799.466415	-0.007967	IEQVRR
16.7	799.455170	0.003278	LEAAIQR
16.7	799.466400	-0.007952	LENLRR
16.7	799.466415	-0.007967	LERAVGR
16.7	799.466400	-0.007952	LERINR

Mascot: http://www.matrixscience.com/

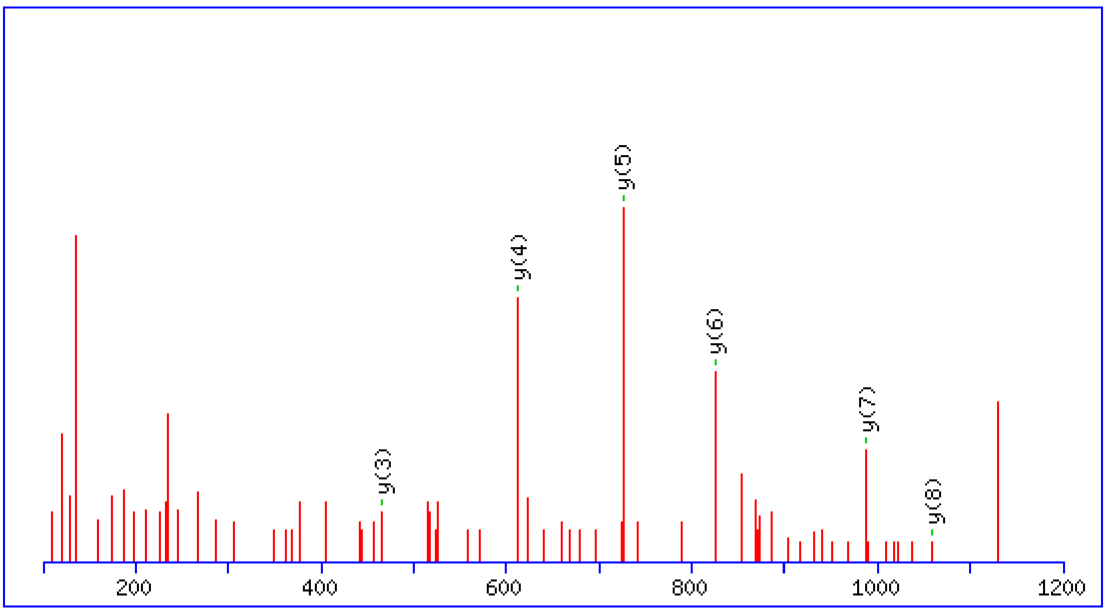
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AAYVLFYQR**
Found in **UBP11_HUMAN**, Ubiquitin carboxyl-terminal hydrolase 11 OS=Homo sapiens GN=USP11 PE=1 SV=3

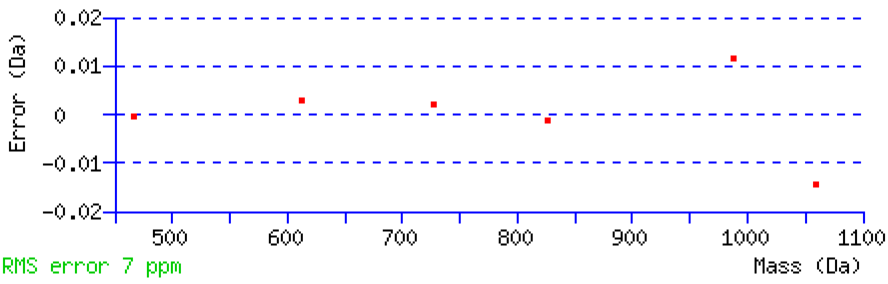
Match to Query 25010: 1129.591688 from(565.803120,2+) rtinseconds(2752) index(36342)
Title: Locus:1.1.1.2451.19
Data file 2011-11-14 - TFD - EP 8-1.mgf

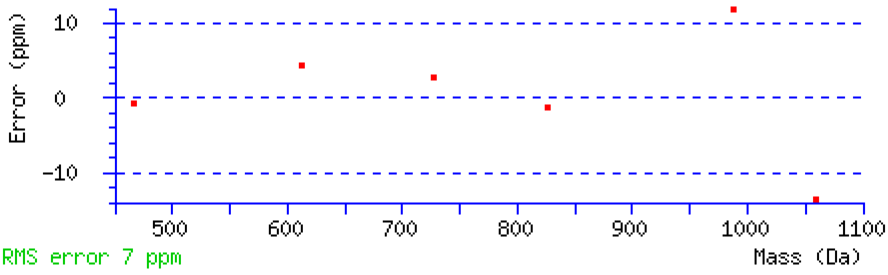
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1129.592010
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.0011
Matches : 6/50 fragment ions using 10 most intense peaks (help)

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	72.044390	36.525833			A					9
2	143.081504	72.044390			A	***1059.562194***	530.284735	1042.535645	521.771461	8
3	306.144833	153.576055			Y	***988.525080***	494.766178	971.498531	486.252904	7
4	405.213247	203.110262			V	***825.461751***	413.234514	808.435202	404.721239	6
5	518.297311	259.652294			L	***726.393337***	363.700307	709.366788	355.187032	5
6	665.365725	333.186501			F	***613.309273***	307.158275	596.282724	298.645000	4
7	828.429054	414.718165			Y	***466.240859***	233.624068	449.214310	225.110793	3
8	956.487632	478.747454	939.461083	470.234179	Q	303.177530	152.092403	286.150981	143.579129	2
9					R	175.118952	88.063114	158.092403	79.549840	1





NCBI **BLAST** search of AAYVLFYQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.3	1129.592010	-0.000322	AAYVLFYQR

Mascot: http://www.matrixscience.com/

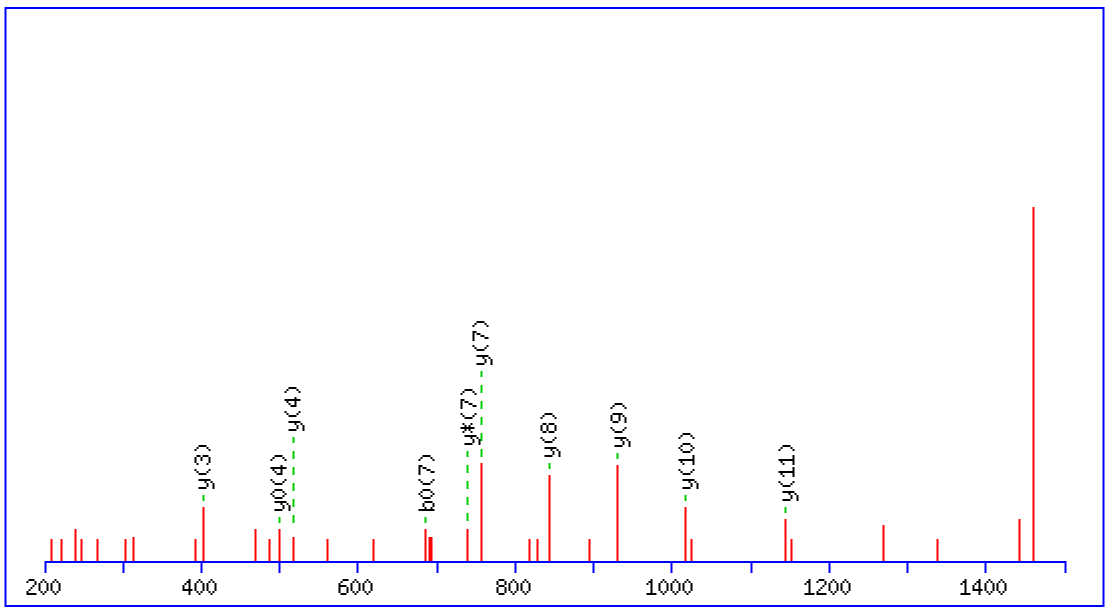
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DAQQSSSPAADNLR**
Found in **UBE4A_HUMAN**, Ubiquitin conjugation factor E4 A OS=Homo sapiens GN=UBE4A PE=1 SV=2

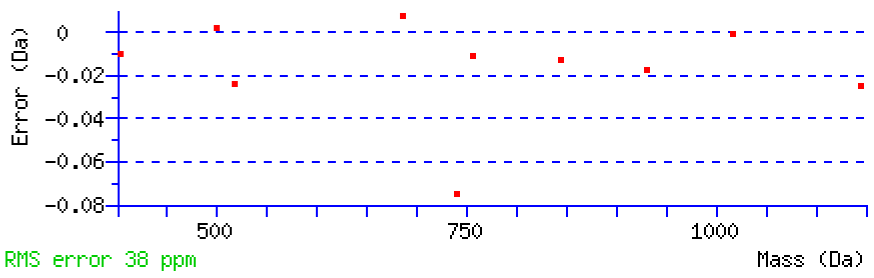
Match to Query 802274: 1458.671928 from(730.343240,2+) rtinseconds(1233) index(248213)
Title: Locus:1.1.1.912.47
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

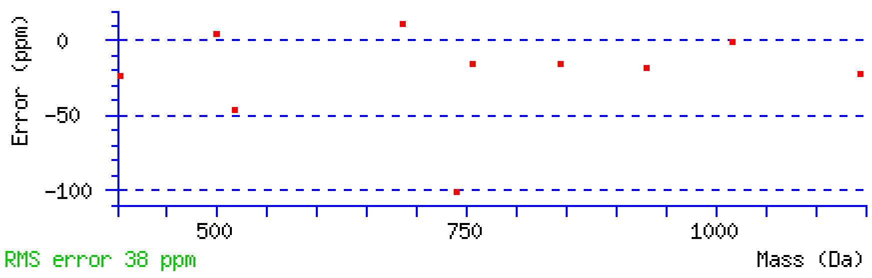
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1458.669876
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.00055
Matches : 10/146 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	116.034219	58.520748			98.023654	49.515465	D							14
2	187.071333	94.039304			169.060768	85.034022	A	1344.650232	672.828754	1327.623683	664.315479	1326.639667	663.823471	13
3	315.129911	158.068593	298.103362	149.555319	297.119346	149.063311	Q	1273.613118	637.310197	1256.586569	628.796922	1255.602553	628.304914	12
4	443.188489	222.097883	426.161940	213.584608	425.177924	213.092600	Q	***1145.554540***	573.280908	1128.527991	564.767633	1127.543975	564.275625	11
5	530.220517	265.613897	513.193968	257.100622	512.209952	256.608614	S	***1017.495962***	509.251619	1000.469413	500.738344	999.485397	500.246336	10
6	617.252545	309.129911	600.225996	300.616636	599.241980	300.124628	S	***930.463934***	465.735605	913.437385	457.222330	912.453369	456.730322	9
7	704.284573	352.645925	687.258024	344.132650	686.274008	343.640642	S	***843.431906***	422.219591	826.405357	413.706316	825.421341	413.214308	8
8	801.337337	401.172307	784.310788	392.659032	783.326772	392.167024	P	***756.399878***	378.703577	739.373329	370.190302	738.389313	369.698294	7
9	872.374451	436.690864	855.347902	428.177589	854.363886	427.685581	A	659.347114	330.177195	642.320565	321.663920	641.336549	321.171912	6
10	943.411565	472.209421	926.385016	463.696146	925.401000	463.204138	A	588.310000	294.658638	571.283451	286.145363	570.299435	285.653355	5
11	1058.438508	529.722892	1041.411959	521.209618	1040.427943	520.717609	D	***517.272886***	259.140081	500.246337	250.626806	499.262321	250.134798	4
12	1172.481435	586.744355	1155.454886	578.231081	1154.470870	577.739073	N	***402.245943***	201.626609	385.219394	193.113335			3
13	1285.565499	643.286387	1268.538950	634.773113	1267.554934	634.281105	L	288.203016	144.605146	271.176467	136.091871			2
14							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of DAQQSSSPAADNLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.8	1458.669876	0.002052	DAQQSSSPAADNLR
1.0	1458.659531	0.012397	QVDGEPCRLAPAM

Mascot: http://www.matrixscience.com/

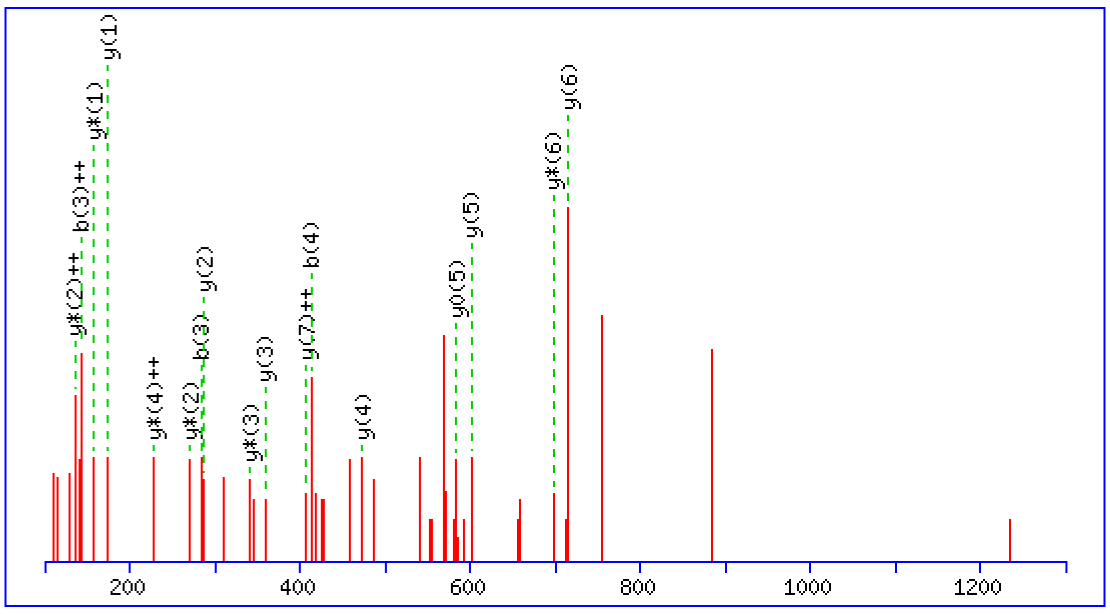
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AVLENALR**
Found in **UFD1_HUMAN**, Ubiquitin fusion degradation protein 1 homolog OS=Homo sapiens GN=UFD1L PE=1 SV=3

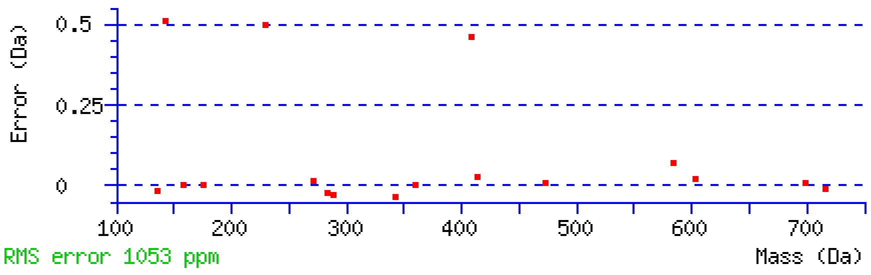
Match to Query 6920: 884.509868 from(443.262210,2+) rtinseconds(1755) index(17928)
Title: Locus:1.1.1.2012.9
Data file 2011-11-10 - TFD - EP 3-4.mgf

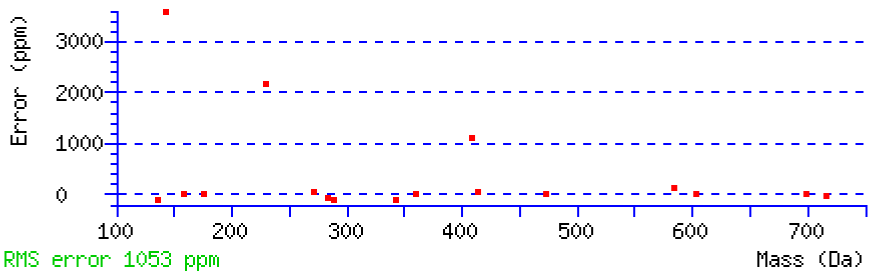
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 884.507935
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 35 **Expect:** 0.0024
Matches : 17/62 fragment ions using 32 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							8
2	171.112804	86.060040					V	814.478128	407.742702	797.451579	399.229428	796.467563	398.737420	7
3	**284.196868**	142.602072					L	***715.409714***	358.208495	698.383165	349.695221	697.399149	349.203213	6
4	**413.239461**	207.123369			395.228896	198.118086	E	***602.325650***	301.666463	585.299101	293.153189	584.315085	292.661181	5
5	527.282388	264.144832	510.255839	255.631558	509.271823	255.139550	N	***473.283057***	237.145167	456.256508	228.631892			4
6	598.319502	299.663389	581.292953	291.150115	580.308937	290.658107	A	***359.240130***	180.123703	342.213581	171.610429			3
7	711.403566	356.205421	694.377017	347.692147	693.393001	347.200139	L	***288.203016***	144.605146	271.176467	136.091872			2
8							R	***175.118952***	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of AVLENALR
(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	884.507935	0.001933	AVLENALR
19.7	884.507950	0.001918	LPGEKLGR
8.0	884.507950	0.001918	AVVEKPAR
6.2	884.507950	0.001918	LTPAQALR
3.4	884.507935	0.001933	NLALEGLR
2.6	884.507950	0.001918	AIDVKSPR
2.6	884.507950	0.001918	ALQDLGLR
0.8	884.507980	0.001888	IGGGGVQLGK
0.4	884.507950	0.001918	KSPLTAPR

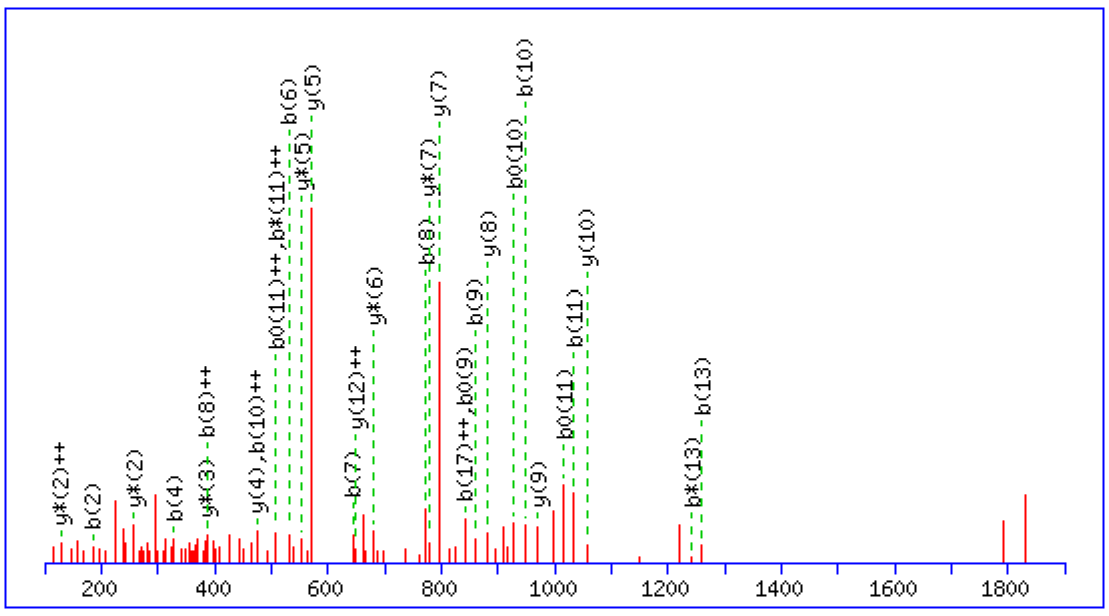
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SPGSSDNQSSSPQPAQQK**
Found in **UBP2L_HUMAN**, Ubiquitin-associated protein 2-like OS=Homo sapiens GN=UBAP2L PE=1 SV=2

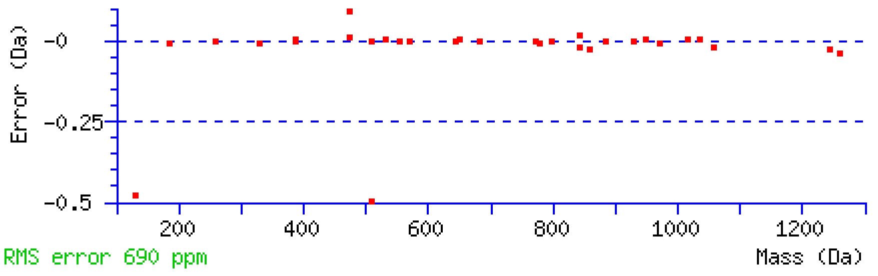
Match to Query 994255: 1828.818312 from(610.613380,3+) rtinseconds(753) index(157360)
Title: Locus:1.1.1.972.2
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

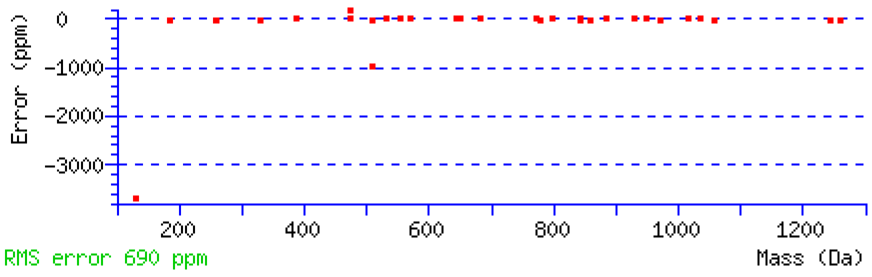
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1828.818741
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 54 **Expect:** 2.7e-005
Matches : 31/178 fragment ions using 44 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							18
2	***185.092068***	93.049672			167.081503	84.044389	P	1742.793996	871.900636	1725.767447	863.387362	1724.783431	862.895354	17
3	242.113532	121.560404			224.102967	112.555121	G	1645.741232	823.374254	1628.714683	814.860980	1627.730667	814.368972	16
4	***329.145560***	165.076418			311.134995	156.071136	S	1588.719768	794.863522	1571.693219	786.350248	1570.709203	785.858240	15
5	416.177588	208.592432			398.167023	199.587149	S	1501.687740	751.347508	1484.661191	742.834234	1483.677175	742.342226	14
6	***531.204531***	266.105904			513.193966	257.100621	D	1414.655712	707.831494	1397.629163	699.318220	1396.645147	698.826212	13
7	***645.247458***	323.127367	628.220909	314.614092	627.236893	314.122084	N	1299.628769	650.318023	1282.602220	641.804748	1281.618204	641.312740	12
8	***773.306036***	**387.156656**	756.279487	378.643381	755.295471	378.151373	Q	1185.585842	593.296559	1168.559293	584.783285	1167.575277	584.291277	11
9	***860.338064***	430.672670	843.311515	422.159395	842.327499	421.667387	S	**1057.527264**	529.267270	1040.500715	520.753996	1039.516699	520.261988	10
10	***947.370092***	**474.188684**	930.343543	465.675409	929.359527	465.183401	S	**970.495236**	485.751256	953.468687	477.237982	952.484671	476.745974	9
11	***1034.402120***	517.704698	1017.375571	509.191423	1016.391555	508.699415	S	**883.463208**	442.235242	866.436659	433.721968	865.452643	433.229960	8
12	1131.454884	566.231080	1114.428335	557.717806	1113.444319	557.225798	P	**796.431180**	398.719228	779.404631	390.205954			7
13	***1259.513462***	630.260369	1242.486913	621.747095	1241.502897	621.255087	Q	699.378416	350.192846	682.351867	341.679572			6
14	1356.566226	678.786751	1339.539677	670.273477	1338.555661	669.781469	P	**571.319838**	286.163557	554.293289	277.650283			5
15	1427.603340	714.305308	1410.576791	705.792034	1409.592775	705.300026	A	**474.267074**	237.637175	457.240525	229.123900			4
16	1555.661918	778.334597	1538.635369	769.821323	1537.651353	769.329315	Q	403.229960	202.118618	386.203411	193.605344			3
17	1683.720496	**842.363886**	1666.693947	833.850612	1665.709931	833.358604	Q	275.171382	138.089329	258.144833	129.576055			2
18							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of SPGSSDNQSSSPQPAQQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
53.6	1828.818741	-0.000429	SPGSSDNQSSSPQPAQQK
5.0	1828.827667	-0.009355	MAAAPPSYCFVAFPPR
0.8	1828.827667	-0.009355	MAAAPPSYCFVAFPPR
0.8	1828.827667	-0.009355	MAAAPPSYCFVAFPPR

Mascot: http://www.matrixscience.com/

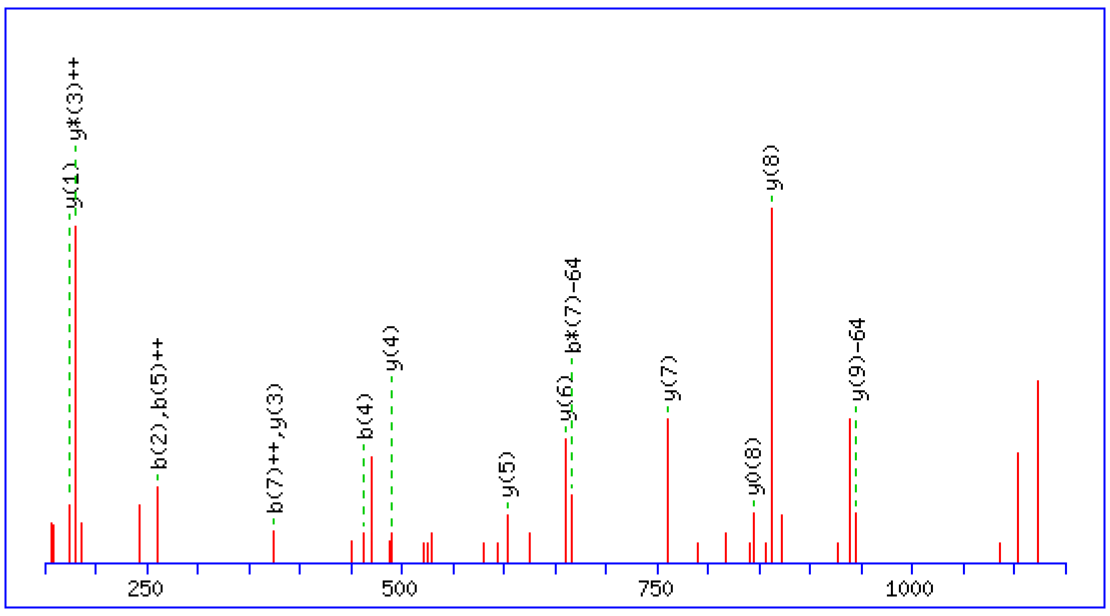
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LMTTGNNTVR**
Found in **UBE2Z_HUMAN**, Ubiquitin-conjugating enzyme E2 Z OS=Homo sapiens GN=UBE2Z PE=1 SV=2

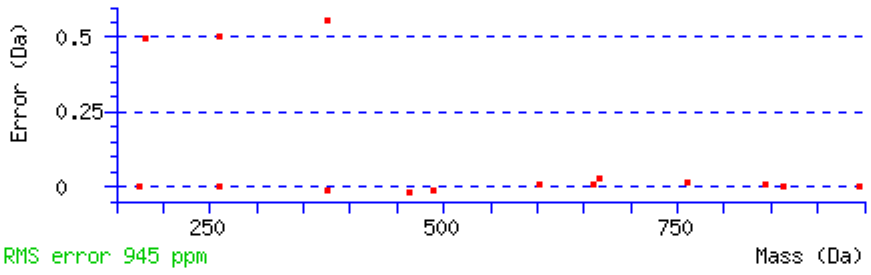
Match to Query 23853: 1121.548828 from(561.781690,2+) rtinseconds(870) index(1703)
Title: Locus:1.1.1.1659.31
Data file 2011-11-10 - TFD - EP 4-4.mgf

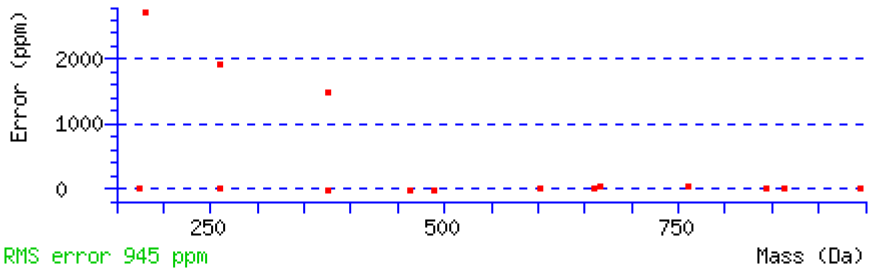
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1121.549911
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M2      : Oxidation (M), with neutral losses 63.998285(shown in table), 0.000000
Ions Score: 52  Expect: 4.6e-005
Matches : 15/134 fragment ions using 22 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							10
2	197.128455	99.067865					M	*945.474836*	473.241056	928.448287	464.727782	927.464271	464.235774	9
3	298.176134	149.591705			280.165569	140.586423	T	*862.437721*	431.722499	845.411172	423.209224	844.427156	422.717216	8
4	399.223813	200.115545			381.213248	191.110262	T	*761.390042*	381.198659	744.363493	372.685385	743.379477	372.193377	7
5	456.245277	228.626277			438.234712	219.620994	G	*660.342363*	330.674820	643.315814	322.161545	642.331798	321.669537	6
6	570.288204	285.647740	553.261655	277.134466	552.277639	276.642458	N	*603.320899*	302.164088	586.294350	293.650813	585.310334	293.158805	5
7	684.331131	342.669204	667.304582	334.155929	666.320566	333.663921	N	*489.277972*	245.142624	472.251423	236.629349	471.267407	236.137341	4
8	785.378810	393.193043	768.352261	384.679769	767.368245	384.187761	T	*375.235045*	188.121161	358.208496	179.607886	357.224480	179.115878	3
9	884.447224	442.727250	867.420675	434.213976	866.436659	433.721968	V	274.187366	137.597321	257.160817	129.084047			2
10							R	*175.118952*	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of LMTTGNNTVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.5	1121.549911	-0.001083	LMTTGNNTVR
5.9	1121.546555	0.002273	VGPGYLGSGGSR
5.4	1121.538651	0.010177	SREDMIDIK
5.3	1121.553925	-0.005097	MLIPFSNPR
4.7	1121.556412	-0.007584	ALSLASSSGSDK
4.5	1121.553925	-0.005097	QGFMEKTGPK
1.0	1121.553925	-0.005097	LFPMSALDGR
0.4	1121.546539	0.002289	FSGTSGPNSLR
0.3	1121.546036	0.002792	MELLECVSK

Mascot: http://www.matrixscience.com/

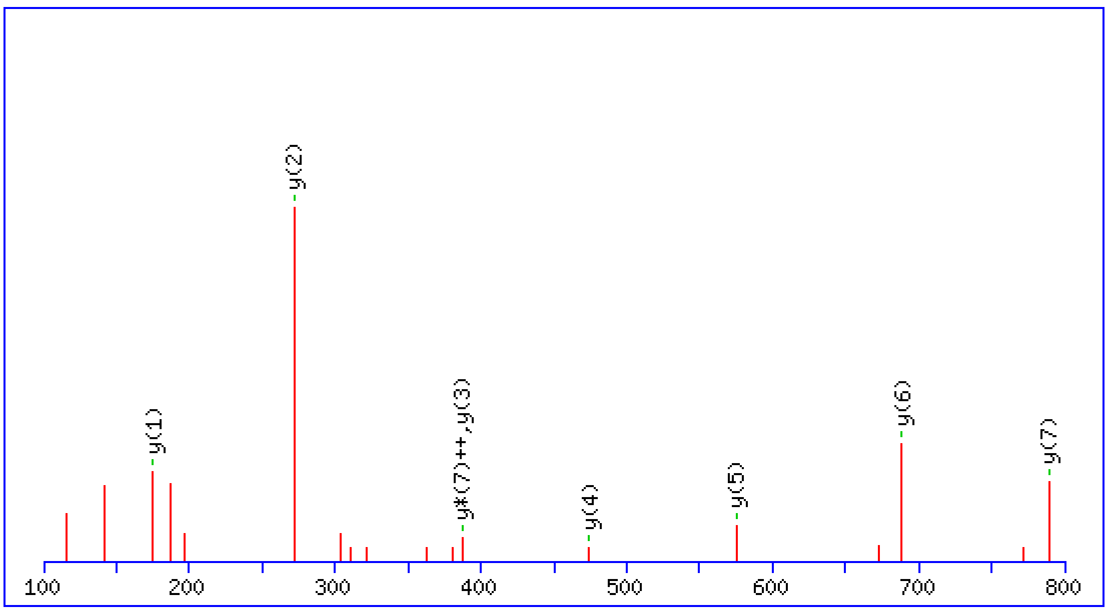
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ITLTSDPR**
Found in **UFM1_HUMAN**, Ubiquitin-fold modifier 1 OS=Homo sapiens GN=UFM1 PE=1 SV=1

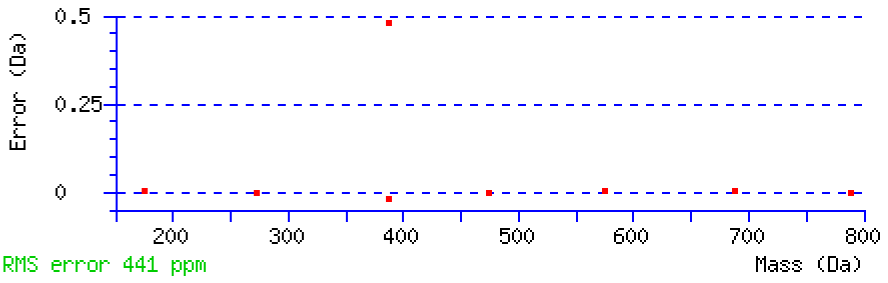
Match to Query 6174: 901.486348 from(451.750450,2+) rtinseconds(1522) index(4262)
Title: Locus:1.1.1.2215.6
Data file 2011-11-12 - TFD - EP 5-8.mgf

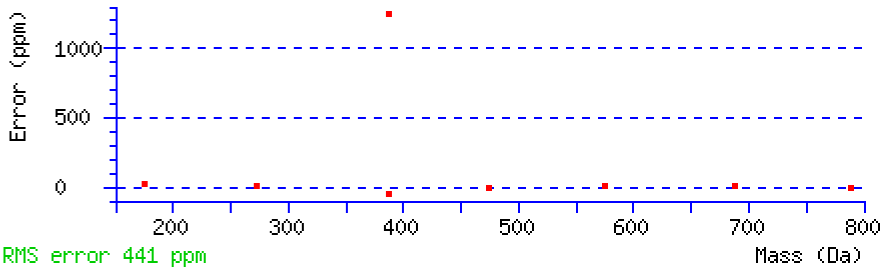
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 901.486893
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 81  Expect: 1.2e-007
Matches : 8/64 fragment ions using 7 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							8
2	215.139019	108.073147	197.128454	99.067865	T	***789.410109***	395.208693	772.383560	386.695418	771.399544	386.203410	7
3	328.223083	164.615179	310.212518	155.609897	L	***688.362430***	344.684853	671.335881	336.171579	670.351865	335.679571	6
4	429.270762	215.139019	411.260197	206.133737	T	***575.278366***	288.142821	558.251817	279.629547	557.267801	279.137539	5
5	516.302790	258.655033	498.292225	249.649751	S	***474.230687***	237.618981	457.204138	229.105707	456.220122	228.613699	4
6	631.329733	316.168505	613.319168	307.163222	D	***387.198659***	194.102967	370.172110	185.589693	369.188094	185.097685	3
7	728.382497	364.694887	710.371932	355.689604	P	***272.171716***	136.589496	255.145167	128.076221			2
8					R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of ITLTSDPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
81.1	901.486893	-0.000545	ITLTSDPR
28.2	901.486893	-0.000545	LTVDEAVR
15.5	901.486893	-0.000545	TLIVDGER
13.4	901.486877	-0.000529	LGEEVSLR
13.4	901.480347	0.006001	LMAIQNGR
13.4	901.486877	-0.000529	LSLDELGR
11.9	901.486862	-0.000514	LEEEVKR
11.6	901.486893	-0.000545	TPPLSSLR
11.2	901.480347	0.006001	KLCNTPR
10.8	901.486862	-0.000514	LELDEKR

Mascot: http://www.matrixscience.com/

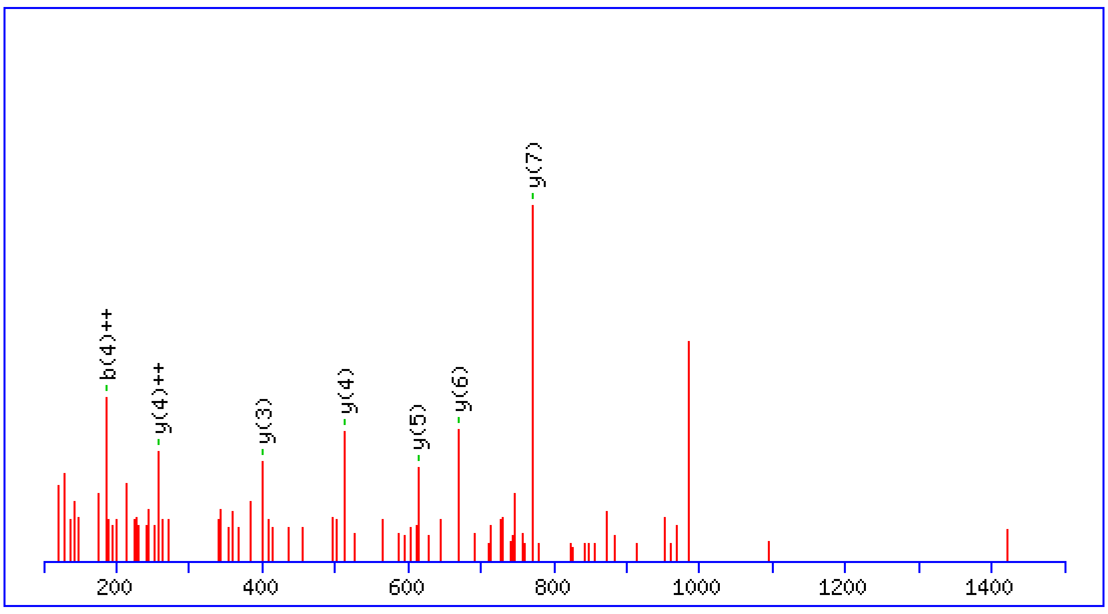
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLTGVLPER**
Found in **UBCP1_HUMAN**, Ubiquitin-like domain-containing CTD phosphatase 1 OS=Homo sapiens GN=UBLCP1 PE=1 SV=2

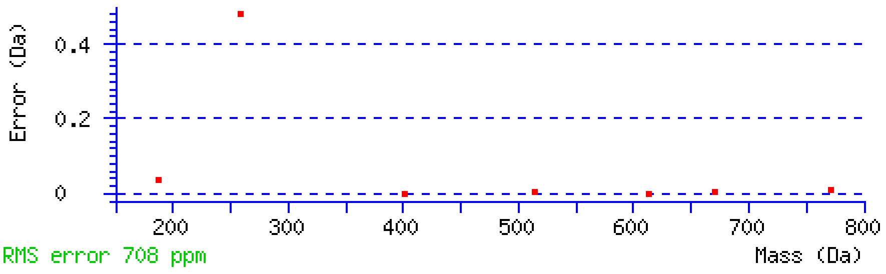
Match to Query 14817: 984.554428 from(493.284490,2+) rtinseconds(1991) index(21904)
Title: Locus:1.1.1.2176.18
Data file 2011-11-12 - TFD - EP 5-4.mgf

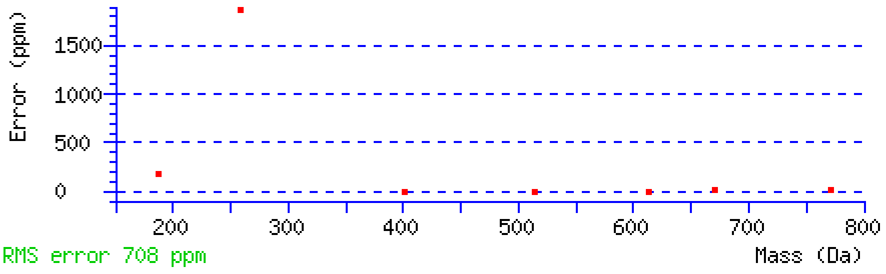
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 984.560394
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 34  Expect: 0.0025
Matches : 7/78 fragment ions using 9 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116	84.044390	42.525833	T							9
2	215.139019	108.073147	197.128454	99.067865	L	884.519994	442.763635	867.493445	434.250361	866.509429	433.758353	8
3	316.186698	158.596987	298.176133	149.591704	T	***771.435930***	386.221603	754.409381	377.708328	753.425365	377.216320	7
4	373.208162	187.107719	355.197597	178.102436	G	***670.388251***	335.697764	653.361702	327.184489	652.377686	326.692481	6
5	472.276576	236.641926	454.266011	227.636643	V	***613.366787***	307.187032	596.340238	298.673757	595.356222	298.181749	5
6	585.360640	293.183958	567.350075	284.178676	L	***514.298373***	257.652825	497.271824	249.139550	496.287808	248.647542	4
7	682.413404	341.710340	664.402839	332.705058	P	***401.214309***	201.110792	384.187760	192.597518	383.203744	192.105510	3
8	811.455997	406.231637	793.445432	397.226354	E	304.161545	152.584410	287.134996	144.071136	286.150980	143.579128	2
9					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of TLTGVLPER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.5	984.560394	-0.005966	TLTGVLPER
5.5	984.546463	0.007965	VSAQRATPR
3.4	984.549149	0.005279	IPPADSLLK
3.3	984.546448	0.007980	IPNLSRNR
2.6	984.560364	-0.005936	ILDAAGANLK
1.8	984.546432	0.007996	LNINARER

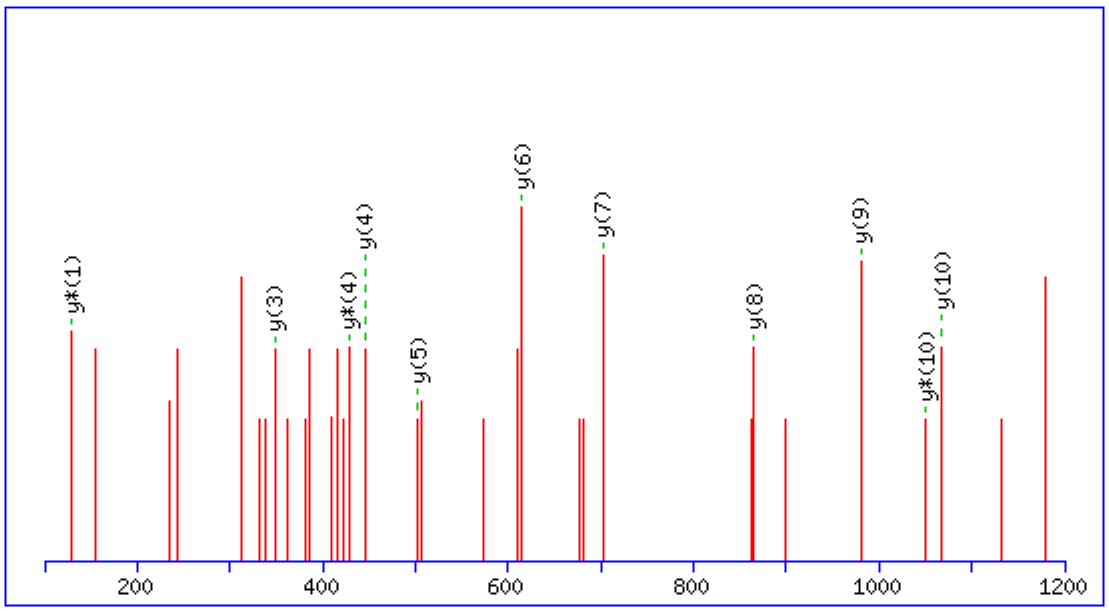
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSDYSIGPNSK**
Found in **UBL4A_HUMAN**, Ubiquitin-like protein 4A OS=Homo sapiens GN=UBL4A PE=1 SV=1

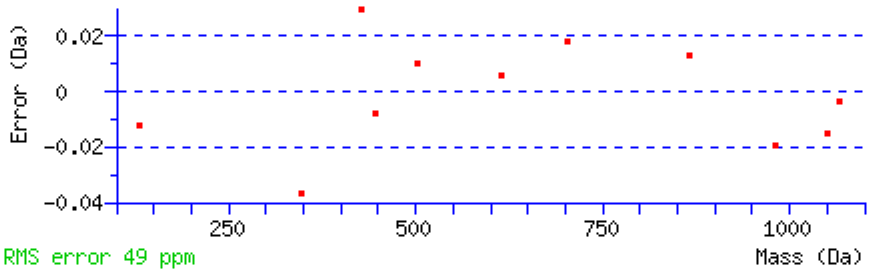
Match to Query 29173: 1179.576308 from(590.795430,2+) rtinseconds(1705) index(15511)
Title: Locus:1.1.1.1800.44
Data file 2011-11-12 - TFD - EP 6-6.mgf

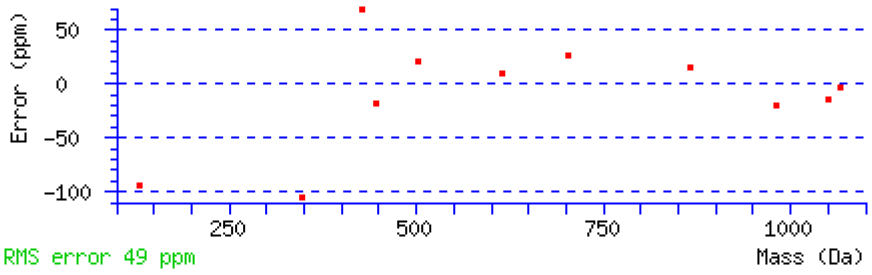
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1179.577148
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 51 **Expect:** 6.1e-005
Matches : 11/100 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							11
2	201.123368	101.065322			183.112803	92.060039	S	***1067.500379***	534.253828	1050.473830	525.740553	1049.489814	525.248545	10
3	316.150311	158.578793			298.139746	149.573511	D	***980.468351***	490.737814	963.441802	482.224539	962.457786	481.732531	9
4	479.213640	240.110458			461.203075	231.105176	Y	***865.441408***	433.224342	848.414859	424.711068	847.430843	424.219060	8
5	566.245668	283.626472			548.235103	274.621190	S	***702.378079***	351.692678	685.351530	343.179403	684.367514	342.687395	7
6	679.329732	340.168504			661.319167	331.163222	I	***615.346051***	308.176664	598.319502	299.663389	597.335486	299.171381	6
7	736.351196	368.679236			718.340631	359.673954	G	***502.261987***	251.634632	485.235438	243.121357	484.251422	242.629349	5
8	833.403960	417.205618			815.393395	408.200336	P	***445.240523***	223.123900	428.213974	214.610625	427.229958	214.118617	4
9	947.446887	474.227082	930.420338	465.713807	929.436322	465.221799	N	***348.187759***	174.597518	331.161210	166.084243	330.177194	165.592235	3
10	1034.478915	517.743096	1017.452366	509.229821	1016.468350	508.737813	S	234.144832	117.576054	217.118283	109.062780	216.134267	108.570772	2
11							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of LSDYSIGPNSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
50.7	1179.577148	-0.000840	LSDYSIGPNSK
5.8	1179.573975	0.002333	LAMTREMNSK

Mascot: http://www.matrixscience.com/

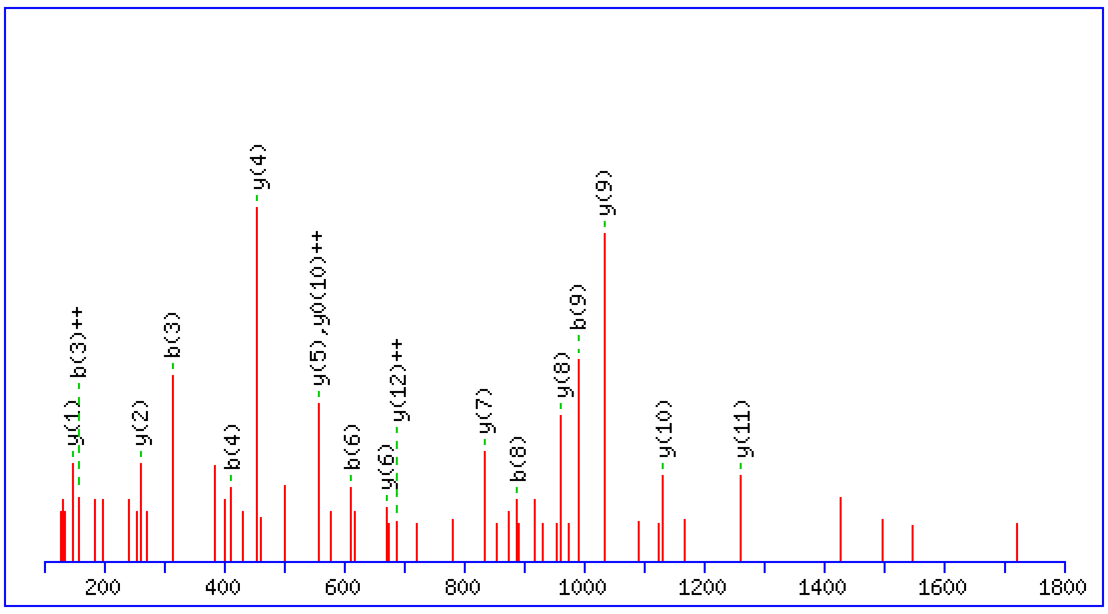
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALEVAEYLTPVLK**
Found in **ATG3_HUMAN**, Ubiquitin-like-conjugating enzyme ATG3 OS=Homo sapiens GN=ATG3 PE=1 SV=1

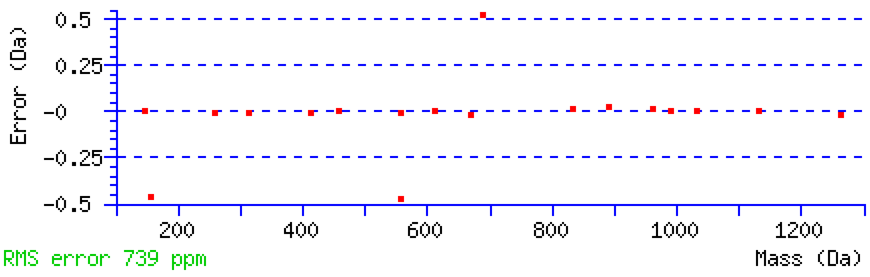
Match to Query 43152: 1444.822148 from(723.418350,2+) rtinseconds(3582) index(52214)
Title: Locus:1.1.1.2789.24
Data file 2011-11-13 - TFD - EP 7-4.mgf

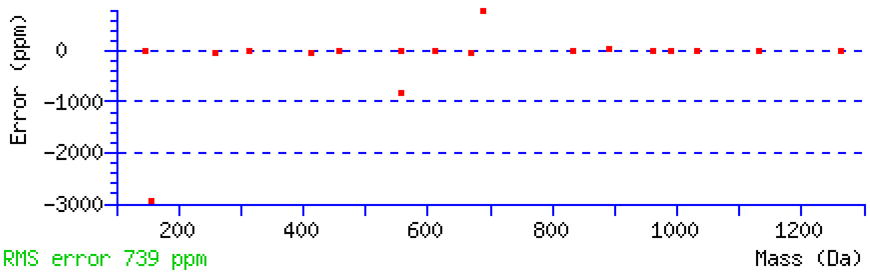
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1444.817703
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 81  Expect: 2.3e-008
Matches : 18/108 fragment ions using 24 most intense peaks   (help)
```

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	72.044390	36.525833			A							13
2	185.128454	93.067865			L	1374.787896	687.897586	1357.761347	679.384312	1356.777331	678.892304	12
3	**314.171047**	157.589161	296.160482	148.583879	E	***1261.703832***	631.355554	1244.677283	622.842280	1243.693267	622.350271	11
4	**413.239461**	207.123369	395.228896	198.118086	V	***1132.661239***	566.834258	1115.634690	558.320983	1114.650674	557.828975	10
5	484.276575	242.641926	466.266010	233.636643	A	***1033.592825***	517.300051	1016.566276	508.786776	1015.582260	508.294768	9
6	**613.319168**	307.163222	595.308603	298.157940	E	***962.555711***	481.781494	945.529162	473.268219	944.545146	472.776211	8
7	776.382497	388.694887	758.371932	379.689604	Y	***833.513118***	417.260197	816.486569	408.746922	815.502553	408.254914	7
8	**889.466561**	445.236919	871.455996	436.231636	L	***670.449789***	335.728533	653.423240	327.215258	652.439224	326.723250	6
9	**990.514240**	495.760758	972.503675	486.755476	T	***557.365725***	279.186501	540.339176	270.673226	539.355160	270.181218	5
10	1087.567004	544.287140	1069.556439	535.281858	P	***456.318046***	228.662661	439.291497	220.149386			4
11	1186.635418	593.821347	1168.624853	584.816065	V	359.265282	180.136279	342.238733	171.623004			3
12	1299.719482	650.363379	1281.708917	641.358096	L	***260.196868***	130.602072	243.170319	122.088797			2
13					K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of ALEVAEYLTPVLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
81.3	1444.817703	0.004445	ALEVAEYLTPVLK
2.1	1444.813675	0.008473	KLLTASDLAASDLK
1.0	1444.811157	0.010991	AHILYMSLEKLK

Mascot: http://www.matrixscience.com/

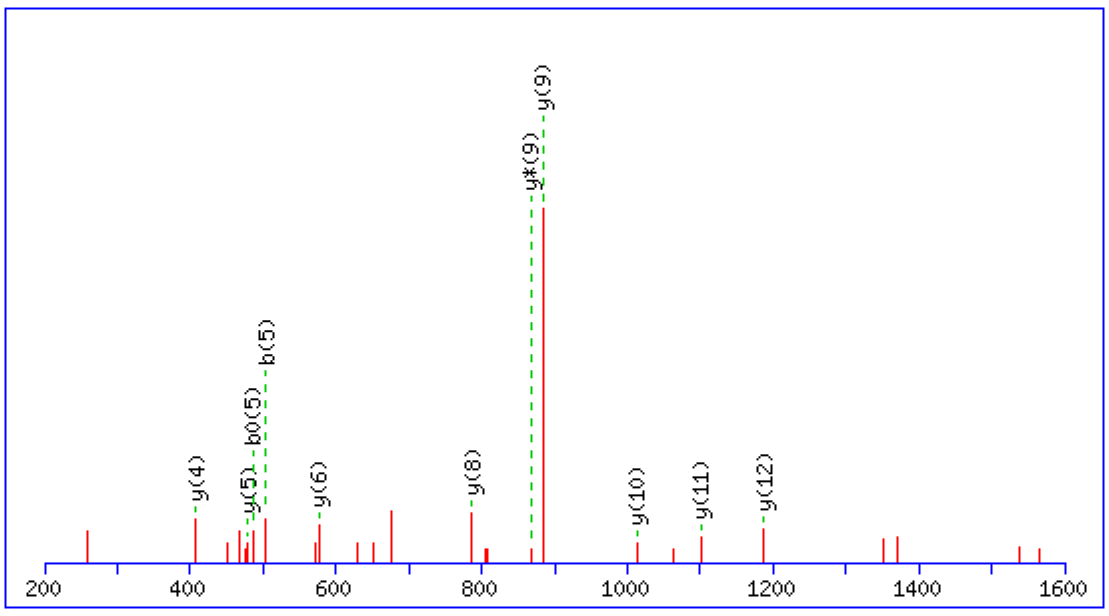
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **VTSSEPPNPASSSK**
Found in **UBXN4_HUMAN**, UBX domain-containing protein 4 OS=Homo sapiens GN=UBXN4 PE=1 SV=2

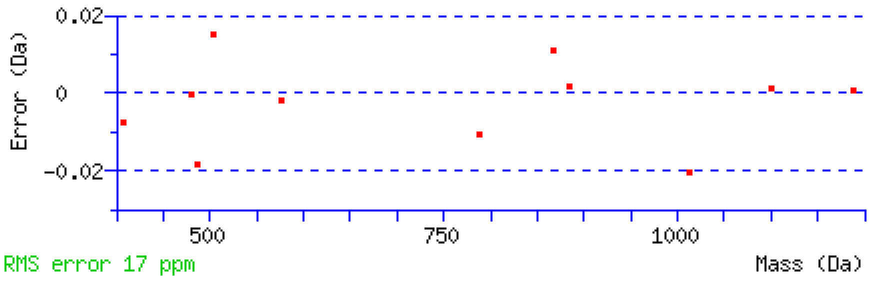
Match to Query 733991: 1386.663688 from(694.339120,2+) rtinseconds(1065) index(159169)
Title: Locus:1.1.1.1090.24
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

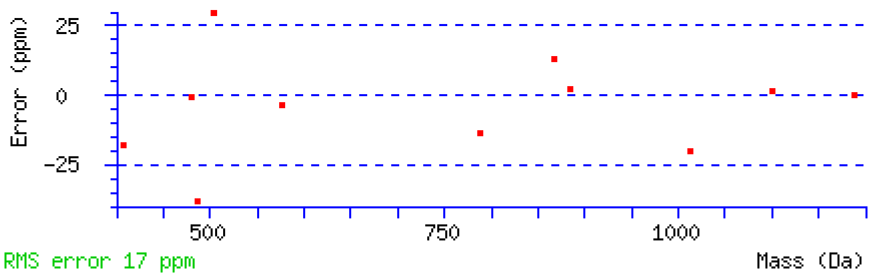
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1386.662674
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 43 **Expect:** 0.0006
Matches : 11/138 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							14
2	201.123369	101.065322			183.112804	92.060040	T	1288.601549	644.804413	1271.575000	636.291138	1270.590984	635.799130	13
3	288.155397	144.581336			270.144832	135.576054	S	***1187.553870***	594.280573	1170.527321	585.767299	1169.543305	585.275291	12
4	375.187425	188.097351			357.176860	179.092068	S	***1100.521842***	550.764559	1083.495293	542.251285	1082.511277	541.759277	11
5	504.230018	252.618647			486.219453	243.613365	E	***1013.489814***	507.248545	996.463265	498.735271	995.479249	498.243263	10
6	601.282782	301.145029			583.272217	292.139747	P	***884.447221***	442.727249	867.420672	434.213974	866.436656	433.721966	9
7	698.335546	349.671411			680.324981	340.666129	P	***787.394457***	394.200867	770.367908	385.687592	769.383892	385.195584	8
8	812.378473	406.692875	795.351924	398.179600	794.367908	397.687592	N	690.341693	345.674485	673.315144	337.161210	672.331128	336.669202	7
9	909.431237	455.219257	892.404688	446.705982	891.420672	446.213974	P	***576.298766***	288.653021	559.272217	280.139747	558.288201	279.647739	6
10	980.468351	490.737814	963.441802	482.224539	962.457786	481.732531	A	***479.246002***	240.126639	462.219453	231.613365	461.235437	231.121357	5
11	1067.500379	534.253828	1050.473830	525.740553	1049.489814	525.248545	S	***408.208888***	204.608082	391.182339	196.094808	390.198323	195.602800	4
12	1154.532407	577.769842	1137.505858	569.256567	1136.521842	568.764559	S	321.176860	161.092068	304.150311	152.578794	303.166295	152.086786	3
13	1241.564435	621.285856	1224.537886	612.772581	1223.553870	612.280573	S	234.144832	117.576054	217.118283	109.062780	216.134267	108.570772	2
14							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of VTSSEPPNPASSSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
43.0	1386.662674	0.001014	VTSSEPPNPASSSK
18.2	1386.656143	0.007545	RTPPNCAAEDIK
18.2	1386.656143	0.007545	RTPPNCAAEDIK
6.5	1386.656143	0.007545	RTINSSQEPAPGM
4.5	1386.673920	-0.010232	KPSDGSPDTKPSR
3.8	1386.667587	-0.003899	VASFVAMAGQFLM
3.2	1386.664001	-0.000313	FNNPATAAPNSQR
3.0	1386.667587	-0.003899	VASFVAMAGQFLM
1.3	1386.662689	0.000999	EPASPAPTPTSLR
1.2	1386.656158	0.007530	ELAAMGPGASGDGVR

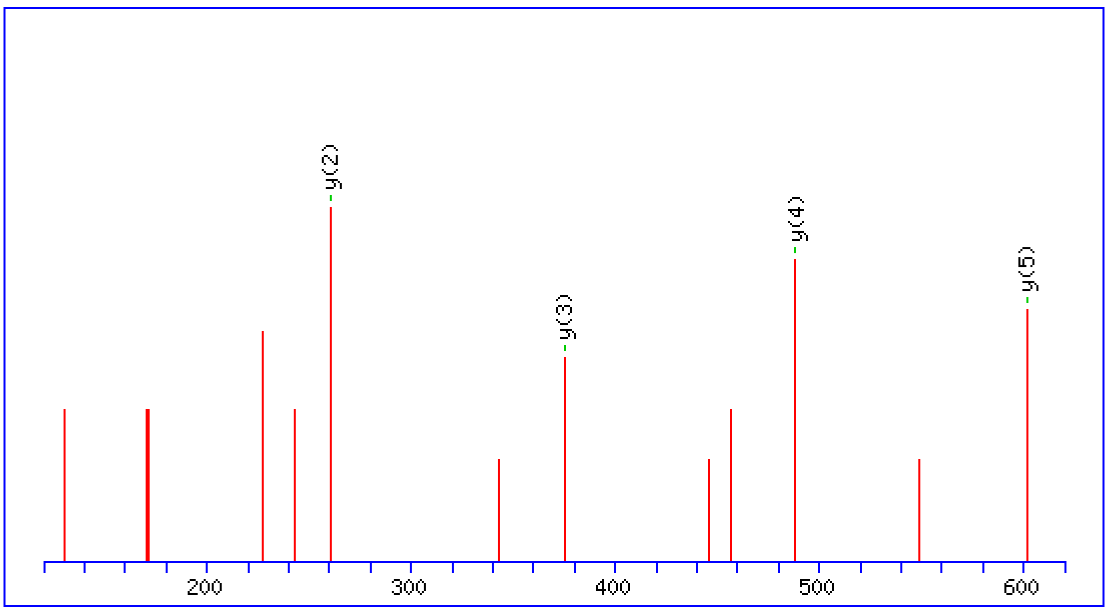
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FLIPDIK**
Found in **UD3A1_HUMAN**, UDP-glucuronosyltransferase 3A1 OS=Homo sapiens GN=UGT3A1 PE=2 SV=1

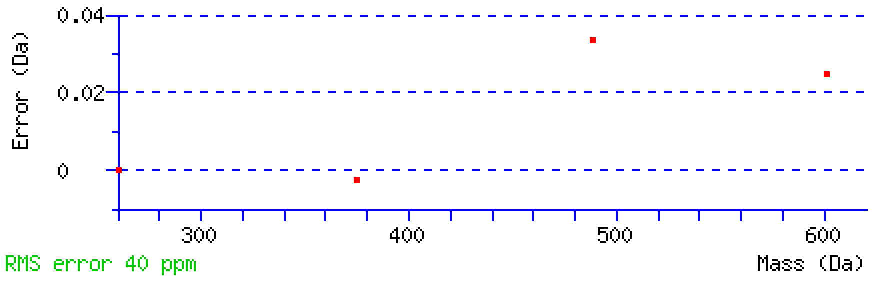
Match to Query 79336: 860.506388 from(431.260470,2+) rtinseconds(1825) index(752303)
Title: Locus:1.1.1.1039.7
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

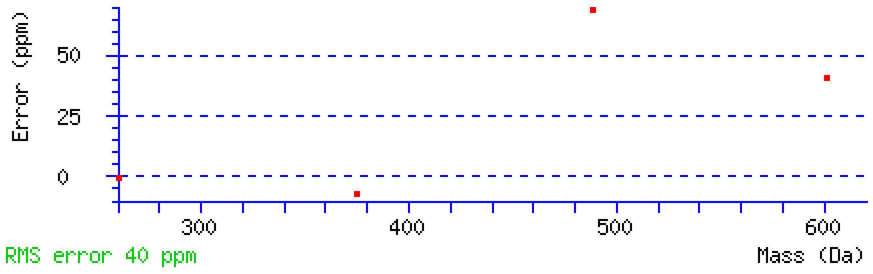
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 120 to 620 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 860.500748
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
P4 : Oxidation (P)
Ions Score: 34 **Expect:** 0.0022
Matches : 4/48 fragment ions using 5 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.075690	74.541483			F							7
2	261.159754	131.083515			L	714.439618	357.723447	697.413069	349.210173	696.429053	348.718165	6
3	374.243818	187.625547			I	*601.355554*	301.181415	584.329005	292.668141	583.344989	292.176133	5
4	487.291497	244.149386			P	*488.271490*	244.639383	471.244941	236.126108	470.260925	235.634100	4
5	602.318440	301.662858	584.307875	292.657576	D	*375.223811*	188.115543	358.197262	179.602269	357.213246	179.110261	3
6	715.402504	358.204890	697.391939	349.199608	I	*260.196868*	130.602072	243.170319	122.088798			2
7					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of FLIPDIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.3	860.500748	0.005640	FLIPDIK
19.5	860.500748	0.005640	LFPDILK
18.6	860.504105	0.002283	MILDLLK
18.6	860.504105	0.002283	MLLDILK
17.8	860.500748	0.005640	FPLLVEK
17.8	860.511978	-0.005590	LFLPLSR
17.8	860.511963	-0.005575	YPLLISR
11.0	860.504105	0.002283	LILMDLK
10.1	860.500748	0.005640	LDFLPLK
3.4	860.504105	0.002283	LLDLIMK

Mascot: http://www.matrixscience.com/

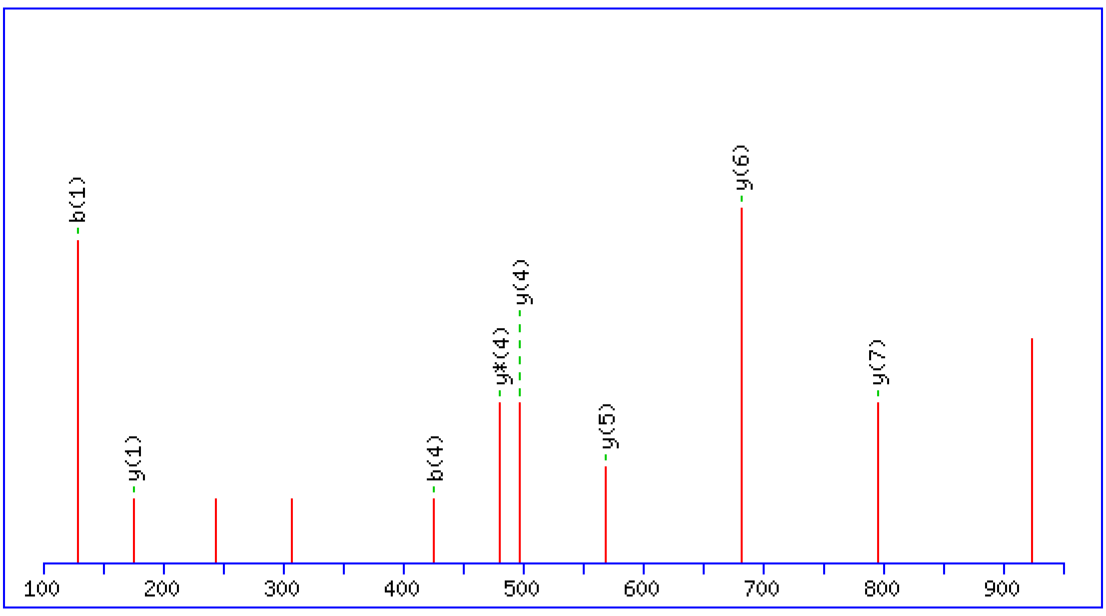
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **KPPAIPIR**
Found in **S35B4_HUMAN**, UDP-xylose and UDP-N-acetylglucosamine transporter OS=Homo sapiens GN=SLC35B4 PE=2 SV=1

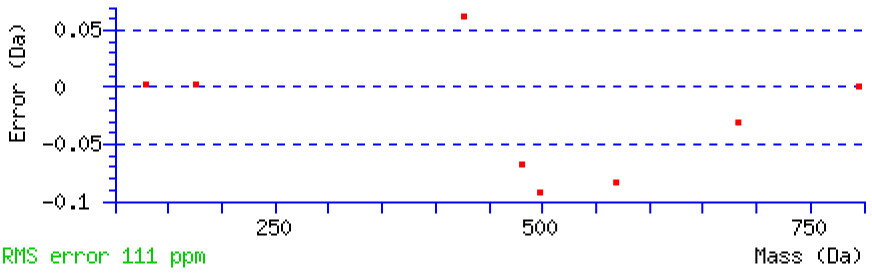
Match to Query 158091: 922.557688 from(462.286120,2+) rtinseconds(1134) index(739948)
Title: Locus:1.1.1.772.10
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

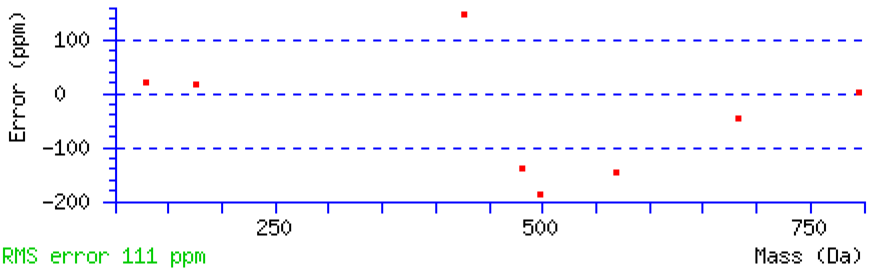
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 922.559982
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
P2      : Oxidation (P)
P3      : Oxidation (P)
Ions Score: 45  Expect: 0.0001
Matches : 8/56 fragment ions using 10 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	**129.102239**	65.054757	112.075690	56.541483	K					8
2	242.149918	121.578597	225.123369	113.065322	P	***795.472316***	398.239796	778.445767	389.726522	7
3	355.197597	178.102436	338.171048	169.589162	P	***682.424637***	341.715957	665.398088	333.202682	6
4	**426.234711**	213.620994	409.208162	205.107719	A	***569.376958***	285.192117	552.350409	276.678843	5
5	539.318775	270.163026	522.292226	261.649751	I	***498.339844***	249.673560	481.313295	241.160285	4
6	636.371539	318.689408	619.344990	310.176133	P	385.255780	193.131528	368.229231	184.618253	3
7	749.455603	375.231440	732.429054	366.718165	I	288.203016	144.605146	271.176467	136.091871	2
8					R	***175.118952***	88.063114	158.092403	79.549839	1





NCBI **BLAST** search of KPPAIPIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.4	922.559982	-0.002294	KPPAIPIR
21.9	922.559982	-0.002294	QILPPLAR
21.9	922.559982	-0.002294	QILPPLAR
15.9	922.559967	-0.002279	KLIPNPNK
15.9	922.559982	-0.002294	KLLHGDIK
12.2	922.548767	0.008921	AGLVLPPPK
11.9	922.559982	-0.002294	KLTSHLPK
11.9	922.559982	-0.002294	KPPAIPIR
5.3	922.548752	0.008936	AGLVIPPEK
4.6	922.548767	0.008921	AGLVLPPPK

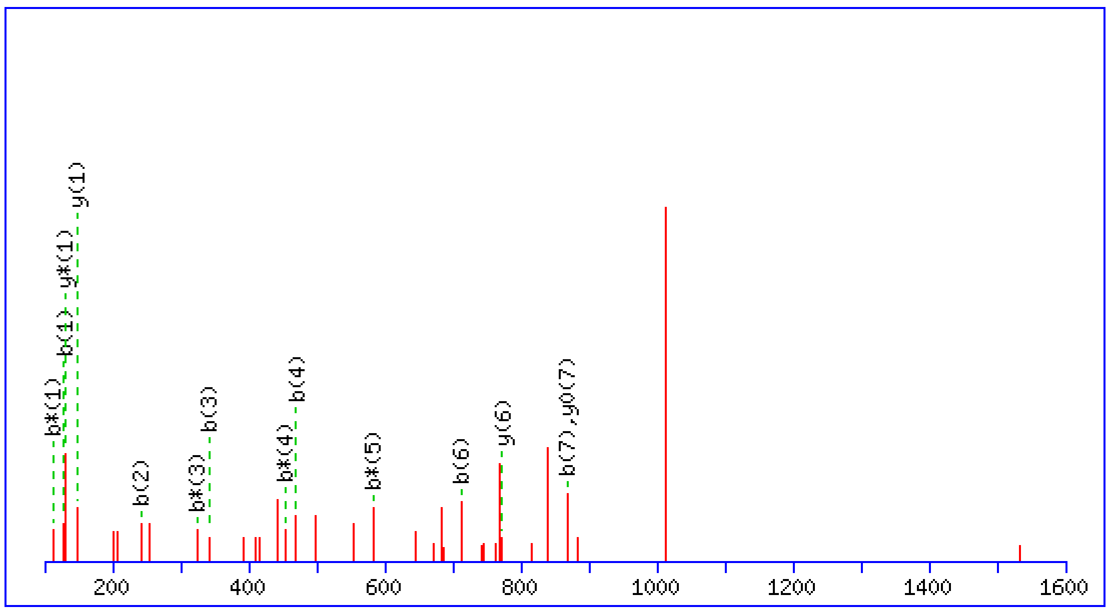
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QLVEEIRK**
Found in **CJ118_HUMAN**, Uncharacterized protein C10orf118 OS=Homo sapiens GN=C10orf118 PE=2 SV=2

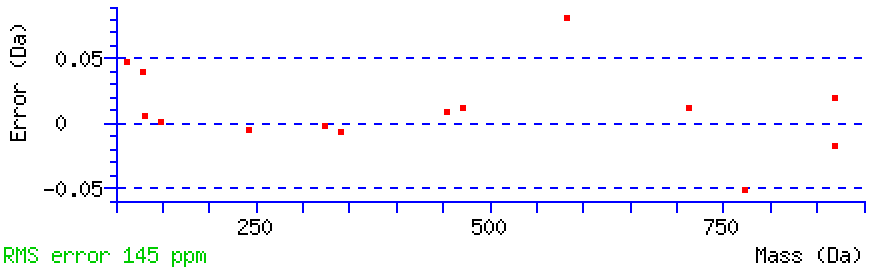
Match to Query 16099: 1013.589208 from(507.801880,2+) rtinseconds(1375) index(10237)
Title: Locus:1.1.1.1956.28
Data file 2011-11-10 - TFD - EP 3-1.mgf

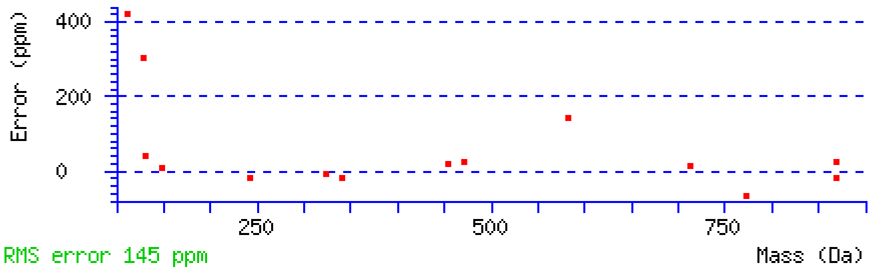
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1013.586914
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 32  Expect: 0.0071
Matches : 14/72 fragment ions using 29 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	*129.065854*	65.036565	112.039305	56.523291			Q							8
2	*242.149918*	121.578597	225.123369	113.065323			L	886.535643	443.771460	869.509094	435.258185	868.525078	434.766177	7
3	*341.218332*	171.112804	324.191783	162.599530			V	**773.451579**	387.229428	756.425030	378.716153	755.441014	378.224145	6
4	*470.260925*	235.634101	453.234376	227.120826	452.250360	226.628818	E	674.383165	337.695221	657.356616	329.181946	656.372600	328.689938	5
5	599.303518	300.155397	582.276969	291.642123	581.292953	291.150115	E	545.340572	273.173924	528.314023	264.660650	527.330007	264.168642	4
6	*712.387582*	356.697429	695.361033	348.184155	694.377017	347.692147	I	416.297979	208.652628	399.271430	200.139353			3
7	*868.488693*	434.747985	851.462144	426.234710	850.478128	425.742702	R	303.213915	152.110596	286.187366	143.597321			2
8							K	**147.112804**	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of QLVEEIRK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.9	1013.586914	0.002294	QLVEEIRK
23.6	1013.586914	0.002294	LRAEIEGVK
17.1	1013.586945	0.002263	AGLVQNVVSK
16.2	1013.594315	-0.005107	IKMLPTPAK
15.7	1013.586914	0.002294	IKVEELQR
14.4	1013.598160	-0.008952	KIQTQLQR
13.6	1013.586914	0.002294	KPREELVK
11.7	1013.598175	-0.008967	QLGVNTVRK
11.7	1013.586914	0.002294	EVIQLKER
11.1	1013.586914	0.002294	QLKELDLR

Mascot: http://www.matrixscience.com/

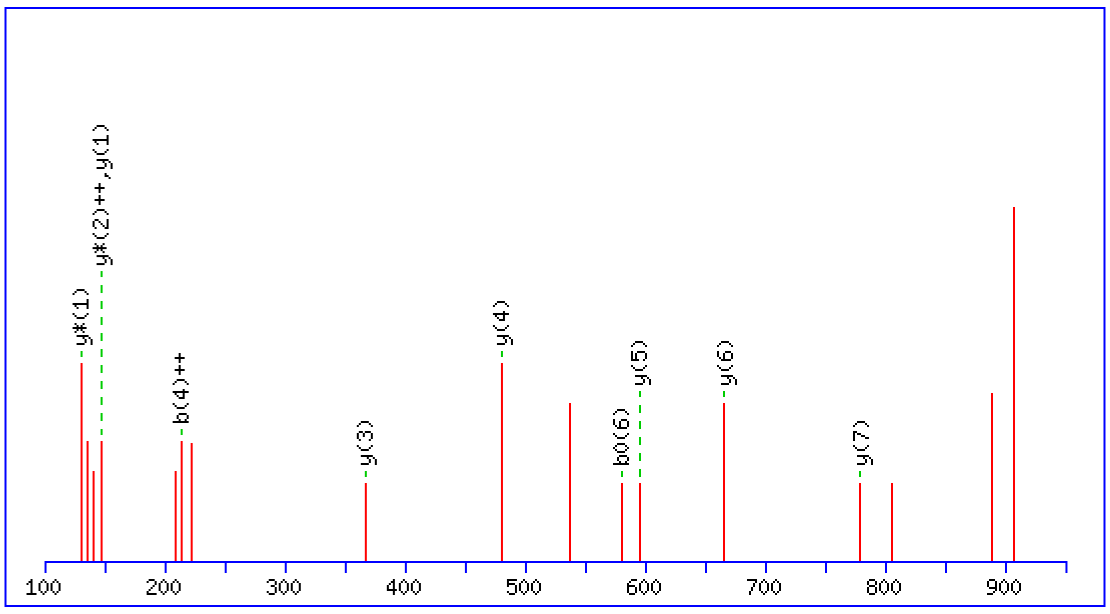
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QLADIGYK**
Found in **CL062_HUMAN**, Uncharacterized protein C12orf62 OS=Homo sapiens GN=C12orf62 PE=2 SV=1

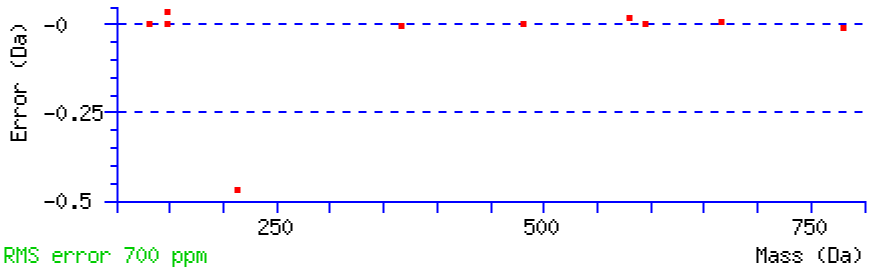
Match to Query 6564: 906.488828 from(454.251690,2+) rtinseconds(1824) index(7460)
Title: Locus:1.1.1.2330.19
Data file 2011-11-12 - TFD - EP 5-8.mgf

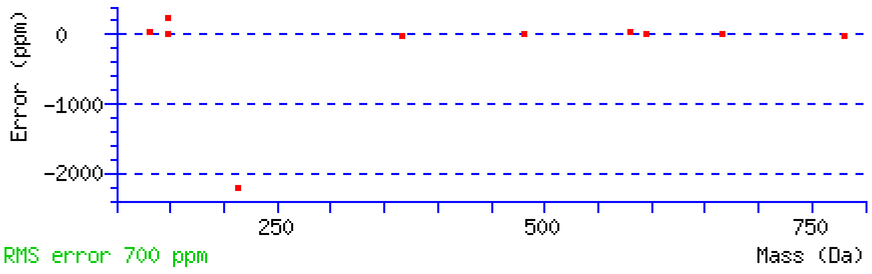
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 906.481064
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 47 **Expect:** 0.00022
Matches : 10/70 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	129.065854	65.036565	112.039305	56.523291			**Q**							8
2	242.149918	121.578597	225.123369	113.065323			**L**	***779.429782***	390.218529	762.403233	381.705255	761.419217	381.213247	7
3	313.187032	157.097154	296.160483	148.583879			**A**	***666.345718***	333.676497	649.319169	325.163223	648.335153	324.671215	6
4	428.213975	214.610626	411.187426	206.097351	410.203410	205.605343	**D**	***595.308604***	298.157940	578.282055	289.644666	577.298039	289.152658	5
5	541.298039	271.152658	524.271490	262.639383	523.287474	262.147375	**I**	***480.281661***	240.644468	463.255112	232.131194			4
6	598.319503	299.663390	581.292954	291.150115	580.308938	290.658107	**G**	***367.197597***	184.102436	350.171048	175.589162			3
7	761.382832	381.195054	744.356283	372.681780	743.372267	372.189772	**Y**	310.176133	155.591704	293.149584	147.078430			2
8							**K**	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of QLADIGYK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.3	906.481064	0.007764	QLADIGYK
20.1	906.492279	-0.003451	QLAEYRK
19.5	906.492310	-0.003482	AGLGAVYTR
15.8	906.492294	-0.003466	QLKESFR
11.2	906.481079	0.007749	AQLDSFVK
11.2	906.484451	0.004377	QVLSVMSK
10.3	906.481049	0.007779	KLFEENK
10.3	906.484436	0.004392	KLISDMGK
10.3	906.481049	0.007779	KPLNYEK
10.3	906.492294	-0.003466	KPREFSK

Mascot: http://www.matrixscience.com/

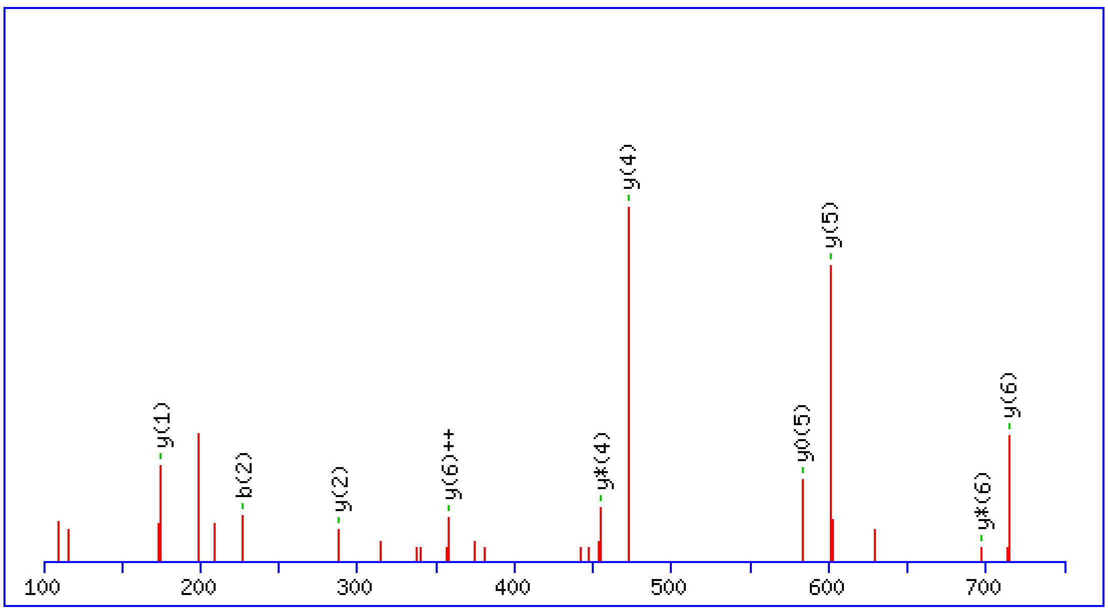
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLEPALR**
Found in **CA087_HUMAN**, Uncharacterized protein C1orf87 OS=Homo sapiens GN=C1orf87 PE=2 SV=1

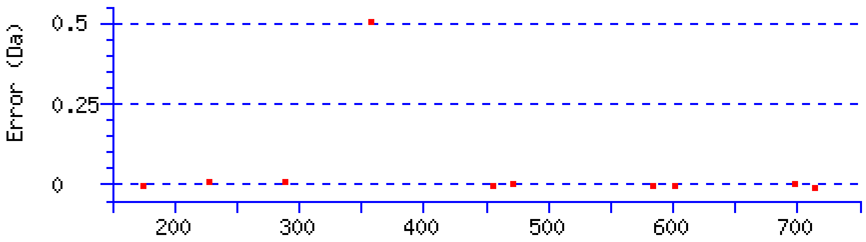
Match to Query 35232: 826.492508 from(414.253530,2+) rtinseconds(1811) index(672838)
Title: Locus:1.1.1.1358.5
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●

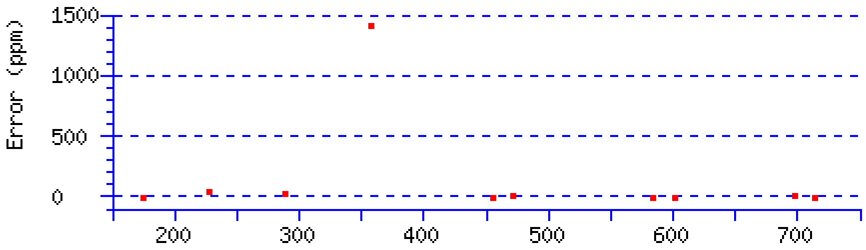


Monoisotopic mass of neutral peptide Mr(calc): 826.491226
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
P4 : Oxidation (P)
Ions Score: 36 **Expect:** 0.0011
Matches : 10/48 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							7
2	227.175404	114.091340			L	***714.414466***	357.710871	697.387917	349.197597	696.403901	348.705589	6
3	356.217997	178.612637	338.207432	169.607354	E	***601.330402***	301.168839	584.303853	292.655565	583.319837	292.163557	5
4	469.265676	235.136476	451.255111	226.131194	P	***472.287809***	236.647542	455.261260	228.134268			4
5	540.302790	270.655033	522.292225	261.649751	A	359.240130	180.123703	342.213581	171.610428			3
6	653.386854	327.197065	635.376289	318.191783	L	***288.203016***	144.605146	271.176467	136.091871			2
7					R	***175.118952***	88.063114	158.092403	79.549839			1



RMS error 444 ppm



RMS error 444 ppm

NCBI **BLAST** search of LLEPALR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.0	826.491226	0.001282	LLEPALR
24.0	826.491226	0.001282	LELPLSR
20.0	826.491241	0.001267	LIPSPLR
20.0	826.491226	0.001282	LPLEALR
20.0	826.491257	0.001251	LPTPVLR
12.2	826.491241	0.001267	ILGPGLNK
10.5	826.491226	0.001282	ILLSPER
10.5	826.491241	0.001267	ILTPEVR
10.5	826.491257	0.001251	IPVVVER
9.7	826.491226	0.001282	EILSPLR

Mascot: http://www.matrixscience.com/

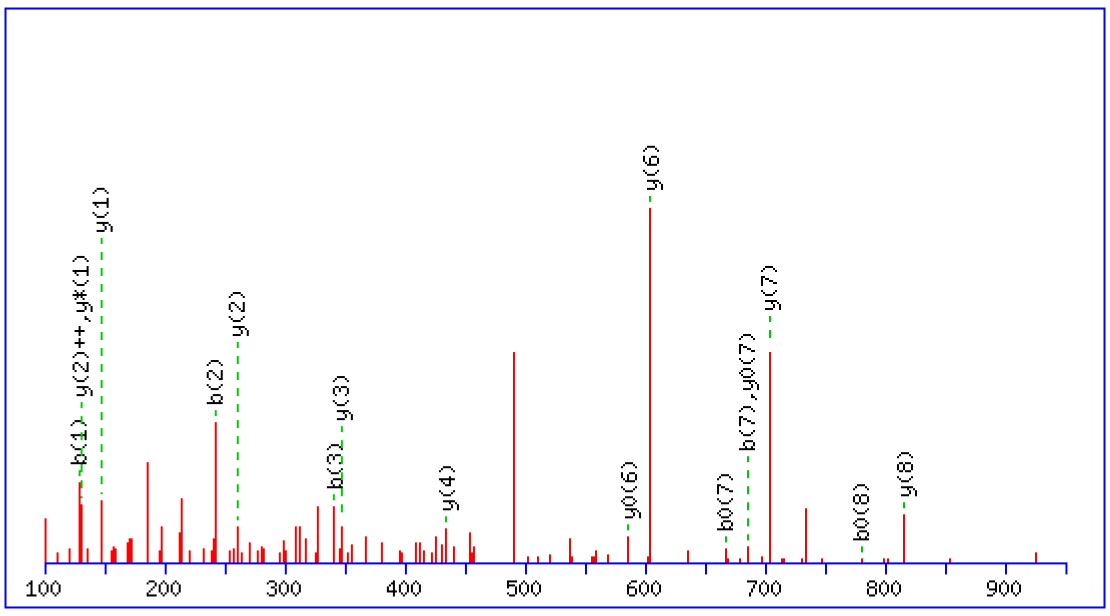
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KPVVASSLK**
Found in **CB042_HUMAN**, Uncharacterized protein C2orf42 OS=Homo sapiens GN=C2orf42 PE=2 SV=1

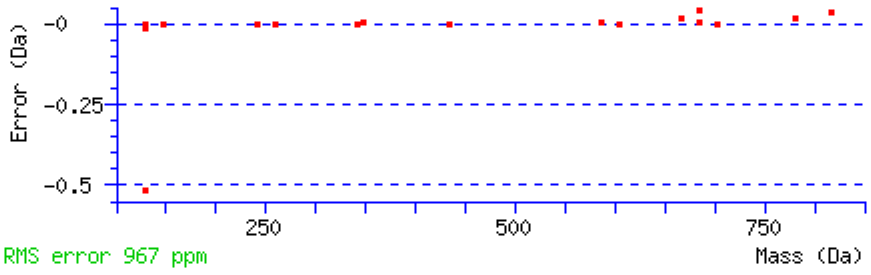
Match to Query 11375: 943.569288 from(472.791920,2+) rtinseconds(2137) index(25011)
Title: Locus:1.1.1.2245.15
Data file 2011-11-13 - TFD - EP 7-4.mgf

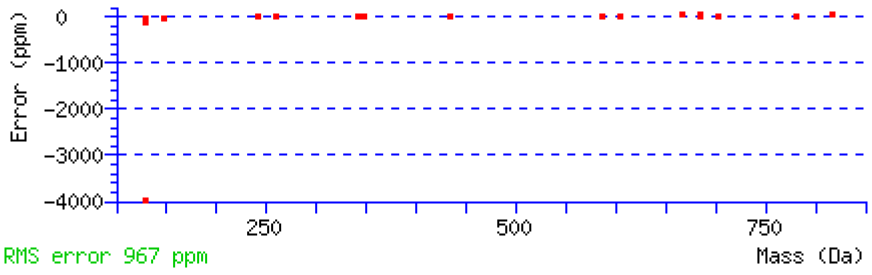
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 943.570221
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P2      : Oxidation (P)
Ions Score: 45  Expect: 0.00014
Matches : 17/82 fragment ions using 33 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	**129.102239**	65.054757	112.075690	56.541483			K							9
2	**242.149918**	121.578597	225.123369	113.065322			P	***816.482545***	408.744911	799.455996	400.231636	798.471980	399.739628	8
3	**341.218332**	171.112804	324.191783	162.599529			V	***703.434866***	352.221071	686.408317	343.707797	685.424301	343.215789	7
4	440.286746	220.647011	423.260197	212.133737			V	***604.366452***	302.686864	587.339903	294.173590	586.355887	293.681582	6
5	511.323860	256.165568	494.297311	247.652294			A	505.298038	253.152657	488.271489	244.639382	487.287473	244.147374	5
6	598.355888	299.681582	581.329339	291.168308	580.345323	290.676300	S	***434.260924***	217.634100	417.234375	209.120825	416.250359	208.628817	4
7	**685.387916**	343.197596	668.361367	334.684322	667.377351	334.192314	S	***347.228896***	174.118086	330.202347	165.604811	329.218331	165.112803	3
8	798.471980	399.739628	781.445431	391.226354	780.461415	390.734346	L	***260.196868***	130.602072	243.170319	122.088798			2
9							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of KPVVASSLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.9	943.570221	-0.000933	GALVLGSSLK
44.9	943.570221	-0.000933	KPVVASSLK
15.9	943.570221	-0.000933	KLGSTLTPK
9.3	943.570206	-0.000918	LQVESLKK
9.1	943.570236	-0.000948	LGSTVGLVAK
9.0	943.570190	-0.000902	EKLINSLK
8.7	943.570221	-0.000933	KVLVEQTK
8.2	943.570221	-0.000933	TAPTSKVIK
5.7	943.570221	-0.000933	KLLDVTQK
5.6	943.570206	-0.000918	ESIQVKLK

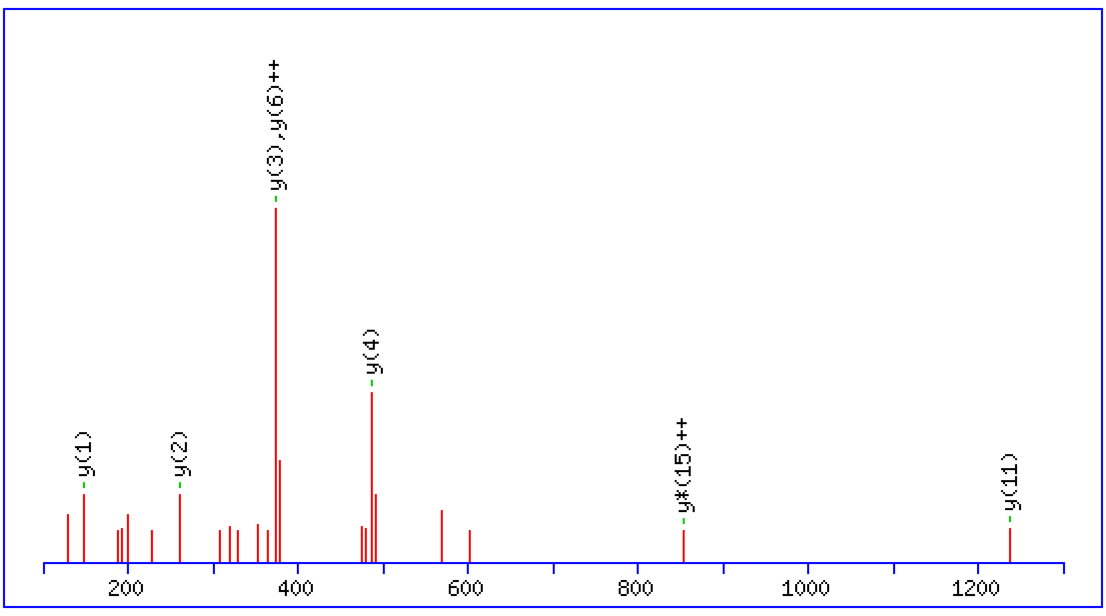
{MATRIX SCIENCE}
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MGIGWKPLAPIFPPLPK**
Found in **CB071_HUMAN**, Uncharacterized protein C2orf71 OS=Homo sapiens GN=C2orf71 PE=1 SV=1

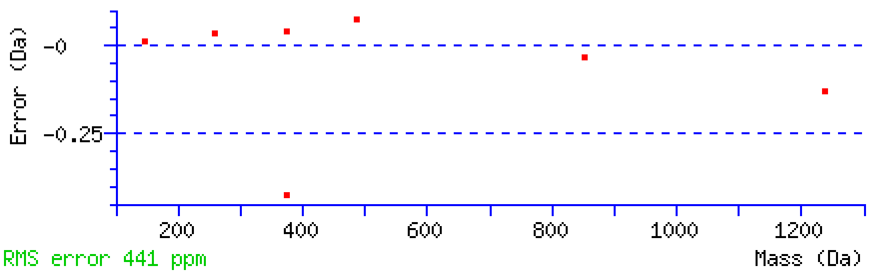
Match to Query 17039: 1909.040592 from(637.354140,3+) rtinseconds(2336) index(8932)
Title: Locus:1.1.1.2503.10
Data file 2011-11-10 - TFD - EP 4-8.mgf

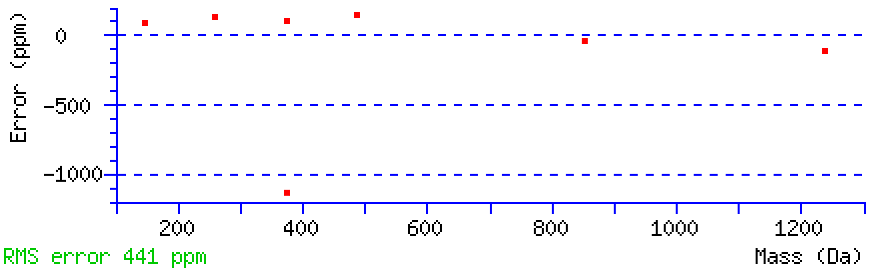
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1909.053558
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P13     : Oxidation (P)
P14     : Oxidation (P)
P16     : Oxidation (P)
Ions Score: 38  Expect: 0.0027
Matches : 7/118 fragment ions using 7 most intense peaks   (help)
```

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	132.047761	66.527518			M					17
2	189.069225	95.038250			G	1779.020357	890.013816	1761.993808	881.500542	16
3	302.153289	151.580282			I	1721.998893	861.503085	1704.972344	852.989810	15
4	359.174753	180.091014			G	1608.914829	804.961052	1591.888280	796.447778	14
5	545.254066	273.130671			W	1551.893365	776.450320	1534.866816	767.937046	13
6	673.349029	337.178153	656.322480	328.664878	K	1365.814052	683.410664	1348.787503	674.897390	12
7	770.401793	385.704535	753.375244	377.191260	P	***1237.719089***	619.363182	1220.692540	610.849908	11
8	883.485857	442.246567	866.459308	433.733292	L	1140.666325	570.836800	1123.639776	562.323526	10
9	954.522971	477.765124	937.496422	469.251849	A	1027.582261	514.294769	1010.555712	505.781494	9
10	1051.575735	526.291505	1034.549186	517.778231	P	956.545147	478.776211	939.518598	470.262937	8
11	1164.659799	582.833537	1147.633250	574.320263	I	859.492383	430.249830	842.465834	421.736555	7
12	1311.728213	656.367744	1294.701664	647.854470	F	746.408319	373.707798	729.381770	365.194523	6
13	1424.775892	712.891584	1407.749343	704.378310	P	599.339905	300.173591	582.313356	291.660316	5
14	1537.823571	769.415423	1520.797022	760.902149	P	***486.292226***	243.649751	469.265677	235.136476	4
15	1650.907635	825.957455	1633.881086	817.444181	L	***373.244547***	187.125911	356.217998	178.612637	3
16	1763.955314	882.481295	1746.928765	873.968020	P	***260.160483***	130.583879	243.133934	122.070605	2
17					K	***147.112804***	74.060040	130.086255	65.546765	1





NCBI **BLAST** search of MGIGWKPLAPIFPPLPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.2	1909.053558	-0.012966	MGIGWKPLAPIFPPLPK
38.2	1909.053558	-0.012966	MGIGWKPLAPIFPPLPK
38.2	1909.053558	-0.012966	MGIGWKPLAPIFPPLPK
23.7	1909.053558	-0.012966	MGIGWKPLAPIFPPLPK
23.7	1909.053558	-0.012966	MGIGWKPLAPIFPPLPK
23.7	1909.053558	-0.012966	MGIGWKPLAPIFPPLPK
21.6	1909.053558	-0.012966	MGIGWKPLAPIFPPLPK
15.4	1909.028381	0.012211	NVFHYLMAFLRELLK
10.8	1909.034241	0.006351	QMIKLTQEHIEALLDK
8.0	1909.053558	-0.012966	MGIGWKPLAPIFPPLPK

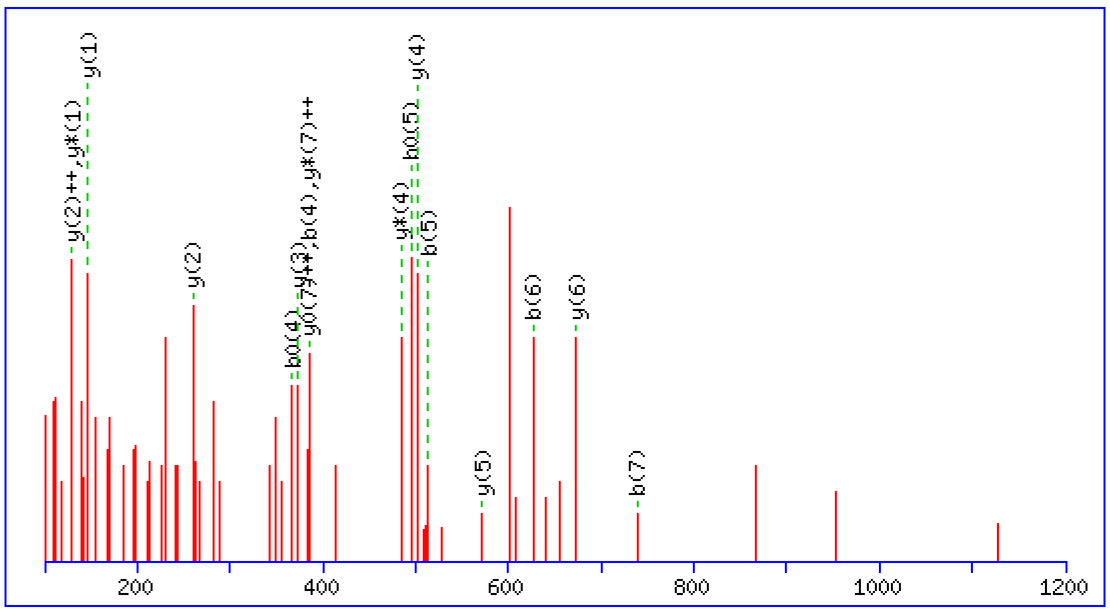
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VITAQPPK**
Found in **CC024_HUMAN**, Uncharacterized protein C3orf24 OS=Homo sapiens GN=C3orf24 PE=2 SV=1

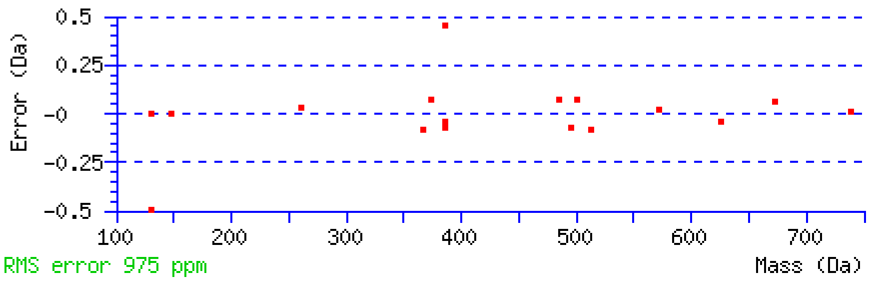
Match to Query 6794: 884.498548 from(443.256550,2+) rtinseconds(2213) index(25368)
Title: Locus:1.1.1.2134.6
Data file 2011-11-12 - TFD - EP 6-5.mgf

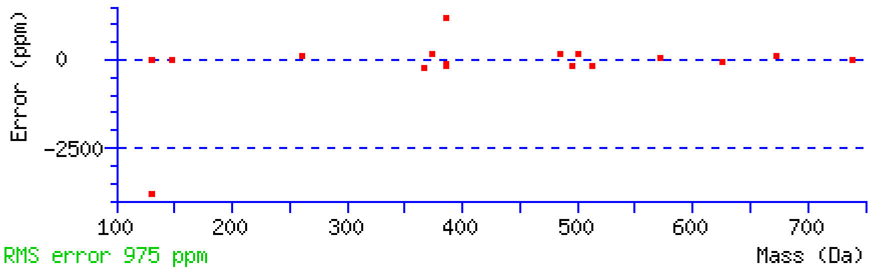
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 884.496735
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P6 : Oxidation (P)
P7 : Oxidation (P)
Ions Score: 51 **Expect:** 4.9e-005
Matches : 17/62 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							8
2	213.159754	107.083515					I	786.435597	393.721437	769.409048	385.208162	768.425032	384.716154	7
3	314.207433	157.607354			296.196868	148.602072	T	*673.351533*	337.179405	656.324984	328.666130	655.340968	328.174122	6
4	**385.244547**	193.125911			367.233982	184.120629	A	*572.303854*	286.655565	555.277305	278.142291			5
5	**513.303125**	257.155201	496.276576	248.641926	495.292560	248.149918	Q	*501.266740*	251.137008	484.240191	242.623734			4
6	**626.350804**	313.679040	609.324255	305.165766	608.340239	304.673758	P	*373.208162*	187.107719	356.181613	178.594445			3
7	**739.398483**	370.202880	722.371934	361.689605	721.387918	361.197597	P	*260.160483*	130.583879	243.133934	122.070605			2
8							K	*147.112804*	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of VITAQPPK
(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	884.496735	0.001813	VITAQPPK
23.7	884.496704	0.001844	QSPEALLK
16.5	884.496704	0.001844	EPLKAAPK
13.4	884.496735	0.001813	GAAPVDVLK
13.2	884.496719	0.001829	TPADPKLK
12.8	884.496719	0.001829	SAQPLPLK
12.3	884.496719	0.001829	ASPAVALPK
10.3	884.490189	0.008359	KPMQLPR
10.3	884.490189	0.008359	KPMQLPR
10.1	884.490189	0.008359	MNKHVLK

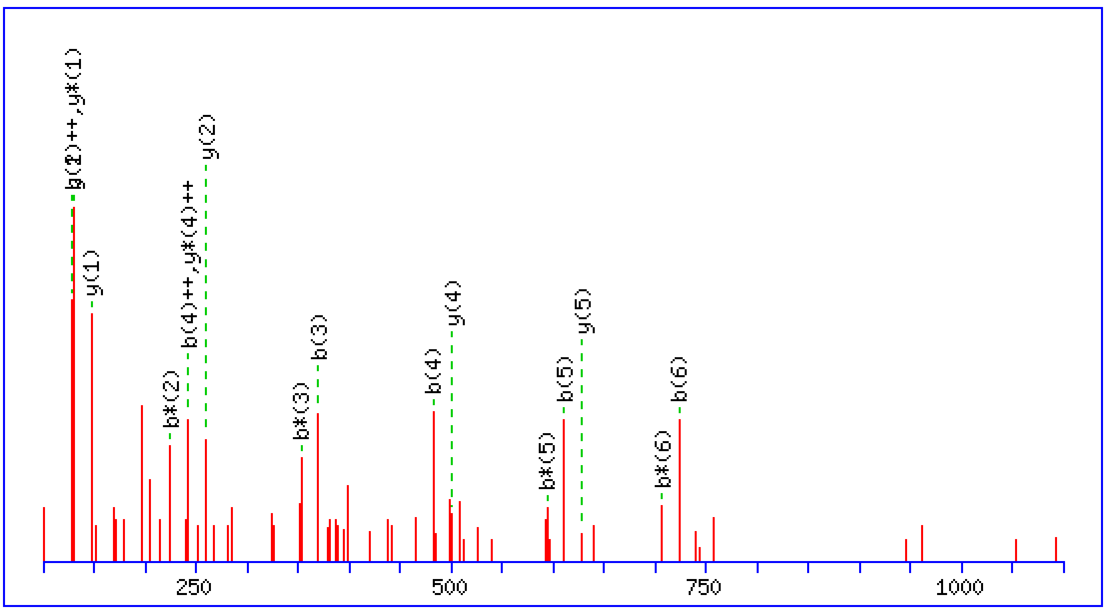
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **KPKPKPK**
Found in **CLD23_HUMAN**, Claudin-23 OS=Homo sapiens GN=CLDN23 PE=1 SV=2

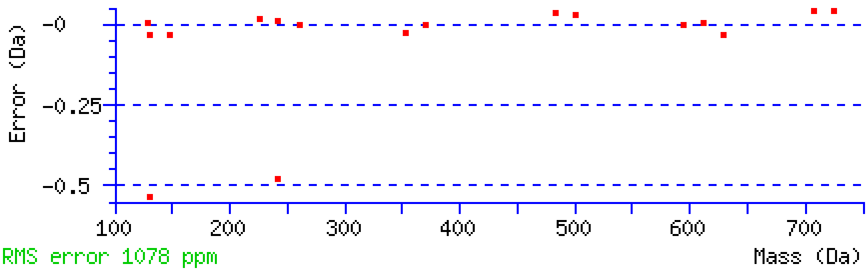
Match to Query 4558: 869.539308 from(435.776930,2+) rtinseconds(1635) index(4252)
Title: Locus:1.1.1.2279.5
Data file 2011-11-13 - TFD - EP 7-8.mgf

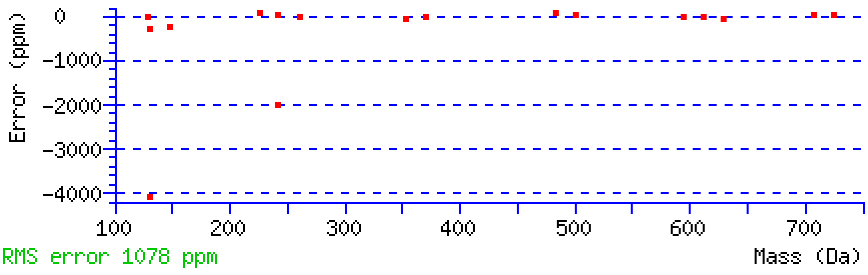
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 869.533432
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P2 : Oxidation (P)
P4 : Oxidation (P)
P6 : Oxidation (P)
Ions Score: 49 **Expect:** 9.2e-005
Matches : 18/48 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	***129.102239***	65.054757	112.075690	56.541483	**K**					7
2	***242.149918***	121.578597	225.123369	113.065322	**P**	742.445767	371.726522	725.419218	363.213247	6
3	***370.244881***	185.626079	353.218332	177.112804	**K**	**629.398088**	315.202682	612.371539	306.689408	5
4	***483.292560***	242.149918	466.266011	233.636644	**P**	**501.303125**	251.155201	484.276576	242.641926	4
5	***611.387523***	306.197400	594.360974	297.684125	**K**	388.255446	194.631361	371.228897	186.118087	3
6	***724.435202***	362.721239	707.408653	354.207965	**P**	**260.160483**	130.583879	243.133934	122.070605	2
7					**K**	**147.112804**	74.060040	130.086255	65.546765	1





NCBI **BLAST** search of KPKPKPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.3	869.533432	0.005876	KPKPKPK
49.3	869.533432	0.005876	QPQLKLK
49.1	869.533432	0.005876	QLQQLLK
41.3	869.533432	0.005876	LKQIGALQ
34.0	869.533432	0.005876	KAAVPQIK
33.7	869.533432	0.005876	QQLQLLK
31.5	869.533432	0.005876	KPLKQPK
31.4	869.533432	0.005876	KLQPIQK
21.4	869.544662	-0.005354	QRPTKLK
20.9	869.533432	0.005876	QKLLGPSK

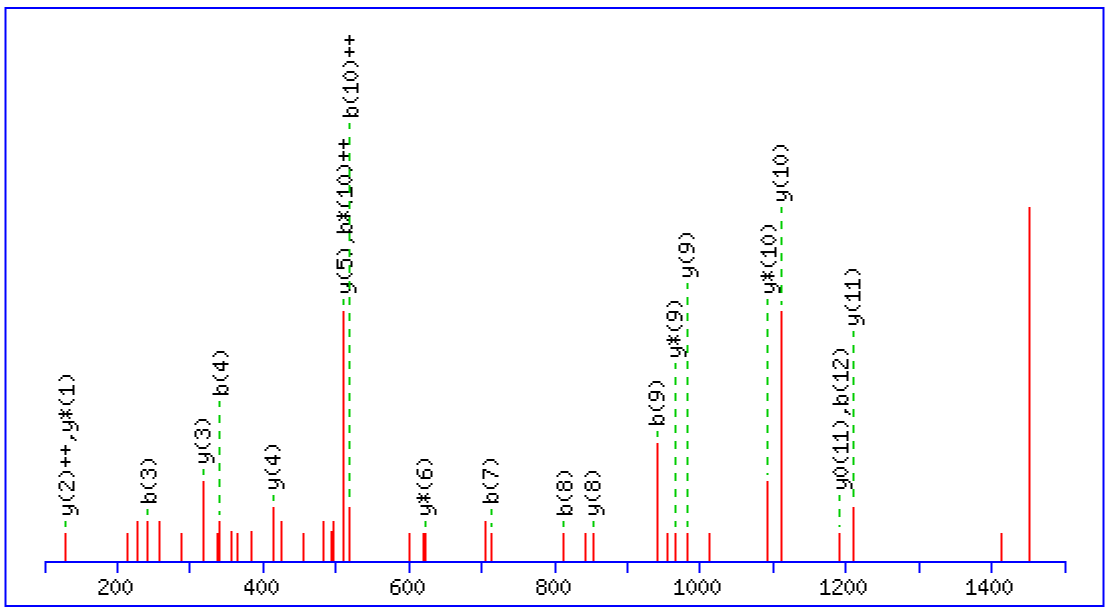
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AGIVQEDVQPPGLK**
Found in **CD052_HUMAN**, Uncharacterized protein C4orf52 OS=Homo sapiens GN=C4orf52 PE=1 SV=2

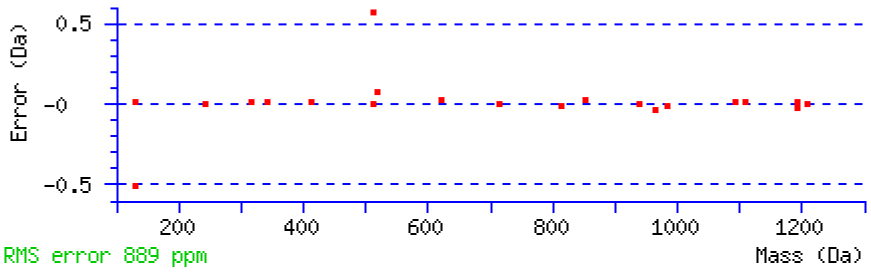
Match to Query 22670: 1449.794728 from(725.904640,2+) rtinseconds(2301) index(13395)
Title: Locus:1.1.1.2599.32
Data file 2011-11-14 - TFD - EP 8-8.mgf

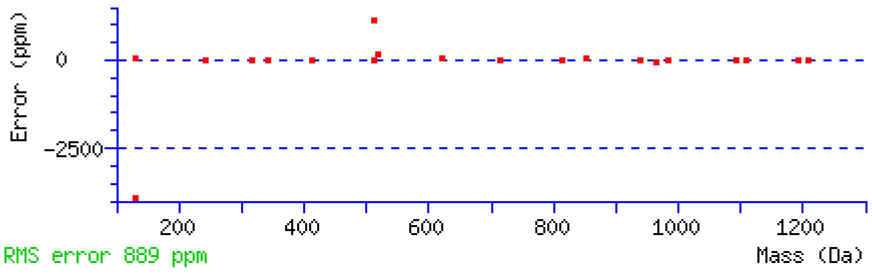
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1449.782745
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 48 **Expect:** 0.00011
Matches : 21/124 fragment ions using 32 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							14
2	129.065854	65.036565					G	1379.752908	690.380092	1362.726359	681.866818	1361.742343	681.374809	13
3	***242.149918***	121.578597					I	1322.731444	661.869360	1305.704895	653.356085	1304.720879	652.864077	12
4	***341.218332***	171.112804					V	***1209.647380***	605.327328	1192.620831	596.814054	1191.636815	596.322045	11
5	469.276910	235.142093	452.250361	226.628819			Q	***1110.578966***	555.793121	1093.552417	547.279846	1092.568401	546.787838	10
6	598.319503	299.663390	581.292954	291.150115	580.308938	290.658107	E	***982.520388***	491.763832	965.493839	483.250557	964.509823	482.758549	9
7	***713.346446***	357.176861	696.319897	348.663587	695.335881	348.171579	D	***853.477795***	427.242535	836.451246	418.729261	835.467230	418.237253	8
8	***812.414860***	406.711068	795.388311	398.197794	794.404295	397.705786	V	738.450852	369.729064	721.424303	361.215789			7
9	***940.473438***	470.740357	923.446889	462.227083	922.462873	461.735075	Q	639.382438	320.194857	622.355889	311.681582			6
10	1037.526202	519.266739	1020.499653	510.753465	1019.515637	510.261457	P	***511.323860***	256.165568	494.297311	247.652293			5
11	1134.578966	567.793121	1117.552417	559.279847	1116.568401	558.787839	P	***414.271096***	207.639186	397.244547	199.125911			4
12	***1191.600430***	596.303853	1174.573881	587.790579	1173.589865	587.298570	G	***317.218332***	159.112804	300.191783	150.599529			3
13	1304.684494	652.845885	1287.657945	644.332610	1286.673929	643.840602	L	260.196868	130.602072	243.170319	122.088797			2
14							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of AGIVQEDVQPPGLK
(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	1449.782745	0.011983	AGIVQEDVQPPGLK
5.5	1449.782715	0.012013	VQIYSIEVRESK
5.1	1449.793976	0.000752	GLPGESGPRGLLGPK

Mascot: http://www.matrixscience.com/

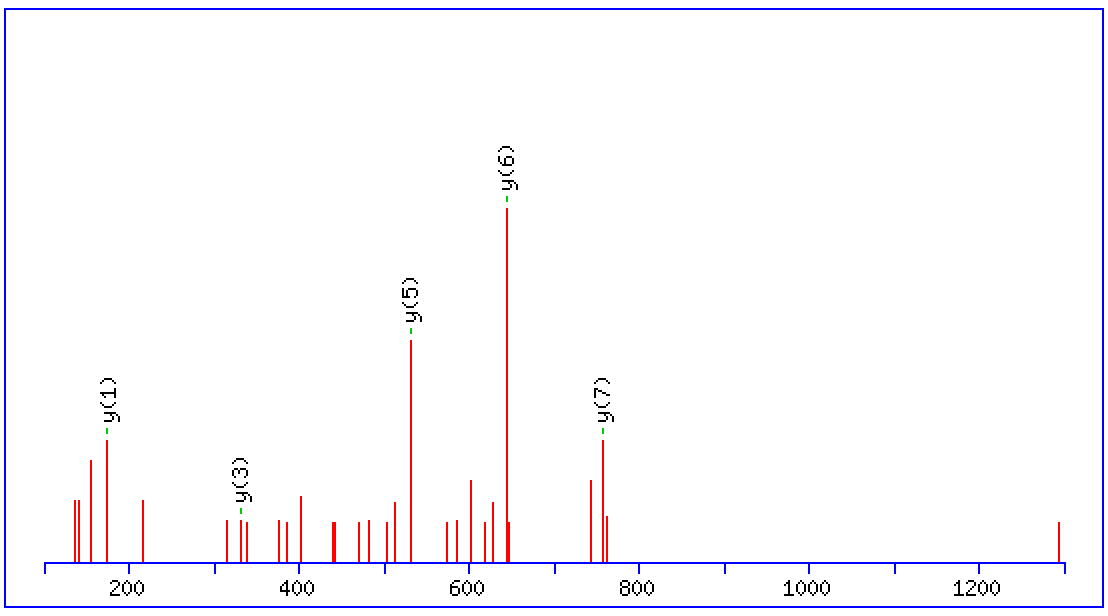
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ESLIPSVGR**
Found in **CE034_HUMAN**, Uncharacterized protein C5orf34 OS=Homo sapiens GN=C5orf34 PE=2 SV=2

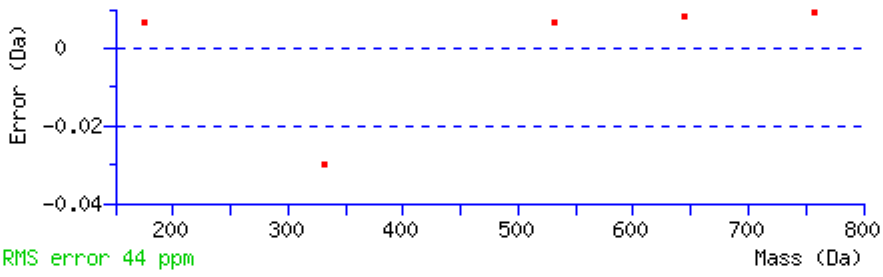
Match to Query 12226: 972.520828 from(487.267690,2+) rtinseconds(2345) index(29227)
Title: Locus:1.1.1.2315.7
Data file 2011-11-14 - TFD - EP 8-3.mgf

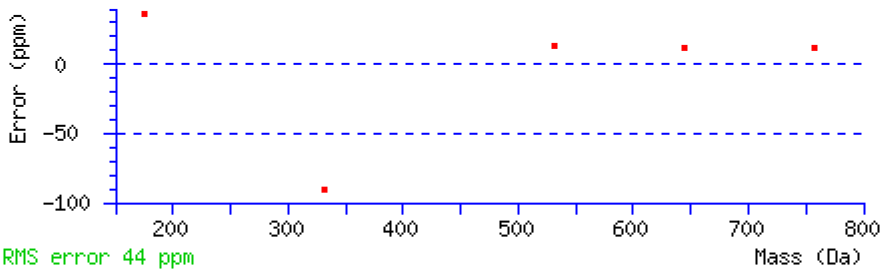
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1300] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 972.524002
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P5      : Oxidation (P)
Ions Score: 41  Expect: 0.0013
Matches : 5/74 fragment ions using 7 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572	112.039304	56.523290	**E**							9
2	217.081897	109.044586	199.071332	100.039304	**S**	844.488693	422.747985	827.462144	414.234710	826.478128	413.742702	8
3	330.165961	165.586618	312.155396	156.581336	**L**	***757.456665***	379.231971	740.430116	370.718696	739.446100	370.226688	7
4	443.250025	222.128650	425.239460	213.123368	**I**	***644.372601***	322.689939	627.346052	314.176664	626.362036	313.684656	6
5	556.297704	278.652490	538.287139	269.647208	**P**	***531.288537***	266.147907	514.261988	257.634632	513.277972	257.142624	5
6	643.329732	322.168504	625.319167	313.163222	**S**	418.240858	209.624067	401.214309	201.110793	400.230293	200.618785	4
7	742.398146	371.702711	724.387581	362.697429	**V**	***331.208830***	166.108053	314.182281	157.594779			3
8	799.419610	400.213443	781.409045	391.208161	**G**	232.140416	116.573846	215.113867	108.060572			2
9					**R**	***175.118952***	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of ESLIPSVGR
(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	972.523972	-0.003144	SEIIELNR
40.9	972.524002	-0.003174	ESLIPSVGR
14.3	972.523987	-0.003159	EIISEVQR
14.3	972.523972	-0.003144	IEISELNR
13.3	972.523987	-0.003159	ELSLVEQR
12.2	972.524002	-0.003174	DLTELVQR
10.3	972.517487	0.003341	VVPPSMRR
7.4	972.523987	-0.003159	LTLDINER
7.3	972.517487	0.003341	VVPPSMRR
5.8	972.524002	-0.003174	LVTEGALDR

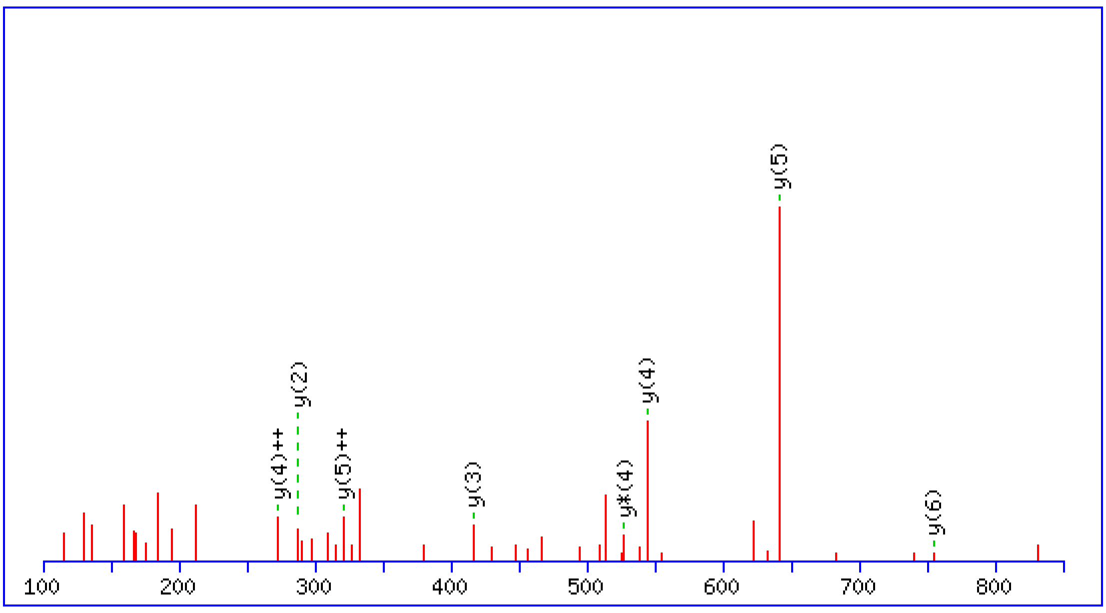
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VPPQKPR**
Found in **CG051_HUMAN**, Uncharacterized protein C7orf51 OS=Homo sapiens GN=C7orf51 PE=1 SV=1

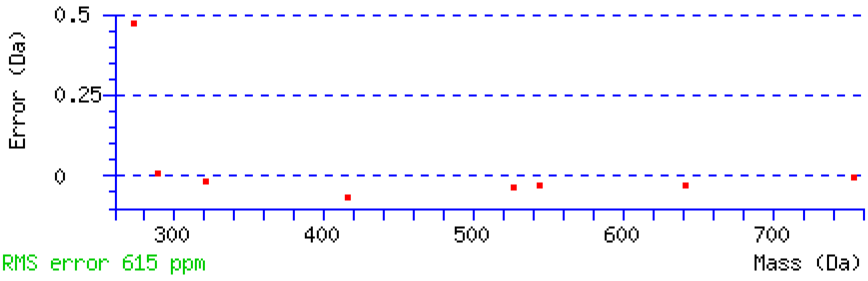
Match to Query 4833: 852.485668 from(427.250110,2+) rtinseconds(1882) index(17518)
Title: Locus:1.1.1.1984.6
Data file 2011-11-10 - TFD - EP 3-6.mgf

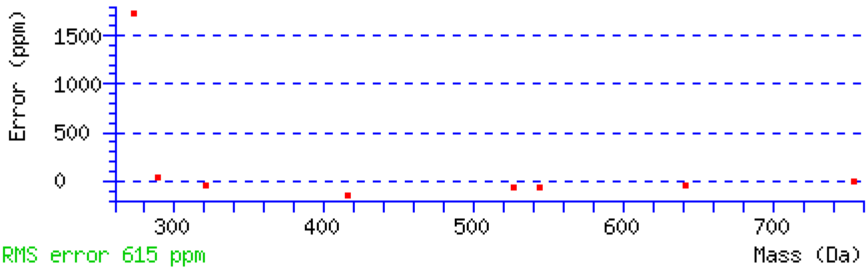
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 852.481750
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P2      : Oxidation (P)
P6      : Oxidation (P)
Ions Score: 32  Expect: 0.0029
Matches : 8/42 fragment ions using 15 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	100.075690	50.541483			V					7
2	213.123369	107.065322			P	*754.420615*	377.713946	737.394066	369.200671	6
3	310.176133	155.591704			P	*641.372936*	321.190106	624.346387	312.676832	5
4	438.234711	219.620994	421.208162	211.107719	Q	*544.320172*	272.663724	527.293623	264.150450	4
5	566.329674	283.668475	549.303125	275.155201	K	*416.261594*	208.634435	399.235045	200.121160	3
6	679.377353	340.192315	662.350804	331.679040	P	*288.166631*	144.586953	271.140082	136.073679	2
7					R	175.118952	88.063114	158.092403	79.549839	1





NCBI **BLAST** search of VPPQKPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.3	852.481750	0.003918	VPPQKPR
23.0	852.485764	-0.000096	VLPPNWK
15.5	852.481750	0.003918	VPPQKPR
12.4	852.481750	0.003918	LVPPAQGR
7.0	852.481750	0.003918	LVTDHLR
3.9	852.481750	0.003918	VIDTLHR

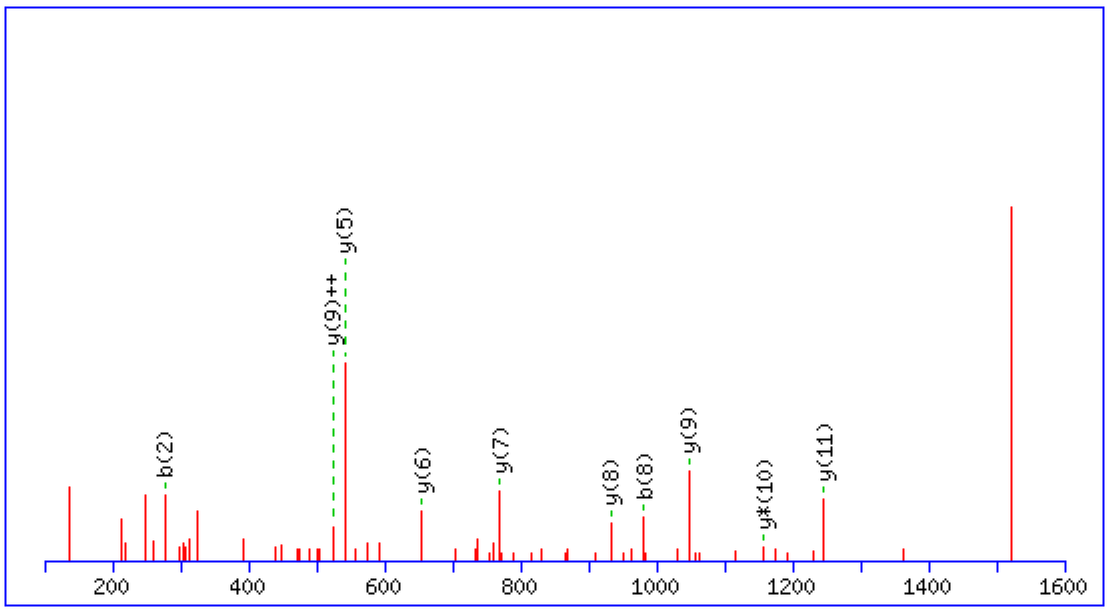
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YLAQNYDIPNLAK**
Found in **CG073_HUMAN**, Uncharacterized protein C7orf73 OS=Homo sapiens GN=C7orf73 PE=4 SV=1

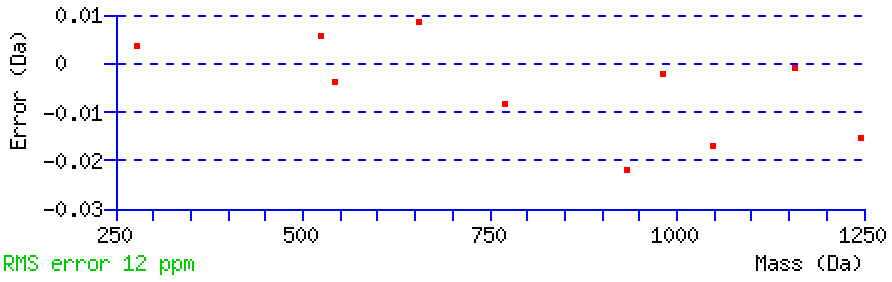
Match to Query 855823: 1521.778708 from(761.896630,2+) rtinseconds(2768) index(1005738)
Title: Locus:1.1.1.1548.44
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

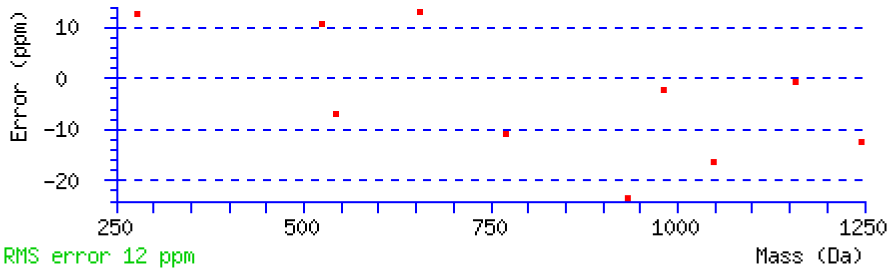
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1521.782700
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 42  Expect: 0.00071
Matches : 10/114 fragment ions using 13 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	164.070605	82.538940					Y							13
2	**277.154669**	139.080973					L	1359.726692	680.366984	1342.700143	671.853710	1341.716127	671.361701	12
3	348.191783	174.599530					A	***1246.642628***	623.824952	1229.616079	615.311678	1228.632063	614.819670	11
4	476.250361	238.628819	459.223812	230.115544			Q	1175.605514	588.306395	1158.578965	579.793121	1157.594949	579.301113	10
5	590.293288	295.650282	573.266739	287.137008			N	***1047.546936***	524.277106	1030.520387	515.763832	1029.536371	515.271823	9
6	753.356617	377.181947	736.330068	368.668672			Y	***933.504009***	467.255643	916.477460	458.742368	915.493444	458.250360	8
7	868.383560	434.695418	851.357011	426.182144	850.372995	425.690136	D	***770.440680***	385.723978	753.414131	377.210703	752.430115	376.718695	7
8	**981.467624**	491.237450	964.441075	482.724176	963.457059	482.232168	I	***655.413737***	328.210507	638.387188	319.697232			6
9	1078.520388	539.763832	1061.493839	531.250558	1060.509823	530.758550	P	***542.329673***	271.668475	525.303124	263.155200			5
10	1192.563315	596.785296	1175.536766	588.272021	1174.552750	587.780013	N	445.276909	223.142092	428.250360	214.628818			4
11	1305.647379	653.327328	1288.620830	644.814053	1287.636814	644.322045	L	331.233982	166.120629	314.207433	157.607354			3
12	1376.684493	688.845885	1359.657944	680.332610	1358.673928	679.840602	A	218.149918	109.578597	201.123369	101.065322			2
13							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of YLAQNYDIPNLAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.2	1521.782700	-0.003992	YLAQNYDIPNLAK

Mascot: http://www.matrixscience.com/

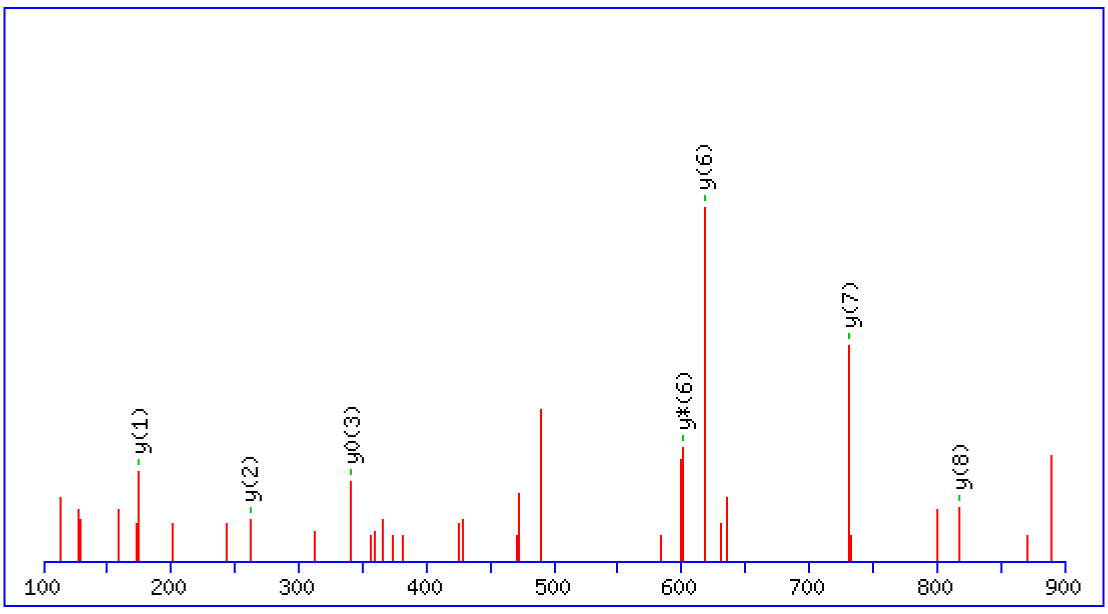
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ASLTGTPSR**
Found in **YM012_HUMAN**, Uncharacterized protein DKFZp434B061 OS=Homo sapiens PE=2 SV=2

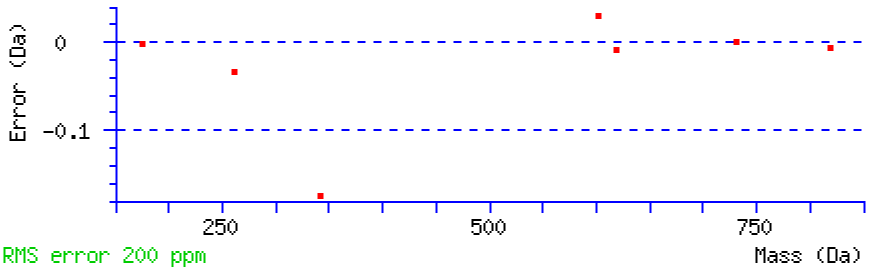
Match to Query 113964: 888.464048 from(445.239300,2+) rtinseconds(1452) index(501735)
Title: Locus:1.1.1.881.6
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

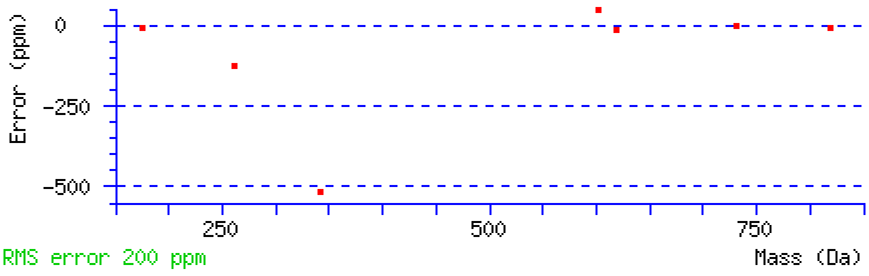
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 888.466492
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 46  Expect: 0.00064
Matches : 7/76 fragment ions using 8 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			A							9
2	159.076418	80.041847	141.065853	71.036564	S	***818.436658***	409.721967	801.410109	401.208693	800.426093	400.716685	8
3	272.160482	136.583879	254.149917	127.578597	L	***731.404630***	366.205953	714.378081	357.692679	713.394065	357.200671	7
4	373.208161	187.107719	355.197596	178.102436	T	***618.320566***	309.663921	601.294017	301.150647	600.310001	300.658639	6
5	430.229625	215.618450	412.219060	206.613168	G	517.272887	259.140082	500.246338	250.626807	499.262322	250.134799	5
6	531.277304	266.142290	513.266739	257.137008	T	460.251423	230.629349	443.224874	222.116075	442.240858	221.624067	4
7	628.330068	314.668672	610.319503	305.663390	P	359.203744	180.105510	342.177195	171.592235	341.193179	171.100227	3
8	715.362096	358.184686	697.351531	349.179404	S	***262.150980***	131.579128	245.124431	123.065853	244.140415	122.573845	2
9					R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of ASLTGTPSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.8	888.466492	-0.002444	ASLTGTPSR
41.8	888.466461	-0.002413	ASLENSLR
26.5	888.466476	-0.002428	ASLLQSDR
14.0	888.455246	0.008802	SALQVEDK
13.3	888.466492	-0.002444	APSTAVTAR
10.2	888.466476	-0.002428	ATSSAALPR
8.7	888.456589	0.007459	ASVDRWR
8.5	888.466461	-0.002413	SANELLSR
8.5	888.466492	-0.002444	SATPATVSR
7.8	888.466476	-0.002428	ATEVKGER

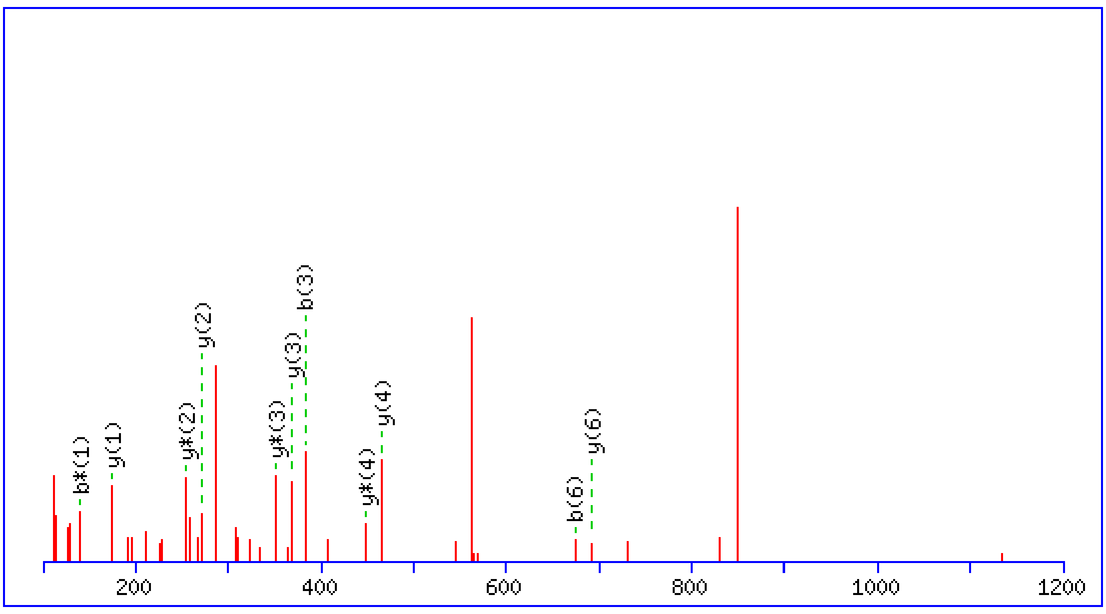
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **RPPPPPR**
Found in **K1522_HUMAN**, Uncharacterized protein KIAA1522 OS=Homo sapiens GN=KIAA1522 PE=1 SV=2

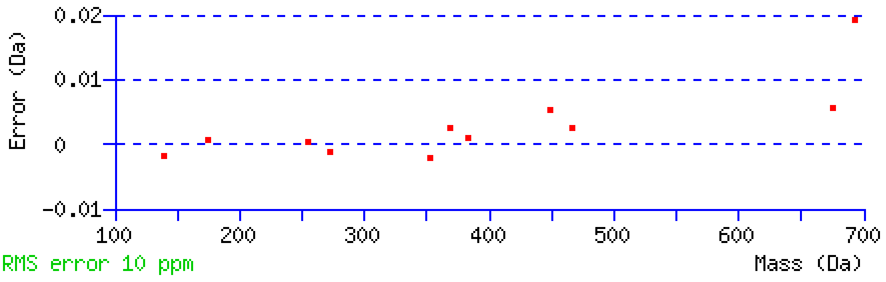
Match to Query 4106: 847.469248 from(424.741900,2+) rtinseconds(743) index(347)
Title: Locus:1.1.1.1626.6
Data file 2011-11-10 - TFD - EP 3-4.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●

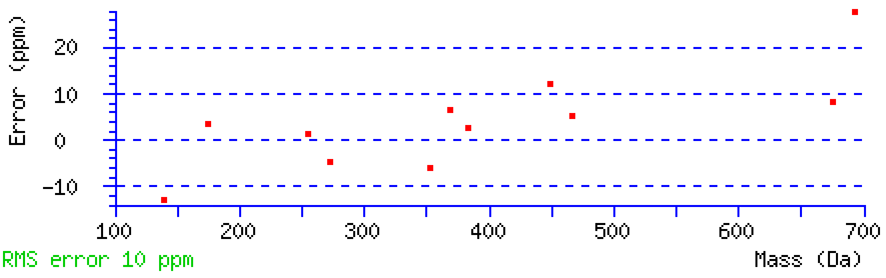


```
Monoisotopic mass of neutral peptide Mr(calc): 847.466431
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P2       : Oxidation (P)
P3       : Oxidation (P)
Ions Score: 36  Expect: 0.0021
Matches : 11/48 fragment ions using 18 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	157.108387	79.057831	140.081838	70.544557	R					7
2	270.156066	135.581671	253.129517	127.068397	P	*692.372602*	346.689939	675.346053	338.176665	6
3	**383.203745**	192.105510	366.177196	183.592236	P	579.324923	290.166100	562.298374	281.652825	5
4	480.256509	240.631892	463.229960	232.118618	P	*466.277244*	233.642260	449.250695	225.128986	4
5	577.309273	289.158275	560.282724	280.645000	P	*369.224480*	185.115878	352.197931	176.602603	3
6	**674.362037**	337.684657	657.335488	329.171382	P	*272.171716*	136.589496	255.145167	128.076221	2
7					R	*175.118952*	88.063114	158.092403	79.549839	1



RMS error 10 ppm



RMS error 10 ppm

NCBI **BLAST** search of RPPPPPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.5	847.466431	0.002817	RPPPPPR
16.0	847.466415	0.002833	REFIQR
14.3	847.466415	0.002833	RELQFR
13.3	847.466431	0.002817	RPPPPPR
13.3	847.466431	0.002817	RPPPPPR
10.5	847.466415	0.002833	ERIGAFR
9.3	847.466400	0.002848	ERKPYR
6.5	847.477646	-0.008398	RTYRPR
6.0	847.466431	0.002817	KVGNFQR
4.8	847.466415	0.002833	RFEIQR

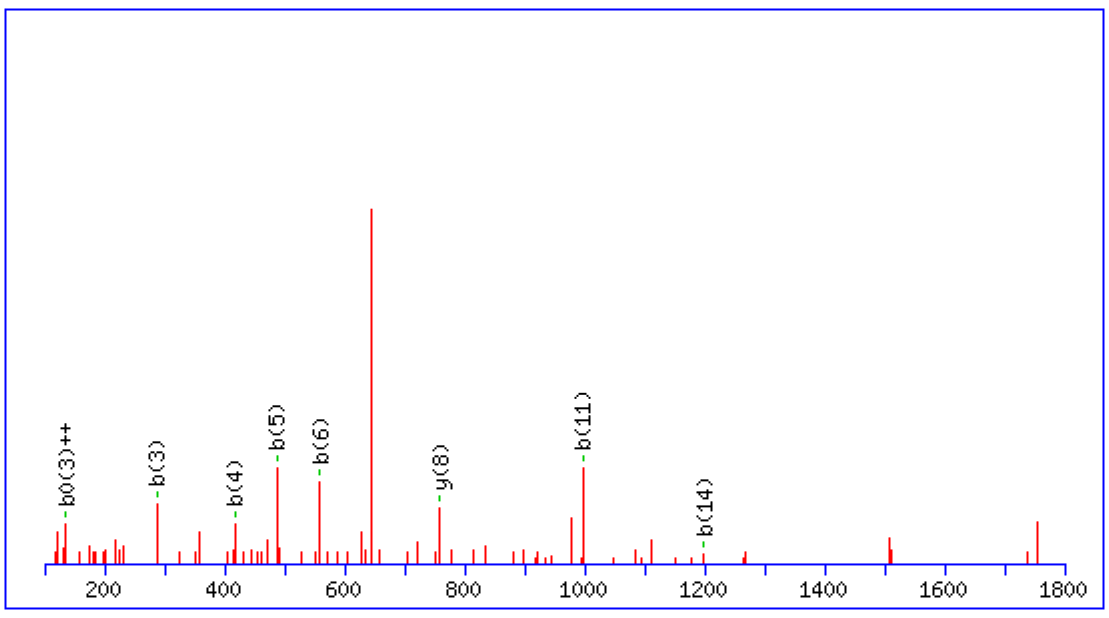
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EGTEAAAAKPAGGSPQGPK**
Found in **K1614_HUMAN**, Uncharacterized protein KIAA1614 OS=Homo sapiens GN=KIAA1614 PE=2 SV=3

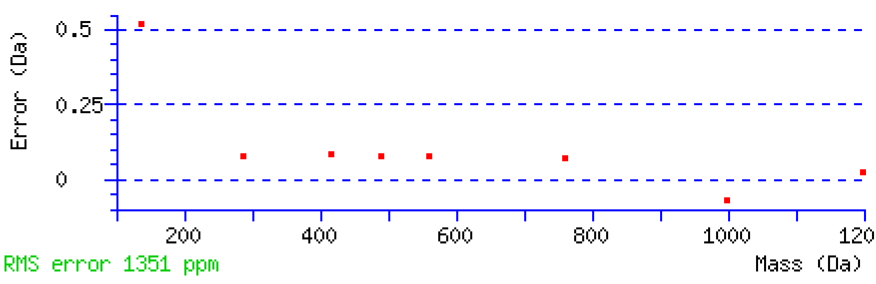
Match to Query 41971: 1754.844162 from(585.955330,3+) rtinseconds(2554) index(26107)
Title: Locus:1.1.1.2302.26
Data file 2011-11-12 - TFD - EP 5-7.mgf

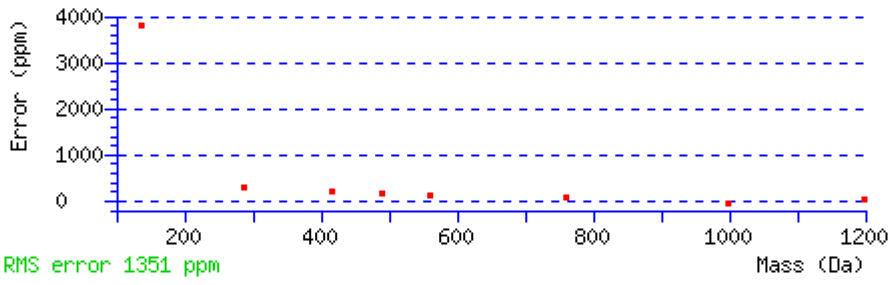
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1754.843491
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P15     : Oxidation (P)
P18     : Oxidation (P)
Ions Score: 31  Expect: 0.0082
Matches : 8/190 fragment ions using 14 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	E							19
2	187.071333	94.039305			169.060768	85.034022	G	1626.808193	813.907735	1609.781644	805.394460	1608.797628	804.902452	18
3	***288.119012***	144.563144			270.108447	135.557862	T	1569.786729	785.397002	1552.760180	776.883728	1551.776164	776.391720	17
4	***417.161605***	209.084441			399.151040	200.079158	E	1468.739050	734.873163	1451.712501	726.359889	1450.728485	725.867880	16
5	***488.198719***	244.602998			470.188154	235.597715	A	1339.696457	670.351867	1322.669908	661.838592	1321.685892	661.346584	15
6	***559.235833***	280.121555			541.225268	271.116272	A	1268.659343	634.833310	1251.632794	626.320035	1250.648778	625.828027	14
7	630.272947	315.640112			612.262382	306.634829	A	1197.622229	599.314752	1180.595680	590.801478	1179.611664	590.309470	13
8	701.310061	351.158669			683.299496	342.153386	A	1126.585115	563.796196	1109.558566	555.282921	1108.574550	554.790913	12
9	829.405024	415.206150	812.378475	406.692876	811.394459	406.200868	K	1055.548001	528.277638	1038.521452	519.764364	1037.537436	519.272356	11
10	926.457788	463.732532	909.431239	455.219258	908.447223	454.727250	P	927.453038	464.230157	910.426489	455.716883	909.442473	455.224875	10
11	***997.494902***	499.251089	980.468353	490.737815	979.484337	490.245807	A	830.400274	415.703775	813.373725	407.190500	812.389709	406.698492	9
12	1054.516366	527.761821	1037.489817	519.248547	1036.505801	518.756539	G	759.363160	380.185218	742.336611	371.671944	741.352595	371.179936	8
13	1111.537830	556.272553	1094.511281	547.759279	1093.527265	547.267271	G	702.341696	351.674486	685.315147	343.161211	684.331131	342.669203	7
14	***1198.569858***	599.788567	1181.543309	591.275293	1180.559293	590.783285	S	645.320232	323.163754	628.293683	314.650480	627.309667	314.158472	6
15	1311.617537	656.312407	1294.590988	647.799132	1293.606972	647.307124	P	558.288204	279.647740	541.261655	271.134465			5
16	1439.676115	720.341696	1422.649566	711.828421	1421.665550	711.336413	Q	445.240525	223.123900	428.213976	214.610626			4
17	1496.697579	748.852427	1479.671030	740.339153	1478.687014	739.847145	G	317.181947	159.094611	300.155398	150.581337			3
18	1609.745258	805.376267	1592.718709	796.862993	1591.734693	796.370984	P	260.160483	130.583879	243.133934	122.070605			2
19							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of EGTEAAAAKPAGGSPQGPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.3	1754.843491	0.000671	EGTEAAAAKPAGGSPQGPK
12.7	1754.843491	0.000671	EGTEAAAAKPAGGSPQGPK
12.7	1754.843491	0.000671	EGTEAAAAKPAGGSPQGPK
9.7	1754.850906	-0.006744	ALSGGGSVASPPPSPAMPK
9.7	1754.850906	-0.006744	ALSGGGSVASPPPSPAMPK
9.7	1754.850906	-0.006744	ALSGGGSVASPPPSPAMPK
9.7	1754.850906	-0.006744	ALSGGGSVASPPPSPAMPK
9.7	1754.850906	-0.006744	ALSGGGSVASPPPSPAMPK
9.7	1754.850906	-0.006744	ALSGGGSVASPPPSPAMPK
2.0	1754.847488	-0.003326	SDEEYRELFDLALR

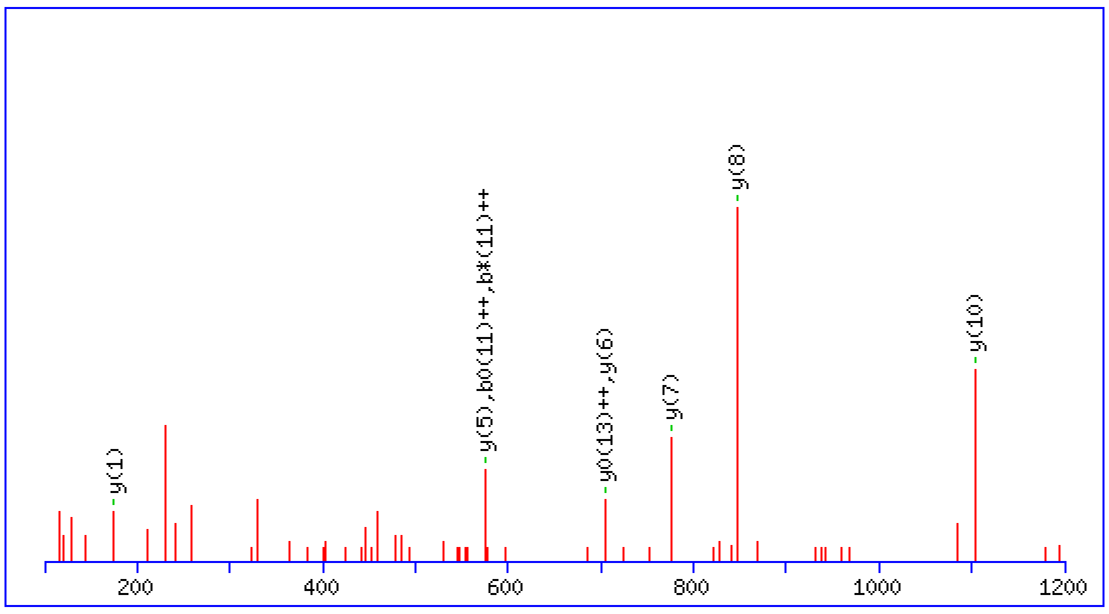
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LDPEPEKAAESPSPR**
Found in **K1671_HUMAN**, Uncharacterized protein KIAA1671 OS=Homo sapiens GN=KIAA1671 PE=1 SV=2

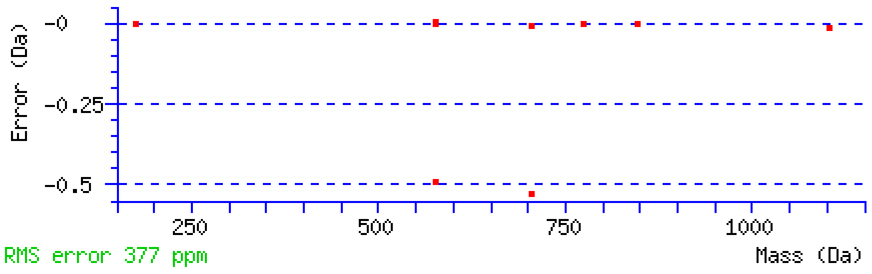
Match to Query 397543: 1653.779442 from(552.267090,3+) rtinseconds(1322) index(417171)
Title: Locus:1.1.1.841.29
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

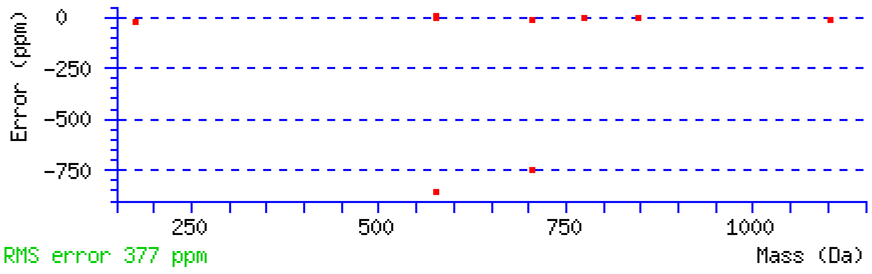
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1653.784561
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
P12     : Oxidation (P)
P14     : Oxidation (P)
Ions Score: 37  Expect: 0.0079
Matches : 9/150 fragment ions using 11 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					L							15
2	229.118283	115.062779			211.107718	106.057497	D	1541.707807	771.357542	1524.681258	762.844267	1523.697242	762.352259	14
3	326.171047	163.589161			308.160482	154.583879	P	1426.680864	713.844070	1409.654315	705.330796	1408.670299	704.838788	13
4	455.213640	228.110458			437.203075	219.105176	E	1329.628100	665.317688	1312.601551	656.804414	1311.617535	656.312406	12
5	552.266404	276.636840			534.255839	267.631558	P	1200.585507	600.796392	1183.558958	592.283117	1182.574942	591.791109	11
6	681.308997	341.158137			663.298432	332.152854	E	*1103.532743*	552.270010	1086.506194	543.756735	1085.522178	543.264727	10
7	809.403960	405.205618	792.377411	396.692344	791.393395	396.200336	K	974.490150	487.748713	957.463601	479.235439	956.479585	478.743431	9
8	880.441074	440.724175	863.414525	432.210901	862.430509	431.718893	A	*846.395187*	423.701232	829.368638	415.187957	828.384622	414.695949	8
9	951.478188	476.242732	934.451639	467.729458	933.467623	467.237450	A	*775.358073*	388.182675	758.331524	379.669400	757.347508	379.177392	7
10	1080.520781	540.764028	1063.494232	532.250754	1062.510216	531.758746	E	*704.320959*	352.664118	687.294410	344.150843	686.310394	343.658835	6
11	1167.552809	584.280043	1150.526260	575.766768	1149.542244	575.274760	S	*575.278366*	288.142821	558.251817	279.629547	557.267801	279.137539	5
12	1280.600488	640.803882	1263.573939	632.290608	1262.589923	631.798600	P	488.246338	244.626807	471.219789	236.113533	470.235773	235.621525	4
13	1367.632516	684.319896	1350.605967	675.806622	1349.621951	675.314614	S	375.198659	188.102968	358.172110	179.589693	357.188094	179.097685	3
14	1480.680195	740.843736	1463.653646	732.330461	1462.669630	731.838453	P	288.166631	144.586953	271.140082	136.073679			2
15							R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LDPEPEKAAESPSPR
(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	1653.784561	-0.005119	LDPEPEKAAESPSPR
2.0	1653.784592	-0.005150	SDEIPATEPPQLPGR
0.2	1653.778046	0.001396	PNATPAPAQPESTAMR

Mascot: http://www.matrixscience.com/

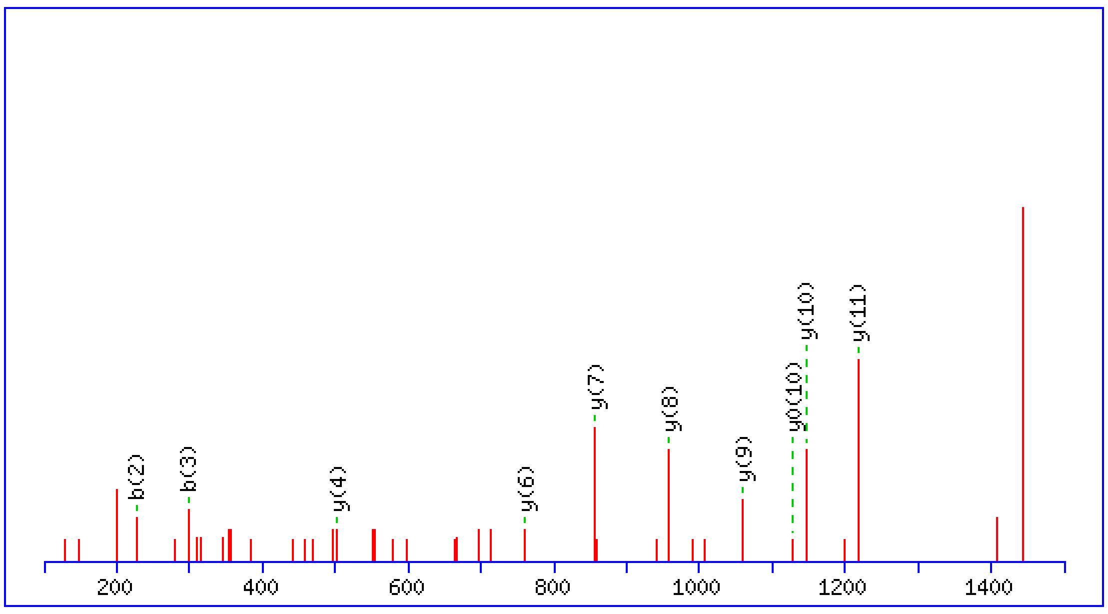
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLASTTPEEILEK**
Found in **CO040_HUMAN**, UPF0235 protein C15orf40 OS=Homo sapiens GN=C15orf40 PE=1 SV=1

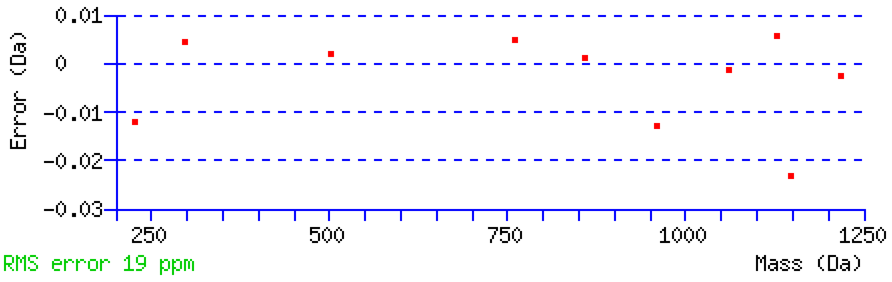
Match to Query 37908: 1442.781208 from(722.397880,2+) rtinseconds(2763) index(27832)
Title: Locus:1.1.1.2510.28
Data file 2011-11-10 - TFD - EP 4-7.mgf

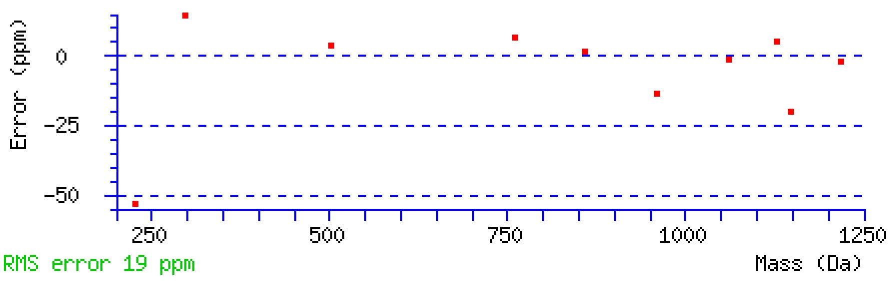
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1442.786789
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 43   Expect: 0.0002
Matches : 10/112 fragment ions using 22 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							13
2	**227.175404**	114.091340			L	1330.710039	665.858658	1313.683490	657.345383	1312.699474	656.853375	12
3	**298.212518**	149.609897			A	***1217.625975***	609.316625	1200.599426	600.803351	1199.615410	600.311343	11
4	385.244546	193.125911	367.233981	184.120628	S	***1146.588861***	573.798069	1129.562312	565.284794	1128.578296	564.792786	10
5	486.292225	243.649750	468.281660	234.644468	T	***1059.556833***	530.282054	1042.530284	521.768780	1041.546268	521.276772	9
6	587.339904	294.173590	569.329339	285.168308	T	***958.509154***	479.758215	941.482605	471.244940	940.498589	470.752932	8
7	684.392668	342.699972	666.382103	333.694690	P	***857.461475***	429.234376	840.434926	420.721101	839.450910	420.229093	7
8	813.435261	407.221269	795.424696	398.215986	E	***760.408711***	380.707993	743.382162	372.194719	742.398146	371.702711	6
9	942.477854	471.742565	924.467289	462.737283	E	631.366118	316.186697	614.339569	307.673422	613.355553	307.181414	5
10	1055.561918	528.284597	1037.551353	519.279315	I	***502.323525***	251.665400	485.296976	243.152126	484.312960	242.660118	4
11	1168.645982	584.826629	1150.635417	575.821347	L	389.239461	195.123368	372.212912	186.610094	371.228896	186.118086	3
12	1297.688575	649.347925	1279.678010	640.342643	E	276.155397	138.581336	259.128848	130.068062	258.144832	129.576054	2
13					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of LLASTTPEEILEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
43.3	1442.786789	-0.005581	LLASTTPEEILEK
3.8	1442.788132	-0.006924	LPEDLKNFRPAK

Mascot: http://www.matrixscience.com/

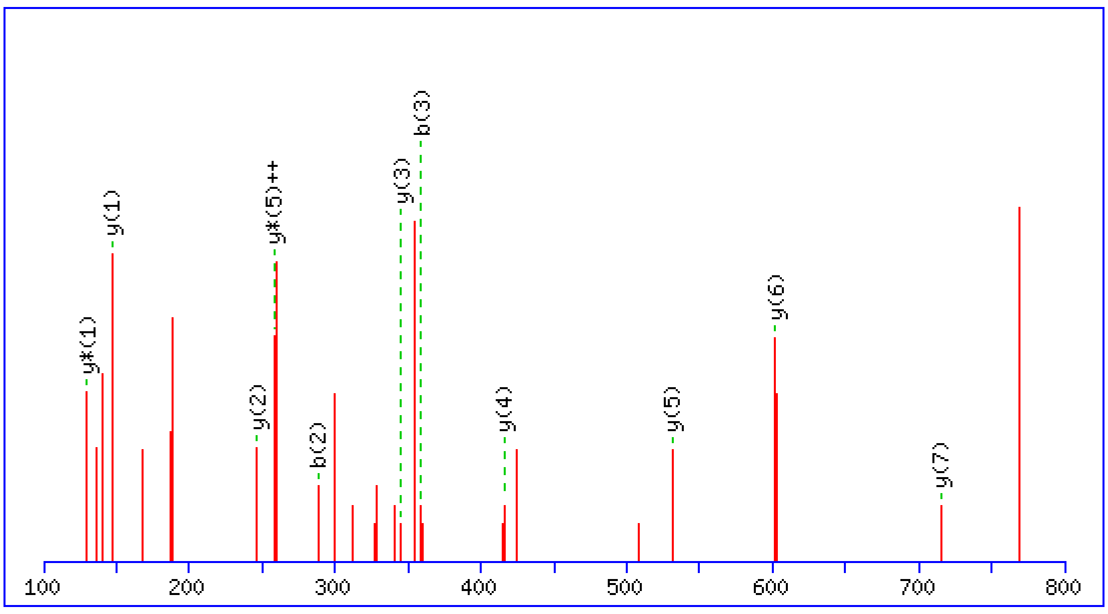
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **CLADAVVK**
Found in **CA151_HUMAN**, UPF0327 protein C1orf151 OS=Homo sapiens GN=C1orf151 PE=1 SV=1

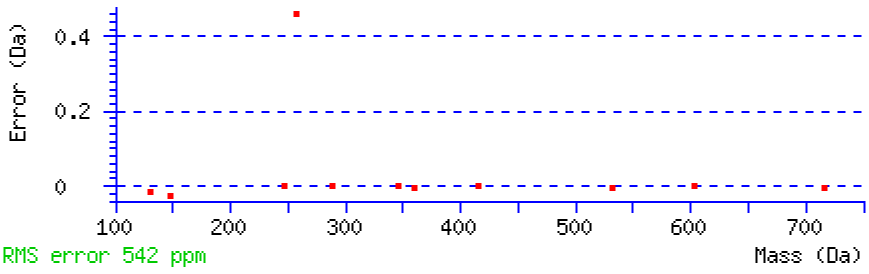
Match to Query 5270: 888.473828 from(445.244190,2+) rtinseconds(1616) index(5039)
Title: Locus:1.1.1.2250.7
Data file 2011-11-12 - TFD - EP 5-8.mgf

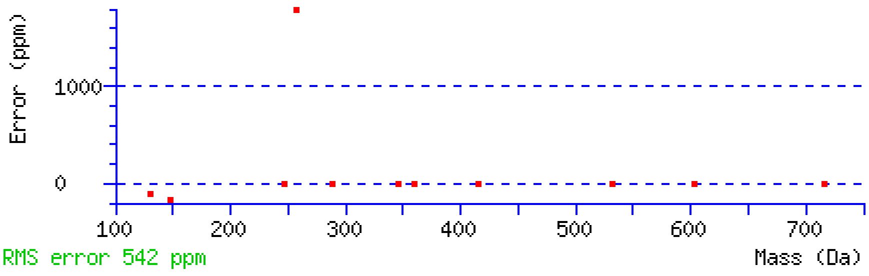
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 888.473877
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 44  Expect: 0.0008
Matches : 11/56 fragment ions using 24 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	175.053575	88.030425			C							8
2	**288.137639**	144.572457			L	***715.434867***	358.221072	698.408318	349.707797	697.424302	349.215789	7
3	**359.174753**	180.091014			A	***602.350803***	301.679040	585.324254	293.165765	584.340238	292.673757	6
4	474.201696	237.604486	456.191131	228.599203	D	***531.313689***	266.160483	514.287140	257.647208	513.303124	257.155200	5
5	545.238810	273.123043	527.228245	264.117761	A	***416.286746***	208.647011	399.260197	200.133736			4
6	644.307224	322.657250	626.296659	313.651968	V	***345.249632***	173.128454	328.223083	164.615179			3
7	743.375638	372.191457	725.365073	363.186174	V	***246.181218***	123.594247	229.154669	115.080972			2
8					K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of CLADAVVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
43.7	888.473877	-0.000049	CLADAVVK
17.6	888.466461	0.007367	EQSEKLR
13.7	888.473877	-0.000049	CSPTGLIK
12.0	888.466476	0.007352	DAASGSLLR
11.1	888.481720	-0.007892	ESARWIK
10.3	888.466476	0.007352	SEAASGVLR
10.1	888.473877	-0.000049	CGLGLDLK
10.1	888.473892	-0.000064	CSVVLGPK
9.6	888.473862	-0.000034	CIINLDK
9.5	888.466476	0.007352	ATSSAALPR

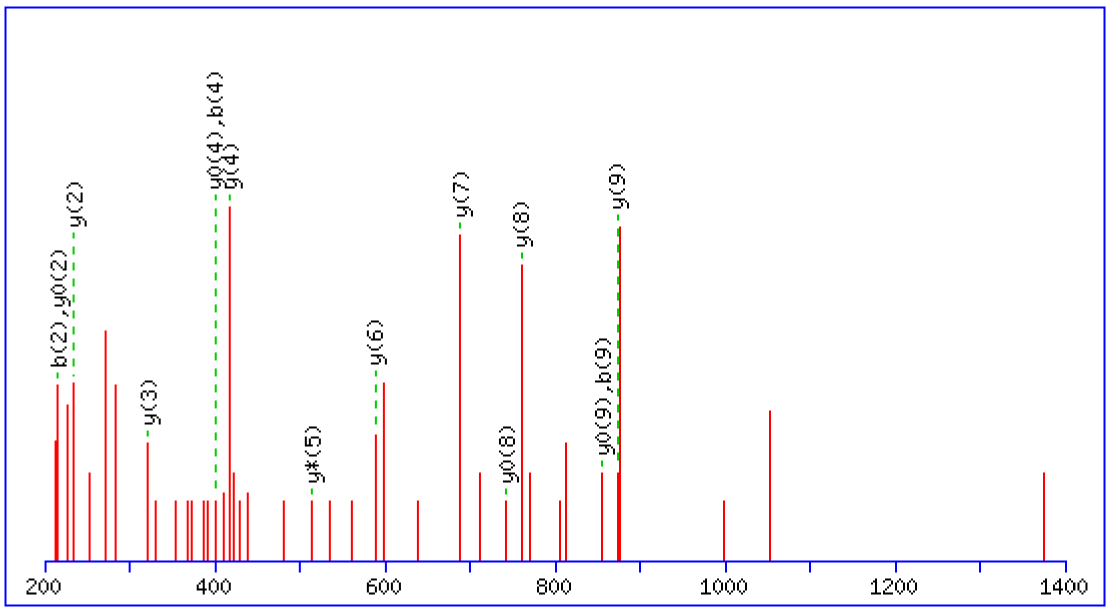
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TNLATGIPSSK**
Found in **CT030_HUMAN**, UPF0414 transmembrane protein C20orf30 OS=Homo sapiens GN=C20orf30 PE=1 SV=1

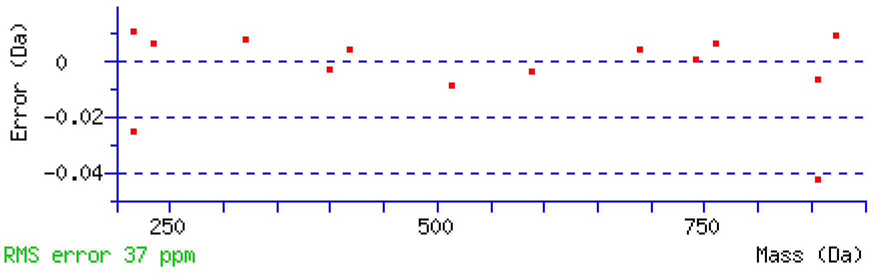
Match to Query 25374: 1087.577308 from(544.795930,2+) rtinseconds(1599) index(13420)
Title: Locus:1.1.1.1827.28
Data file 2011-11-12 - TFD - EP 5-6.mgf

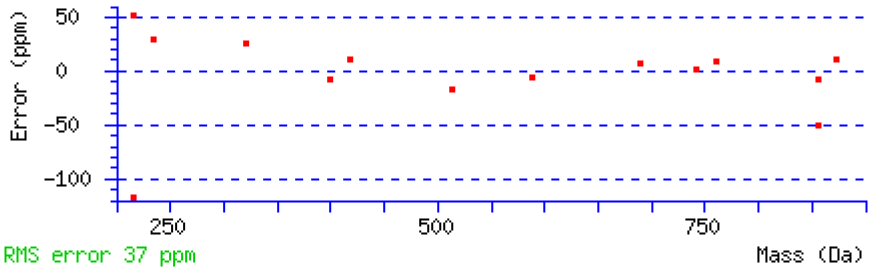
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1087.587326
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.00042
Matches : 15/116 fragment ions using 28 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							11
2	**216.097882**	108.552579	199.071333	100.039305	198.087317	99.547296	N	987.546936	494.277106	970.520387	485.763832	969.536371	485.271824	10
3	329.181946	165.094611	312.155397	156.581336	311.171381	156.089328	L	***873.504009***	437.255643	856.477460	428.742368	855.493444	428.250360	9
4	**400.219060**	200.613168	383.192511	192.099893	382.208495	191.607885	A	***760.419945***	380.713611	743.393396	372.200336	742.409380	371.708328	8
5	501.266739	251.137007	484.240190	242.623733	483.256174	242.131725	T	***689.382831***	345.195054	672.356282	336.681779	671.372266	336.189771	7
6	558.288203	279.647740	541.261654	271.134465	540.277638	270.642457	G	***588.335152***	294.671214	571.308603	286.157940	570.324587	285.665932	6
7	671.372267	336.189772	654.345718	327.676497	653.361702	327.184489	I	531.313688	266.160482	514.287139	257.647208	513.303123	257.155200	5
8	768.425031	384.716154	751.398482	376.202879	750.414466	375.710871	P	***418.229624***	209.618450	401.203075	201.105176	400.219059	200.613168	4
9	**855.457059**	428.232168	838.430510	419.718893	837.446494	419.226885	S	***321.176860***	161.092068	304.150311	152.578794	303.166295	152.086786	3
10	942.489087	471.748182	925.462538	463.234907	924.478522	462.742899	S	***234.144832***	117.576054	217.118283	109.062780	216.134267	108.570772	2
11							K	147.112804	74.060040	130.086255	65.546766			1





NCBI **BLAST** search of TNLATGIPSSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.1	1087.587326	-0.010018	TNLATGIPSSK
3.1	1087.569595	0.007713	LVVVGDGACGK

Mascot: http://www.matrixscience.com/

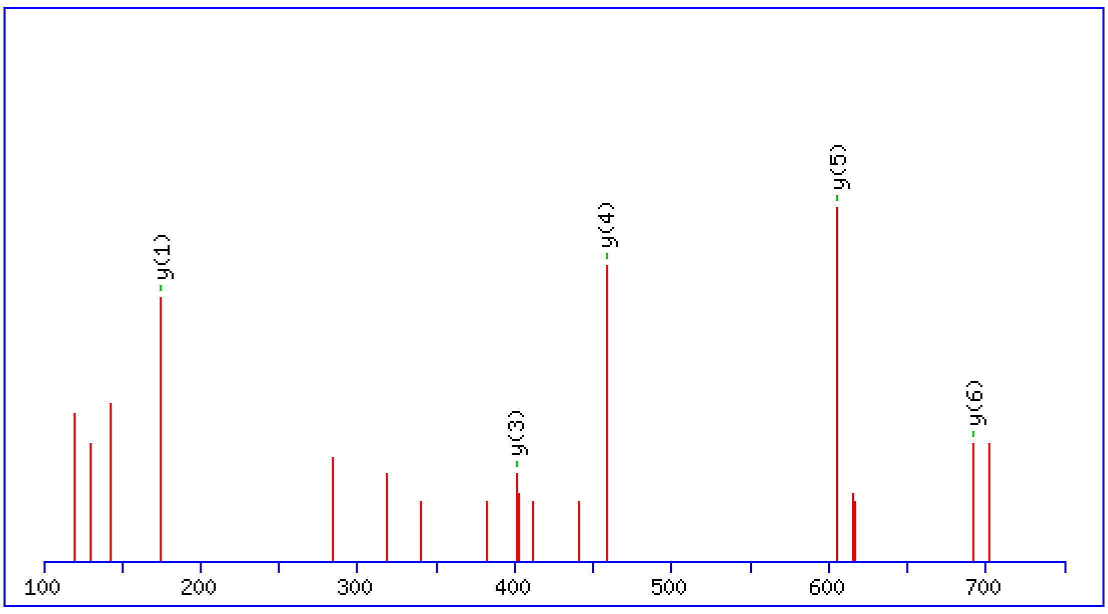
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MSFGLLR**
Found in **CV032_HUMAN**, UPF0466 protein C22orf32, mitochondrial OS=Homo sapiens GN=C22orf32 PE=2 SV=1

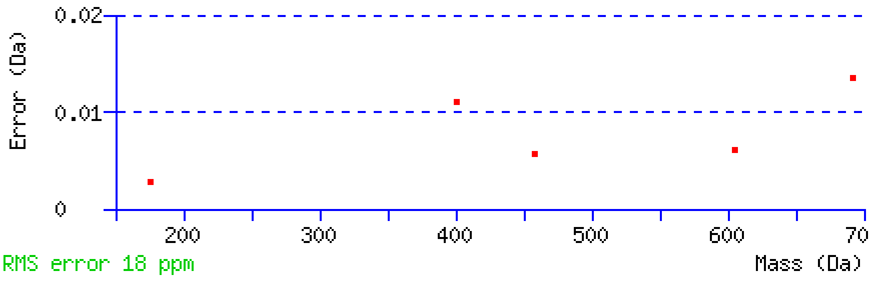
Match to Query 2698: 838.444008 from(420.229280,2+) rtinseconds(2392) index(13562)
Title: Locus:1.1.1.2426.5
Data file 2011-11-12 - TFD - EP 6-8.mgf

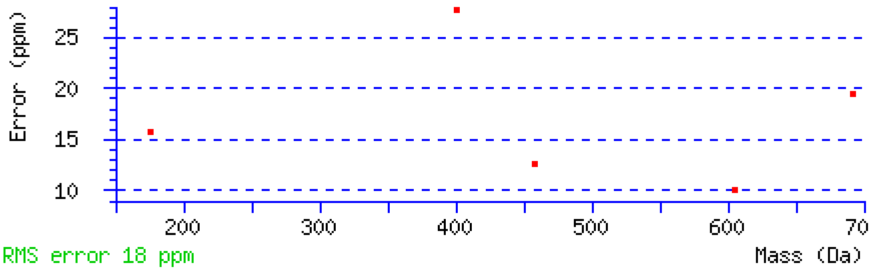
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 838.437103
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M1      : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 47  Expect: 5.4e-005
Matches : 5/70 fragment ions using 6 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.042676	74.524976			M							7
2	235.074704	118.040990	217.064139	109.035707	S	***692.408986***	346.708131	675.382437	338.194857	674.398421	337.702849	6
3	382.143118	191.575197	364.132553	182.569914	F	***605.376958***	303.192117	588.350409	294.678843			5
4	439.164582	220.085929	421.154017	211.080646	G	***458.308544***	229.657910	441.281995	221.144636			4
5	552.248646	276.627961	534.238081	267.622679	L	***401.287080***	201.147178	384.260531	192.633904			3
6	665.332710	333.169993	647.322145	324.164711	L	288.203016	144.605146	271.176467	136.091872			2
7					R	***175.118952***	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of MSFGLLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.4	838.437103	0.006905	MSFGLLR
1.8	838.440933	0.003075	PHSQKSR
1.4	838.440933	0.003075	QPRPADR
0.8	838.437103	0.006905	MLPPPPR
0.8	838.437103	0.006905	MLPPPPR
0.8	838.437103	0.006905	MLPPPPR
0.6	838.437103	0.006905	MLGFLSR

Mascot: http://www.matrixscience.com/

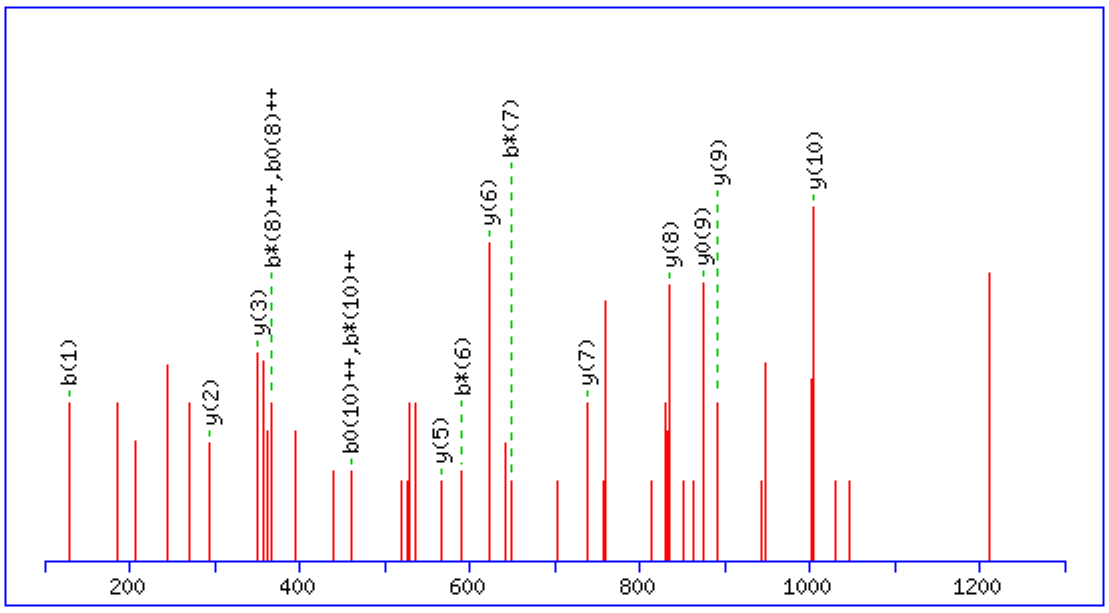
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QPLGPDGSQGFK**
Found in **CA144_HUMAN**, UPF0485 protein C1orf144 OS=Homo sapiens GN=C1orf144 PE=1 SV=1

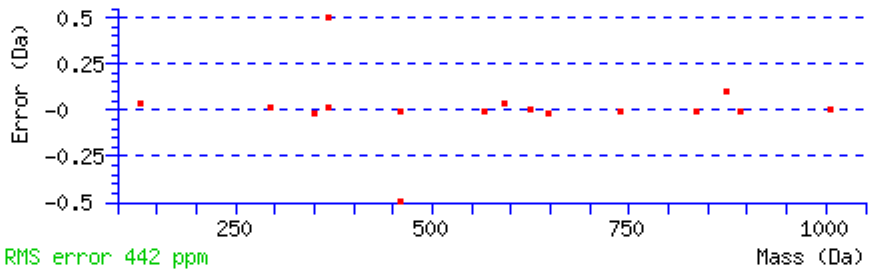
Match to Query 37035: 1229.603508 from(615.809030,2+) rtinseconds(1716) index(15523)
Title: Locus:1.1.1.1908.41
Data file 2011-11-10 - TFD - EP 4-6.mgf

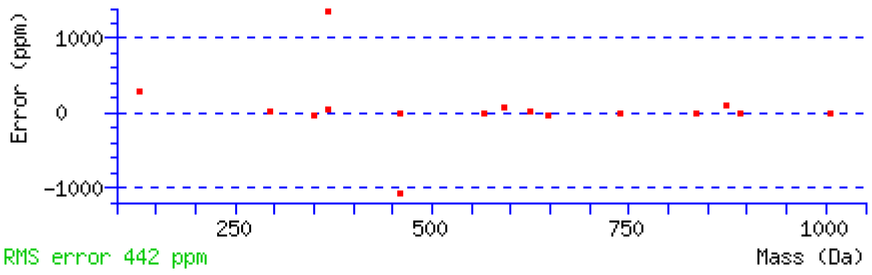
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1229.604065
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.0097
Matches : 16/114 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	129.065854	65.036565	112.039305	56.523291			**Q**							12
2	226.118618	113.562947	209.092069	105.049673			**P**	1102.552751	551.780014	1085.526202	543.266739	1084.542186	542.774731	11
3	339.202682	170.104979	322.176133	161.591704			**L**	***1005.499987***	503.253632	988.473438	494.740357	987.489422	494.248349	10
4	396.224146	198.615711	379.197597	190.102436			**G**	***892.415923***	446.711600	875.389374	438.198325	874.405358	437.706317	9
5	493.276910	247.142093	476.250361	238.628818			**P**	***835.394459***	418.200868	818.367910	409.687593	817.383894	409.195585	8
6	608.303853	304.655565	591.277304	296.142290	590.293288	295.650282	**D**	***738.341695***	369.674486	721.315146	361.161211	720.331130	360.669203	7
7	665.325317	333.166297	648.298768	324.653022	647.314752	324.161014	**G**	***623.314752***	312.161014	606.288203	303.647740	605.304187	303.155732	6
8	752.357345	376.682311	735.330796	368.169036	734.346780	367.677028	**S**	***566.293288***	283.650282	549.266739	275.137008	548.282723	274.645000	5
9	880.415923	440.711600	863.389374	432.198325	862.405358	431.706317	**Q**	479.261260	240.134268	462.234711	231.620994			4
10	937.437387	469.222332	920.410838	460.709057	919.426822	460.217049	**G**	***351.202682***	176.104979	334.176133	167.591704			3
11	1084.505801	542.756539	1067.479252	534.243264	1066.495236	533.751256	**F**	***294.181218***	147.594247	277.154669	139.080972			2
12							**K**	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of QPLGPDGSQGFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.5	1229.604065	-0.000557	QPLGPDGSQGFK

Mascot: http://www.matrixscience.com/

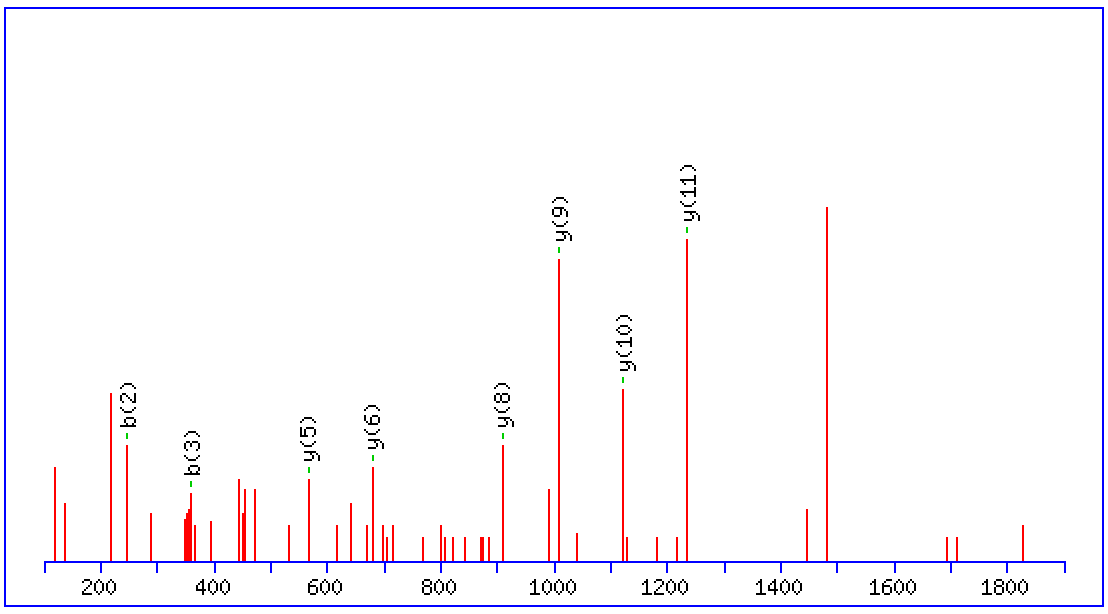
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FVLITDILDTFGK**
Found in **CP062_HUMAN**, UPF0505 protein C16orf62 OS=Homo sapiens GN=C16orf62 PE=1 SV=2

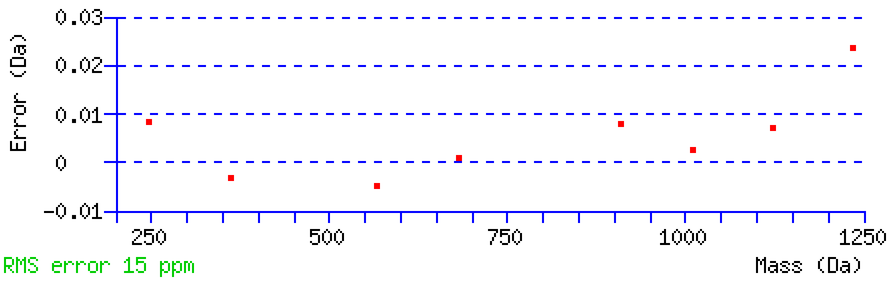
Match to Query 46156: 1480.822228 from(741.418390,2+) rtinseconds(4821) index(70355)
Title: Locus:1.1.1.3205.10
Data file 2011-11-12 - TFD - EP 6-2.mgf

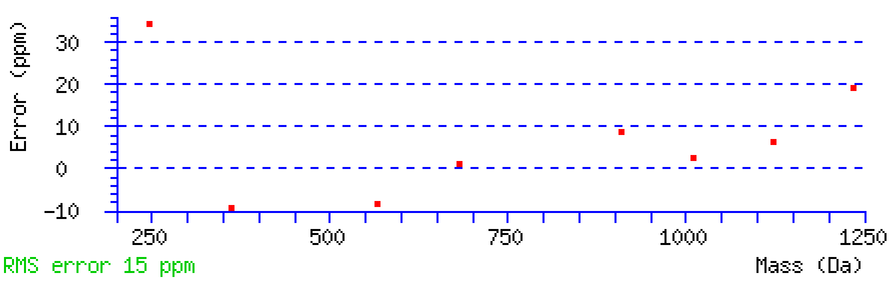
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1480.817749
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 42  Expect: 0.00021
Matches : 8/106 fragment ions using 13 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.075690	74.541483			F							13
2	**247.144104**	124.075690			V	1334.756596	667.881936	1317.730047	659.368662	1316.746031	658.876653	12
3	**360.228168**	180.617722			L	***1235.688182***	618.347729	1218.661633	609.834455	1217.677617	609.342447	11
4	473.312232	237.159754			I	***1122.604118***	561.805697	1105.577569	553.292423	1104.593553	552.800414	10
5	574.359911	287.683594	556.349346	278.678311	T	***1009.520054***	505.263665	992.493505	496.750391	991.509489	496.258383	9
6	689.386854	345.197065	671.376289	336.191782	D	***908.472375***	454.739826	891.445826	446.226551	890.461810	445.734543	8
7	802.470918	401.739097	784.460353	392.733814	I	793.445432	397.226354	776.418883	388.713080	775.434867	388.221072	7
8	915.554982	458.281129	897.544417	449.275847	L	***680.361368***	340.684322	663.334819	332.171048	662.350803	331.679040	6
9	1030.581925	515.794601	1012.571360	506.789318	D	***567.277304***	284.142290	550.250755	275.629016	549.266739	275.137008	5
10	1131.629604	566.318440	1113.619039	557.313157	T	452.250361	226.628818	435.223812	218.115544	434.239796	217.623536	4
11	1278.698018	639.852647	1260.687453	630.847365	F	351.202682	176.104979	334.176133	167.591704			3
12	1335.719482	668.363379	1317.708917	659.358096	G	204.134268	102.570772	187.107719	94.057497			2
13					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of FVLITDILDTFGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.1	1480.817749	0.004479	FVLITDILDTFGK
2.9	1480.819077	0.003151	FVIFDLHRPPPK
2.9	1480.819077	0.003151	FVIFDLHRPPPK
2.9	1480.819077	0.003151	FVIFDLHRPPPK

Mascot: http://www.matrixscience.com/

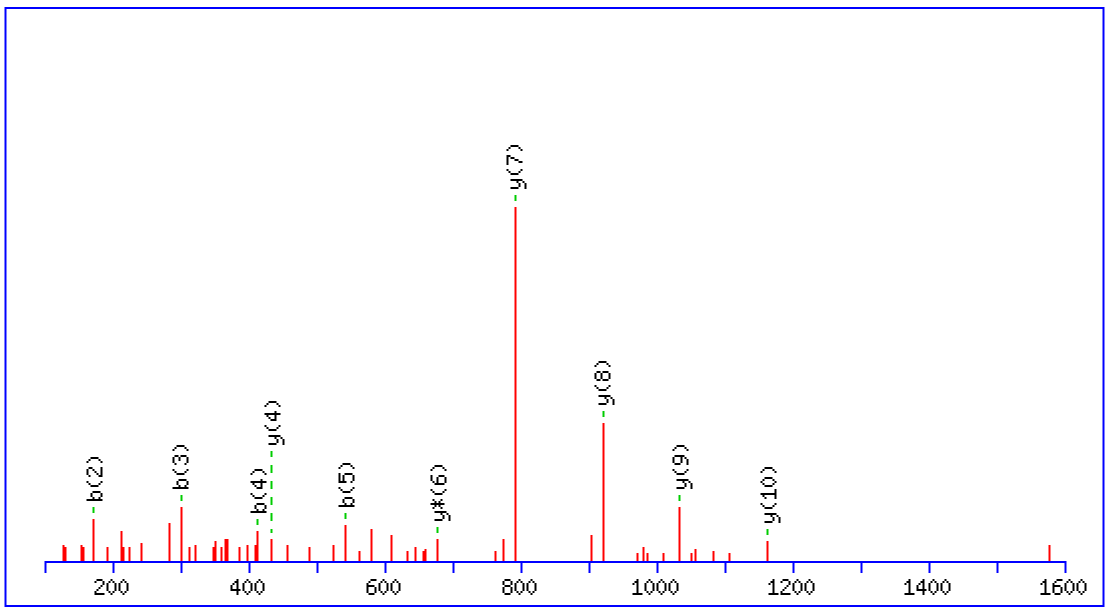
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GNEIEPNFSATR**
Found in **CO038_HUMAN**, UPF0552 protein C15orf38 OS=Homo sapiens GN=C15orf38 PE=1 SV=1

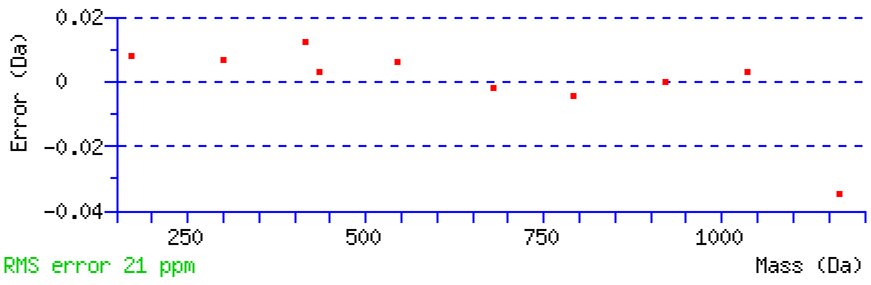
Match to Query 36331: 1333.626588 from(667.820570,2+) rtinseconds(1984) index(18155)
Title: Locus:1.1.1.2341.40
Data file 2011-11-12 - TFD - EP 5-5.mgf

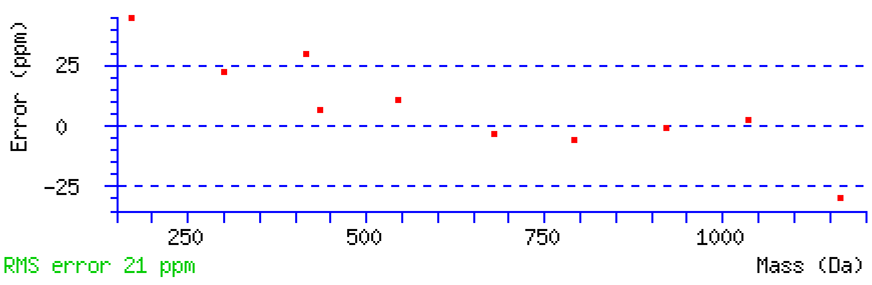
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1333.626221
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 43 **Expect:** 0.00058
Matches : 10/124 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							12
2	**172.071667**	86.539471	155.045118	78.026197			N	1277.612055	639.309666	1260.585506	630.796391	1259.601490	630.304383	11
3	**301.114260**	151.060768	284.087711	142.547494	283.103695	142.055486	E	***1163.569128***	582.288202	1146.542579	573.774927	1145.558563	573.282919	10
4	**414.198324**	207.602800	397.171775	199.089526	396.187759	198.597518	I	***1034.526535***	517.766906	1017.499986	509.253631	1016.515970	508.761623	9
5	**543.240917**	272.124097	526.214368	263.610822	525.230352	263.118814	E	***921.442471***	461.224874	904.415922	452.711599	903.431906	452.219591	8
6	640.293681	320.650479	623.267132	312.137204	622.283116	311.645196	P	***792.399878***	396.703577	775.373329	388.190302	774.389313	387.698294	7
7	754.336608	377.671942	737.310059	369.158668	736.326043	368.666660	N	695.347114	348.177195	678.320565	339.663920	677.336549	339.171912	6
8	901.405022	451.206149	884.378473	442.692875	883.394457	442.200867	F	581.304187	291.155732	564.277638	282.642457	563.293622	282.150449	5
9	988.437050	494.722163	971.410501	486.208889	970.426485	485.716881	S	***434.235773***	217.621524	417.209224	209.108250	416.225208	208.616242	4
10	1059.474164	530.240720	1042.447615	521.727446	1041.463599	521.235437	A	347.203745	174.105510	330.177196	165.592236	329.193180	165.100228	3
11	1160.521843	580.764560	1143.495294	572.251285	1142.511278	571.759277	T	276.166631	138.586953	259.140082	130.073679	258.156066	129.581671	2
12							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of GNEIEPNFSATR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.5	1333.626221	0.000367	GNEIEPNFSATR
11.2	1333.626282	0.000306	GPSGPQGPGGPPGPK
4.8	1333.629593	-0.003005	INSVEQNDMLR
3.8	1333.618393	0.008195	GVCVPNGLSLSSD
2.7	1333.626282	0.000306	GPSGPQGPGGPPGPK

Mascot: http://www.matrixscience.com/

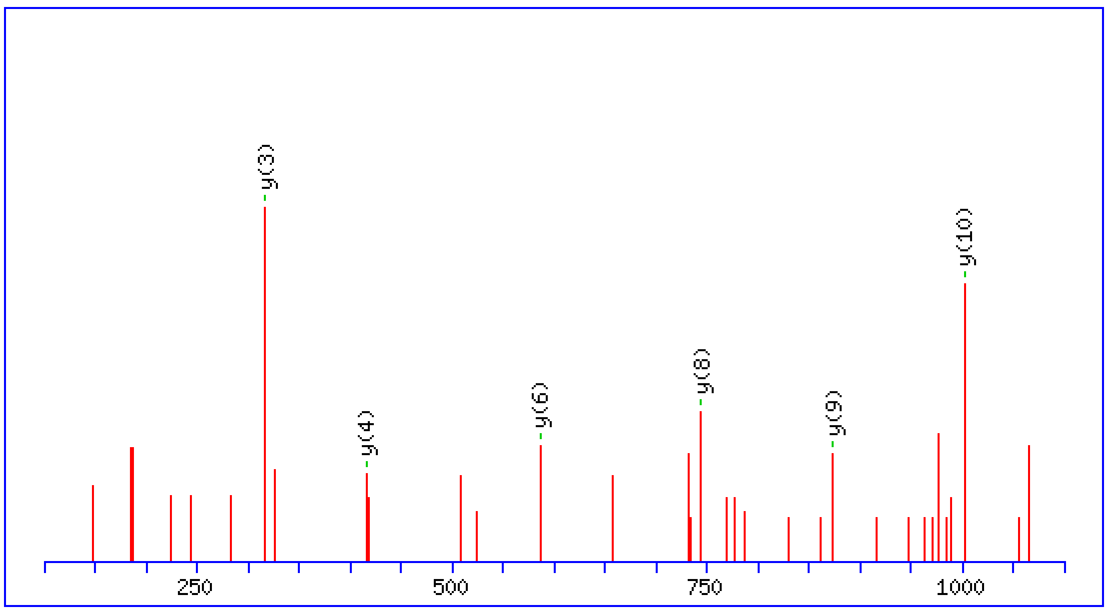
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SVEESAGLVGLK**
Found in **CG055_HUMAN**, UPF0562 protein C7orf55 OS=Homo sapiens GN=C7orf55 PE=1 SV=2

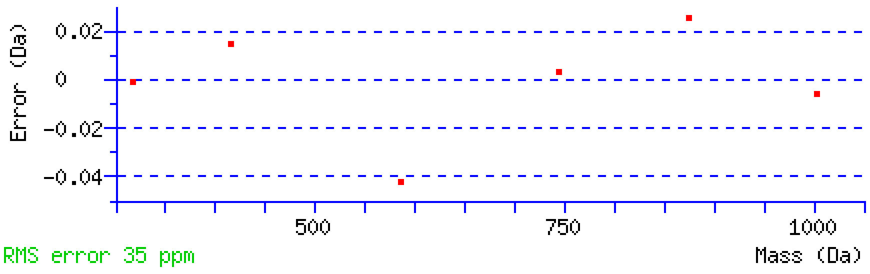
Match to Query 25951: 1187.630188 from(594.822370,2+) rtinseconds(2248) index(20953)
Title: Locus:1.1.1.2184.20
Data file 2011-11-12 - TFD - EP 5-7.mgf

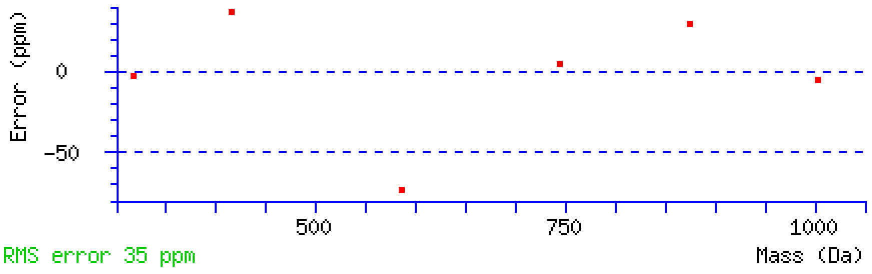
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1100] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1187.639755
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 42  Expect: 0.00095
Matches : 6/96 fragment ions using 10 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	S							12
2	187.107718	94.057497	169.097153	85.052214	V	1101.615016	551.311146	1084.588467	542.797872	1083.604451	542.305863	11
3	316.150311	158.578793	298.139746	149.573511	E	***1002.546602***	501.776939	985.520053	493.263665	984.536037	492.771657	10
4	445.192904	223.100090	427.182339	214.094808	E	***873.504009***	437.255643	856.477460	428.742368	855.493444	428.250360	9
5	532.224932	266.616104	514.214367	257.610822	S	***744.461416***	372.734346	727.434867	364.221072	726.450851	363.729064	8
6	603.262046	302.134661	585.251481	293.129379	A	657.429388	329.218332	640.402839	320.705058			7
7	660.283510	330.645393	642.272945	321.640111	G	***586.392274***	293.699775	569.365725	285.186501			6
8	773.367574	387.187425	755.357009	378.182143	L	529.370810	265.189043	512.344261	256.675769			5
9	872.435988	436.721632	854.425423	427.716350	V	***416.286746***	208.647011	399.260197	200.133736			4
10	929.457452	465.232364	911.446887	456.227082	G	***317.218332***	159.112804	300.191783	150.599529			3
11	1042.541516	521.774396	1024.530951	512.769114	L	260.196868	130.602072	243.170319	122.088797			2
12					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of SVEESAGLVGLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.5	1187.639755	-0.009567	SVEESAGLVGLK
8.7	1187.618622	0.011566	WLEEVSQVAK
6.3	1187.626694	0.003494	IVRCICPSR
3.8	1187.629852	0.000336	DPNFEALVRK
0.3	1187.629868	0.000320	QIGKQEGGPFK

Mascot: http://www.matrixscience.com/

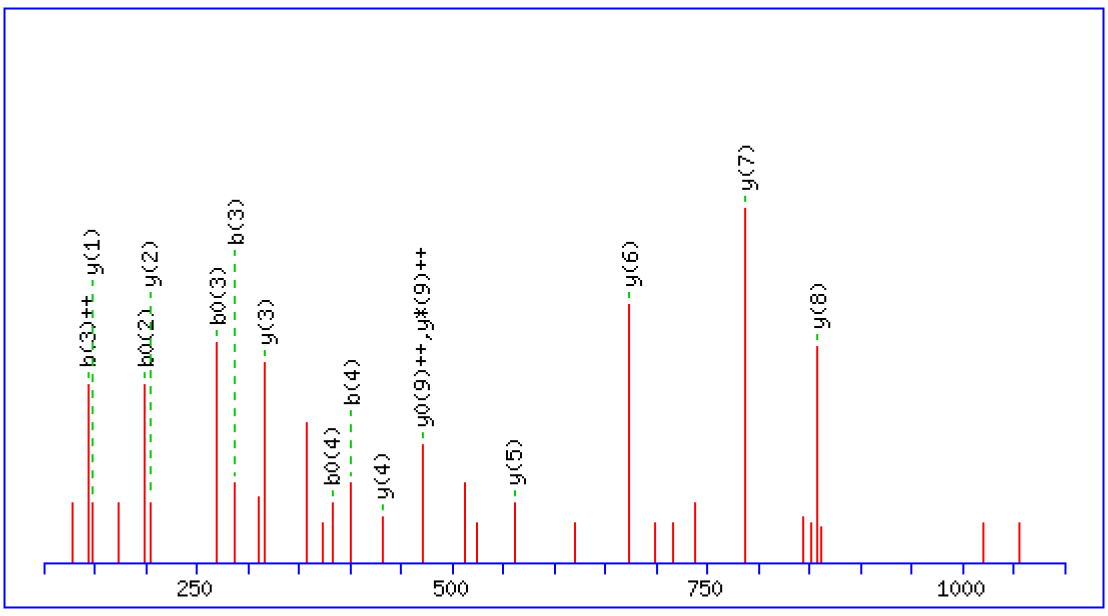
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DTALLEDLGK**
Found in **CP013_HUMAN**, UPF0585 protein C16orf13 OS=Homo sapiens GN=C16orf13 PE=1 SV=2

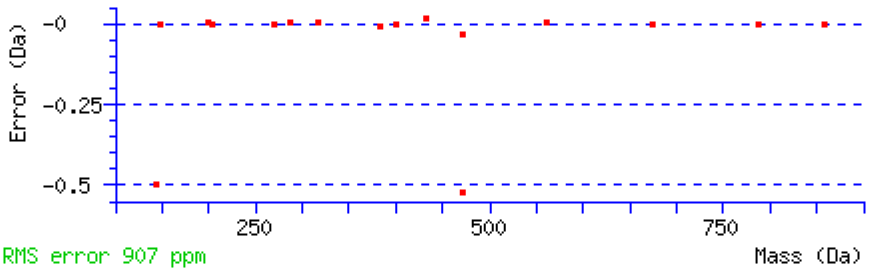
Match to Query 21659: 1073.557528 from(537.786040,2+) rtinseconds(2762) index(35446)
Title: Locus:1.1.1.2366.15
Data file 2011-11-10 - TFD - EP 4-5.mgf

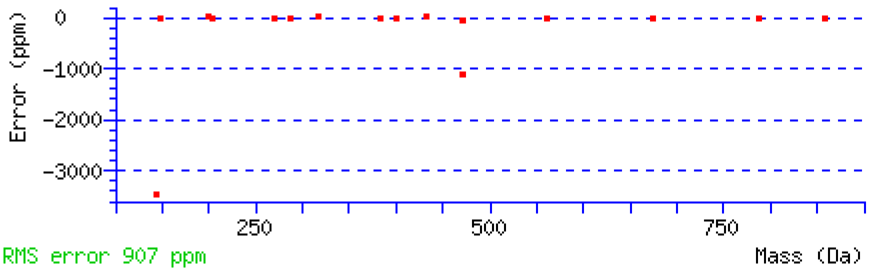
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1073.560440
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 57 **Expect:** 4.6e-005
Matches : 16/84 fragment ions using 29 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.034219	58.520748	98.023654	49.515465	D							10
2	217.081898	109.044587	199.071333	100.039304	T	959.540789	480.274033	942.514240	471.760758	941.530224	471.268750	9
3	**288.119012**	144.563144	270.108447	135.557862	A	***858.493110***	429.750193	841.466561	421.236919	840.482545	420.744911	8
4	**401.203076**	201.105176	383.192511	192.099894	L	***787.455996***	394.231636	770.429447	385.718362	769.445431	385.226354	7
5	514.287140	257.647208	496.276575	248.641926	L	***674.371932***	337.689604	657.345383	329.176330	656.361367	328.684322	6
6	643.329733	322.168505	625.319168	313.163222	E	***561.287868***	281.147572	544.261319	272.634298	543.277303	272.142290	5
7	758.356676	379.681976	740.346111	370.676694	D	***432.245275***	216.626276	415.218726	208.113001	414.234710	207.620993	4
8	871.440740	436.224008	853.430175	427.218726	L	***317.218332***	159.112804	300.191783	150.599530			3
9	928.462204	464.734740	910.451639	455.729458	G	***204.134268***	102.570772	187.107719	94.057498			2
10					K	***147.112804***	74.060040	130.086255	65.546766			1





NCBI **BLAST** search of DTALLEDLGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.7	1073.560440	-0.002912	DTALLEDLGK
17.7	1073.550537	0.006991	EGTLWEALR
11.2	1073.565125	-0.007597	SLGANMAAALR
9.2	1073.563126	-0.005598	RWGHHLPR
6.7	1073.550552	0.006976	VNEWKTPGK
1.9	1073.550552	0.006976	EFVNPSLPR
1.6	1073.560440	-0.002912	TDAETLPALK
0.4	1073.550552	0.006976	DTLASLPWR
0.3	1073.565140	-0.007612	RECLTPIR
0.3	1073.565125	-0.007597	SNLMNNILR

Mascot: http://www.matrixscience.com/

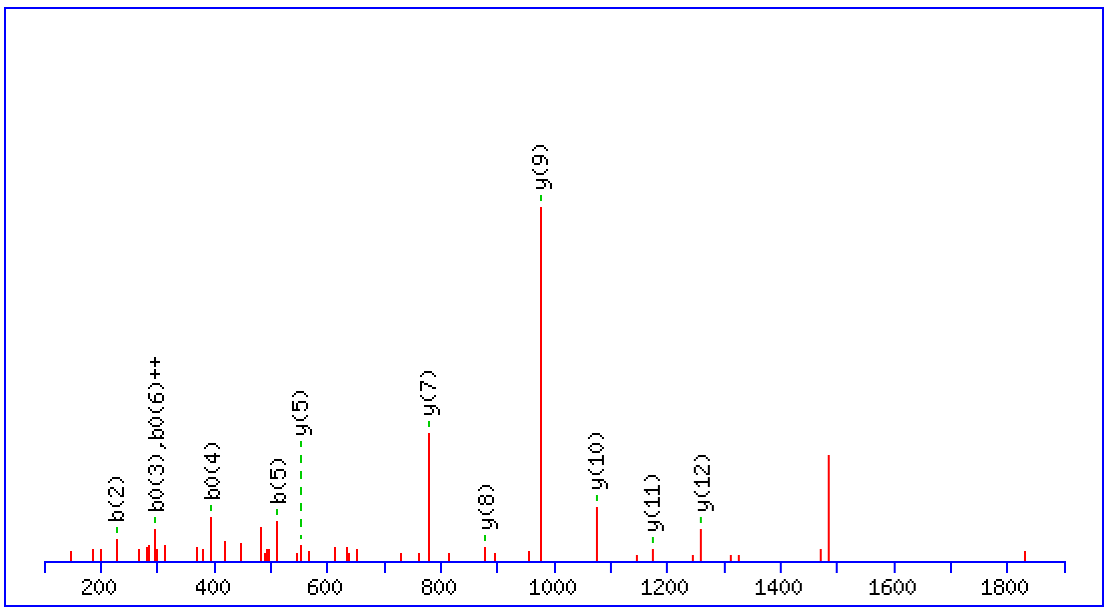
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLSVVPVPEGYSVK**
Found in **CT027_HUMAN**, UPF0687 protein C20orf27 OS=Homo sapiens GN=C20orf27 PE=1 SV=3

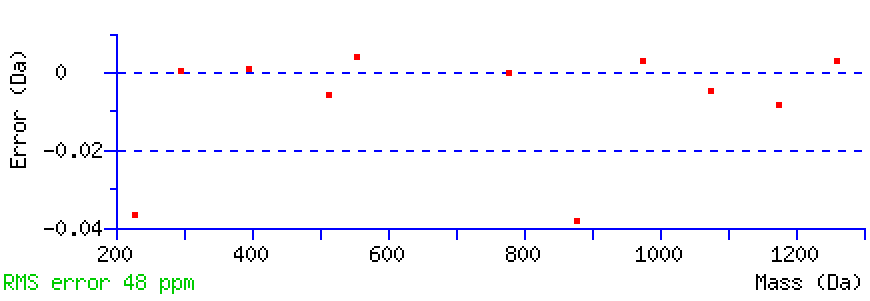
Match to Query 44654: 1485.846168 from(743.930360,2+) rtinseconds(2956) index(38942)
Title: Locus:1.1.1.2277.42
Data file 2011-11-12 - TFD - EP 6-6.mgf

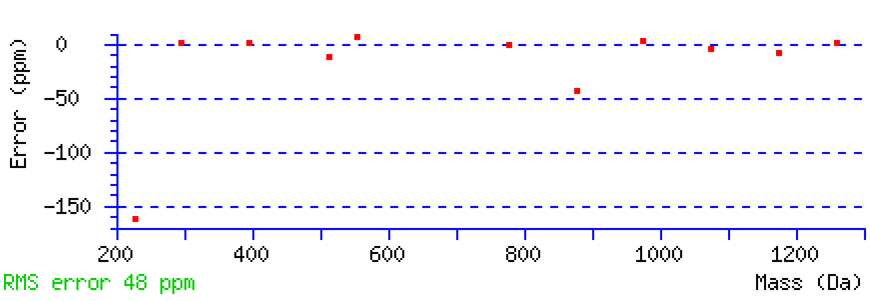
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1485.844284
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 66  Expect: 1.1e-006
Matches : 12/122 fragment ions using 13 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							14
2	**227.175404**	114.091340			L	1373.767494	687.387385	1356.740945	678.874111	1355.756929	678.382103	13
3	314.207432	157.607354	296.196867	148.602071	S	***1260.683430***	630.845353	1243.656881	622.332079	1242.672865	621.840071	12
4	413.275846	207.141561	395.265281	198.136279	V	***1173.651402***	587.329339	1156.624853	578.816065	1155.640837	578.324057	11
5	**512.344260**	256.675768	494.333695	247.670486	V	***1074.582988***	537.795132	1057.556439	529.281858	1056.572423	528.789850	10
6	609.397024	305.202150	591.386459	296.196868	P	***975.514574***	488.260925	958.488025	479.747651	957.504009	479.255643	9
7	708.465438	354.736357	690.454873	345.731075	V	***878.461810***	439.734543	861.435261	431.221269	860.451245	430.729261	8
8	805.518202	403.262739	787.507637	394.257457	P	***779.393396***	390.200336	762.366847	381.687062	761.382831	381.195054	7
9	934.560795	467.784036	916.550230	458.778753	E	682.340632	341.673954	665.314083	333.160680	664.330067	332.668672	6
10	991.582259	496.294768	973.571694	487.289485	G	***553.298039***	277.152658	536.271490	268.639383	535.287474	268.147375	5
11	1154.645588	577.826432	1136.635023	568.821150	Y	496.276575	248.641926	479.250026	240.128651	478.266010	239.636643	4
12	1241.677616	621.342446	1223.667051	612.337164	S	333.213246	167.110261	316.186697	158.596987	315.202681	158.104979	3
13	1340.746030	670.876653	1322.735465	661.871371	V	246.181218	123.594247	229.154669	115.080973			2
14					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of LLSVVPVPEGYSVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
66.2	1485.844284	0.001884	LLSVVPVPEGYSVK

Mascot: http://www.matrixscience.com/

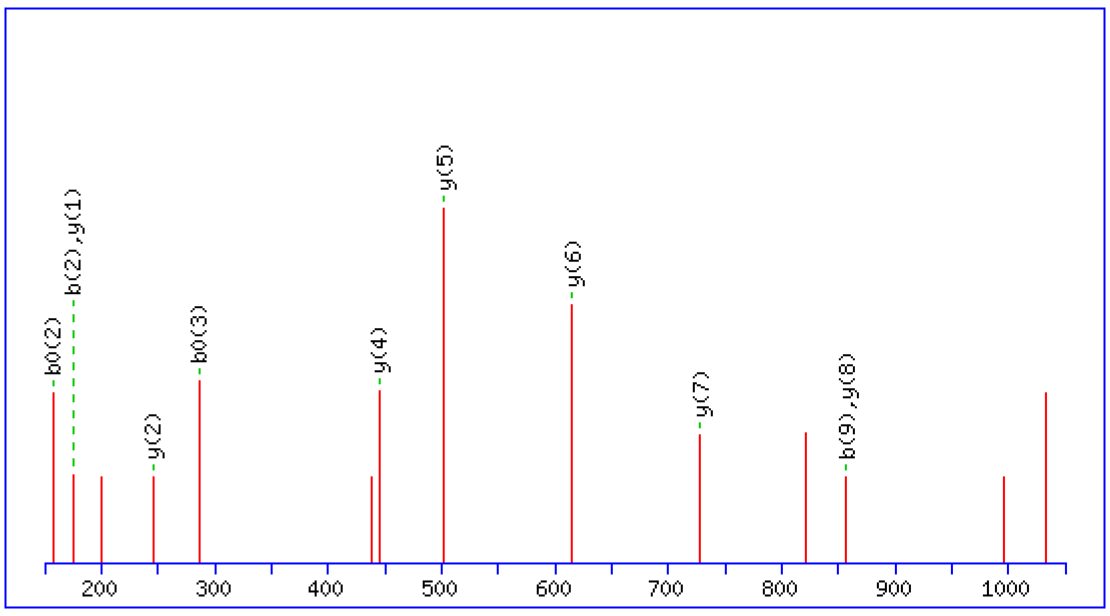
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SSELLGQAAR**
Found in **CJ032_HUMAN**, UPF0693 protein C10orf32 OS=Homo sapiens GN=C10orf32 PE=1 SV=1

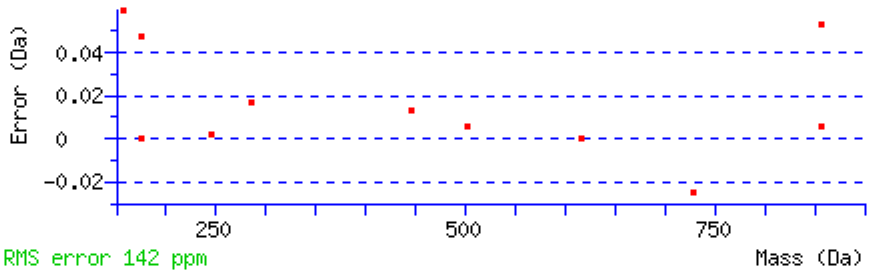
Match to Query 17931: 1030.543048 from(516.278800,2+) rtinseconds(1535) index(9152)
Title: Locus:1.1.1.1939.28
Data file 2011-11-14 - TFD - EP 8-7.mgf

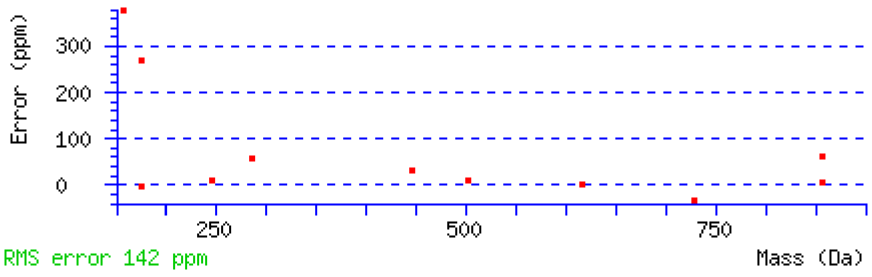
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1030.540695
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 66 **Expect:** 3.5e-006
Matches : 11/82 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							10
2	**175.071332**	88.039304			157.060767	79.034021	S	944.515971	472.761624	927.489422	464.248349	926.505406	463.756341	9
3	304.113925	152.560600			286.103360	143.555318	E	***857.483943***	429.245610	840.457394	420.732335	839.473378	420.240327	8
4	417.197989	209.102633			399.187424	200.097350	L	***728.441350***	364.724313	711.414801	356.211039			7
5	530.282053	265.644665			512.271488	256.639382	L	***615.357286***	308.182281	598.330737	299.669007			6
6	587.303517	294.155397			569.292952	285.150114	G	***502.273222***	251.640249	485.246673	243.126975			5
7	715.362095	358.184686	698.335546	349.671411	697.351530	349.179403	Q	***445.251758***	223.129517	428.225209	214.616243			4
8	786.399209	393.703243	769.372660	385.189968	768.388644	384.697960	A	317.193180	159.100228	300.166631	150.586953			3
9	**857.436323**	429.221800	840.409774	420.708525	839.425758	420.216517	A	***246.156066***	123.581671	229.129517	115.068397			2
10							R	***175.118952***	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of SSELLGQAAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
65.7	1030.540695	0.002353	SSELLGQAAR
18.6	1030.540695	0.002353	SSAEVIAQAR
15.3	1030.534180	0.008868	RPMLAAAGGR
13.9	1030.544739	-0.001691	RFLPPEPK
11.7	1030.534180	0.008868	RMIDVQNR
11.4	1030.540695	0.002353	ELTRDLER
8.1	1030.551926	-0.008878	AELTATNRR
6.7	1030.540695	0.002353	LSKEAPGSAR
6.5	1030.545410	-0.002362	RPVRASCR
3.0	1030.534180	0.008868	CVGQIERR

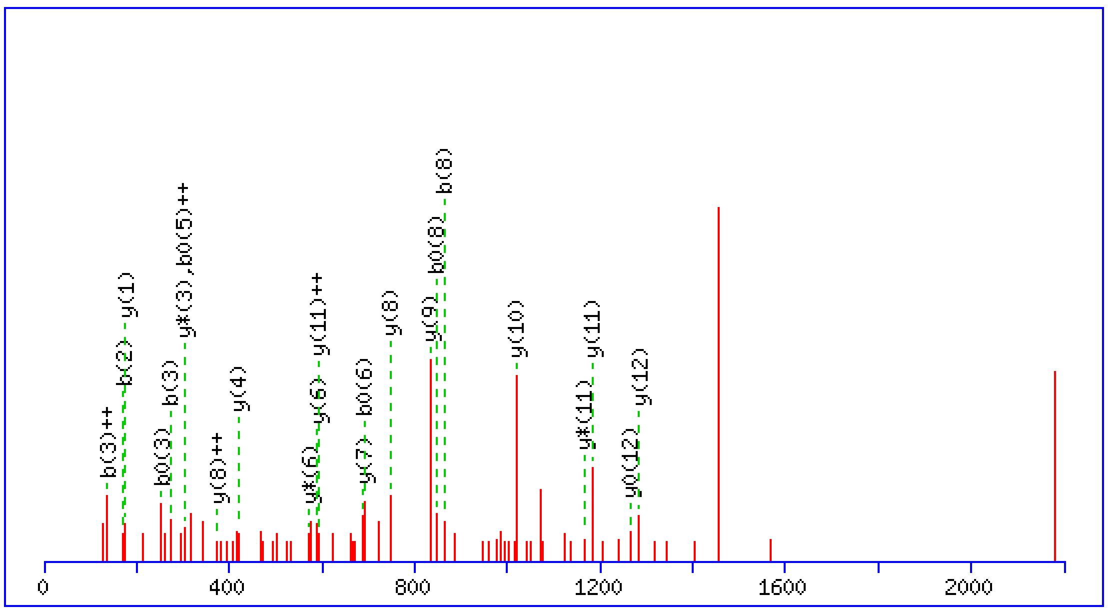
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VATYWSGVGLTGSR**
Found in **NUD14_HUMAN**, Uridine diphosphate glucose pyrophosphatase OS=Homo sapiens GN=NUDT14 PE=1 SV=2

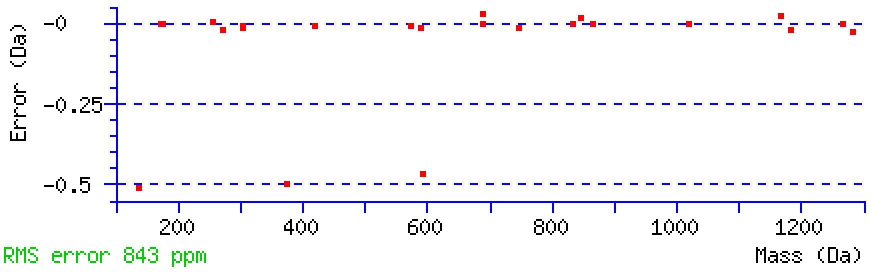
Match to Query 43203: 1452.726828 from(727.370690,2+) rtinseconds(2776) index(35721)
Title: Locus:1.1.1.2371.40
Data file 2011-11-10 - TFD - EP 4-5.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●

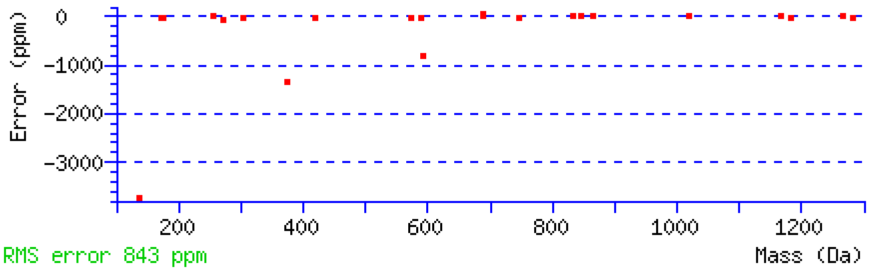


```
Monoisotopic mass of neutral peptide Mr(calc): 1452.736145
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 43  Expect: 0.00055
Matches : 23/124 fragment ions using 47 most intense peaks   (help)
```

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	100.075690	50.541483			V							14
2	**171.112804**	86.060040			A	1354.674992	677.841134	1337.648443	669.327860	1336.664427	668.835851	13
3	**272.160483**	136.583879	254.149918	127.578597	T	***1283.637878***	642.322577	1266.611329	633.809303	1265.627313	633.317295	12
4	435.223812	218.115544	417.213247	209.110262	Y	***1182.590199***	591.798738	1165.563650	583.285463	1164.579634	582.793455	11
5	621.303125	311.155201	603.292560	302.149918	W	***1019.526870***	510.267073	1002.500321	501.753799	1001.516305	501.261791	10
6	708.335153	354.671215	690.324588	345.665932	S	***833.447557***	417.227417	816.421008	408.714142	815.436992	408.222134	9
7	765.356617	383.181947	747.346052	374.176664	G	***746.415529***	373.711403	729.388980	365.198128	728.404964	364.706120	8
8	**864.425031**	432.716154	846.414466	423.710871	V	***689.394065***	345.200671	672.367516	336.687396	671.383500	336.195388	7
9	921.446495	461.226886	903.435930	452.221603	G	***590.325651***	295.666464	573.299102	287.153189	572.315086	286.661181	6
10	1034.530559	517.768918	1016.519994	508.763635	L	533.304187	267.155732	516.277638	258.642457	515.293622	258.150449	5
11	1135.578238	568.292757	1117.567673	559.287475	T	***420.220123***	210.613699	403.193574	202.100425	402.209558	201.608417	4
12	1192.599702	596.803489	1174.589137	587.798206	G	319.172444	160.089860	302.145895	151.576585	301.161879	151.084577	3
13	1279.631730	640.319503	1261.621165	631.314221	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
14					R	***175.118952***	88.063114	158.092403	79.549839			1



RMS error 843 ppm



RMS error 843 ppm

NCBI **BLAST** search of VATYWSGVGLTGSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
43.3	1452.736145	-0.009317	VATYWSGVGLTGSR

Mascot: http://www.matrixscience.com/

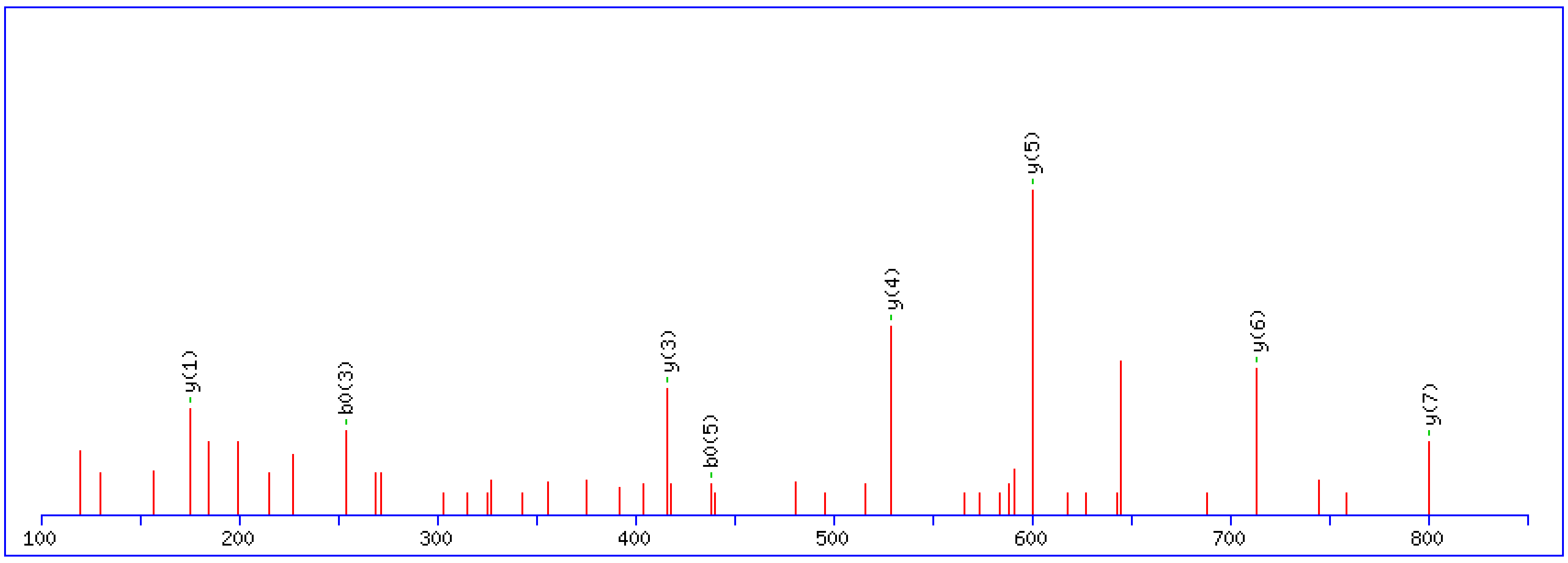
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ASLALLQR**
Found in **VPS29_HUMAN**, Vacuolar protein sorting-associated protein 29 OS=Homo sapiens GN=VPS29 PE=1 SV=1

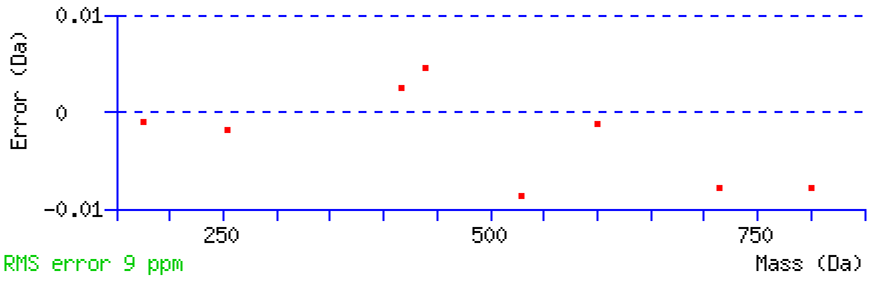
Match to Query 4464: 870.524448 from(436.269500,2+) rtinseconds(2165) index(26342)
Title: Locus:1.1.1.1214.5
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 1.mgf

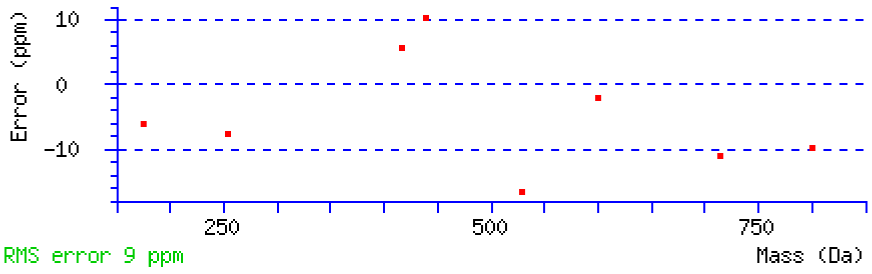
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 850 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 870.528671
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.0018
Matches : 8/58 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							8
2	159.076418	80.041847			141.065853	71.036564	S	***800.498864***	400.753070	783.472315	392.239796	782.488299	391.747788	7
3	272.160482	136.583879			254.149917	127.578597	L	***713.466836***	357.237056	696.440287	348.723782			6
4	343.197596	172.102436			325.187031	163.097154	A	***600.382772***	300.695024	583.356223	292.181750			5
5	456.281660	228.644468			438.271095	219.639186	L	***529.345658***	265.176467	512.319109	256.663193			4
6	569.365724	285.186500			551.355159	276.181218	L	***416.261594***	208.634435	399.235045	200.121160			3
7	697.424302	349.215789	680.397753	340.702515	679.413737	340.210507	Q	303.177530	152.092403	286.150981	143.579128			2
8							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of ASLALLQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.4	870.528671	-0.004223	ASLALLQR
24.5	870.528671	-0.004223	ASAIIIQR
12.5	870.528671	-0.004223	ALSQLALR
9.7	870.528687	-0.004239	AAVVDKIR
9.7	870.528671	-0.004223	ALLSALQR
9.7	870.528687	-0.004239	AVEGVLKR
8.9	870.528671	-0.004223	LLENVKR
8.2	870.517441	0.007007	LLEELVR
7.3	870.528671	-0.004223	LNDLIKR
5.9	870.517441	0.007007	LLEIVER

Mascot: http://www.matrixscience.com/

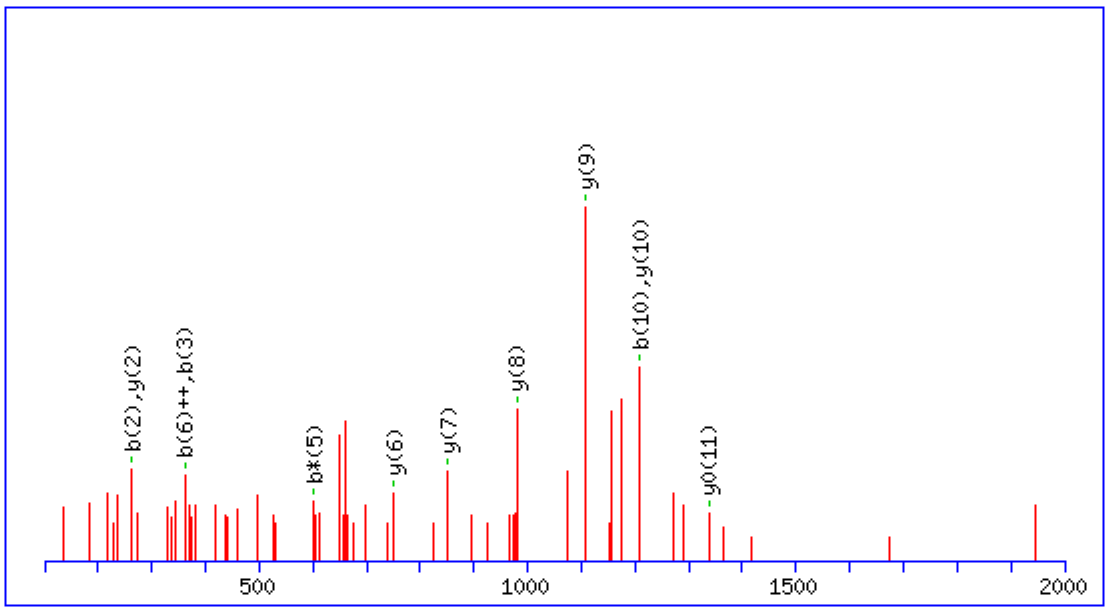
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NFVEETVYLLSR**
Found in **VPS41_HUMAN**, Vacuolar protein sorting-associated protein 41 homolog OS=Homo sapiens GN=VPS41 PE=1 SV=3

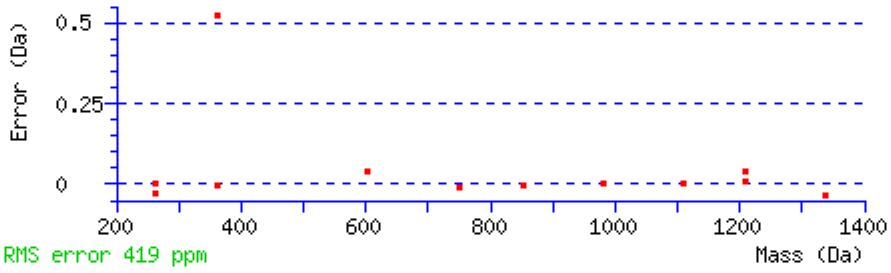
Match to Query 46986: 1468.766228 from(735.390390,2+) rtinseconds(4359) index(64333)
Title: Locus:1.1.1.3068.9
Data file 2011-11-14 - TFD - EP 8-2.mgf

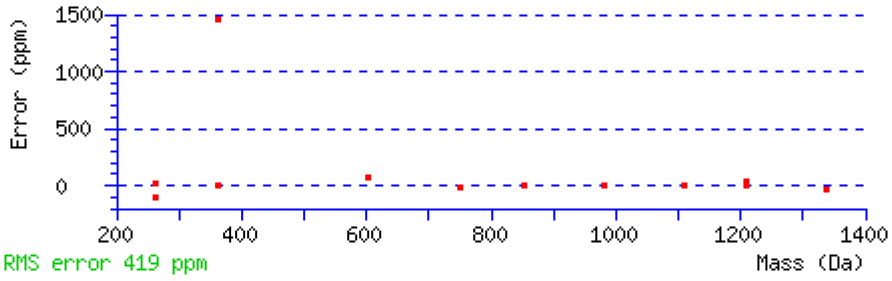
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1468.756180
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 40  Expect: 0.0011
Matches : 12/124 fragment ions using 13 most intense peaks   (help)
```

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			N							12
2	**262.118617**	131.562946	245.092068	123.049672			F	1355.720544	678.363910	1338.693995	669.850636	1337.709979	669.358628	11
3	**361.187031**	181.097153	344.160482	172.583879			V	***1208.652130***	604.829703	1191.625581	596.316429	1190.641565	595.824420	10
4	490.229624	245.618450	473.203075	237.105176	472.219059	236.613168	E	***1109.583716***	555.295496	1092.557167	546.782221	1091.573151	546.290213	9
5	619.272217	310.139747	602.245668	301.626472	601.261652	301.134464	E	***980.541123***	490.774200	963.514574	482.260925	962.530558	481.768917	8
6	720.319896	360.663586	703.293347	352.150312	702.309331	351.658304	T	***851.498530***	426.252903	834.471981	417.739628	833.487965	417.247620	7
7	819.388310	410.197793	802.361761	401.684519	801.377745	401.192511	V	***750.450851***	375.729064	733.424302	367.215789	732.440286	366.723781	6
8	982.451639	491.729458	965.425090	483.216183	964.441074	482.724175	Y	651.382437	326.194857	634.355888	317.681582	633.371872	317.189574	5
9	1095.535703	548.271490	1078.509154	539.758215	1077.525138	539.266207	L	488.319108	244.663192	471.292559	236.149917	470.308543	235.657909	4
10	**1208.619767**	604.813521	1191.593218	596.300247	1190.609202	595.808239	L	375.235044	188.121160	358.208495	179.607885	357.224479	179.115877	3
11	1295.651795	648.329536	1278.625246	639.816261	1277.641230	639.324253	S	***262.150980***	131.579128	245.124431	123.065854	244.140415	122.573846	2
12							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of NFVEETVYLLSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.3	1468.756180	0.010048	NFVEETVYLLSR

Mascot: http://www.matrixscience.com/

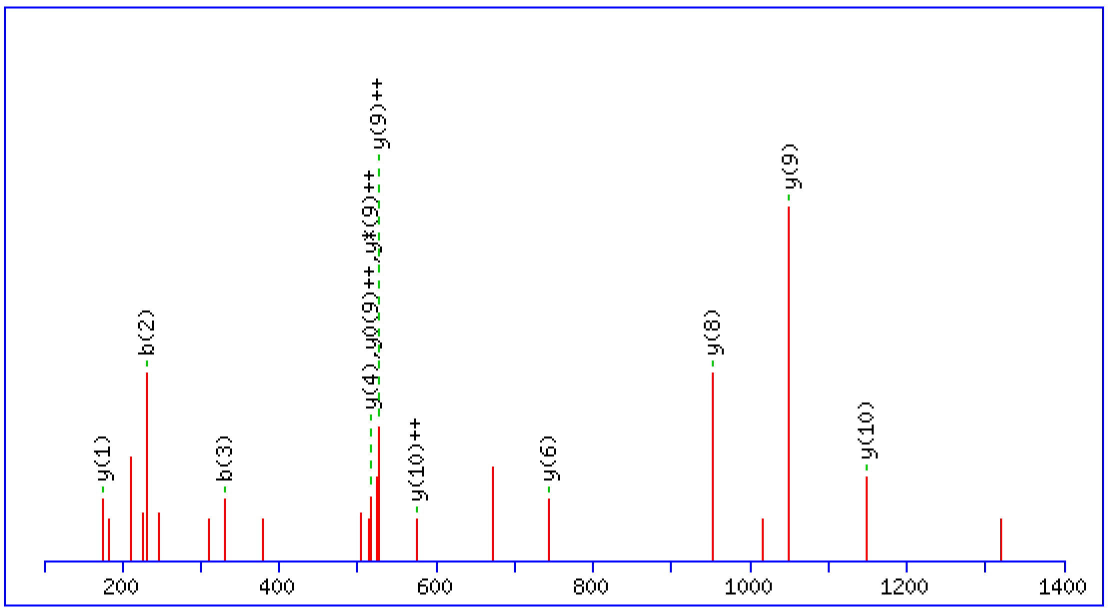
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **TEVPPLLLILDR**
Found in **VPS45_HUMAN**, Vacuolar protein sorting-associated protein 45 OS=Homo sapiens GN=VPS45 PE=1 SV=1

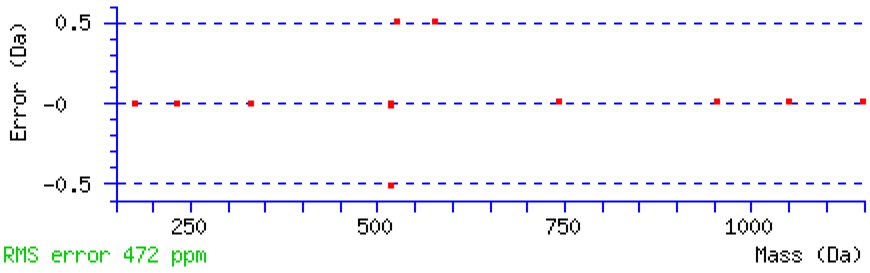
Match to Query 37428: 1377.829468 from(689.922010,2+) rtinseconds(4394) index(67622)
Title: Locus:1.1.1.3222.18
Data file 2011-11-13 - TFD - EP 7-3.mgf

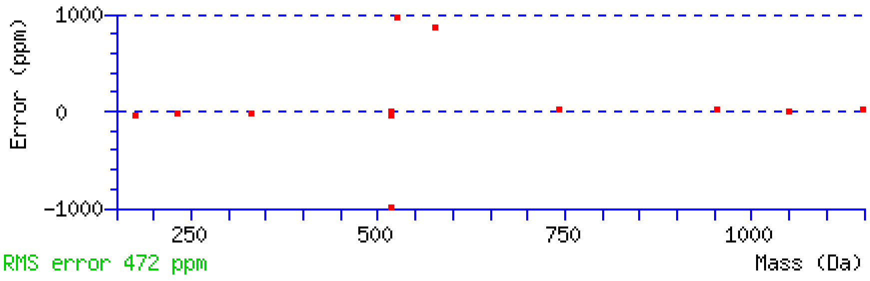
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1377.823135
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 44 **Expect:** 4.4e-005
Matches : 12/108 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116	84.044390	42.525833	T							12
2	**231.097548**	116.052412	213.086983	107.047130	E	1277.782750	639.395013	1260.756201	630.881739	1259.772185	630.389731	11
3	**330.165962**	165.586619	312.155397	156.581337	V	***1148.740157***	574.873717	1131.713608	566.360442	1130.729592	565.868434	10
4	427.218726	214.113001	409.208161	205.107719	P	***1049.671743***	525.339510	1032.645194	516.826235	1031.661178	516.334227	9
5	524.271490	262.639383	506.260925	253.634101	P	***952.618979***	476.813128	935.592430	468.299853	934.608414	467.807845	8
6	637.355554	319.181415	619.344989	310.176133	L	855.566215	428.286746	838.539666	419.773471	837.555650	419.281463	7
7	750.439618	375.723447	732.429053	366.718165	L	***742.482151***	371.744714	725.455602	363.231439	724.471586	362.739431	6
8	863.523682	432.265479	845.513117	423.260197	L	629.398087	315.202682	612.371538	306.689407	611.387522	306.197399	5
9	976.607746	488.807511	958.597181	479.802229	I	***516.314023***	258.660650	499.287474	250.147375	498.303458	249.655367	4
10	1089.691810	545.349543	1071.681245	536.344261	L	403.229959	202.118617	386.203410	193.605343	385.219394	193.113335	3
11	1204.718753	602.863015	1186.708188	593.857732	D	290.145895	145.576585	273.119346	137.063311	272.135330	136.571303	2
12					R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of TEVPPLLLILDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
43.6	1377.823135	0.006333	TEVPPLLLILDR

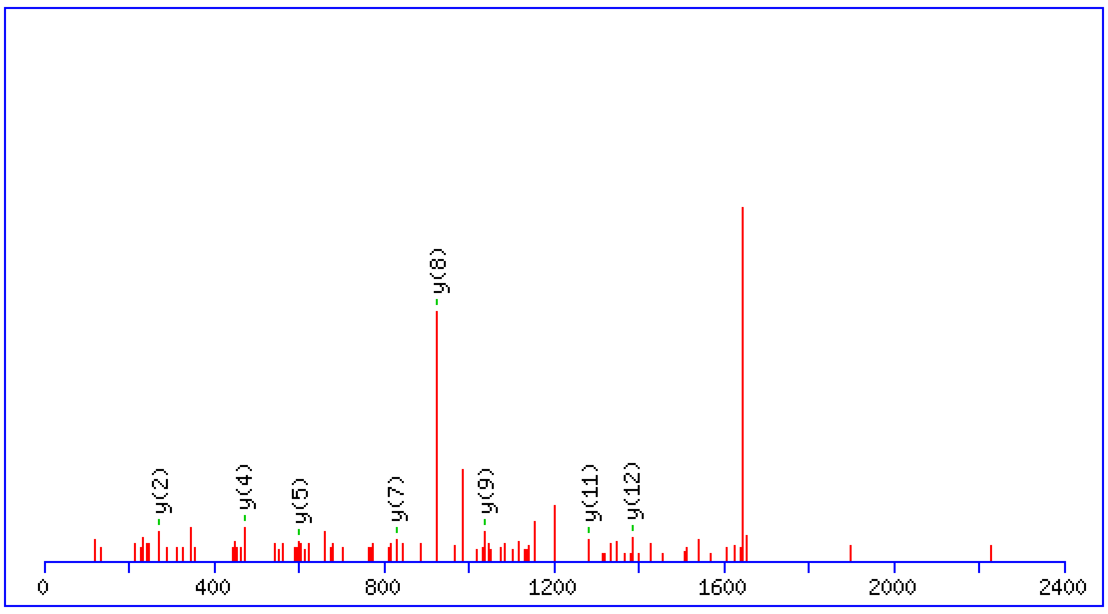
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IFTEDLPEVESLPR**
Found in **VPS39_HUMAN**, Vam6/Vps39-like protein OS=Homo sapiens GN=VPS39 PE=1 SV=2

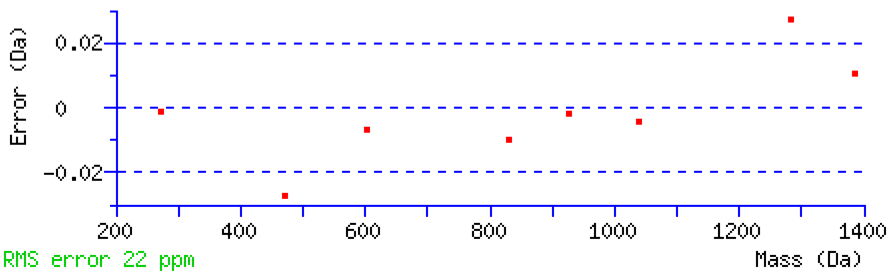
Match to Query 50837: 1643.842188 from(822.928370,2+) rtinseconds(3196) index(41488)
Title: Locus:1.1.1.2852.41
Data file 2011-11-12 - TFD - EP 5-2.mgf

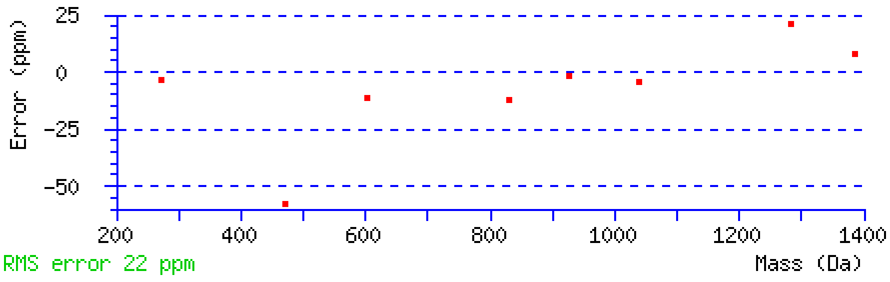
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1643.840637
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 52 **Expect:** 8.4e-005
Matches : 8/120 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							14
2	261.159754	131.083515			F	1531.763865	766.385571	1514.737316	757.872296	1513.753300	757.380288	13
3	362.207433	181.607354	344.196868	172.602072	T	***1384.695451***	692.851364	1367.668902	684.338089	1366.684886	683.846081	12
4	491.250026	246.128651	473.239461	237.123369	E	***1283.647772***	642.327524	1266.621223	633.814250	1265.637207	633.322242	11
5	606.276969	303.642123	588.266404	294.636840	D	1154.605179	577.806227	1137.578630	569.292953	1136.594614	568.800945	10
6	719.361033	360.184155	701.350468	351.178872	L	***1039.578236***	520.292756	1022.551687	511.779482	1021.567671	511.287474	9
7	816.413797	408.710537	798.403232	399.705254	P	***926.494172***	463.750724	909.467623	455.237450	908.483607	454.745442	8
8	945.456390	473.231833	927.445825	464.226551	E	***829.441408***	415.224342	812.414859	406.711068	811.430843	406.219060	7
9	1044.524804	522.766040	1026.514239	513.760758	V	700.398815	350.703046	683.372266	342.189771	682.388250	341.697763	6
10	1173.567397	587.287337	1155.556832	578.282054	E	***601.330401***	301.168838	584.303852	292.655564	583.319836	292.163556	5
11	1260.599425	630.803351	1242.588860	621.798068	S	***472.287808***	236.647542	455.261259	228.134267	454.277243	227.642259	4
12	1373.683489	687.345383	1355.672924	678.340100	L	385.255780	193.131528	368.229231	184.618253			3
13	1470.736253	735.871765	1452.725688	726.866482	P	***272.171716***	136.589496	255.145167	128.076221			2
14					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of IFTEDLPEVESLPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.9	1643.840637	0.001551	IFTEDLPEVESLPR
11.7	1643.837448	0.004740	VAAAESMPLLLECAR

Mascot: http://www.matrixscience.com/

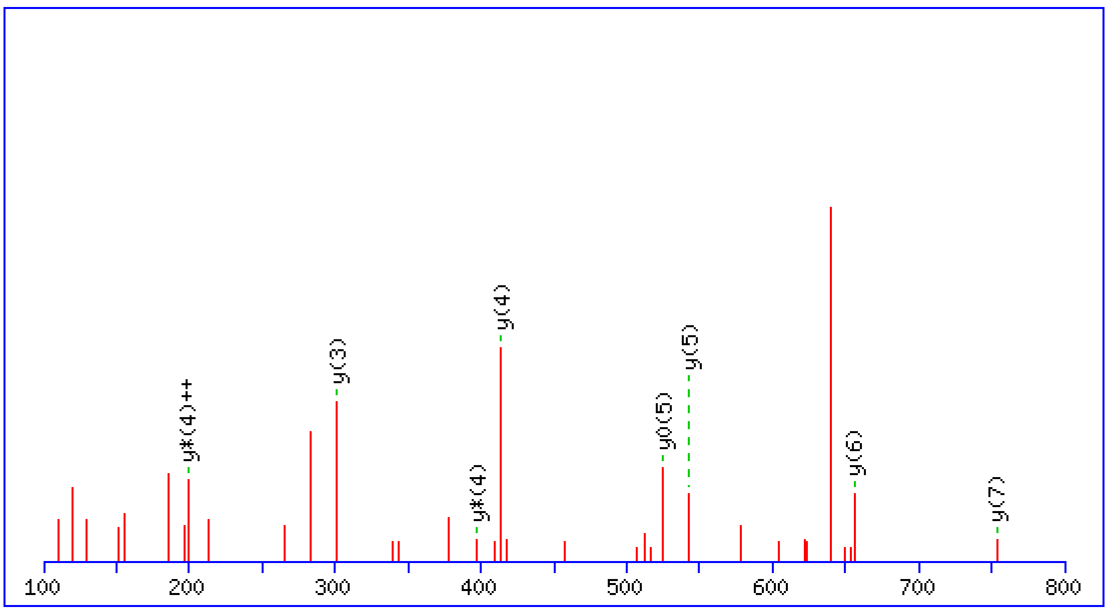
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VPLEPGPK**
Found in **VASN_HUMAN**, Vasorin OS=Homo sapiens GN=VASN PE=1 SV=1

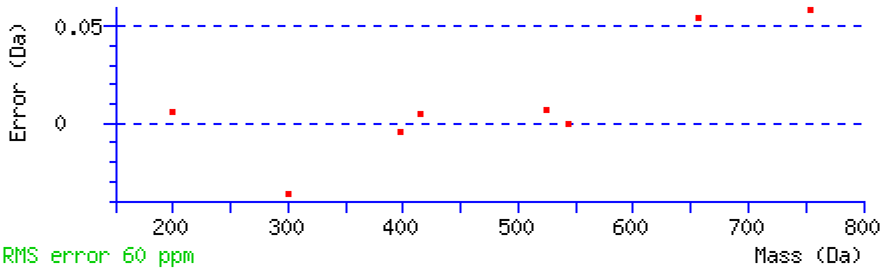
Match to Query 4416: 851.479888 from(426.747220,2+) rtinseconds(1899) index(20675)
Title: Locus:1.1.1.2067.6
Data file 2011-11-10 - TFD - EP 3-4.mgf

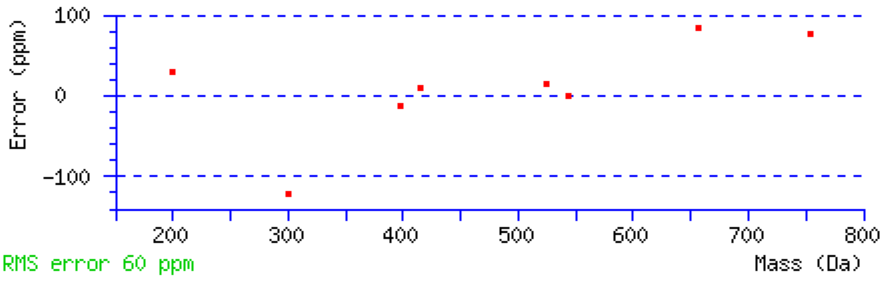
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 851.475266
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P5      : Oxidation (P)
Ions Score: 38  Expect: 0.00087
Matches : 8/56 fragment ions using 13 most intense peaks   (help)
```

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	100.075690	50.541483			V							8
2	197.128454	99.067865			P	***753.414132***	377.210704	736.387583	368.697430	735.403567	368.205422	7
3	310.212518	155.609897			L	***656.361368***	328.684322	639.334819	320.171048	638.350803	319.679040	6
4	439.255111	220.131193	421.244546	211.125911	E	***543.277304***	272.142290	526.250755	263.629016	525.266739	263.137008	5
5	552.302790	276.655033	534.292225	267.649751	P	***414.234711***	207.620994	397.208162	199.107719			4
6	609.324254	305.165765	591.313689	296.160483	G	***301.187032***	151.097154	284.160483	142.583880			3
7	706.377018	353.692147	688.366453	344.686865	P	244.165568	122.586422	227.139019	114.073148			2
8					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of VPLEPGPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.9	851.475266	0.004622	VPLEPGPK
23.6	851.475266	0.004622	VPLEPGPK
13.6	851.486496	-0.006608	VLPAPAPR
12.8	851.475266	0.004622	VPLEPGPK
11.7	851.486496	-0.006608	VLPAPAPR
9.5	851.486496	-0.006608	VPPPALSR
6.5	851.486496	-0.006608	VLPAPAPR
6.4	851.486496	-0.006608	VPPPALSR
3.5	851.486496	-0.006608	VLKHPDK
1.3	851.475266	0.004622	DPPIPVAK

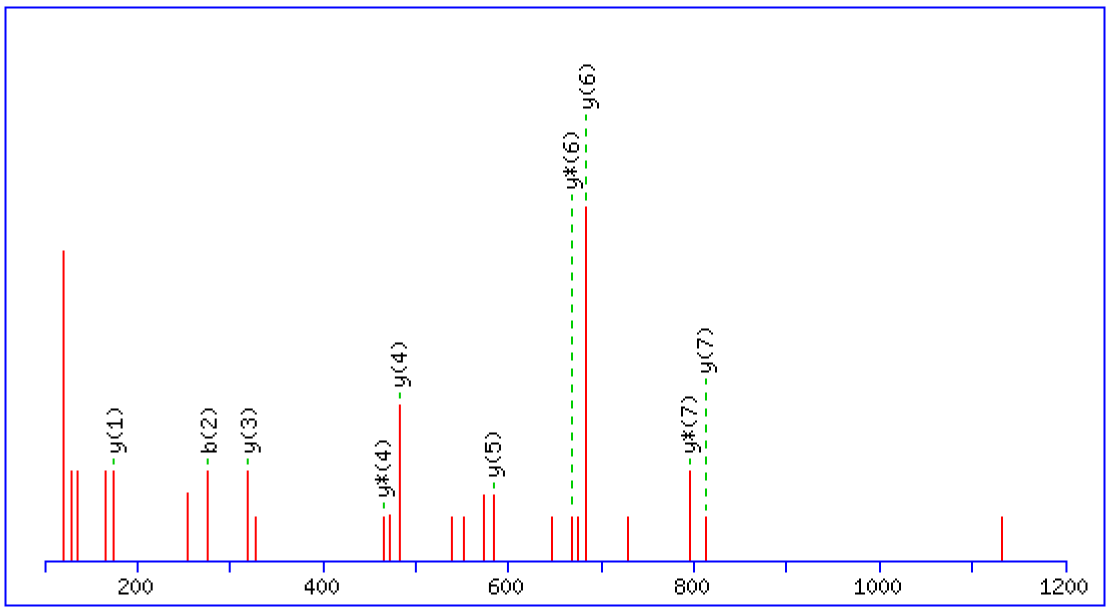
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FQTTYGSR**
Found in **VAMP7_HUMAN**, Vesicle-associated membrane protein 7 OS=Homo sapiens GN=VAMP7 PE=1 SV=3

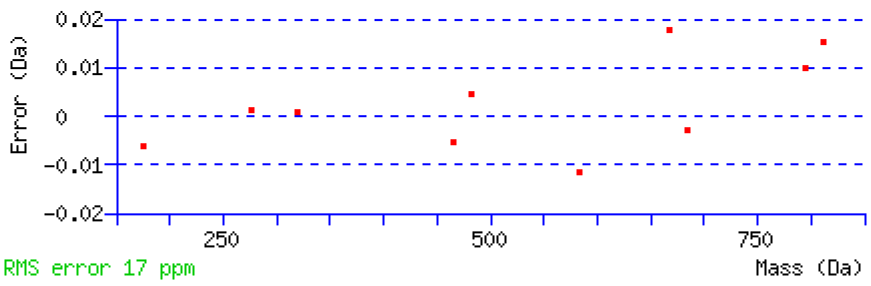
Match to Query 13135: 958.455088 from(480.234820,2+) rtinseconds(1304) index(6534)
Title: Locus:1.1.1.1763.20
Data file 2011-11-10 - TFD - EP 3-6.mgf

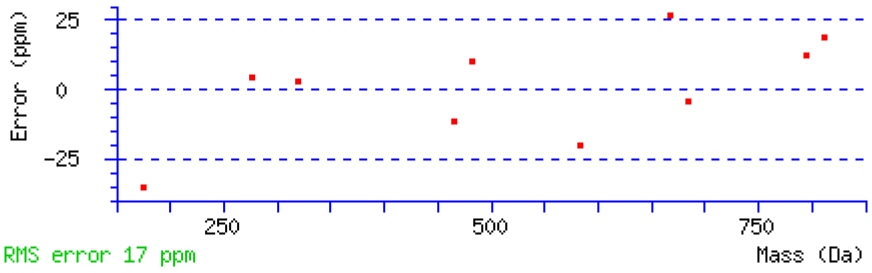
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 958.450851
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.0018
Matches : 10/76 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.075690	74.541483					**F**							8
2	276.134268	138.570772	259.107719	130.057497			**Q**	***812.389709***	406.698493	795.363160	398.185218	794.379144	397.693210	7
3	377.181947	189.094611	360.155398	180.581337	359.171382	180.089329	**T**	***684.331131***	342.669204	667.304582	334.155929	666.320566	333.663921	6
4	478.229626	239.618451	461.203077	231.105177	460.219061	230.613169	**T**	***583.283452***	292.145364	566.256903	283.632090	565.272887	283.140082	5
5	641.292955	321.150116	624.266406	312.636841	623.282390	312.144833	**Y**	***482.235773***	241.621524	465.209224	233.108250	464.225208	232.616242	4
6	698.314419	349.660848	681.287870	341.147573	680.303854	340.655565	**G**	***319.172444***	160.089860	302.145895	151.576585	301.161879	151.084577	3
7	785.346447	393.176862	768.319898	384.663587	767.335882	384.171579	**S**	262.150980	131.579128	245.124431	123.065853	244.140415	122.573845	2
8							**R**	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of FQTTYGSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.6	958.450851	0.004237	FQTTYGSR
6.2	958.454224	0.000864	MPGPSPGLR
5.8	958.454208	0.000880	MQGPIPER
5.8	958.454208	0.000880	MQGPIPER
4.5	958.446808	0.008280	EEGDPRTR

Mascot: http://www.matrixscience.com/

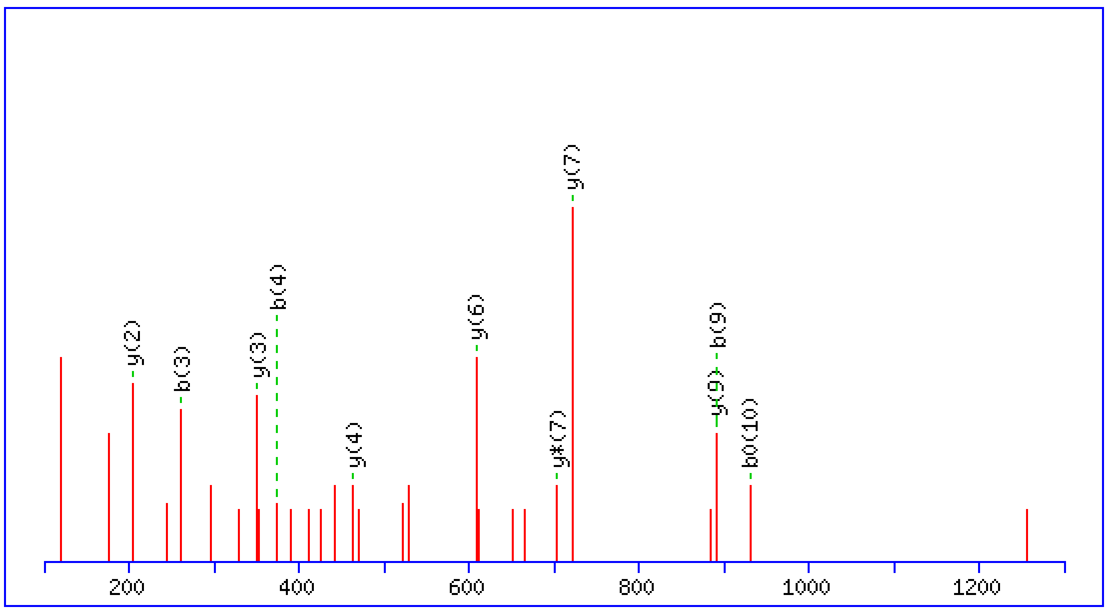
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GFGLLGSIFGK**
Found in **VKORL_HUMAN**, Vitamin K epoxide reductase complex subunit 1-like protein 1 OS=Homo sapiens GN=VKORC1L1 PE=1 SV=2

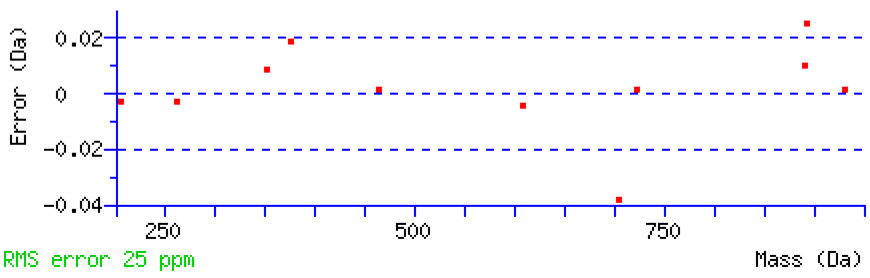
Match to Query 22630: 1094.608888 from(548.311720,2+) rtinseconds(4077) index(60836)
Title: Locus:1.1.1.2941.17
Data file 2011-11-14 - TFD - EP 8-1.mgf

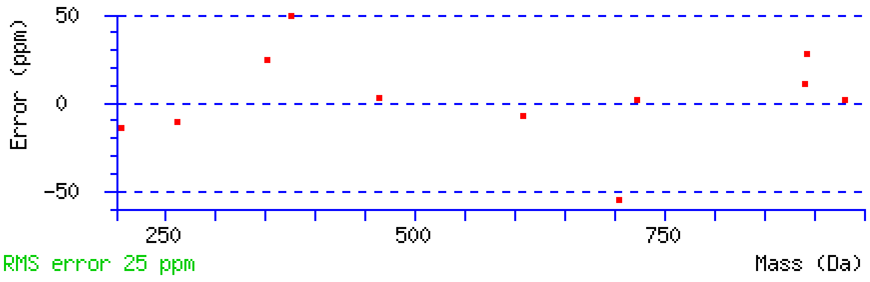
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1094.612442
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 48  Expect: 6.9e-005
Matches : 11/80 fragment ions using 16 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008			G							11
2	205.097154	103.052215			F	1038.598244	519.802760	1021.571695	511.289486	1020.587679	510.797478	10
3	**262.118618**	131.562947			G	***891.529830***	446.268553	874.503281	437.755278	873.519265	437.263270	9
4	**375.202682**	188.104979			L	834.508366	417.757821	817.481817	409.244547	816.497801	408.752539	8
5	488.286746	244.647011			L	***721.424302***	361.215789	704.397753	352.702514	703.413737	352.210506	7
6	545.308210	273.157743			G	***608.340238***	304.673757	591.313689	296.160483	590.329673	295.668475	6
7	632.340238	316.673757	614.329673	307.668475	S	551.318774	276.163025	534.292225	267.649750	533.308209	267.157742	5
8	745.424302	373.215789	727.413737	364.210507	I	***464.286746***	232.647011	447.260197	224.133736			4
9	**892.492716**	446.749996	874.482151	437.744713	F	***351.202682***	176.104979	334.176133	167.591704			3
10	949.514180	475.260728	931.503615	466.255446	G	***204.134268***	102.570772	187.107719	94.057497			2
11					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of GFGLLGSIFGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.7	1094.612442	-0.003554	GFGLLGSIFGK
3.1	1094.598495	0.010393	APRPWPSLR
1.4	1094.608414	0.000474	RVPDPSPVTK
1.0	1094.608383	0.000505	EPKPVGLNNK

Mascot: http://www.matrixscience.com/

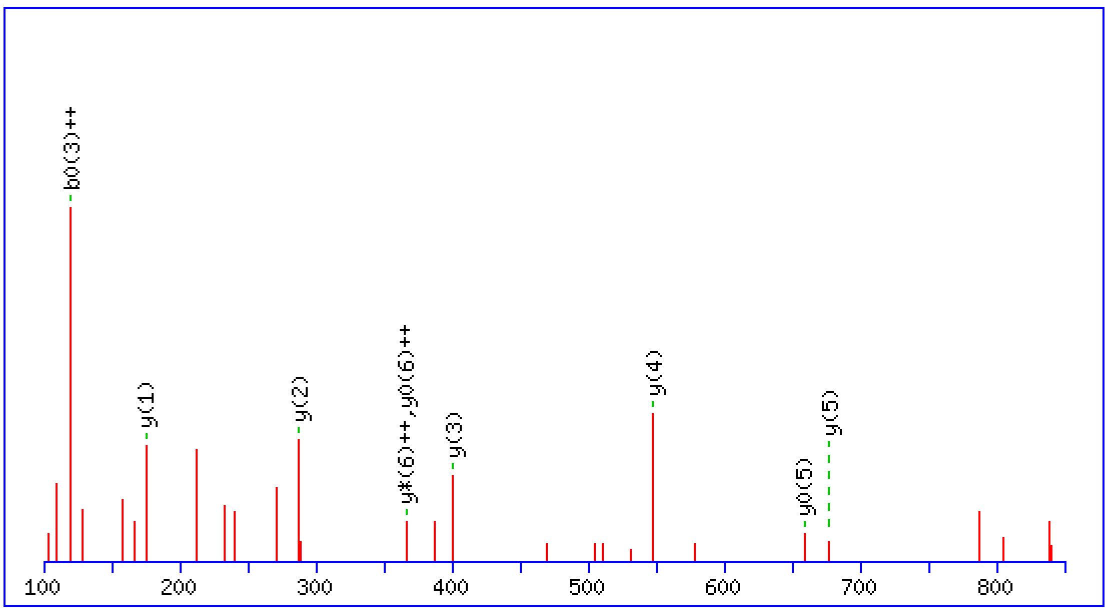
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GAEFLLR**
Found in **CCG6_HUMAN**, Voltage-dependent calcium channel gamma-6 subunit OS=Homo sapiens GN=CACNG6 PE=2 SV=1

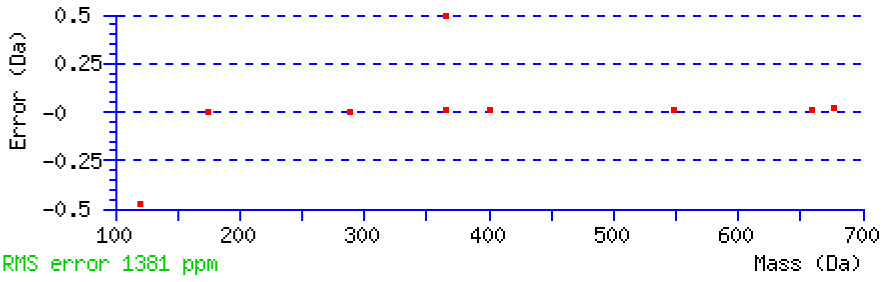
Match to Query 826: 804.446268 from(403.230410,2+) rtinseconds(2167) index(25297)
Title: Locus:1.1.1.2254.2
Data file 2011-11-14 - TFD - EP 8-2.mgf

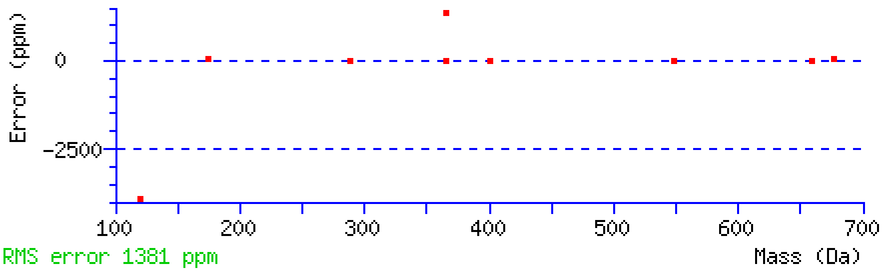
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 804.449371
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 37 **Expect:** 0.0041
Matches : 9/48 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008			G							7
2	129.065854	65.036565			A	748.435201	374.721239	731.408652	366.207964	730.424636	365.715956	6
3	258.108447	129.557862	240.097882	120.552579	E	***677.398087***	339.202682	660.371538	330.689407	659.387522	330.197399	5
4	405.176861	203.092068	387.166296	194.086786	F	***548.355494***	274.681385	531.328945	266.168111			4
5	518.260925	259.634101	500.250360	250.628818	L	***401.287080***	201.147178	384.260531	192.633904			3
6	631.344989	316.176133	613.334424	307.170850	L	***288.203016***	144.605146	271.176467	136.091872			2
7					R	***175.118952***	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of GAEFLLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.4	804.449371	-0.003103	GAEFLLR
34.4	804.449371	-0.003103	QEFLLR
9.8	804.452728	-0.006460	EMKILR
9.8	804.452728	-0.006460	EMKLLR
9.8	804.452744	-0.006476	MALSVLR
9.1	804.452728	-0.006460	KLMELR
8.6	804.449356	-0.003088	KYLEPR
7.9	804.452728	-0.006460	MEKLLR
7.9	804.452728	-0.006460	MKELLR
7.9	804.449387	-0.003119	VFASPLR

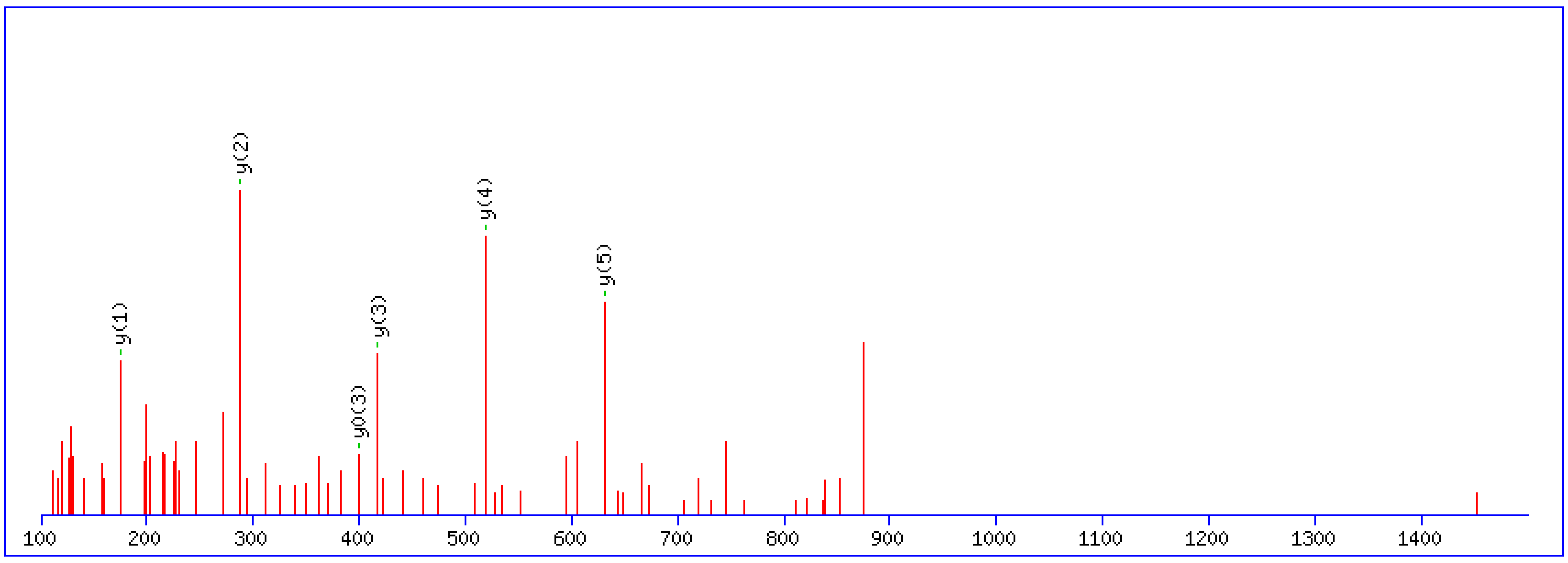
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DKITELR**
Found in **VSIG4_HUMAN**, V-set and immunoglobulin domain-containing protein 4 OS=Homo sapiens GN=VSIG4 PE=1 SV=1

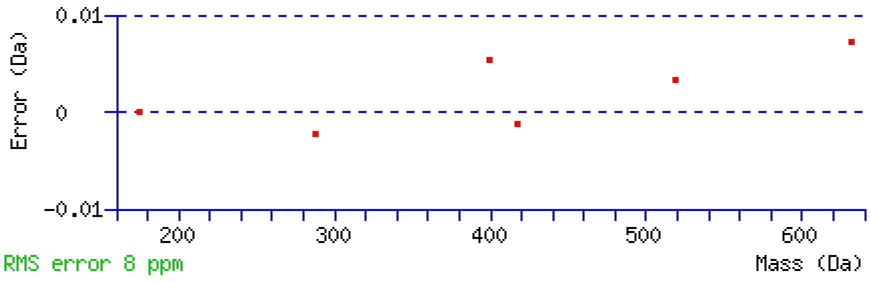
Match to Query 4649: 873.483328 from(437.748940,2+) rtinseconds(1602) index(15592)
Title: Locus:1.1.1.999.5
Data file 2012-01-27 - TFD - Epitel - IEC - 10ul - 1.mgf

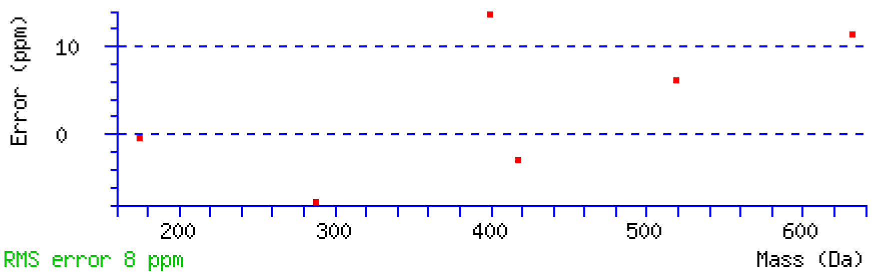
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 1500 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 873.491959
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 42 **Expect:** 0.0011
Matches : 6/66 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.034219	58.520748			98.023654	49.515465	**D**							7
2	244.129182	122.568229	227.102633	114.054955	226.118617	113.562947	**K**	759.472315	380.239796	742.445766	371.726521	741.461750	371.234513	6
3	357.213246	179.110261	340.186697	170.596987	339.202681	170.104979	**I**	***631.377352***	316.192314	614.350803	307.679040	613.366787	307.187032	5
4	458.260925	229.634101	441.234376	221.120826	440.250360	220.628818	**T**	***518.293288***	259.650282	501.266739	251.137008	500.282723	250.645000	4
5	587.303518	294.155397	570.276969	285.642123	569.292953	285.150115	**E**	***417.245609***	209.126443	400.219060	200.613168	399.235044	200.121160	3
6	700.387582	350.697429	683.361033	342.184155	682.377017	341.692147	**L**	***288.203016***	144.605146	271.176467	136.091872			2
7							**R**	***175.118952***	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of DKITELR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.3	873.491959	-0.008631	DKITELR
25.0	873.491959	-0.008631	KEVTLER
12.6	873.491943	-0.008615	ELSKEIR
12.6	873.491959	-0.008631	TDLKELR
9.3	873.480713	0.002615	KDLELEK
9.3	873.480713	0.002615	KDLLEEK
9.3	873.491974	-0.008646	KDLSGVQK
9.2	873.482071	0.001257	KHYGTIR
9.2	873.491959	-0.008631	KLEDTIR
6.3	873.482071	0.001257	KLFSSHR

Mascot: http://www.matrixscience.com/

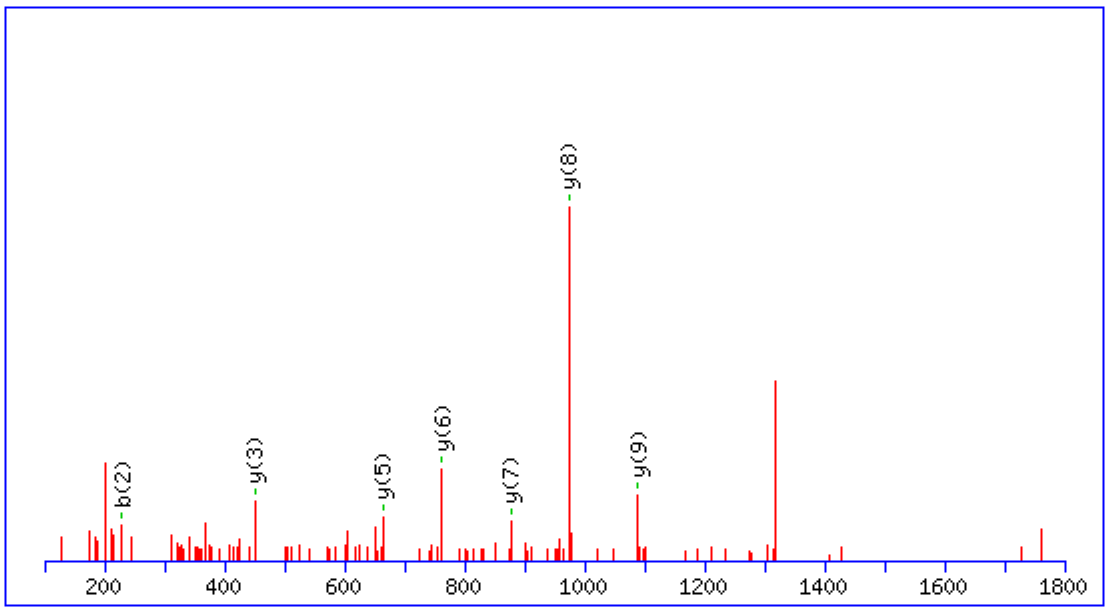
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DLNPDVNVFQR**
Found in **VPP1_HUMAN**, V-type proton ATPase 116 kDa subunit a isoform 1 OS=Homo sapiens GN=ATP6V0A1 PE=1 SV=3

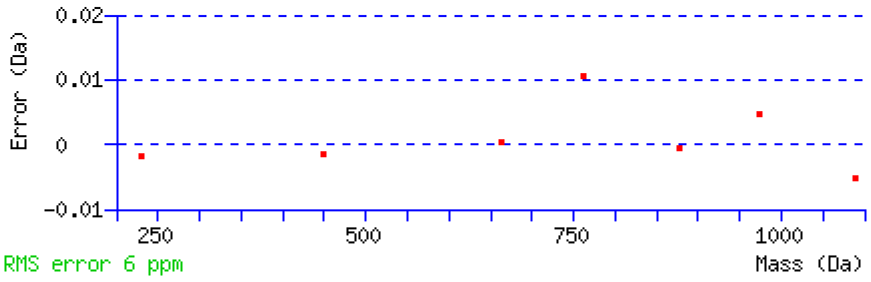
Match to Query 36859: 1315.661268 from(658.837910,2+) rtinseconds(2642) index(33826)
Title: Locus:1.1.1.2350.31
Data file 2011-11-10 - TFD - EP 4-1.mgf

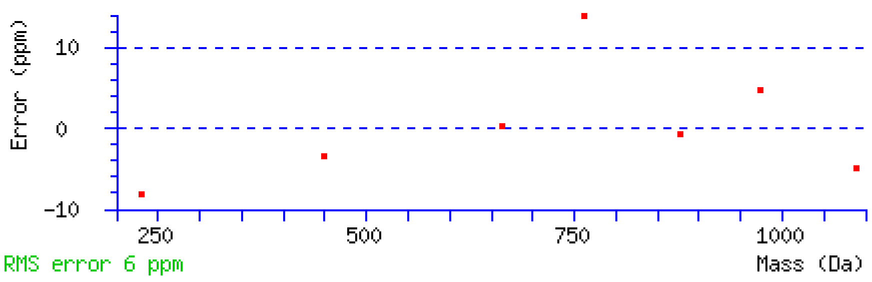
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1315.652069
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.00084
Matches : 7/104 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.034219	58.520748			98.023654	49.515465	D							11
2	229.118283	115.062779			211.107718	106.057497	L	1201.632397	601.319836	1184.605848	592.806562	1183.621832	592.314554	10
3	343.161210	172.084243	326.134661	163.570968	325.150645	163.078960	N	***1088.548333***	544.777805	1071.521784	536.264530	1070.537768	535.772522	9
4	440.213974	220.610625	423.187425	212.097350	422.203409	211.605342	P	***974.505406***	487.756341	957.478857	479.243067	956.494841	478.751059	8
5	555.240917	278.124097	538.214368	269.610822	537.230352	269.118814	D	***877.452642***	439.229959	860.426093	430.716684	859.442077	430.224676	7
6	654.309331	327.658303	637.282782	319.145029	636.298766	318.653021	V	***762.425699***	381.716488	745.399150	373.203213			6
7	768.352258	384.679767	751.325709	376.166492	750.341693	375.674484	N	***663.357285***	332.182281	646.330736	323.669006			5
8	867.420672	434.213974	850.394123	425.700699	849.410107	425.208691	V	549.314358	275.160817	532.287809	266.647543			4
9	1014.489086	507.748181	997.462537	499.234906	996.478521	498.742898	F	***450.245944***	225.626610	433.219395	217.113336			3
10	1142.547664	571.777470	1125.521115	563.264196	1124.537099	562.772187	Q	303.177530	152.092403	286.150981	143.579129			2
11							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of DLNPDVNVFQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.3	1315.652069	0.009199	DLNPDVNVFQR
3.5	1315.652039	0.009229	KTPYEEQLHR

Mascot: http://www.matrixscience.com/

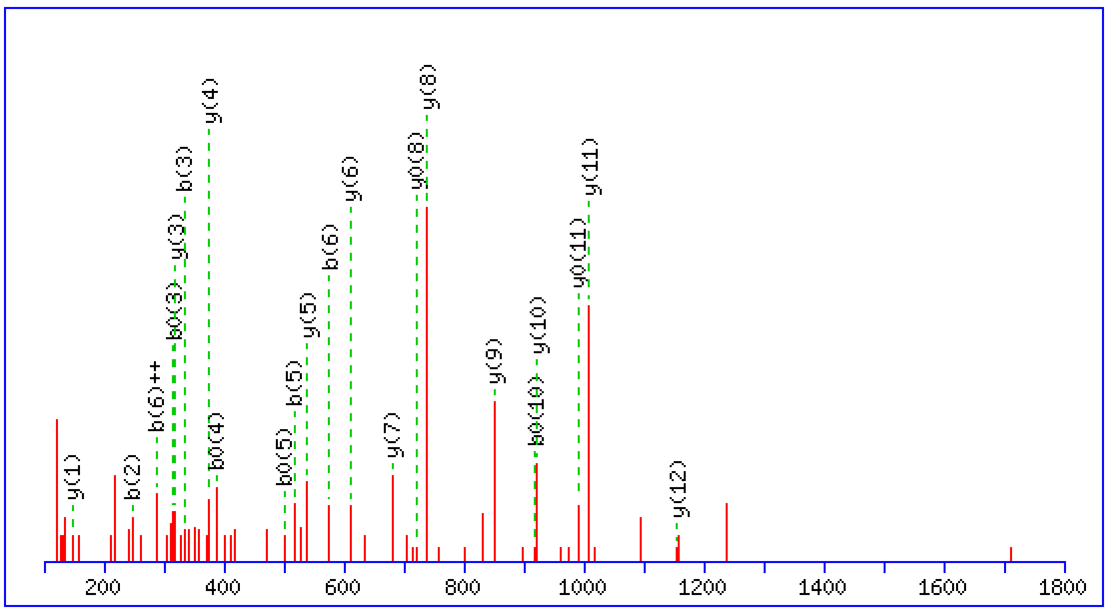
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VFSALGAAYGTAK**
Found in **VATL_HUMAN**, V-type proton ATPase 16 kDa proteolipid subunit OS=Homo sapiens GN=ATP6V0C PE=1 SV=1

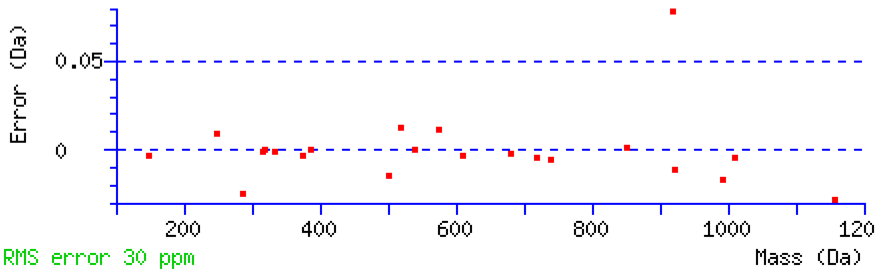
Match to Query 587795: 1254.657728 from(628.336140,2+) rtinseconds(2399) index(999008)
Title: Locus:1.1.1.1407.35
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

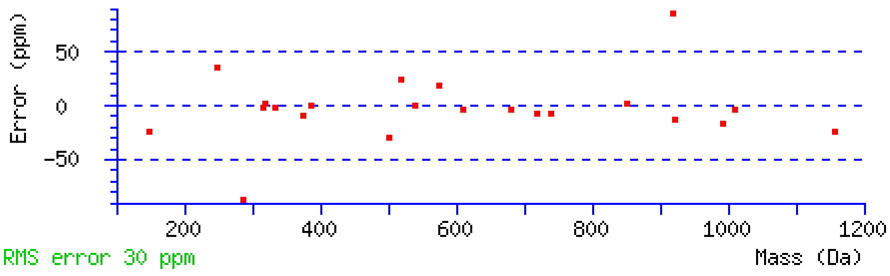
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1254.660828
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 76 **Expect:** 4e-007
Matches : 22/112 fragment ions using 44 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483			V							13
2	**247.144104**	124.075690			F	***1156.599702***	578.803489	1139.573153	570.290215	1138.589137	569.798206	12
3	**334.176132**	167.591704	316.165567	158.586422	S	***1009.531288***	505.269282	992.504739	496.756008	991.520723	496.264000	11
4	405.213246	203.110261	387.202681	194.104978	A	***922.499260***	461.753268	905.472711	453.239994	904.488695	452.747986	10
5	**518.297310**	259.652293	500.286745	250.647011	L	***851.462146***	426.234711	834.435597	417.721437	833.451581	417.229429	9
6	**575.318774**	288.163025	557.308209	279.157743	G	***738.378082***	369.692679	721.351533	361.179405	720.367517	360.687397	8
7	646.355888	323.681582	628.345323	314.676300	A	***681.356618***	341.181947	664.330069	332.668673	663.346053	332.176665	7
8	717.393002	359.200139	699.382437	350.194857	A	***610.319504***	305.663390	593.292955	297.150116	592.308939	296.658108	6
9	880.456331	440.731804	862.445766	431.726521	Y	***539.282390***	270.144833	522.255841	261.631559	521.271825	261.139551	5
10	937.477795	469.242536	919.467230	460.237253	G	***376.219061***	188.613168	359.192512	180.099894	358.208496	179.607886	4
11	1038.525474	519.766375	1020.514909	510.761093	T	***319.197597***	160.102436	302.171048	151.589162	301.187032	151.097154	3
12	1109.562588	555.284932	1091.552023	546.279650	A	218.149918	109.578597	201.123369	101.065322			2
13					K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of VFSALGAAYGTAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
75.5	1254.660828	-0.003100	VFSALGAAYGTAK
7.7	1254.668045	-0.010317	SLRLGPGGLDDR
7.5	1254.668243	-0.010515	VFSAFITVLQM
6.9	1254.660828	-0.003100	SYPGLTSYLVR
2.8	1254.664200	-0.006472	TPPGSPQLAMLK
1.2	1254.664200	-0.006472	TPPGSPQLAMLK

Mascot: http://www.matrixscience.com/

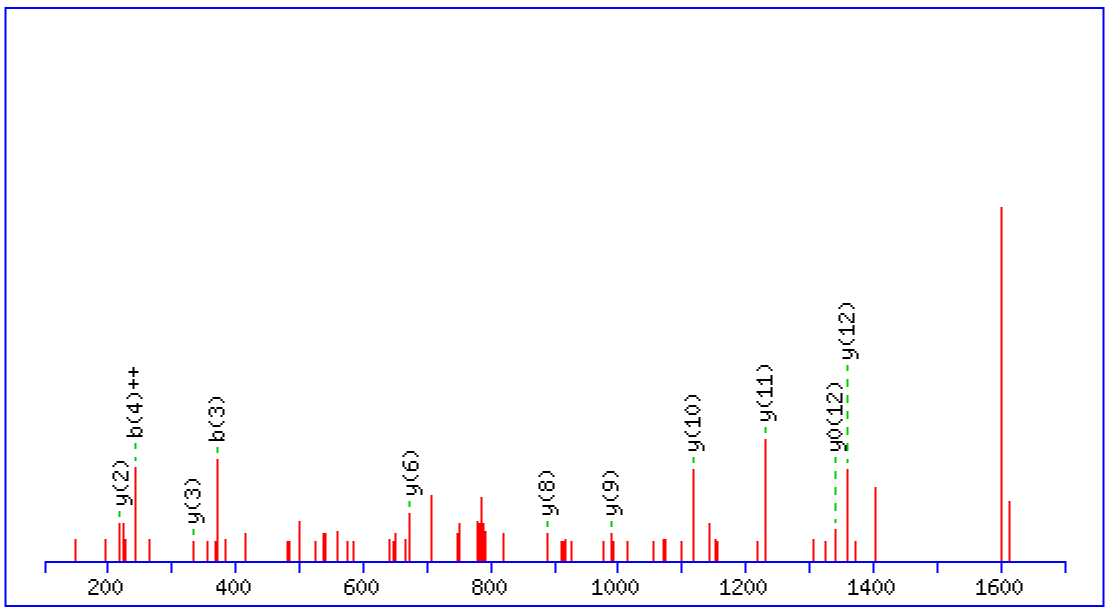
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IQQIETTLNILDAK**
Found in **CCD53_HUMAN**, WASH complex subunit CCDC53 OS=Homo sapiens GN=CCDC53 PE=1 SV=1

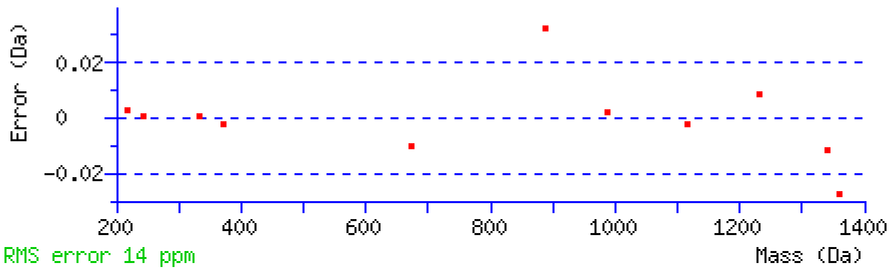
Match to Query 46514: 1598.885228 from(800.449890,2+) rtinseconds(3213) index(41258)
Title: Locus:1.1.1.2808.37
Data file 2011-11-12 - TFD - EP 5-5.mgf

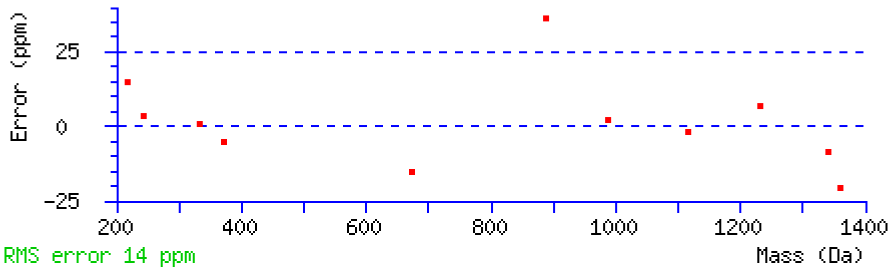
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1598.887909
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 40  Expect: 0.00027
Matches : 12/142 fragment ions using 26 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					I							14
2	**242.149918**	121.578597	225.123369	113.065323			Q	1486.811151	743.909214	1469.784602	735.395939	1468.800586	734.903931	13
3	**370.208496**	185.607886	353.181947	177.094612			Q	***1358.752573***	679.879925	1341.726024	671.366650	1340.742008	670.874642	12
4	483.292560	242.149918	466.266011	233.636644			I	***1230.693995***	615.850635	1213.667446	607.337361	1212.683430	606.845353	11
5	612.335153	306.671215	595.308604	298.157940	594.324588	297.665932	E	***1117.609931***	559.308604	1100.583382	550.795329	1099.599366	550.303321	10
6	713.382832	357.195054	696.356283	348.681780	695.372267	348.189772	T	***988.567338***	494.787307	971.540789	486.274032	970.556773	485.782024	9
7	814.430511	407.718894	797.403962	399.205619	796.419946	398.713611	T	***887.519659***	444.263467	870.493110	435.750193	869.509094	435.258185	8
8	927.514575	464.260926	910.488026	455.747651	909.504010	455.255643	L	786.471980	393.739628	769.445431	385.226353	768.461415	384.734345	7
9	1041.557502	521.282389	1024.530953	512.769115	1023.546937	512.277107	N	***673.387916***	337.197596	656.361367	328.684321	655.377351	328.192313	6
10	1154.641566	577.824421	1137.615017	569.311147	1136.631001	568.819139	I	559.344989	280.176132	542.318440	271.662858	541.334424	271.170850	5
11	1267.725630	634.366453	1250.699081	625.853179	1249.715065	625.361170	L	446.260925	223.634100	429.234376	215.120826	428.250360	214.628818	4
12	1382.752573	691.879925	1365.726024	683.366650	1364.742008	682.874642	D	***333.176861***	167.092069	316.150312	158.578794	315.166296	158.086786	3
13	1453.789687	727.398482	1436.763138	718.885207	1435.779122	718.393199	A	***218.149918***	109.578597	201.123369	101.065322			2
14							K	147.112804	74.060040	130.086255	65.546765			1



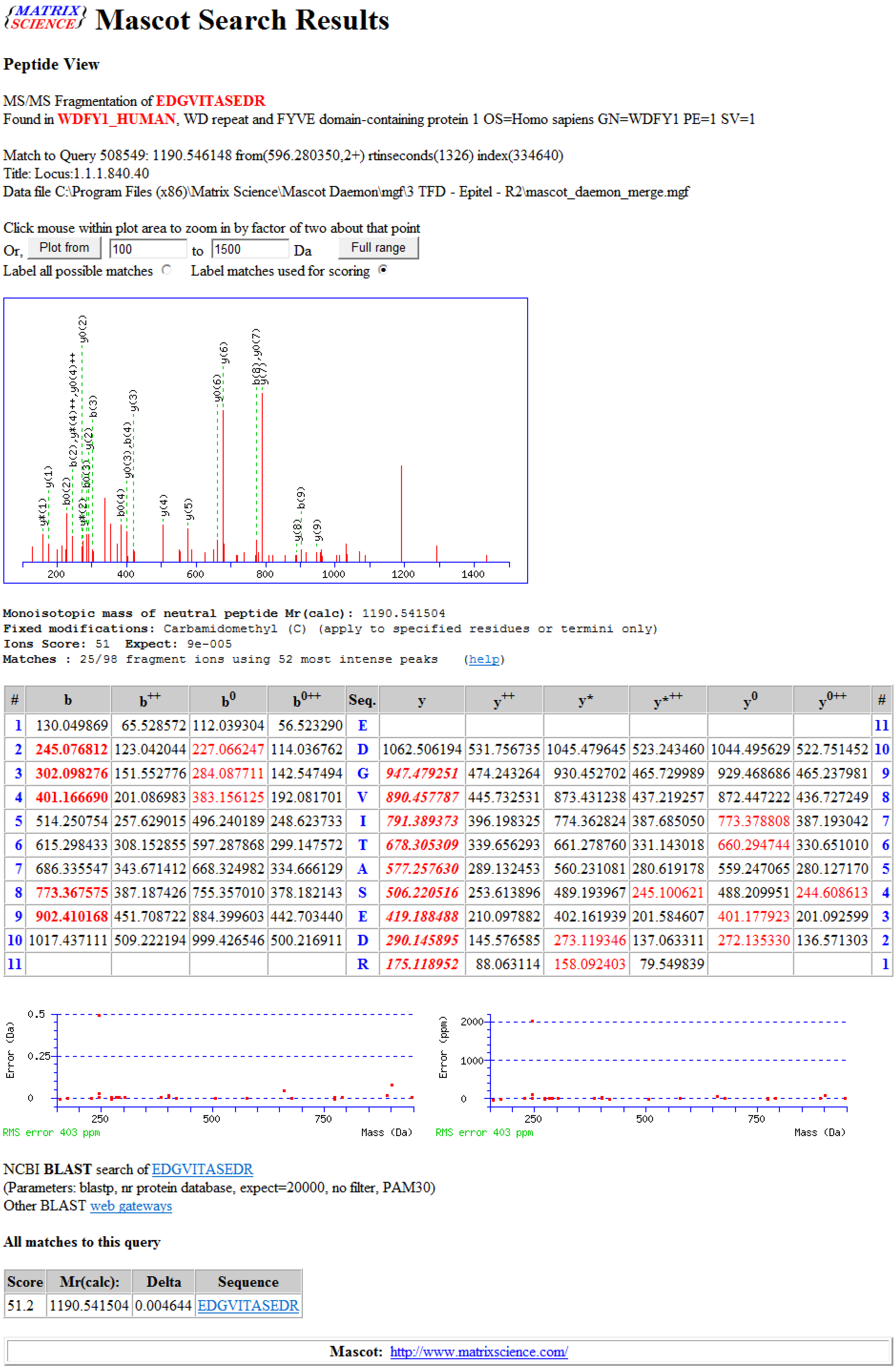


NCBI **BLAST** search of IQQIETTLNILDAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.7	1598.887909	-0.002681	IQQIETTLNILDAK
1.6	1598.887924	-0.002696	LQKQTDLDLSPLTK
1.1	1598.870163	0.015065	LLQQCETLKVPPK

Mascot: http://www.matrixscience.com/



Mascot Search Results

Peptide View

MS/MS Fragmentation of **EDGVITASEDR**
Found in **WDFY1_HUMAN**, WD repeat and FYVE domain-containing protein 1 OS=Homo sapiens GN=WDFY1 PE=1 SV=1

Match to Query 508549: 1190.546148 from(596.280350,2+) rtinseconds(1326) index(334640)
Title: Locus:1.1.1.840.40
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●

```
Monoisotopic mass of neutral peptide Mr(calc): 1190.541504
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 51  Expect: 9e-005
Matches : 25/98 fragment ions using 52 most intense peaks   (help)
```

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	130.049869	65.528572	112.039304	56.523290	E							11
2	**245.076812**	123.042044	227.066247	114.036762	D	1062.506194	531.756735	1045.479645	523.243460	1044.495629	522.751452	10
3	**302.098276**	151.552776	284.087711	142.547494	G	***947.479251***	474.243264	930.452702	465.729989	929.468686	465.237981	9
4	**401.166690**	201.086983	383.156125	192.081701	V	***890.457787***	445.732531	873.431238	437.219257	872.447222	436.727249	8
5	514.250754	257.629015	496.240189	248.623733	I	***791.389373***	396.198325	774.362824	387.685050	773.378808	387.193042	7
6	615.298433	308.152855	597.287868	299.147572	T	***678.305309***	339.656293	661.278760	331.143018	660.294744	330.651010	6
7	686.335547	343.671412	668.324982	334.666129	A	***577.257630***	289.132453	560.231081	280.619178	559.247065	280.127170	5
8	**773.367575**	387.187426	755.357010	378.182143	S	***506.220516***	253.613896	489.193967	245.100621	488.209951	244.608613	4
9	**902.410168**	451.708722	884.399603	442.703440	E	***419.188488***	210.097882	402.161939	201.584607	401.177923	201.092599	3
10	1017.437111	509.222194	999.426546	500.216911	D	***290.145895***	145.576585	273.119346	137.063311	272.135330	136.571303	2
11					R	***175.118952***	88.063114	158.092403	79.549839			1

RMS error 403 ppm

RMS error 403 ppm

NCBI **BLAST** search of EDGVITASEDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.2	1190.541504	0.004644	EDGVITASEDR

Mascot: http://www.matrixscience.com/

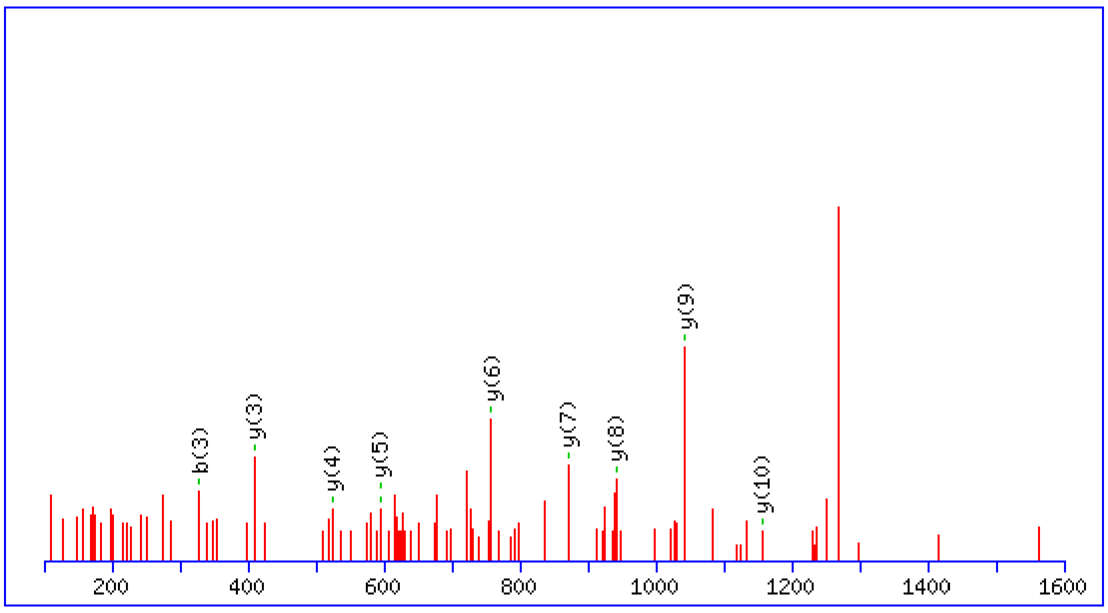
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LITAIYADYAR**
Found in **WDR11_HUMAN**, WD repeat-containing protein 11 OS=Homo sapiens GN=WDR11 PE=1 SV=1

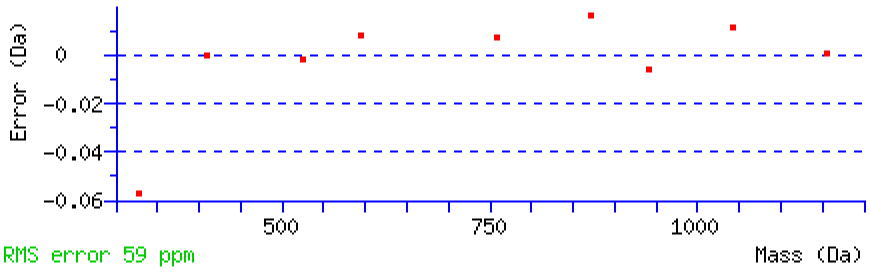
Match to Query 30608: 1268.672228 from(635.343390,2+) rtinseconds(2764) index(33703)
Title: Locus:1.1.1.2603.30
Data file 2011-11-12 - TFD - EP 5-1.mgf

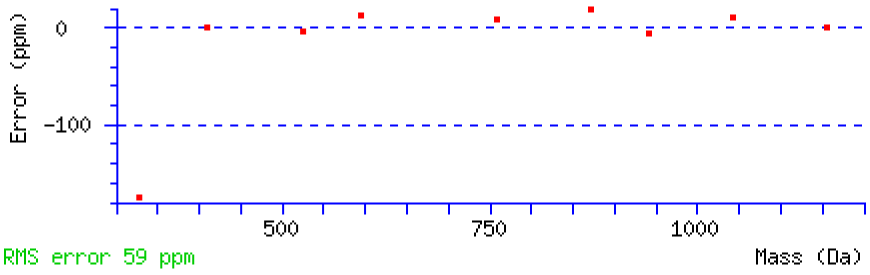
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1268.676453
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.00018
Matches : 9/90 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							11
2	227.175404	114.091340			I	***1156.599702***	578.803489	1139.573153	570.290215	1138.589137	569.798206	10
3	328.223083	164.615179	310.212518	155.609897	T	***1043.515638***	522.261457	1026.489089	513.748182	1025.505073	513.256174	9
4	399.260197	200.133737	381.249632	191.128454	A	***942.467959***	471.737617	925.441410	463.224343	924.457394	462.732335	8
5	512.344261	256.675769	494.333696	247.670486	I	***871.430845***	436.219060	854.404296	427.705786	853.420280	427.213778	7
6	675.407590	338.207433	657.397025	329.202151	Y	***758.346781***	379.677028	741.320232	371.163754	740.336216	370.671746	6
7	746.444704	373.725990	728.434139	364.720708	A	***595.283452***	298.145364	578.256903	289.632089	577.272887	289.140081	5
8	861.471647	431.239462	843.461082	422.234179	D	***524.246338***	262.626807	507.219789	254.113532	506.235773	253.621524	4
9	1024.534976	512.771126	1006.524411	503.765843	Y	***409.219395***	205.113335	392.192846	196.600061			3
10	1095.572090	548.289683	1077.561525	539.284400	A	246.156066	123.581671	229.129517	115.068396			2
11					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LITAIYADYAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.2	1268.676453	-0.004225	LITAIYADYAR
1.4	1268.662582	0.009646	RTSQGFGFTLR

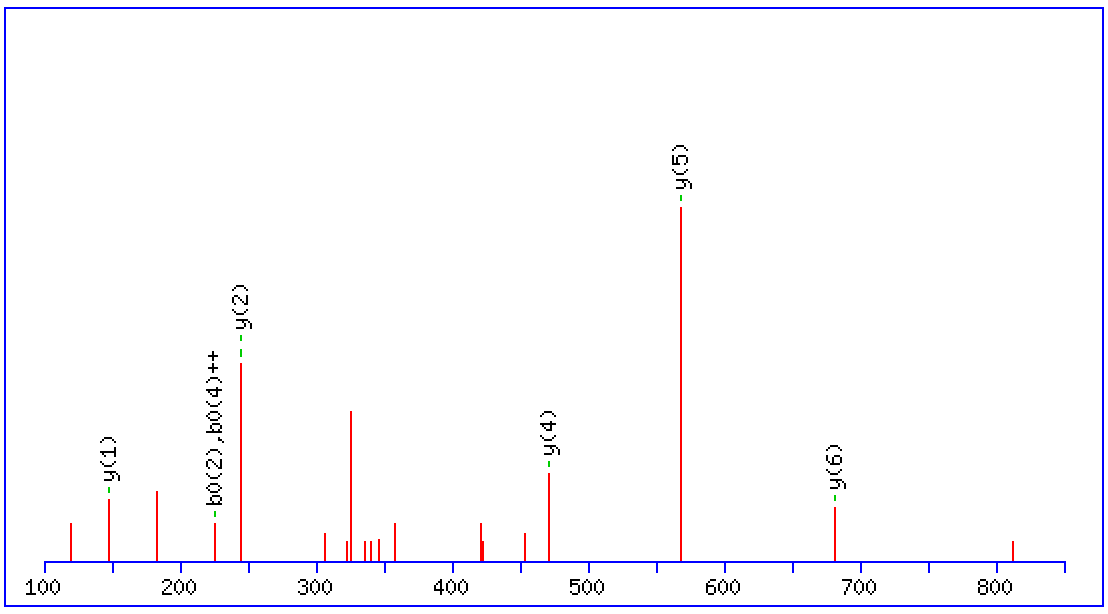
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EPPKVPK**
Found in **WDR36_HUMAN**, WD repeat-containing protein 36 OS=Homo sapiens GN=WDR36 PE=1 SV=1

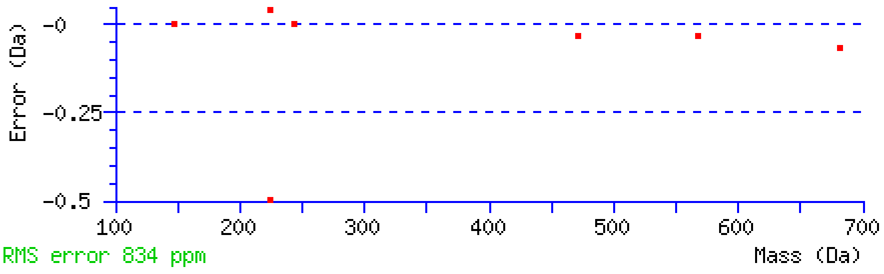
Match to Query 881: 809.467028 from(405.740790,2+) rtinseconds(2199) index(8309)
Title: Locus:1.1.1.2451.2
Data file 2011-11-10 - TFD - EP 4-8.mgf

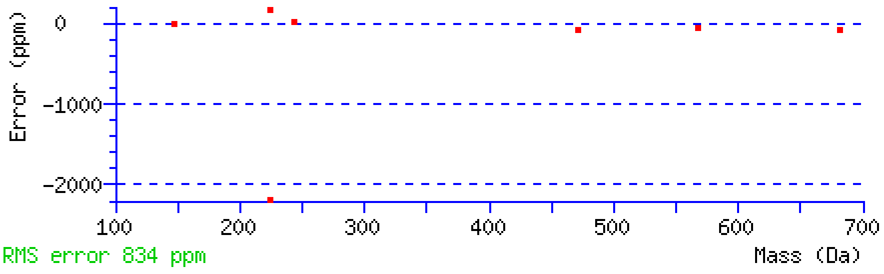
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 809.464691
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P2      : Oxidation (P)
Ions Score: 35  Expect: 0.00069
Matches : 7/54 fragment ions using 10 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	130.049869	65.528572			112.039304	56.523290	E					7
2	243.097548	122.052412			225.086983	113.047129	P	***681.429388***	341.218332	664.402839	332.705058	6
3	340.150312	170.578794			322.139747	161.573512	P	***568.381709***	284.694493	551.355160	276.181218	5
4	468.245275	234.626275	451.218726	226.113001	450.234710	225.620993	K	***471.328945***	236.168111	454.302396	227.654836	4
5	567.313689	284.160483	550.287140	275.647208	549.303124	275.155200	V	343.233982	172.120629	326.207433	163.607355	3
6	664.366453	332.686865	647.339904	324.173590	646.355888	323.681582	P	***244.165568***	122.586422	227.139019	114.073148	2
7							K	***147.112804***	74.060040	130.086255	65.546765	1





NCBI **BLAST** search of EPPKVPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.3	809.464691	0.002337	EPPKVPK
21.1	809.464676	0.002352	ELPPNLK
19.7	809.464691	0.002337	EPPKVPK
13.7	809.464691	0.002337	EKVPPPK
13.7	809.464691	0.002337	EKVPPPK
13.7	809.464691	0.002337	EVKPPPK
13.7	809.464691	0.002337	EVKPPPK
1.9	809.464691	0.002337	EKVPPPK
1.9	809.464691	0.002337	EVKPPPK
0.7	809.464691	0.002337	LPGGLEPK

{MATRIX SCIENCE}

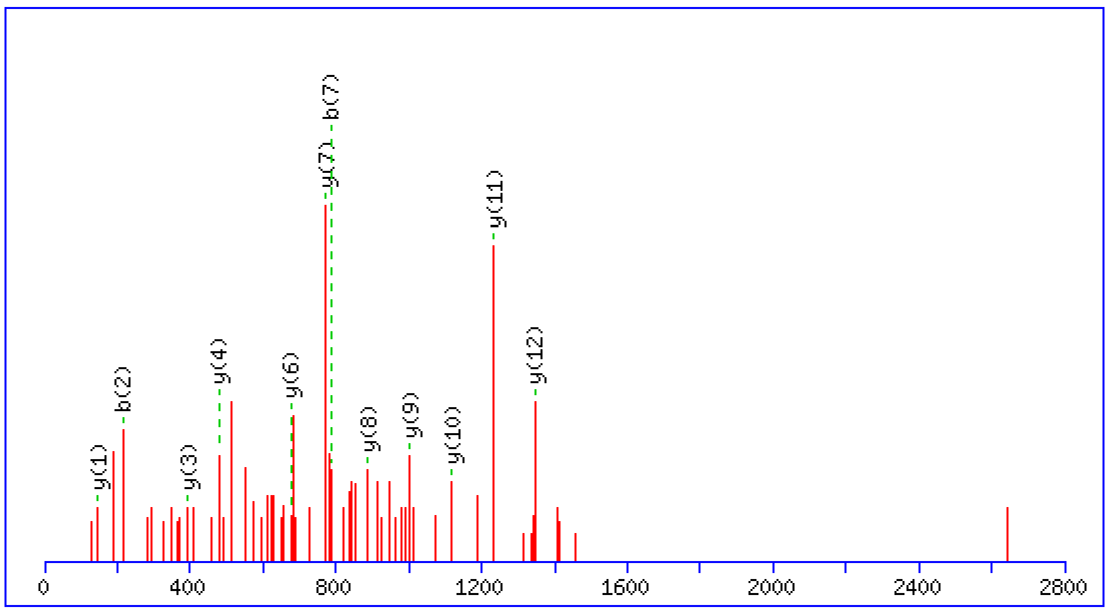
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLIDDDNPPVSFVK**
Found in **WDR5_HUMAN**, WD repeat-containing protein 5 OS=Homo sapiens GN=WDR5 PE=1 SV=1

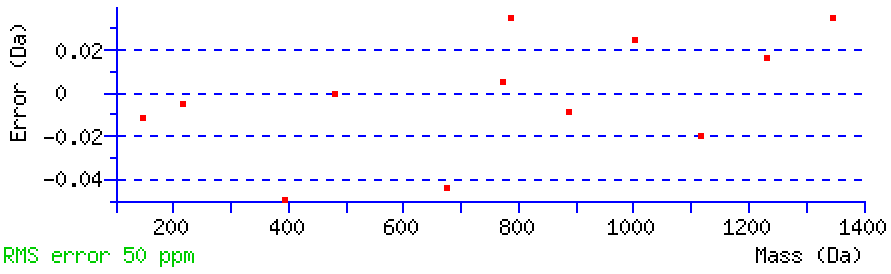
Match to Query 49808: 1558.783188 from(780.398870,2+) rtinseconds(2822) index(37581)
Title: Locus:1.1.1.2489.45
Data file 2011-11-12 - TFD - EP 5-4.mgf

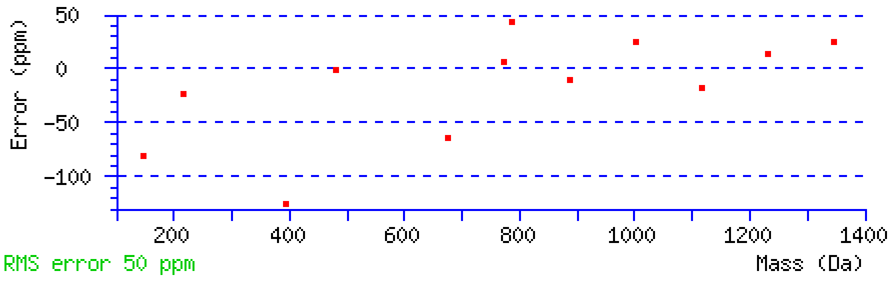
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1558.787903
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 43  Expect: 0.00037
Matches : 12/138 fragment ions using 36 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							14
2	215.139019	108.073147			197.128454	99.067865	L	1458.747486	729.877381	1441.720937	721.364107	1440.736921	720.872099	13
3	328.223083	164.615179			310.212518	155.609897	I	***1345.663422***	673.335349	1328.636873	664.822075	1327.652857	664.330067	12
4	443.250026	222.128651			425.239461	213.123369	D	***1232.579358***	616.793317	1215.552809	608.280043	1214.568793	607.788035	11
5	558.276969	279.642123			540.266404	270.636840	D	***1117.552415***	559.279846	1100.525866	550.766571	1099.541850	550.274563	10
6	673.303912	337.155594			655.293347	328.150311	D	***1002.525472***	501.766374	985.498923	493.253100	984.514907	492.761092	9
7	787.346839	394.177057	770.320290	385.663783	769.336274	385.171775	N	***887.498529***	444.252903	870.471980	435.739628	869.487964	435.247620	8
8	884.399603	442.703440	867.373054	434.190165	866.389038	433.698157	P	***773.455602***	387.231439	756.429053	378.718165	755.445037	378.226157	7
9	981.452367	491.229822	964.425818	482.716547	963.441802	482.224539	P	***676.402838***	338.705057	659.376289	330.191783	658.392273	329.699775	6
10	1080.520781	540.764028	1063.494232	532.250754	1062.510216	531.758746	V	579.350074	290.178675	562.323525	281.665401	561.339509	281.173393	5
11	1167.552809	584.280043	1150.526260	575.766768	1149.542244	575.274760	S	***480.281660***	240.644468	463.255111	232.131194	462.271095	231.639186	4
12	1314.621223	657.814250	1297.594674	649.300975	1296.610658	648.808967	F	***393.249632***	197.128454	376.223083	188.615180			3
13	1413.689637	707.348457	1396.663088	698.835182	1395.679072	698.343174	V	246.181218	123.594247	229.154669	115.080973			2
14							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of TLIDDDNPPVSFVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.7	1558.787903	-0.004715	TLIDDDNPPVSFVK
5.9	1558.796616	-0.013428	TIRFLHSFTMYK
3.3	1558.784714	-0.001526	MASSMKQVPNPLPK

Mascot: http://www.matrixscience.com/

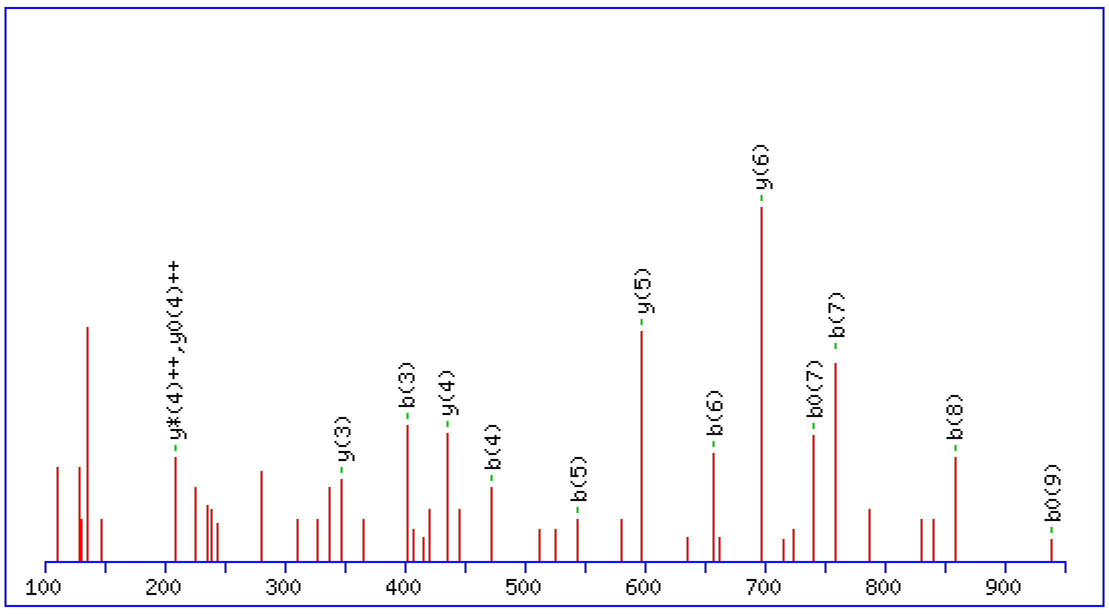
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YTHAANTVVYSSNK**
Found in **WDR82_HUMAN**, WD repeat-containing protein 82 OS=Homo sapiens GN=WDR82 PE=1 SV=1

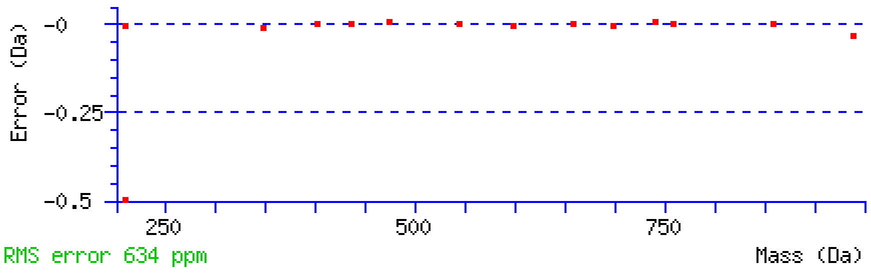
Match to Query 878778: 1553.747892 from(518.923240,3+) rtinseconds(1109) index(496073)
Title: Locus:1.1.1.747.22
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●

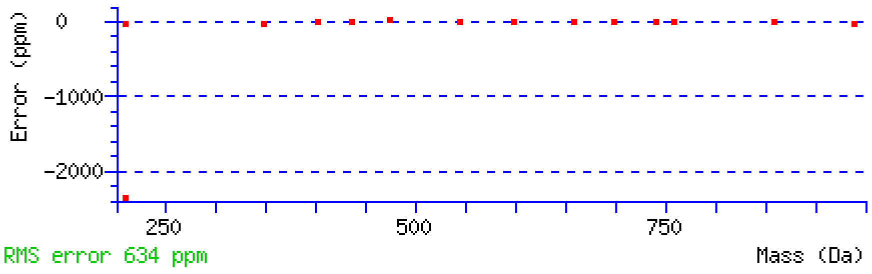


Monoisotopic mass of neutral peptide Mr(calc): 1553.747406
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 52 **Expect:** 9.1e-005
Matches : 14/140 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	164.070605	82.538940					Y							14
2	265.118284	133.062780			247.107719	124.057498	T	1391.691369	696.349323	1374.664820	687.836048	1373.680804	687.344040	13
3	***402.177196***	201.592236			384.166631	192.586954	H	1290.643690	645.825483	1273.617141	637.312209	1272.633125	636.820201	12
4	***473.214310***	237.110793			455.203745	228.105511	A	1153.584778	577.296027	1136.558229	568.782753	1135.574213	568.290745	11
5	***544.251424***	272.629350			526.240859	263.624068	A	1082.547664	541.777470	1065.521115	533.264196	1064.537099	532.772188	10
6	***658.294351***	329.650814	641.267802	321.137539	640.283786	320.645531	N	1011.510550	506.258913	994.484001	497.745639	993.499985	497.253631	9
7	***759.342030***	380.174653	742.315481	371.661379	741.331465	371.169371	T	897.467623	449.237450	880.441074	440.724175	879.457058	440.232167	8
8	***858.410444***	429.708860	841.383895	421.195585	840.399879	420.703577	V	796.419944	398.713610	779.393395	390.200336	778.409379	389.708328	7
9	957.478858	479.243067	940.452309	470.729792	939.468293	470.237784	V	***697.351530***	349.179403	680.324981	340.666129	679.340965	340.174121	6
10	1120.542187	560.774732	1103.515638	552.261457	1102.531622	551.769449	Y	***598.283116***	299.645196	581.256567	291.131922	580.272551	290.639914	5
11	1207.574215	604.290746	1190.547666	595.777471	1189.563650	595.285463	S	***435.219787***	218.113532	418.193238	209.600257	417.209222	209.108249	4
12	1294.606243	647.806760	1277.579694	639.293485	1276.595678	638.801477	S	***348.187759***	174.597518	331.161210	166.084243	330.177194	165.592235	3
13	1408.649170	704.828223	1391.622621	696.314949	1390.638605	695.822941	N	261.155731	131.081503	244.129182	122.568229			2
14							K	147.112804	74.060040	130.086255	65.546765			1



RMS error 634 ppm



RMS error 634 ppm

NCBI **BLAST** search of YTHAANTVVYSSNK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.7	1553.747406	0.000486	YTHAANTVVYSSNK

Mascot: http://www.matrixscience.com/

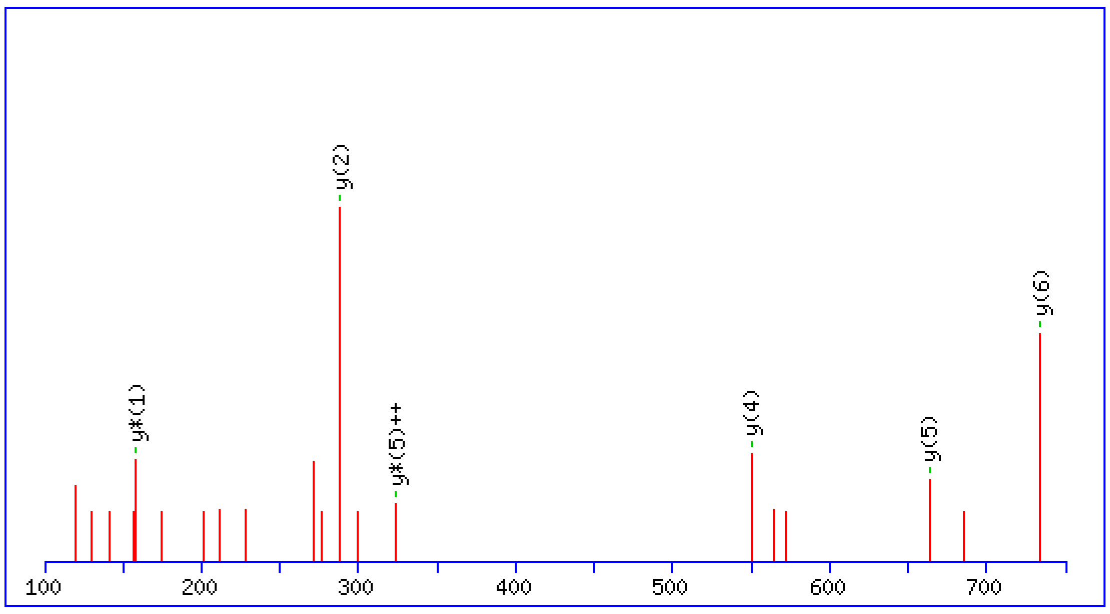
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NLAIFDLR**
Found in **MIO_HUMAN**, WD repeat-containing protein mio OS=Homo sapiens GN=MIOS PE=1 SV=2

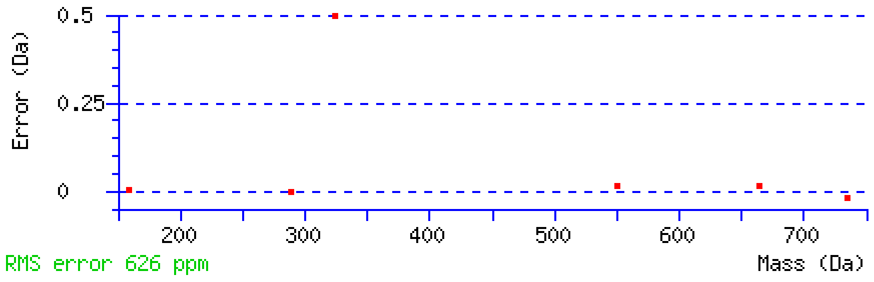
Match to Query 12958: 960.539548 from(481.277050,2+) rtinseconds(3308) index(46871)
Title: Locus:1.1.1.2693.4
Data file 2011-11-10 - TFD - EP 3-2.mgf

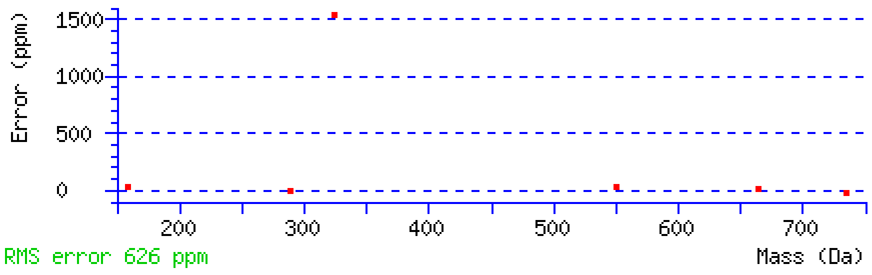
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 960.539246
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.0022
Matches : 6/70 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			N							8
2	228.134267	114.570771	211.107718	106.057497			L	847.503615	424.255446	830.477066	415.742171	829.493050	415.250163	7
3	299.171381	150.089328	282.144832	141.576054			A	***734.419551***	367.713414	717.393002	359.200139	716.408986	358.708131	6
4	412.255445	206.631361	395.228896	198.118086			I	***663.382437***	332.194857	646.355888	323.681582	645.371872	323.189574	5
5	559.323859	280.165568	542.297310	271.652293			F	***550.298373***	275.652825	533.271824	267.139550	532.287808	266.647542	4
6	674.350802	337.679039	657.324253	329.165765	656.340237	328.673757	D	403.229959	202.118617	386.203410	193.605343	385.219394	193.113335	3
7	787.434866	394.221071	770.408317	385.707797	769.424301	385.215789	L	***288.203016***	144.605146	271.176467	136.091871			2
8							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of NLAIFDLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.1	960.539246	0.000302	NLAIFDLR
15.0	960.539246	0.000302	NLLGLYPR
10.0	960.539246	0.000302	APNIYLVR
6.9	960.539246	0.000302	ALNIFVER
3.6	960.542603	-0.003055	AINIMKQK
0.5	960.542603	-0.003055	ELAMTKLR
0.1	960.542618	-0.003070	QMITALLR
0.1	960.539261	0.000287	TPFTLNLR
0.1	960.539276	0.000272	VTFQTPLR

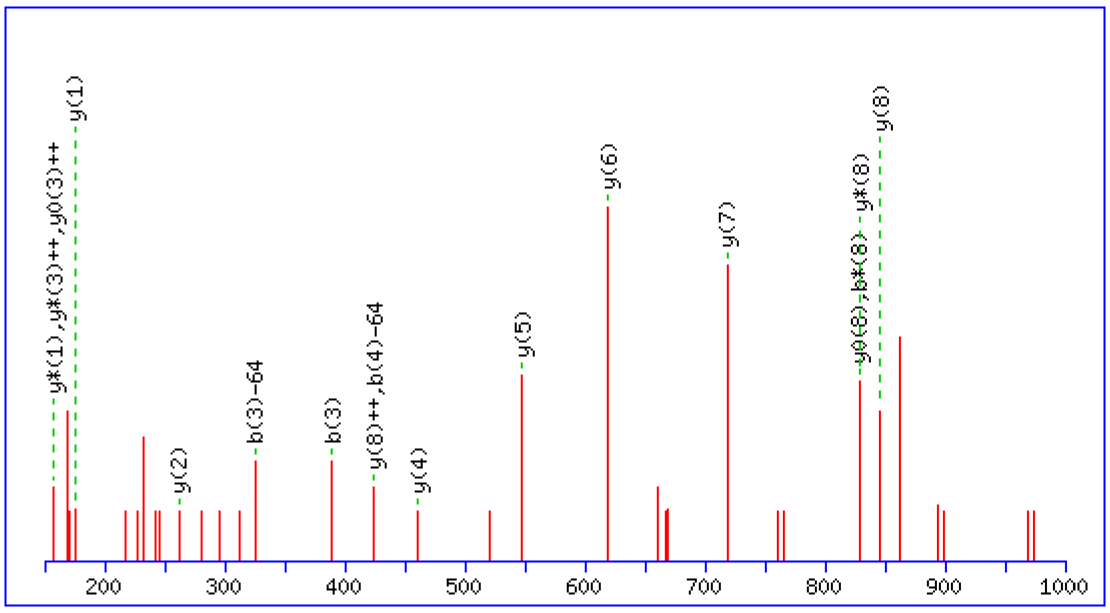
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MLQVASQASR**
Found in **WBP2_HUMAN**, WW domain-binding protein 2 OS=Homo sapiens GN=WBP2 PE=1 SV=1

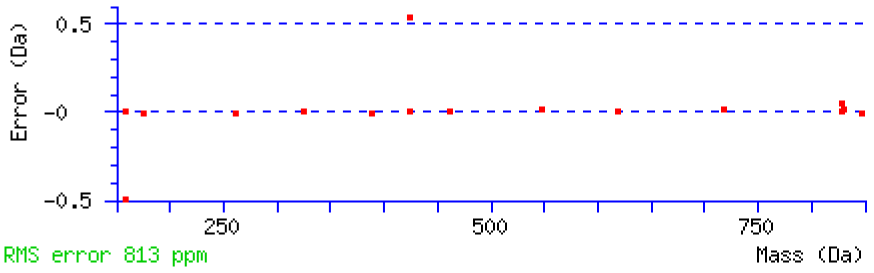
Match to Query 23749: 1105.560728 from(553.787640,2+) rtinseconds(1121) index(5807)
Title: Locus:1.1.1.1769.38
Data file 2011-11-10 - TFD - EP 3-4.mgf

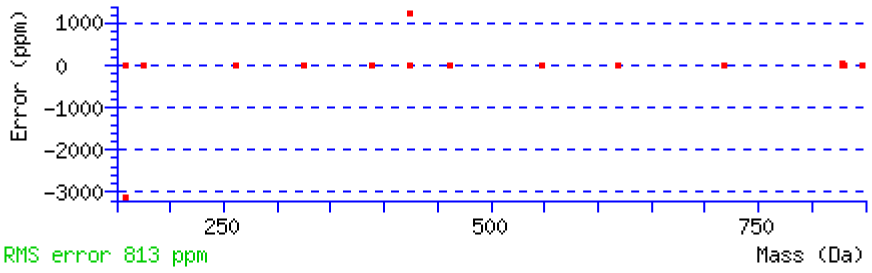
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1105.554977
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 63.998285(shown in table), 0.000000
Ions Score: 41 **Expect:** 0.0011
Matches : 17/132 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	84.044391	42.525833					M							10
2	197.128455	99.067865					L	959.526870	480.267073	942.500321	471.753799	941.516305	471.261791	9
3	**325.187033**	163.097154	308.160484	154.583880			Q	***846.442806***	423.725041	829.416257	415.211767	828.432241	414.719759	8
4	**424.255447**	212.631362	407.228898	204.118087			V	***718.384228***	359.695752	701.357679	351.182478	700.373663	350.690470	7
5	495.292561	248.149919	478.266012	239.636644			A	***619.315814***	310.161545	602.289265	301.648271	601.305249	301.156263	6
6	582.324589	291.665933	565.298040	283.152658	564.314024	282.660650	S	***548.278700***	274.642988	531.252151	266.129714	530.268135	265.637706	5
7	710.383167	355.695222	693.356618	347.181947	692.372602	346.689939	Q	***461.246672***	231.126974	444.220123	222.613700	443.236107	222.121692	4
8	781.420281	391.213779	764.393732	382.700504	763.409716	382.208496	A	333.188094	167.097685	316.161545	158.584410	315.177529	158.092402	3
9	868.452309	434.729793	851.425760	426.216518	850.441744	425.724510	S	***262.150980***	131.579128	245.124431	123.065854	244.140415	122.573846	2
10							R	***175.118952***	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of MLQVASQASR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.1	1105.554977	0.005751	MLQVASQASR

Mascot: http://www.matrixscience.com/

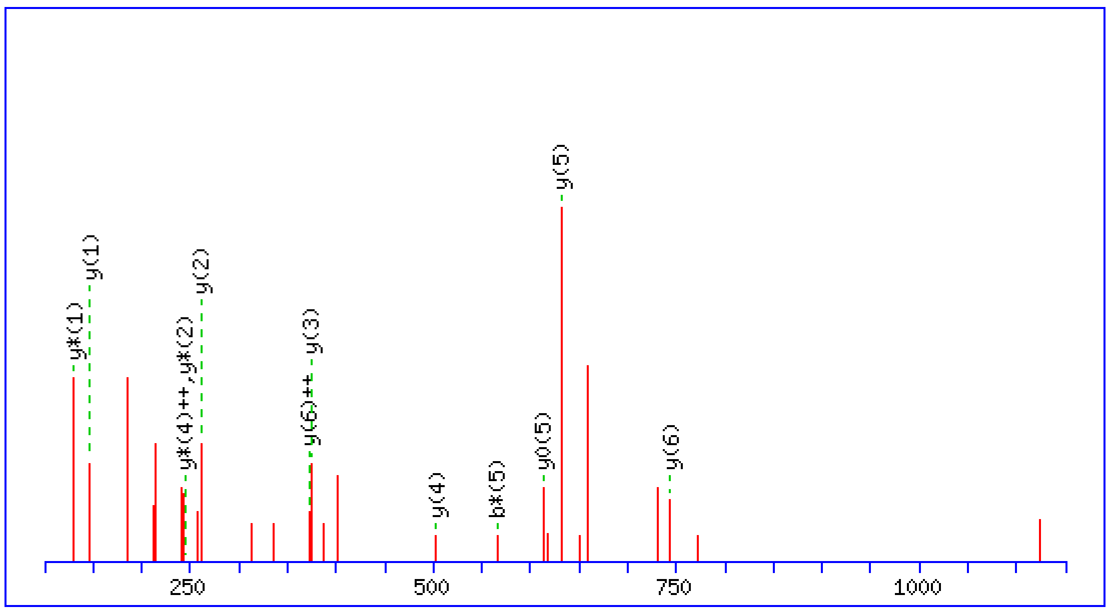
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLQELNK**
Found in **ZBT48_HUMAN**, Zinc finger and BTB domain-containing protein 48 OS=Homo sapiens GN=ZBTB48 PE=1 SV=2

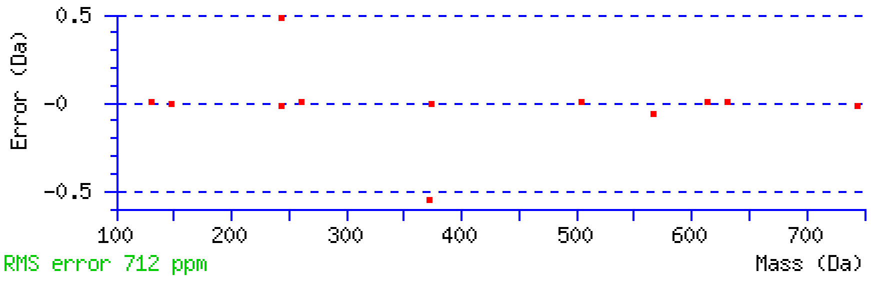
Match to Query 3101: 842.486448 from(422.250500,2+) rtinseconds(1187) index(7517)
Title: Locus:1.1.1.1865.12
Data file 2011-11-10 - TFD - EP 3-3.mgf

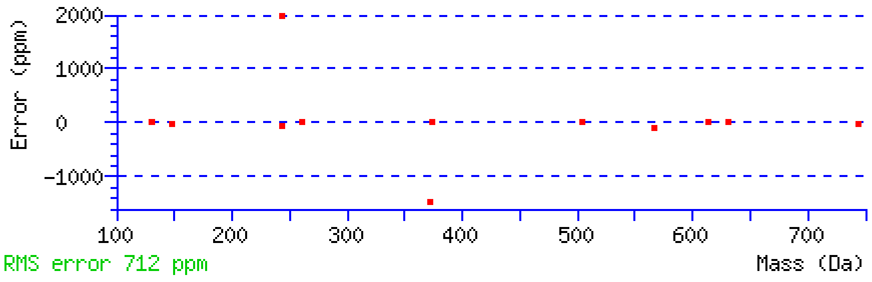
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 842.486145
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.0043
Matches : 12/56 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					**V**							7
2	213.159754	107.083515					**L**	*744.425030*	372.716153	727.398481	364.202879	726.414465	363.710871	6
3	341.218332	171.112804	324.191783	162.599529			**Q**	*631.340966*	316.174121	614.314417	307.660847	613.330401	307.168839	5
4	470.260925	235.634100	453.234376	227.120826	452.250360	226.628818	**E**	*503.282388*	252.144832	486.255839	243.631557	485.271823	243.139549	4
5	583.344989	292.176133	566.318440	283.662858	565.334424	283.170850	**L**	*374.239795*	187.623535	357.213246	179.110261			3
6	697.387916	349.197596	680.361367	340.684322	679.377351	340.192314	**N**	*261.155731*	131.081503	244.129182	122.568229			2
7							**K**	*147.112804*	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of VLQELNK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.7	842.486145	0.000303	VLQELNK
21.8	842.486160	0.000288	VLQDQLK
21.0	842.486160	0.000288	VIEQLGGK
18.9	842.486145	0.000303	LAGLDINK
18.7	842.486145	0.000303	ALLDGLNK
14.6	842.486145	0.000303	AIVGNLEK
13.2	842.486160	0.000288	APVGVEKK
11.5	842.486145	0.000303	ILNQVEK
8.1	842.486160	0.000288	LPNSVLGK
7.9	842.486130	0.000318	LLLENNK

Mascot: http://www.matrixscience.com/

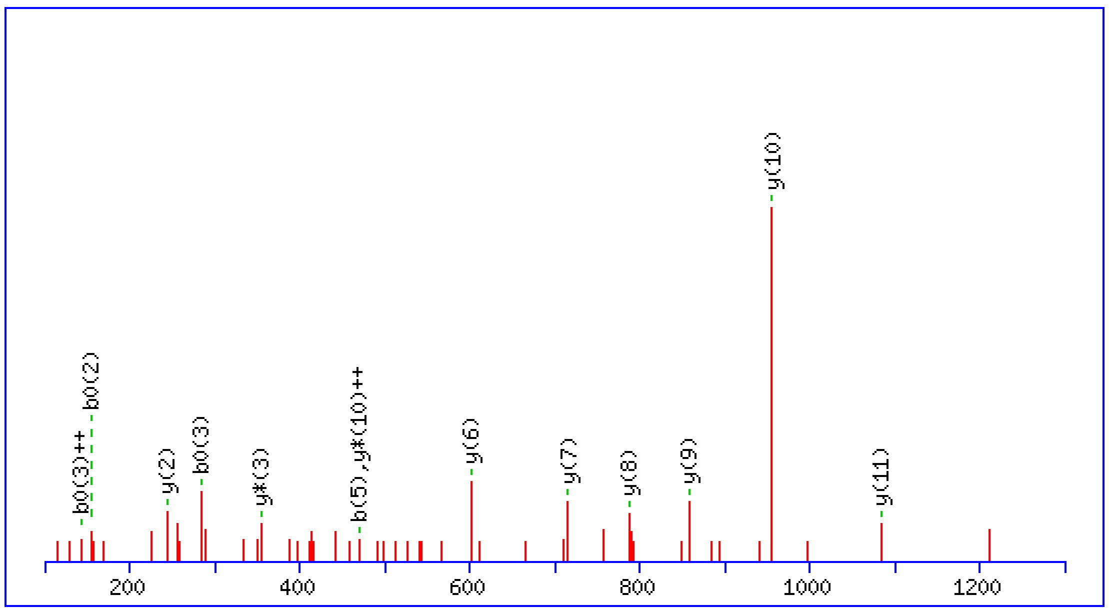
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ATEPAADTGAQPK**
Found in **ZC3H4_HUMAN**, Zinc finger CCCH domain-containing protein 4 OS=Homo sapiens GN=ZC3H4 PE=1 SV=3

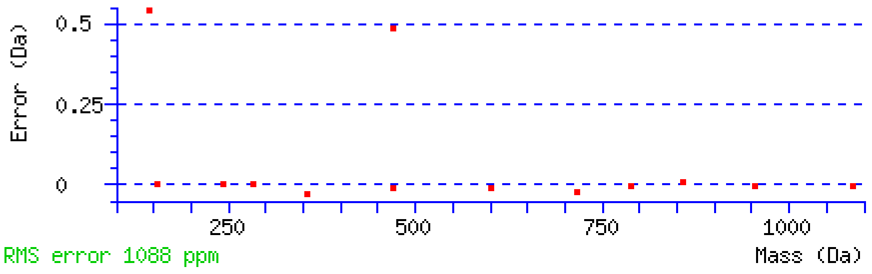
Match to Query 588416: 1255.603008 from(628.808780,2+) rtinseconds(891) index(157726)
Title: Locus:1.1.1.1024.12
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

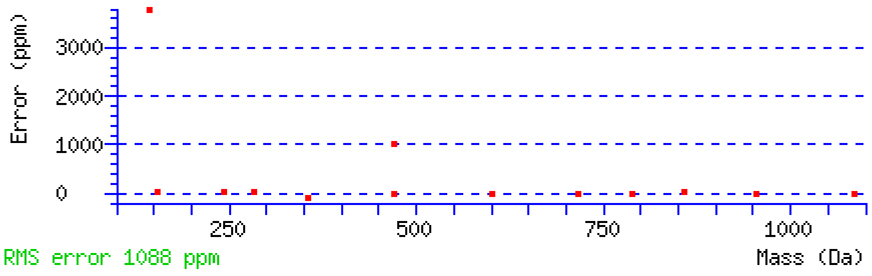
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1255.604431
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 40 **Expect:** 0.0005
Matches : 13/112 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							13
2	173.092069	87.049672			155.081504	78.044390	T	1185.574610	593.290943	1168.548061	584.777669	1167.564045	584.285661	12
3	302.134662	151.570969			284.124097	142.565687	E	***1084.526931***	542.767104	1067.500382	534.253829	1066.516366	533.761821	11
4	399.187426	200.097351			381.176861	191.092069	P	***955.484338***	478.245807	938.457789	469.732533	937.473773	469.240525	10
5	470.224540	235.615908			452.213975	226.610626	A	***858.431574***	429.719425	841.405025	421.206151	840.421009	420.714143	9
6	541.261654	271.134465			523.251089	262.129183	A	***787.394460***	394.200868	770.367911	385.687594	769.383895	385.195586	8
7	656.288597	328.647937			638.278032	319.642654	D	***716.357346***	358.682311	699.330797	350.169037	698.346781	349.677029	7
8	757.336276	379.171776			739.325711	370.166494	T	***601.330403***	301.168840	584.303854	292.655565	583.319838	292.163557	6
9	814.357740	407.682508			796.347175	398.677226	G	500.282724	250.645000	483.256175	242.131726			5
10	885.394854	443.201065			867.384289	434.195783	A	443.261260	222.134268	426.234711	213.620994			4
11	1013.453432	507.230354	996.426883	498.717080	995.442867	498.225072	Q	372.224146	186.615711	355.197597	178.102437			3
12	1110.506196	555.756736	1093.479647	547.243462	1092.495631	546.751454	P	***244.165568***	122.586422	227.139019	114.073148			2
13							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of ATEPAADTGAQPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.5	1255.604431	-0.001423	ATEPAADTGAQPK
4.1	1255.593185	0.009823	AAEVEPSSPEPK
1.5	1255.604431	-0.001423	QPTANEVEQPK

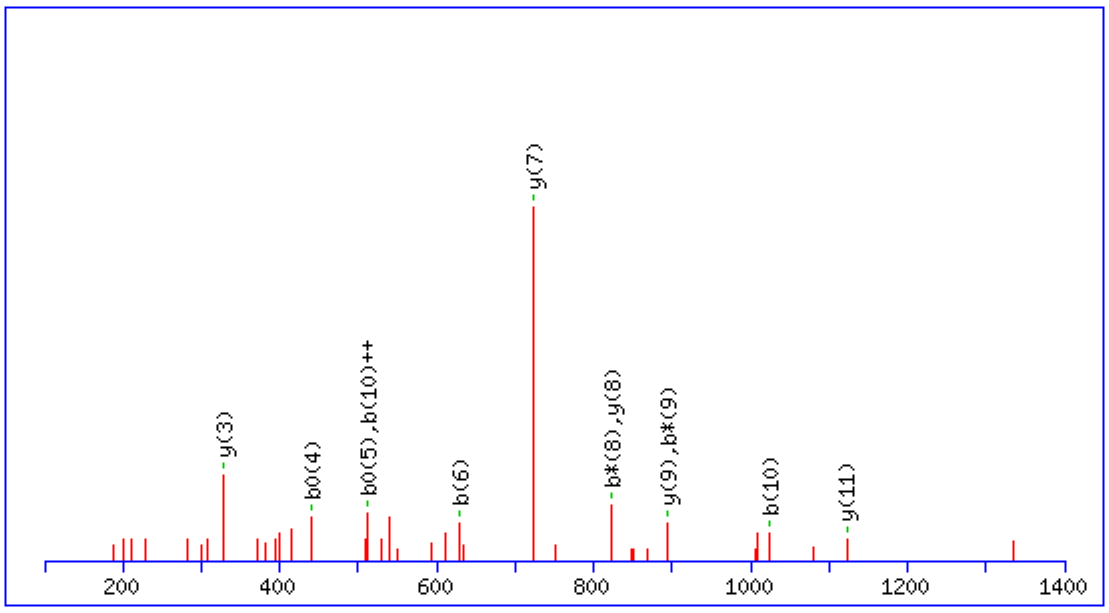
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ETIDAVPNAIPGR**
Found in **ZN207_HUMAN**, Zinc finger protein 207 OS=Homo sapiens GN=ZNF207 PE=1 SV=1

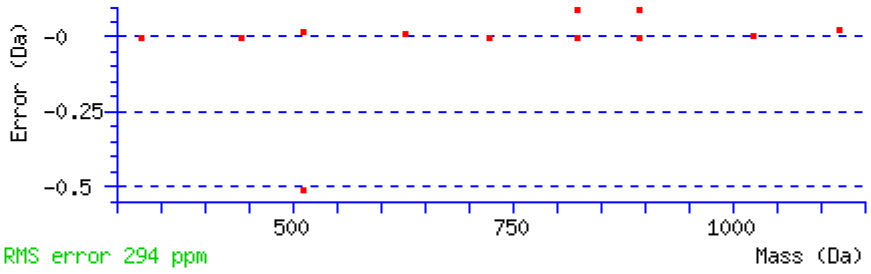
Match to Query 697435: 1351.713548 from(676.864050,2+) rtinseconds(2278) index(435090)
Title: Locus:1.1.1.1211.44
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

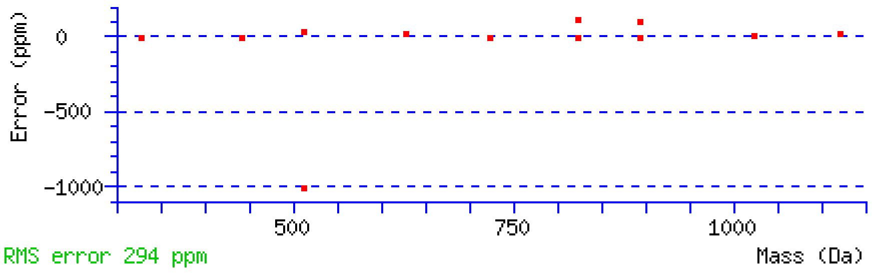
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1351.709564
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 43 **Expect:** 0.00051
Matches : 12/112 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	E							13
2	231.097548	116.052412			213.086983	107.047130	T	1223.674263	612.340770	1206.647714	603.827495	1205.663698	603.335487	12
3	344.181612	172.594444			326.171047	163.589162	I	***1122.626584***	561.816930	1105.600035	553.303655	1104.616019	552.811647	11
4	459.208555	230.107916			441.197990	221.102633	D	1009.542520	505.274898	992.515971	496.761623	991.531955	496.269615	10
5	530.245669	265.626473			512.235104	256.621190	A	***894.515577***	447.761426	877.489028	439.248152			9
6	**629.314083**	315.160680			611.303518	306.155397	V	***823.478463***	412.242869	806.451914	403.729595			8
7	726.366847	363.687062			708.356282	354.681779	P	***724.410049***	362.708663	707.383500	354.195388			7
8	840.409774	420.708525	823.383225	412.195251	822.399209	411.703243	N	627.357285	314.182280	610.330736	305.669006			6
9	911.446888	456.227082	894.420339	447.713808	893.436323	447.221800	A	513.314358	257.160817	496.287809	248.647542			5
10	**1024.530952**	512.769114	1007.504403	504.255839	1006.520387	503.763831	I	442.277244	221.642260	425.250695	213.128985			4
11	1121.583716	561.295496	1104.557167	552.782222	1103.573151	552.290214	P	***329.193180***	165.100228	312.166631	156.586953			3
12	1178.605180	589.806228	1161.578631	581.292954	1160.594615	580.800946	G	232.140416	116.573846	215.113867	108.060571			2
13							R	175.118952	88.063114	158.092403	79.549839			1



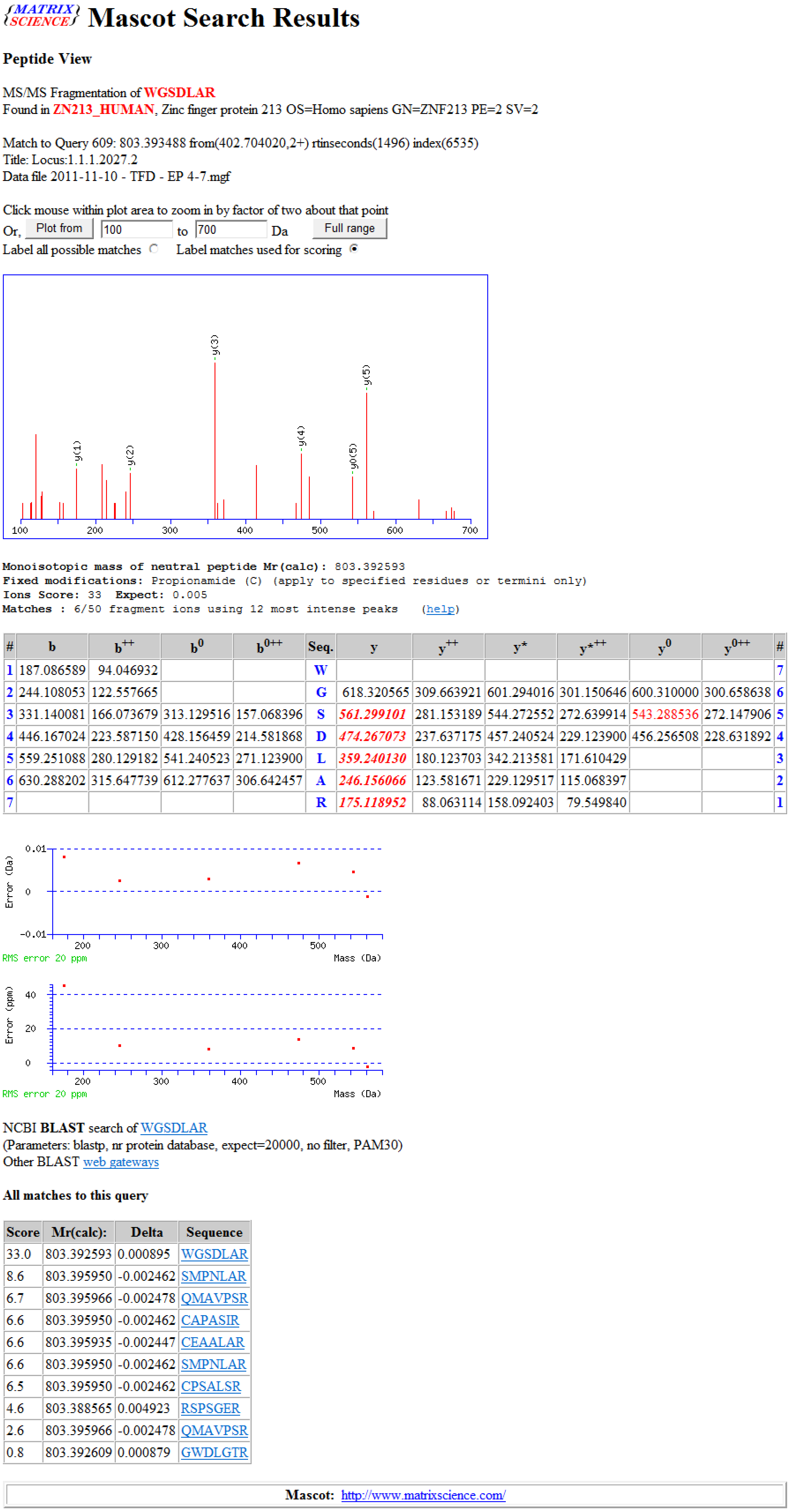


NCBI **BLAST** search of ETIDAVPNAIPGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.9	1351.709564	0.003984	ETIDAVPNAIPGR

Mascot: http://www.matrixscience.com/



Mascot Search Results

Peptide View

MS/MS Fragmentation of **WGSDLAR**
Found in **ZN213_HUMAN**, Zinc finger protein 213 OS=Homo sapiens GN=ZNF213 PE=2 SV=2

Match to Query 609: 803.393488 from(402.704020,2+) rtinseconds(1496) index(6535)
Title: Locus:1.1.1.2027.2
Data file 2011-11-10 - TFD - EP 4-7.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
Label all possible matches ○ Label matches used for scoring ●

```
Monoisotopic mass of neutral peptide Mr(calc): 803.392593
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 33  Expect: 0.005
Matches : 6/50 fragment ions using 12 most intense peaks   (help)
```

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	187.086589	94.046932			W							7
2	244.108053	122.557665			G	618.320565	309.663921	601.294016	301.150646	600.310000	300.658638	6
3	331.140081	166.073679	313.129516	157.068396	S	***561.299101***	281.153189	544.272552	272.639914	543.288536	272.147906	5
4	446.167024	223.587150	428.156459	214.581868	D	***474.267073***	237.637175	457.240524	229.123900	456.256508	228.631892	4
5	559.251088	280.129182	541.240523	271.123900	L	***359.240130***	180.123703	342.213581	171.610429			3
6	630.288202	315.647739	612.277637	306.642457	A	***246.156066***	123.581671	229.129517	115.068397			2
7					R	***175.118952***	88.063114	158.092403	79.549840			1

NCBI **BLAST** search of WGSDLAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.0	803.392593	0.000895	WGSDLAR
8.6	803.395950	-0.002462	SMPNLAR
6.7	803.395966	-0.002478	QMAVPSR
6.6	803.395950	-0.002462	CAPASIR
6.6	803.395935	-0.002447	CEAALAR
6.6	803.395950	-0.002462	SMPNLAR
6.5	803.395950	-0.002462	CPSALSR
4.6	803.388565	0.004923	RSPSGER
2.6	803.395966	-0.002478	QMAVPSR
0.8	803.392609	0.000879	GWDLGTR

Mascot: http://www.matrixscience.com/

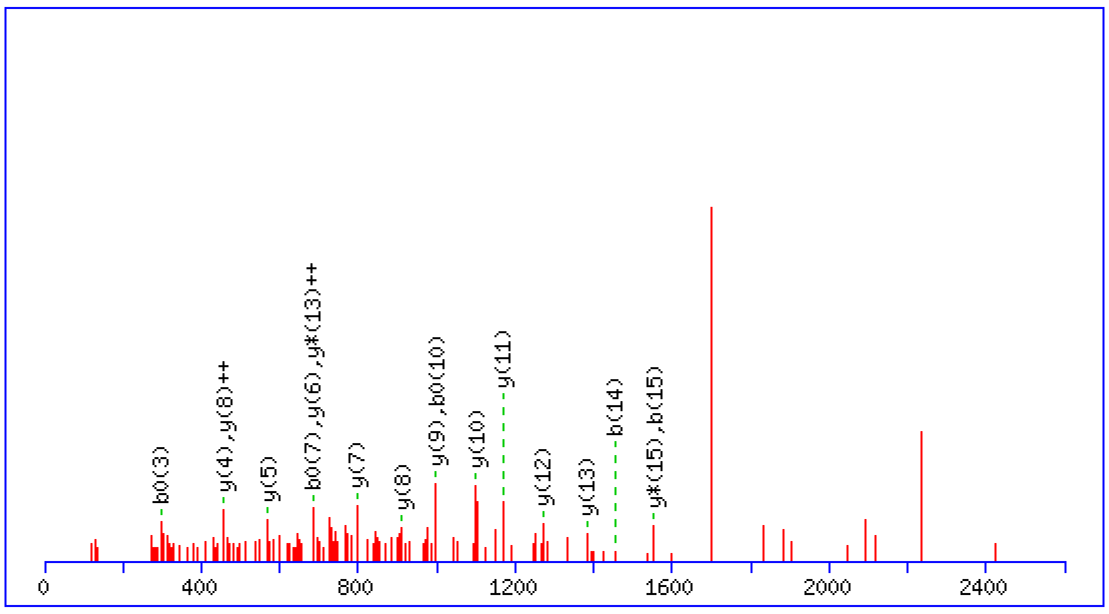
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ESVLTATSILNNPIVK**
Found in **ZN326_HUMAN**, Zinc finger protein 326 OS=Homo sapiens GN=ZNF326 PE=1 SV=2

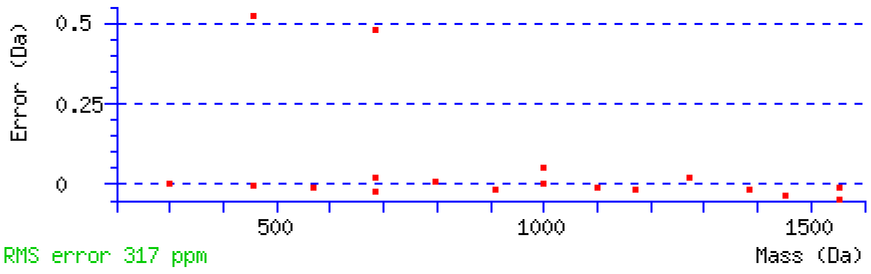
Match to Query 55282: 1697.958588 from(849.986570,2+) rtinseconds(3402) index(48050)
Title: Locus:1.1.1.2678.48
Data file 2011-11-12 - TFD - EP 6-2.mgf

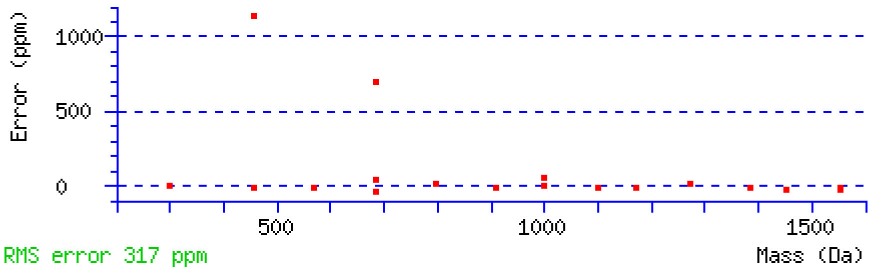
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1697.956329
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 92 **Expect:** 2.7e-009
Matches : 18/144 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	E							16
2	217.081897	109.044586			199.071332	100.039304	S	1569.921034	785.464155	1552.894485	776.950881	1551.910469	776.458873	15
3	316.150311	158.578793			298.139746	149.573511	V	1482.889006	741.948141	1465.862457	733.434867	1464.878441	732.942859	14
4	429.234375	215.120826			411.223810	206.115543	L	***1383.820592***	692.413934	1366.794043	683.900660	1365.810027	683.408652	13
5	530.282054	265.644665			512.271489	256.639383	T	***1270.736528***	635.871902	1253.709979	627.358628	1252.725963	626.866620	12
6	601.319168	301.163222			583.308603	292.157940	A	***1169.688849***	585.348063	1152.662300	576.834788	1151.678284	576.342780	11
7	702.366847	351.687062			684.356282	342.681779	T	***1098.651735***	549.829506	1081.625186	541.316231	1080.641170	540.824223	10
8	789.398875	395.203076			771.388310	386.197793	S	***997.604056***	499.305666	980.577507	490.792392	979.593491	490.300384	9
9	902.482939	451.745108			884.472374	442.739825	I	***910.572028***	455.789652	893.545479	447.276378			8
10	1015.567003	508.287140			997.556438	499.281857	L	***797.487964***	399.247620	780.461415	390.734346			7
11	1129.609930	565.308603	1112.583381	556.795329	1111.599365	556.303321	N	***684.403900***	342.705588	667.377351	334.192314			6
12	1243.652857	622.330067	1226.626308	613.816792	1225.642292	613.324784	N	***570.360973***	285.684125	553.334424	277.170850			5
13	1340.705621	670.856449	1323.679072	662.343174	1322.695056	661.851166	P	***456.318046***	228.662661	439.291497	220.149386			4
14	**1453.789685**	727.398481	1436.763136	718.885206	1435.779120	718.393198	I	359.265282	180.136279	342.238733	171.623004			3
15	**1552.858099**	776.932688	1535.831550	768.419413	1534.847534	767.927405	V	246.181218	123.594247	229.154669	115.080973			2
16							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of ESVLTATSILNNPIVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
92.2	1697.956329	0.002259	ESVLTATSILNNPIVK

Mascot: http://www.matrixscience.com/

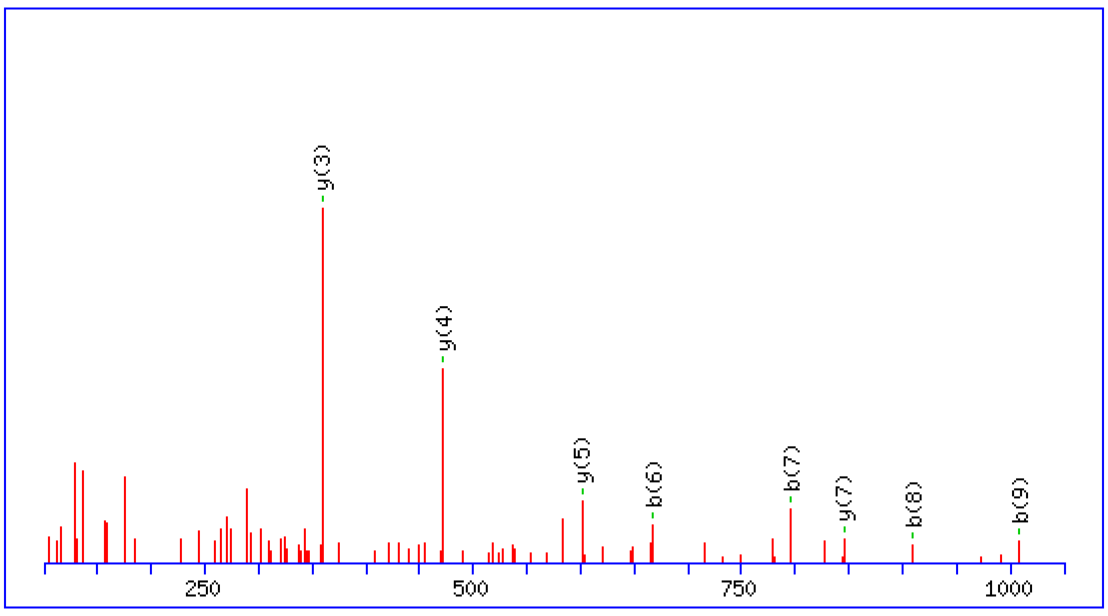
Mascot Search Results

Peptide View

MS/MS Fragmentation of **STYADEELVIK**
Found in **ZN398_HUMAN**, Zinc finger protein 398 OS=Homo sapiens GN=ZNF398 PE=2 SV=1

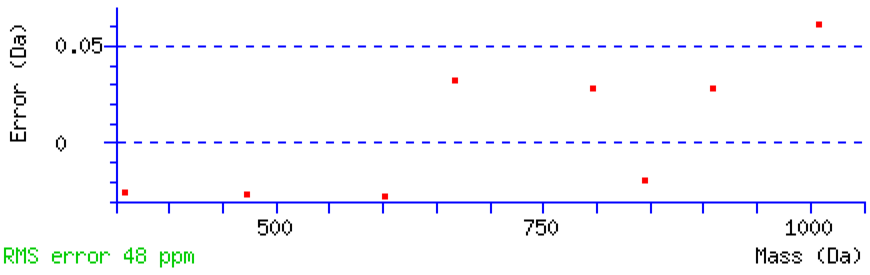
Match to Query 30883: 1266.633462 from(423.218430,3+) rtinseconds(2075) index(24305)
Title: Locus:1.1.1.2160.5
Data file 2011-11-12 - TFD - EP 6-3.mgf

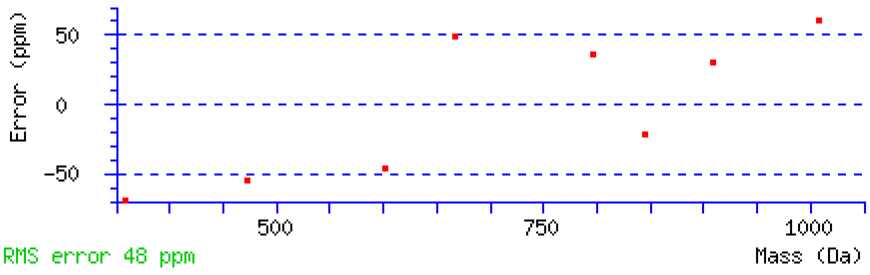
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1266.634323
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.0054
Matches : 8/92 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	S							11
2	189.086983	95.047129	171.076418	86.041847	T	1180.609597	590.808436	1163.583048	582.295162	1162.599032	581.803154	10
3	352.150312	176.578794	334.139747	167.573512	Y	1079.561918	540.284597	1062.535369	531.771323	1061.551353	531.279315	9
4	423.187426	212.097351	405.176861	203.092069	A	916.498589	458.752933	899.472040	450.239658	898.488024	449.747650	8
5	538.214369	269.610823	520.203804	260.605540	D	***845.461475***	423.234376	828.434926	414.721101	827.450910	414.229093	7
6	***667.256962***	334.132119	649.246397	325.126837	E	730.434532	365.720904	713.407983	357.207630	712.423967	356.715622	6
7	***796.299555***	398.653416	778.288990	389.648133	E	***601.391939***	301.199608	584.365390	292.686333	583.381374	292.194325	5
8	***909.383619***	455.195448	891.373054	446.190165	L	***472.349346***	236.678311	455.322797	228.165036			4
9	***1008.452033***	504.729655	990.441468	495.724372	V	***359.265282***	180.136279	342.238733	171.623004			3
10	1121.536097	561.271686	1103.525532	552.266404	I	260.196868	130.602072	243.170319	122.088797			2
11					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of STYADEELVIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.2	1266.634323	-0.000861	STYADEELVIK
9.9	1266.627823	0.005639	YMGDLSGGQVLK
7.2	1266.642899	-0.009437	TGQGPGSRAPSPR
6.6	1266.631668	0.001794	GATPPAPPRAPR
5.0	1266.631668	0.001794	LGHNEIGDTGVR
4.8	1266.631653	0.001809	APVRGDEAPPAR
4.5	1266.639053	-0.005591	TLGSKCGDFLR
4.2	1266.642868	-0.009406	RNSNSNPPLPR
3.3	1266.642868	-0.009406	SAEKRPHSPSR
3.2	1266.625107	0.008355	RNQHMPLESR

Mascot: http://www.matrixscience.com/

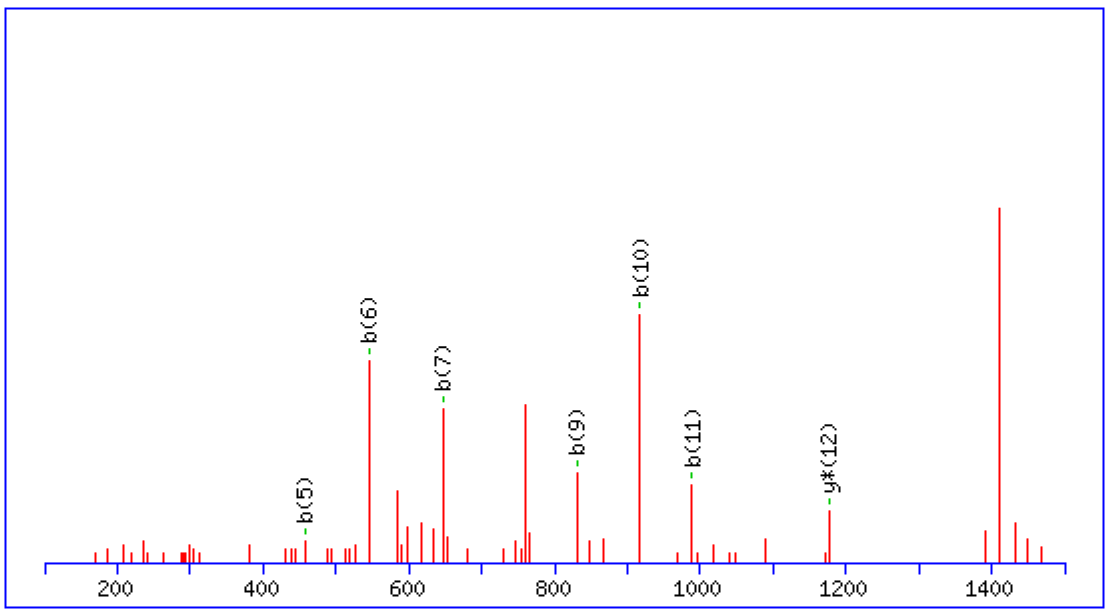
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AEGPSSTPSSAAGPRPPR**
Found in **ZN580_HUMAN**, Zinc finger protein 580 OS=Homo sapiens GN=ZNF580 PE=2 SV=1

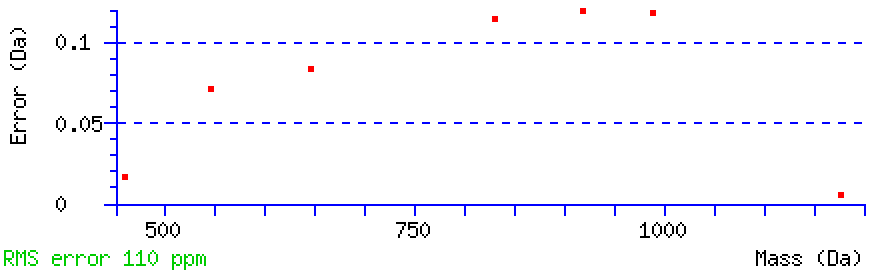
Match to Query 972389: 1736.848308 from(869.431430,2+) rtinseconds(2085) index(513560)
Title: Locus:1.1.1.1127.45
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

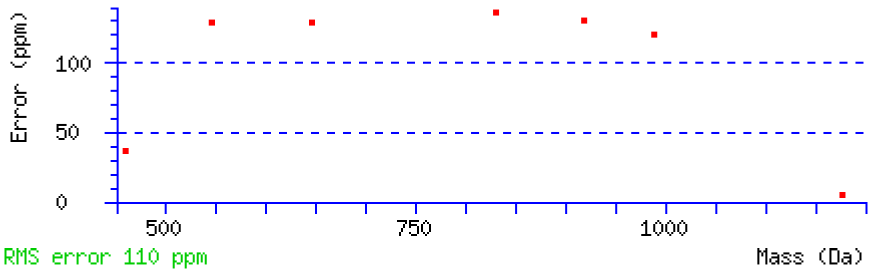
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1500] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1736.844162
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
P4      : Oxidation (P)
Ions Score: 31  Expect: 0.0044
Matches : 7/158 fragment ions using 12 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							18
2	201.086983	101.047130			183.076418	92.041847	E	1666.814338	833.910807	1649.787789	825.397533	1648.803773	824.905524	17
3	258.108447	129.557862			240.097882	120.552579	G	1537.771745	769.389510	1520.745196	760.876236	1519.761180	760.384228	16
4	371.156126	186.081701			353.145561	177.076419	P	1480.750281	740.878778	1463.723732	732.365504	1462.739716	731.873496	15
5	***458.188154***	229.597715			440.177589	220.592433	S	1367.702602	684.354939	1350.676053	675.841664	1349.692037	675.349656	14
6	***545.220182***	273.113729			527.209617	264.108447	S	1280.670574	640.838925	1263.644025	632.325651	1262.660009	631.833643	13
7	***646.267861***	323.637569			628.257296	314.632286	T	1193.638546	597.322911	1176.611997	588.809637	1175.627981	588.317628	12
8	743.320625	372.163951			725.310060	363.158668	P	1092.590867	546.799071	1075.564318	538.285797	1074.580302	537.793789	11
9	***830.352653***	415.679965			812.342088	406.674682	S	995.538103	498.272689	978.511554	489.759415	977.527538	489.267407	10
10	***917.384681***	459.195979			899.374116	450.190696	S	908.506075	454.756675	891.479526	446.243401	890.495510	445.751393	9
11	***988.421795***	494.714536			970.411230	485.709253	A	821.474047	411.240661	804.447498	402.727387			8
12	1059.458909	530.233093			1041.448344	521.227810	A	750.436933	375.722105	733.410384	367.208830			7
13	1116.480373	558.743824			1098.469808	549.738542	G	679.399819	340.203548	662.373270	331.690273			6
14	1213.533137	607.270206			1195.522572	598.264924	P	622.378355	311.692816	605.351806	303.179541			5
15	1369.634248	685.320762	1352.607699	676.807487	1351.623683	676.315479	R	525.325591	263.166434	508.299042	254.653159			4
16	1466.687012	733.847144	1449.660463	725.333869	1448.676447	724.841861	P	369.224480	185.115878	352.197931	176.602603			3
17	1563.739776	782.373526	1546.713227	773.860252	1545.729211	773.368243	P	272.171716	136.589496	255.145167	128.076221			2
18							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of AEGPSSTPSSAAGPRPPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.3	1736.844162	0.004146	AEGPSSTPSSAAGPRPPR
6.1	1736.832932	0.015376	SSEKPTGLWSTASSQR
1.4	1736.844162	0.004146	AEGPSSTPSSAAGPRPPR

Mascot: http://www.matrixscience.com/

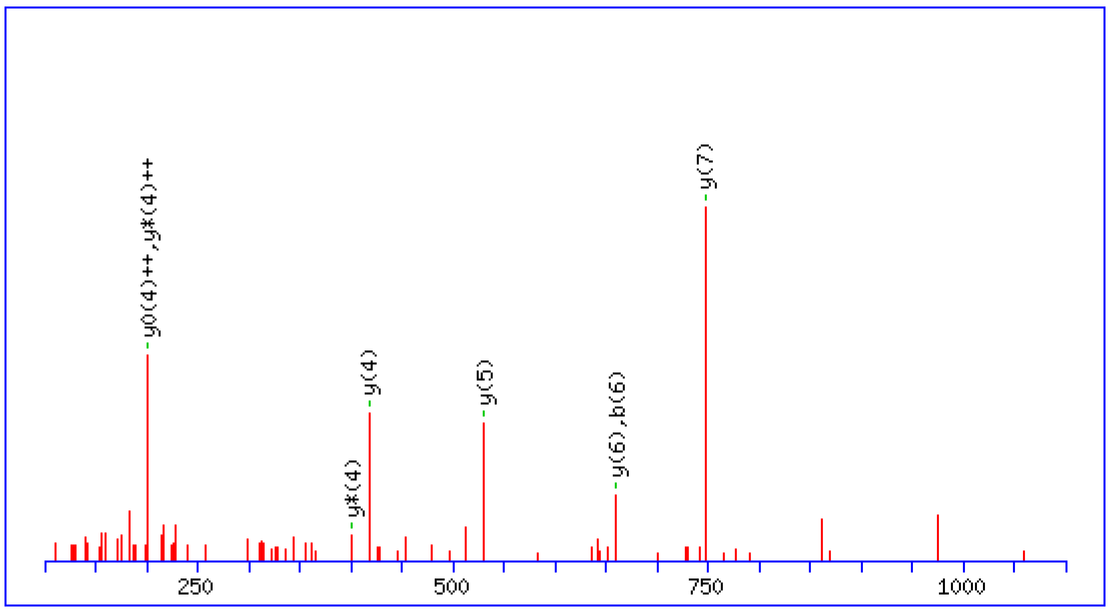
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QTSELTLGK**
Found in **ZN624_HUMAN**, Zinc finger protein 624 OS=Homo sapiens GN=ZNF624 PE=2 SV=3

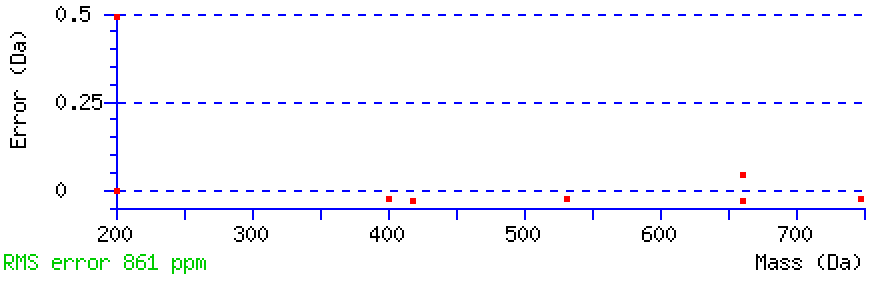
Match to Query 14035: 975.520668 from(488.767610,2+) rtinseconds(2128) index(24254)
Title: Locus:1.1.1.2159.9
Data file 2011-11-10 - TFD - EP 4-1.mgf

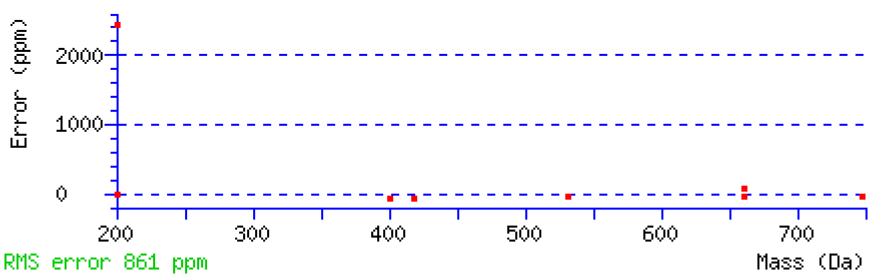
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 975.523666
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.0093
Matches : 8/88 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	129.065854	65.036565	112.039305	56.523291			**Q**							9
2	230.113533	115.560405	213.086984	107.047130	212.102968	106.555122	**T**	848.472375	424.739826	831.445826	416.226551	830.461810	415.734543	8
3	317.145561	159.076418	300.119012	150.563144	299.134996	150.071136	**S**	***747.424696***	374.215986	730.398147	365.702712	729.414131	365.210704	7
4	446.188154	223.597715	429.161605	215.084441	428.177589	214.592433	**E**	***660.392668***	330.699972	643.366119	322.186698	642.382103	321.694690	6
5	559.272218	280.139747	542.245669	271.626473	541.261653	271.134465	**L**	***531.350075***	266.178676	514.323526	257.665401	513.339510	257.173393	5
6	660.319897	330.663587	643.293348	322.150312	642.309332	321.658304	**T**	***418.266011***	209.636644	401.239462	201.123369	400.255446	200.631361	4
7	773.403961	387.205619	756.377412	378.692344	755.393396	378.200336	**L**	317.218332	159.112804	300.191783	150.599530			3
8	830.425425	415.716351	813.398876	407.203076	812.414860	406.711068	**G**	204.134268	102.570772	187.107719	94.057498			2
9							**K**	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of QTSELTLGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.9	975.523666	-0.002998	QTSELTLGK
8.8	975.513763	0.006905	VAKFPENR
5.8	975.525009	-0.004341	GPPPPPRSR
2.1	975.523666	-0.002998	SSTLGPSALK

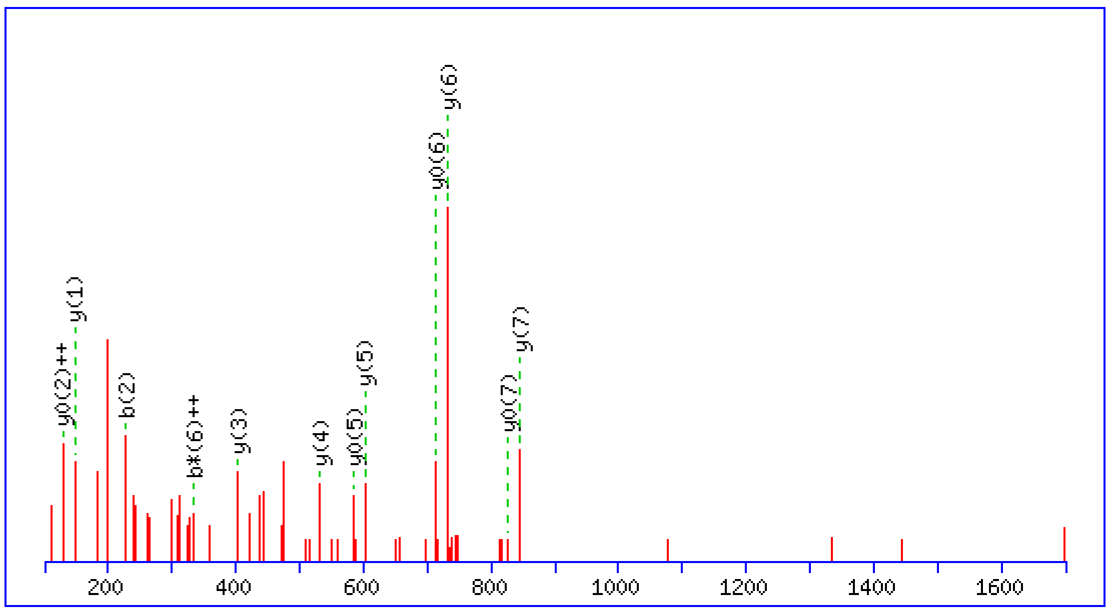
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLEAKQEK**
Found in **ZN770_HUMAN**, Zinc finger protein 770 OS=Homo sapiens GN=ZNF770 PE=2 SV=1

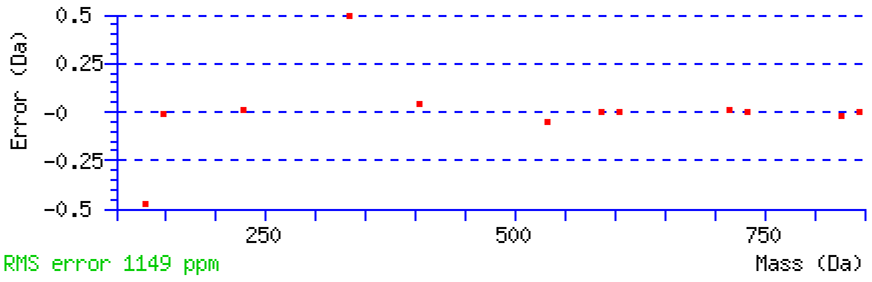
Match to Query 12835: 957.553008 from(479.783780,2+) rtinseconds(1612) index(15185)
Title: Locus:1.1.1.1957.16
Data file 2011-11-10 - TFD - EP 3-4.mgf

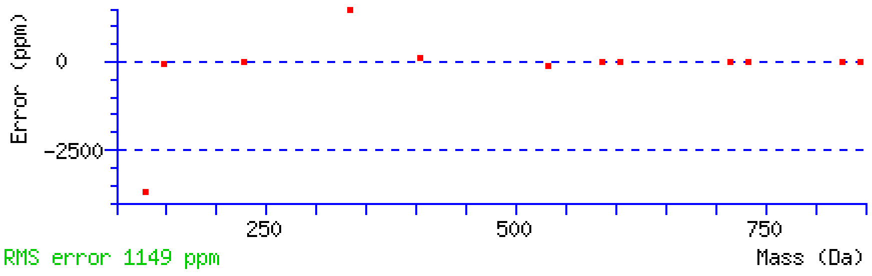
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 957.549454
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 32  Expect: 0.0074
Matches : 12/70 fragment ions using 24 most intense peaks   (help)
```

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					L							8
2	227.175404	114.091340					L	***845.472709***	423.239993	828.446160	414.726718	827.462144	414.234710	7
3	356.217997	178.612637			338.207432	169.607354	E	***732.388645***	366.697961	715.362096	358.184686	714.378080	357.692678	6
4	427.255111	214.131193			409.244546	205.125911	A	***603.346052***	302.176664	586.319503	293.663390	585.335487	293.171382	5
5	555.350074	278.178675	538.323525	269.665401	537.339509	269.173393	K	***532.308938***	266.658107	515.282389	258.144833	514.298373	257.652825	4
6	683.408652	342.207964	666.382103	333.694690	665.398087	333.202682	Q	***404.213975***	202.610626	387.187426	194.097351	386.203410	193.605343	3
7	812.451245	406.729261	795.424696	398.215986	794.440680	397.723978	E	276.155397	138.581336	259.128848	130.068062	258.144832	129.576054	2
8							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of LLEAKQEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.2	957.549454	0.003554	LLEAKQEK
31.0	957.549469	0.003539	LLEQAGSLK
10.4	957.549484	0.003524	LVLTQEQK
7.6	957.549469	0.003539	LLLEVSER
2.2	957.560715	-0.007707	LQGQVSAKK
2.0	957.560699	-0.007691	NLKQIQSK
1.9	957.549484	0.003524	KLDPSGTLK
1.1	957.560715	-0.007707	LSRVQDIK
0.1	957.556885	-0.003877	LPLVPMLK

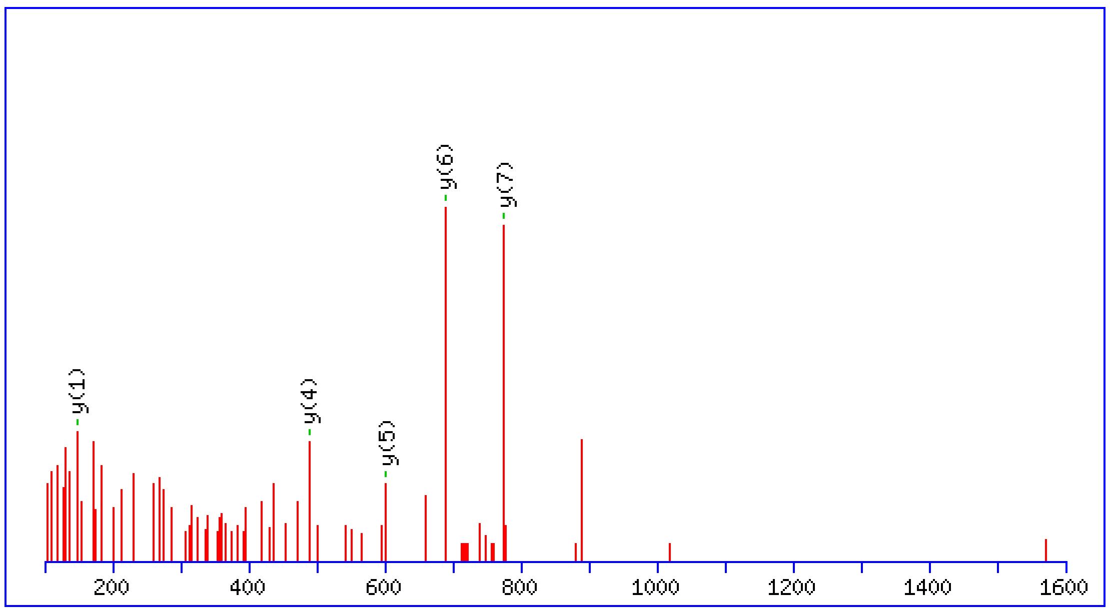
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NSSLLTQK**
Found in **ZN813_HUMAN**, Zinc finger protein 813 OS=Homo sapiens GN=ZNF813 PE=2 SV=2

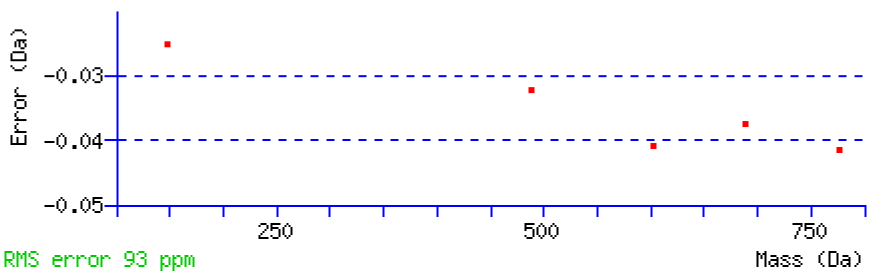
Match to Query 4865: 889.488168 from(445.751360,2+) rtinseconds(1638) index(15826)
Title: Locus:1.1.1.2111.10
Data file 2011-11-10 - TFD - EP 4-3.mgf

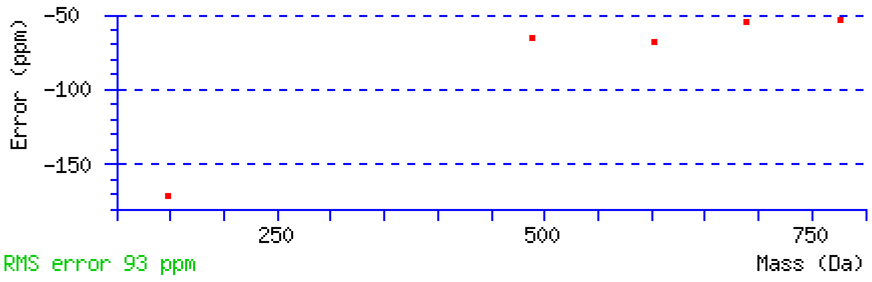
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 889.486877
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 36  Expect: 0.0024
Matches : 5/78 fragment ions using 8 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			N							8
2	202.082231	101.544753	185.055682	93.031479	184.071666	92.539471	S	***776.451245***	388.729261	759.424696	380.215986	758.440680	379.723978	7
3	289.114259	145.060768	272.087710	136.547493	271.103694	136.055485	S	***689.419217***	345.213247	672.392668	336.699972	671.408652	336.207964	6
4	402.198323	201.602800	385.171774	193.089525	384.187758	192.597517	L	***602.387189***	301.697233	585.360640	293.183958	584.376624	292.691950	5
5	515.282387	258.144832	498.255838	249.631557	497.271822	249.139549	L	***489.303125***	245.155201	472.276576	236.641926	471.292560	236.149918	4
6	616.330066	308.668671	599.303517	300.155397	598.319501	299.663389	T	376.219061	188.613169	359.192512	180.099894	358.208496	179.607886	3
7	744.388644	372.697960	727.362095	364.184686	726.378079	363.692678	Q	275.171382	138.089329	258.144833	129.576055			2
8							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of NSSLLTQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.7	889.486877	0.001291	NSSLLTQK
21.6	889.486877	0.001291	NSLSTAAVK
9.8	889.494278	-0.006110	SMLAIVPK
9.6	889.494263	-0.006095	LMGLEALK
4.6	889.486862	0.001306	TASNKEIK
4.3	889.486877	0.001291	LKSSQSPK
2.7	889.494293	-0.006125	GDVLVMLK
2.4	889.494247	-0.006079	KMEELIK
2.1	889.490906	-0.002738	SFEPAVLK
2.1	889.490921	-0.002753	LLFSPGPK

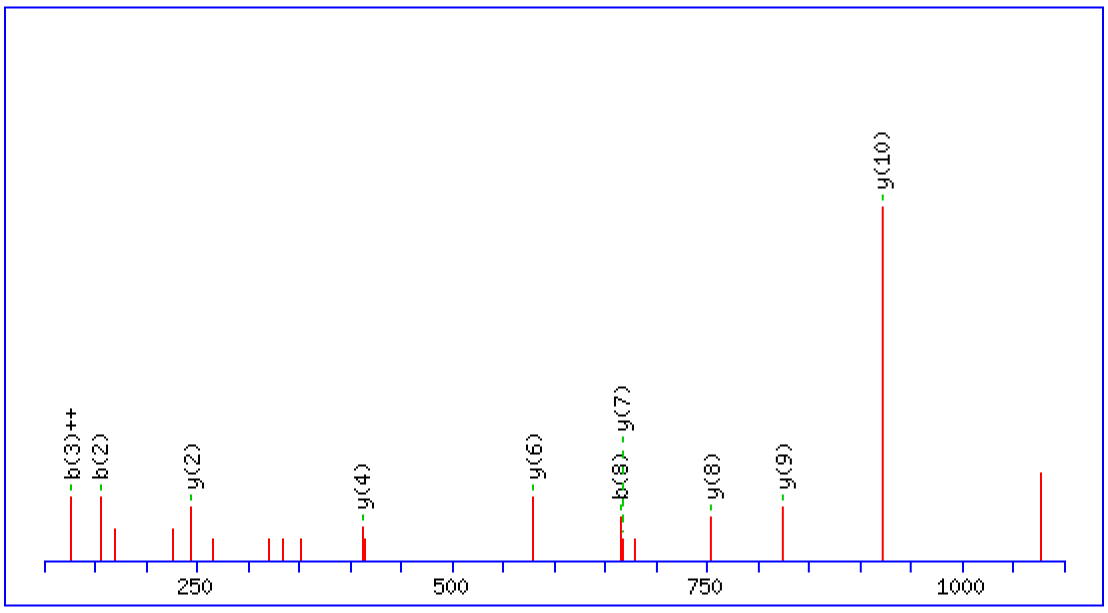
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GPPASSPAPAPK**
Found in **ZYX_HUMAN**, Zyxin OS=Homo sapiens GN=ZYX PE=1 SV=1

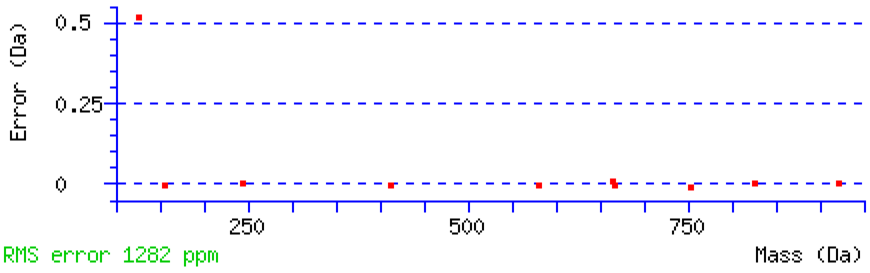
Match to Query 362451: 1075.567888 from(538.791220,2+) rtinseconds(969) index(158189)
Title: Locus:1.1.1.1054.5
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\3 TFD - Epitel - R2\mascot_daemon_merge.mgf

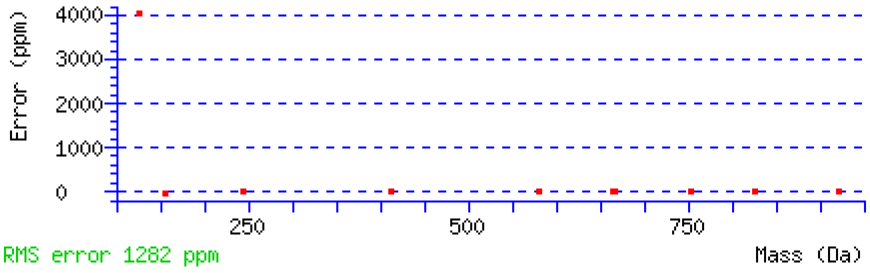
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1075.566193
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 58  Expect: 3e-005
Matches : 10/90 fragment ions using 13 most intense peaks   (help)
```

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	58.028740	29.518008			G							12
2	**155.081504**	78.044390			P	1019.552022	510.279649	1002.525473	501.766374	1001.541457	501.274366	11
3	252.134268	126.570772			P	***922.499258***	461.753267	905.472709	453.239993	904.488693	452.747985	10
4	323.171382	162.089329			A	***825.446494***	413.226885	808.419945	404.713611	807.435929	404.221603	9
5	410.203410	205.605343	392.192845	196.600061	S	***754.409380***	377.708328	737.382831	369.195054	736.398815	368.703046	8
6	497.235438	249.121357	479.224873	240.116075	S	***667.377352***	334.192314	650.350803	325.679039	649.366787	325.187031	7
7	594.288202	297.647739	576.277637	288.642457	P	***580.345324***	290.676300	563.318775	282.163026			6
8	**665.325316**	333.166296	647.314751	324.161014	A	483.292560	242.149918	466.266011	233.636643			5
9	762.378080	381.692678	744.367515	372.687396	P	***412.255446***	206.631361	395.228897	198.118086			4
10	833.415194	417.211235	815.404629	408.205953	A	315.202682	158.104979	298.176133	149.591704			3
11	930.467958	465.737617	912.457393	456.732335	P	***244.165568***	122.586422	227.139019	114.073147			2
12					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of GPPASSPAPAPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
57.9	1075.566193	0.001695	GPPASSPAPAPK

Mascot: http://www.matrixscience.com/